2019 KSBS & SABRAO International Conference on Plant Breeding for Sustainable Development

50th Anniversary Symposium of the Korean Society of Breeding Science and 14th Conference of Society for the Advancement of the Breeding Research in Asia and Oceania

- **Date**: 2nd (Tues) - 5th (Fri) July, 2019
- **Venue**: Kimdaejung Convention Center, Gwangju, Republic of Korea

**Host Organizer**

- The Korean Society of Breeding Science
- Society for the Advancement of the Breeding Research in Asia and Oceania
- Rural Development Administration
- The Agricultural Genome Center
- Agricultural Biotechnology Research Center
- Plant Molecular Breeding Center
- Systems & Synthetic Agrobiotech Center
- GSP Vegetable Seed Center
- Center of Horticultural Seed Development of GSP
- National Agency for Crop Seed Improvement
Sponsors by

National Institute of Agricultural Sciences (NIAS, RDA)
National Institute of Crop Science (NICS, RDA)
National Institute of Horticultural and Herbal Science (NIHHS, RDA)
National Institute of Forest Science
Korea Seed & Variety Service
Korea Atomic Energy Research Institute
The Korean Federation of Science and Technology Societies
Gwangju Convention & Visitors Bureau
Gyeongsang National University
Agricultural Biotechnology Center for Innovative Future Brains, Kyung Hee University
Vegetable Breeding Research Center, Seoul National University
Chungnam National University
Kyungpook National University
Nongwoobio Co., Ltd.
LG Chem
CropLife Korea

Exhibition & Advertisement by

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This work was supported by the Korean Federation of Science and Technology Societies (KOFST) Grant funded by the Korean Government.
President of the KSBS
Prof. Soo-Chul Park
Seoul Natl. Univ.

Chairman of the Organizing Committee
Dr. Si-Yong Kang
KAERI

Plenary Session
Dr. Jeong-Dong Lee
Kyungpook Natl. Univ.
Dr. Jong-Wook Chung
Chungbuk Natl. Univ.

Concurrent Session
CS1. Dr. Joong Hyoun Chin
Sejong Univ.
CS2. Dr. Chang-Soo Kim
Chungnam Natl. Univ.
CS3. Dr. Ki-Hong Jung
Kyung Hee Univ.
CS4. Dr. In-Hwa Yeam
Andong Natl. Univ.
CS5. Dr. Sun-Hwa Ha
Kyung Hee Univ.
CS6. Dr. Kyung-Hwan Kim
NIAS, RDA
CS7. Dr. Je-Min Lee
Kyungpook Natl. Univ.
CS8. Dr. Joo-Hyun Lee
Konkuk University
CS9. Dr. Dong-Yul Sung
LG Chem, Co., Ltd.,
CS10. Dr. Haeng-Hoon Kim
Sunchon Natl. Univ.
CS11. Dr. Jin-Baek Kim
KAERI
CS12. Dr. Jae-Yean Kim
Gyeongsang Natl. Univ.

President of the SABRAO
Prof. Sang-Nag Ahn
Chungnam Natl. Univ.

Chief of Scientific Program Organizer
Dr. Byoung-Cheorl Kang
Seoul Natl. Univ.

Special Session
SS1. Dr. Young-Chan Cho
NIICS, RDA
SS2. Dr. Myeong-Cheoul Cho
NIHHS, RDA
SS3. Dr. Seok-Woo Lee
NIFS
SS4. Dr. Seung-In Yi
KSVS

Poster Session
Dr. Sung-Chur Sim
Sejong University
Dr. Jong-Yeon Lee
NIAS, RDA
Dr. Cheol-Seong Jang
Kangwon Natl. Univ.

Abstract Curator & Editing
Dr. Soon-Wook Kwon
Pusan Natl. Univ.
Dr. Jae-Yoon Kim
Kongju Natl. Univ.
Dr. Jun-Dae Lee
Chonbuk Natl. Univ.

Tour & Local
Dr. Bo-Keun Ha
Chonnam Natl. Univ.
Dr. Tae-Ho Han
Chonnam Natl. Univ.
Dr. Sung-Gil Kim
Chonnam Natl. Univ.

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2019년 (사)한국육종학회 국제공동심포지엄 조직위원회

한국육종학회장 박수철  SABRAO 회장 안상낙

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강서영(한국육종학회), 안상낙(SABRAO), 문중경(농생물게놈활용연구사업단), 박순기(농업생명공학연구단), 고희종(식물분자육종사업단), 이상열(시스템합성농생명공학연구사업단), 임용표(GSP 체소종자사업단), 노일섭(GSP 원예종자사업단), 정진철(GSP 식량종자사업단), 이용범(국립농업과학원), 김두호(국립식량과학원), 황정환(국립원예특작과학원)

총괄총무위원
이강섭(국립농업과학원)

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자문위원
김용권(농협종묘센터), 김종석(충북대학교), 서호남(고려대학교), 오대근(한국농수산대학교), 정영수(동아대학교), 조용구(충북대학교), 임상종(국립식량과학원)
Welcome Address of 2019 KSBS & SABRAO International Conference

It’s our great honor to host the 2019 KSBS (The Korean Society of Breeding Science) & SABRAO (Society for the Advancement of the Breeding Research in Asia and Oceania) International Conferences on Plant Breeding for Sustainable Development. On behalf of joint Conference Organizing Committee and the KSBS, we warmly welcome all participants of this conference. This joint meeting is very meaningful because it is the event in celebration of the 50th Anniversary Symposium of the KSBS and also the 14th International Conference of SABRAO. This is the second time that Korea hosts this important SABRAO Congress and we hosted the 8th Congress in Seoul during September, 1997 when SABRAO was 29 years old.

Population growth and climate change are increasingly adversely affecting global food security, particularly in the Asia–Pacific region. Enhancing crop productivity and quality is an eternal challenge for sustainable development through problem solving caused by population growth and climate change. Plant breeding technology has been playing a key role in creating new crop varieties and useful genetic resources over the past 100 years. Recently, new breeding techniques such as genome editing and Phenomics are being developed, and they are expected to greatly help solve the global problems mentioned above.

In that sense, we tried to provide exciting scientific programs to deal with all aspects of plant breeding and genomics: from the basics to their applications. As part of these efforts, we invited distinguished speakers for plenary lectures and concurrent sessions. We also organized various special sessions such as a Memorial workshop for the 50th anniversary of the KSBS. We are sure that this conference will be a good opportunity for students, post-doctoral colleagues, and established scientists and breeders from other countries to share ideas and experiences.

Finally, we would like to express our deep gratitude to joint organizing agencies, Next-Generation Bio–Green 21 Programs and Golden Seed Project which are supported from Ministry of Agriculture, Food and Rural Affairs (MAFRA) and Rural Development Administration (RDA). We also express our sincere gratitude to many sponsoring companies, institutions and universities.

We wish all of you would have a fruitful time and enjoy a pleasant stay in Gwangju, Korea. Thank you for your participation and attention.

Dr. Si-Yong Kang
Chairperson, Organizing Committee
Korea Atomic Energy Res.Institute

Prof. Soo-Chul Park
President of KSBS
Seoul National Univ.

Prof. Sang-Nag Ahn
President of SABRAO
Chungnam National Univ.
한국육종학회 창립 50주년 기념 국제학술대회를 축하드립니다. 동시에 SABRAO(아시아-오세애니아육종학회) 14차 대회를 한국에서 개최하게 된 것을 매우 놀랍게 생각합니다.

이렇게 좋은 국제 공동 심포지엄을 준비해주신 한국육종학회 박수철 회장님, SABRAO 안상낙 위원장님과 관계자 여러분께 감사드립니다. 한국육종학회 50주년 기념 국제학술대회를 한국에서 개최하게 된 것에 대해 감사드립니다.

종자는 인류의 역사와 함께온 생명의 원천입니다. 농경의 시작은 문명 태동의 원동력이 되었고, 끊임없는 종자 개발과 농업기술의 발전으로 우리는 풍요의 시대에 살고 있습니다. 현대적인 연구로 멜서스의 「인구론」은 가우였음을 증명해온 동서고금의 육종학자들에게 감사의 마음을 전하고 싶습니다.

과거 전통 육종 기술을 이용한 품종개발에는 시간과 노력이 많이 소요되었습니다. 그러나 최근에는 생명공학기술 기반의 육종이 실험실의 연구개발 수준을 넘어져 종자산업을 통해 실용화가 활발히 이루어지고 있으며, 바이오, 에너지 산업 등으로 응용 분야를 확장하고 있습니다. 육종이야말로 식량안보 확보, 적물재배 및 가공 등 식품관련 산업의 효율성을 높이고, 식품자원의 영양학적 가치와 국제경쟁력 향상에 기여하여 농업혁신을 이룰 수 있게 하는 핵심 기술이라고 할 수 있습니다.

이러한 상황에서 열리는 한국육종학회 50주년 국제공동심포지엄은 그 의미가 크다고 생각합니다. 이번 행사를 통해 대한민국 육종 기술의 위상을 확고히 하고, 산·학·연 전체가 더욱 발전할 수 있는 계기가 될 것으로 기대합니다.

올해는 우장춘 박사의 서거 60주년이 되는 해입니다. 우장춘 박사는 ‘종의 합성이론’이라는 논문으로 세계가 주목하는 탁월한 업적을 이루셨습니다. 우리나라 육종연구와 원예연구의 기틀을 마련하고 식량난 해결과 해초종자 자급에도 크게 기여하였습니다. 그 분의 정신을 이어받은 한국육종학회는 지난 50년간의 노력으로 바, 배추, 고추 등에 대하여 우리나라가 세계 최고 수준의 육종기술을 갖출 수 있게 되었습니다. 글로벌 석학이 모이는 이번 행사를 통해 미래세대를 위한 농업혁신을 지속해 나갈 수 있도록 지혜를 모아주시기를 당부 드립니다.

다시 한 번 육종기술의 발전을 위해 한산하신 한국육종학회의 50주년을 축하드리며, 농림축산식품부도 종자산업과 대한민국 농업 발전을 위해 끊임없이 노력할 것을 약속드립니다. 감사합니다.
# 2019 KSBS–SABRAO International Conference Program [1]

## Day 1 (July 2, Tuesday)

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
<th>Location</th>
</tr>
</thead>
<tbody>
<tr>
<td>10:00~</td>
<td>Registration</td>
<td>Lobby Counter</td>
</tr>
<tr>
<td>13:20~13:40</td>
<td>Opening Ceremony</td>
<td>Convention Hall</td>
</tr>
<tr>
<td>13:40~17:00</td>
<td>Plenary Session 1. New Technology and Recent Trends on Plant Breeding</td>
<td>Convention Hall</td>
</tr>
<tr>
<td>17:00~17:40</td>
<td>Poster Session I (Odd Number)</td>
<td>Lobby</td>
</tr>
<tr>
<td>17:40~18:20</td>
<td>KSBS’s General Meeting &amp; Award</td>
<td>Convention Hall</td>
</tr>
<tr>
<td>17:00~18:20</td>
<td>SABRAO Meeting</td>
<td>C3 Room(308-309)</td>
</tr>
<tr>
<td>18:30~20:00</td>
<td>Banquet</td>
<td>Multi-Purpose Auditorium</td>
</tr>
</tbody>
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## Day 2 (July 3, Wednesday)

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
<th>Location</th>
</tr>
</thead>
<tbody>
<tr>
<td>09:00~12:00</td>
<td>CS-1. Abiotic Stress &amp; Yield</td>
<td>Convention Hall 1</td>
</tr>
<tr>
<td>12:00~13:00</td>
<td>Lunch</td>
<td>Convention Hall 2</td>
</tr>
<tr>
<td>13:30~15:30</td>
<td>Poster Change I → II (Odd Number → Even Number)</td>
<td>Convention Hall 3</td>
</tr>
<tr>
<td>15:30~16:00</td>
<td>Coffee Break</td>
<td>Convention Hall 3</td>
</tr>
<tr>
<td>16:00~18:00</td>
<td>CS-7. Quality and Function</td>
<td>Convention Hall 3</td>
</tr>
<tr>
<td>18:00~18:30</td>
<td>Introduction of NPBT Project</td>
<td>C3 Room(308-309)</td>
</tr>
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</table>

## Day 3 (July 4, Thursday)

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
<th>Location</th>
</tr>
</thead>
<tbody>
<tr>
<td>09:00~12:00</td>
<td>CS-10. Genetic Resources</td>
<td>Convention Hall 1</td>
</tr>
<tr>
<td>12:00~13:00</td>
<td>Lunch</td>
<td>Convention Hall 2</td>
</tr>
<tr>
<td>13:00~13:30</td>
<td>Poster Session II (Even Number)</td>
<td>Convention Hall 3</td>
</tr>
<tr>
<td>13:30~14:05</td>
<td>Plenary Session 2. Breeding Strategies for Sustainable Agriculture</td>
<td>Convention Hall 2+3</td>
</tr>
<tr>
<td>16:50~17:30</td>
<td>Awards Ceremony and Closing Ceremony</td>
<td>Convention Hall 2+3</td>
</tr>
</tbody>
</table>

## Day 4 (July 5, Friday)

### Technical & Culture Tour

#### Course-1. Gwangju & Jeonnam Tour


#### Course-2. Jeonju Tour

KDJ [09:00] > Rural Development Administration(RDA) > Lunch > Jeonju-Hanok Village > KDJ [16:30]
# 2019 KSBS–SABRAO International Conference Program [2]

## Day 1 (July 02, 2019, Tuesday)

<table>
<thead>
<tr>
<th>Time</th>
<th>Activity</th>
<th>Venue</th>
</tr>
</thead>
<tbody>
<tr>
<td>10:00~</td>
<td>Registration</td>
<td>Lobby Counter</td>
</tr>
<tr>
<td>13:20~13:40</td>
<td>Opening Ceremony</td>
<td>Convention Hall</td>
</tr>
<tr>
<td>13:20~13:40</td>
<td>- Opening Address</td>
<td>Convention Hall</td>
</tr>
<tr>
<td>13:20~13:40</td>
<td>- Welcome Address</td>
<td>Convention Hall</td>
</tr>
<tr>
<td>13:20~13:40</td>
<td>- Congratulatory Address</td>
<td>Convention Hall</td>
</tr>
<tr>
<td>13:40~17:00</td>
<td><strong>Plenary Session 1, New Technology and Recent Trends on Plant Breeding</strong></td>
<td></td>
</tr>
<tr>
<td>13:40~14:15</td>
<td><strong>Chair</strong> Yong-Pyo Lim (Chungnam National University)</td>
<td></td>
</tr>
<tr>
<td>13:40~14:15</td>
<td>Andrew H. Paterson (Georgia University, USA)</td>
<td></td>
</tr>
<tr>
<td>13:40~14:15</td>
<td>- Length Matters: How Might We Narrow the Quality Gap between Cotton and Synthetic Fibers</td>
<td></td>
</tr>
<tr>
<td>14:15~14:50</td>
<td>Masao Watanabe (Tohoku University, Japan)</td>
<td></td>
</tr>
<tr>
<td>14:15~14:50</td>
<td>- Molecular Mechanism of Self-Incompatibility in Brassicaceae</td>
<td></td>
</tr>
<tr>
<td>14:50~15:10</td>
<td>Coffee Break</td>
<td></td>
</tr>
<tr>
<td>14:50~15:10</td>
<td><strong>Chair</strong> Chee-Hark Harn (Toolgen Inc.,)</td>
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<tr>
<td>15:10~15:45</td>
<td>Jin-Soo Kim (Institute of Basic Science, Korea)</td>
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<tr>
<td>15:10~15:45</td>
<td>- CRISPR Genome Editing in Plants, Animals, and Human Cells</td>
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<tr>
<td>15:45~16:20</td>
<td>Caixia Gao (Chinese Academy of Science, China)</td>
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<tr>
<td>15:45~16:20</td>
<td>- How CRISPR is Changing Agriculture?</td>
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<tr>
<td>16:20~16:55</td>
<td>Jihyun F. Kim (Yonsei University, Korea)</td>
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<tr>
<td>16:20~16:55</td>
<td>- The Microbiome and Host Immunity Interplay in Health and Disease</td>
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<tr>
<td>17:00~17:40</td>
<td><strong>Poster Session I (Odd Number)</strong></td>
<td>Lobby</td>
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<tr>
<td>17:00~17:40</td>
<td><strong>Organizer</strong> Sung-Chul Shim (Sejong University)</td>
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<tr>
<td>17:00~17:40</td>
<td><strong>Organizer</strong> Jong-Yeol Lee (National Institute of Agricultural Sciences)</td>
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<tr>
<td>17:40~18:20</td>
<td><strong>KSBS’s General Meeting &amp; Award</strong></td>
<td>Convention Hall</td>
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<tr>
<td>17:00~18:20</td>
<td><strong>SABRAO Meeting</strong></td>
<td>C3 Room(308-309)</td>
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<tr>
<td>18:30~20:00</td>
<td><strong>Banquet</strong></td>
<td>Multi-Purpose Auditorium</td>
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### Day 2 (July 03, 2019, Wednesday)

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
<th>Location</th>
<th>Chair</th>
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<tbody>
<tr>
<td>09:00~12:00</td>
<td>CS-1. Abiotic Stress &amp; Yiled Convention Hall 1</td>
<td></td>
<td>Joong-Hyoun Chin (Sejong University)</td>
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<tr>
<td></td>
<td>Co-chair Prof. Glenn Gregorio (University of Philippines, Philippines)</td>
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<tr>
<td></td>
<td>CS-2. Genomics Convention Hall 2</td>
<td>Chang-Soo Kim (Chungnam University)</td>
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<td></td>
<td>Chair</td>
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<tr>
<td></td>
<td>CS-3. Bioinformatics Convention Hall 3</td>
<td>Ki-Hong Jung (Kyung Hee University)</td>
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<td></td>
<td>Chair</td>
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<tr>
<td></td>
<td>SS-1* Overview and Food Crops C3 Room(308-309)</td>
<td>Young-Chan Cho (National Institute of Crop Science)</td>
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<td>Chair</td>
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<tr>
<td>12:00~13:30</td>
<td>Lunch</td>
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<td>12:30~13:00</td>
<td>Poster Change I → II (Odd Number → Even Number)</td>
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<tr>
<td>13:30~15:30</td>
<td>CS-4. Biotic Stress Convention Hall 1</td>
<td>In-Hwa Yeam (Andong National University)</td>
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<td></td>
<td>CS-5. Biotechnology Convention Hall 2</td>
<td>Soon-Ki Park (Kyungpook National University)</td>
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<td>Co-chair Soon-Ki Park (Kyungpook National University)</td>
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<td>Young-Soo Chung (Dong-A university)</td>
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<td>Chair</td>
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<td></td>
<td>CS-6. Phenomics Convention Hall 3</td>
<td>Kyung-Hwan Kim (National Institute of Agricultural Sciences)</td>
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<td></td>
<td>SS-2. Horticultural &amp; Herbal Crops C3 Room(308-309)</td>
<td>Myeong-Cheoul Cho (National Institute of Horticultural and Herbal Science)</td>
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<td>Chair</td>
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<tr>
<td>15:30~16:00</td>
<td>Coffee Break</td>
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<tr>
<td>16:00~18:00</td>
<td>CS-7. Quality and Function Convention Hall 1</td>
<td>Je-Min Lee (Kyungpook National University)</td>
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<td>(18:30)</td>
<td>Chair</td>
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<td>CS-8. Genome-Assisted Selection Convention Hall 2</td>
<td>Joo-Hyun Lee (Konkuk University)</td>
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<td>CS-9. Seed Company &amp; Marketing Convention Hall 3</td>
<td>Dong-Yul Sung (LG Chem, Co., Ltd.,)</td>
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<td>Chair</td>
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<td>SS-3. Forest Plants C3 Room(308-309)</td>
<td>Seok-Woo Lee (National Institute of Forest Science)</td>
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<td>Chair</td>
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<tr>
<td>18:00~18:30</td>
<td>Introduction of R&amp;D Project for NPBT Convention Hall 3</td>
<td>Prof. Young Hee Joung (Chonnam Natl. Univ.)</td>
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</table>

* The Special Session entitled “100 years of Variety Development and 50 years of KSBS – Main Achievement and Prospects” will be held in Korean.
<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
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<tbody>
<tr>
<td>09:00~12:00</td>
<td>CS-10. Genetic Resources</td>
<td>Convention Hall 1</td>
<td>Haeng-Hun Kim (Sunchon National University)</td>
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<td></td>
<td>CS-11. Mutation Breeding</td>
<td>Convention Hall 2</td>
<td>Bo-Keun Ha (Chonnam National University)</td>
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<tr>
<td></td>
<td>CS-12. Genome Editing</td>
<td>Convention Hall 3</td>
<td>Jae-Yean Kim (Gyeongsang National University)</td>
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<td></td>
<td>SS-4. Technology and Policy</td>
<td>C3 Room(308-309)</td>
<td>Seung-In Yi (The Korea Seed &amp; Variety Service)</td>
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<tr>
<td>12:00~13:30</td>
<td>Lunch</td>
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<tr>
<td>13:00~13:30</td>
<td>Poster Session II (Even Number)</td>
<td>Lobby</td>
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<tr>
<td>13:30~16:45</td>
<td>Plenary Session 2. Breeding Strategies for Sustainable Agriculture</td>
<td>Convention Hall 2+3</td>
<td>Soon-Ki Park (Kyungpook National University)</td>
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<tr>
<td>13:30~14:05</td>
<td>Hon-Ming Lam (The Chinese University of HongKong)</td>
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<tr>
<td></td>
<td>- Exploring the Genome of Wild Soybean</td>
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<tr>
<td>14:05~14:40</td>
<td>David Honys (Institute of Experimental Botany CAS, Czech)</td>
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<tr>
<td></td>
<td>- Plant Reproduction Success: A Tale of Three-Omes</td>
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<tr>
<td>14:40~15:15</td>
<td>Michael Allen Gore (Cornell University, USA)</td>
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<tr>
<td></td>
<td>- Insights into the Genetic Basis of Crop Nutritional Quality and Stress Resilience</td>
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<tr>
<td>15:15~16:45</td>
<td>Coffee Break</td>
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<tr>
<td></td>
<td>Chair Jin-Cheol Jeong (National Institute of Crop Sciences)</td>
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<tr>
<td>15:35~16:10</td>
<td>Yusaku Uga (National Agriculture and Food Research Organization, Japan)</td>
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<tr>
<td></td>
<td>- Towards Genetic Improvement of Root System Architecture for Developing of Climate-Resilient Rice</td>
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<tr>
<td>16:10~16:45</td>
<td>Ju-Kon Kim (Seoul National University, Korea)</td>
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<tr>
<td></td>
<td>- Identification of a Key Player on Nitrogen-Use-Efficiency of Rice</td>
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### Day 3 (July 04, 2019, Thursday)

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
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<tbody>
<tr>
<td>13:30-16:30</td>
<td><strong>Special Session 5: Science-based Policy for Gene Edited Crops</strong> C3 Room(308-309)</td>
</tr>
<tr>
<td></td>
<td>유전자교정 작물의 합리적 정책방향</td>
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<tr>
<td></td>
<td>- Policy in USDA (Mr. Ibrahim Shagir, USDA-APHIS) Organized by Green-bio Forum</td>
</tr>
<tr>
<td></td>
<td>- Policy in Japan (Dr. Yutaka Tabei, NARO)</td>
</tr>
<tr>
<td></td>
<td>- Policy in EU &amp; Latin America (Dr. CHA Jin, CORTEVA) &amp; ILSI Korea</td>
</tr>
<tr>
<td></td>
<td>- Policy in Korea (Dr. JANG Ho Min, KBCH)</td>
</tr>
<tr>
<td>16:50-17:30</td>
<td><strong>Awards Ceremony and Closing Ceremony</strong> Convention Hall 2+3</td>
</tr>
</tbody>
</table>

**Other Special Session**

- 13:30-15:00 : Illumina Korea Convention Hall 1
- 15:00-15:30 : YOUNG IN Frontier

### Day 4 (July 5, 2019, Friday)

**Technical & Culture Tour**

**[ 1 COURSE ] Gwangju & Jeonnam Tour**


**[2 COURSE] Jeonju Tour**

KDJ [09:00] > Rural Development Administration(RDA) > National Institute of Agricultural Sciences(NAS) > Lunch > Jeonju-Hanok Village > KDJ [16:30]
# 2019 KSBS-SABRAO Concurrent sessions Program [3]

**Day 2 (July 3, Wednesday) (Convention Hall 1)**

<table>
<thead>
<tr>
<th>CS-1. Abiotic stress &amp; Yiled</th>
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</thead>
<tbody>
<tr>
<td><strong>Chair</strong></td>
<td>Joong-Hyoun Chin (Sejong University)</td>
<td>Co-chair: Prof. Glenn Gregorio (University of Philippines, Philippines)</td>
</tr>
<tr>
<td>09:00-09:25</td>
<td>CS01-01</td>
<td>Benildo G. de los Reyes (Texas Tech University, USA)</td>
</tr>
<tr>
<td>09:25-09:45</td>
<td>CS01-02</td>
<td>Sung-Ryul Kim (International Rice Research Institute, Philippines)</td>
</tr>
<tr>
<td>09:45-10:00</td>
<td>CS01-03</td>
<td>Ki-Yoon Kang (Seoul National University, Korea)</td>
</tr>
<tr>
<td>10:00-10:15</td>
<td>CS01-04</td>
<td>Hyun-Sook Lee (Chungnam National University, Korea)</td>
</tr>
<tr>
<td>10:15-10:30</td>
<td>CS01-05</td>
<td>Md. Motiar ROHMAN (Bangladesh Agricultural Research Institute, Bangladesh)</td>
</tr>
<tr>
<td>10:30-10:45</td>
<td>CS01-06</td>
<td>Jung Hyun SHIM (Research Scientist, Plant &amp; Soil Science, USA)</td>
</tr>
<tr>
<td>10:45-11:00</td>
<td>CS01-07</td>
<td>Christos MICHAILDIS (Institute of Experimental Botany CAS, Czech)</td>
</tr>
<tr>
<td>11:00-11:15</td>
<td>CS01-08</td>
<td>Taeklim LEE (Dankook University, Korea)</td>
</tr>
<tr>
<td>11:15-11:30</td>
<td>CS01-09</td>
<td>Bambang Sapta PURWOKO (Bogor Agricultural University, Indonesia)</td>
</tr>
<tr>
<td>11:30-11:45</td>
<td>CS01-10</td>
<td>Hae Koo KIM (National Institute of Agricultural Sciences, Korea)</td>
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</table>

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<table>
<thead>
<tr>
<th>CS-4. Biotic Stress</th>
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<tbody>
<tr>
<td><strong>Chair</strong></td>
<td>In-Hwa Yeam (Andong National University)</td>
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<tr>
<td>13:30-13:55</td>
<td>CS04-01</td>
<td>Jin-Ho Kang (Seoul National University, Korea)</td>
</tr>
<tr>
<td>13:55-14:20</td>
<td>CS04-02</td>
<td>Hyung-Gon Mang (Seoul National University, Korea)</td>
</tr>
<tr>
<td>14:20-14:45</td>
<td>CS04-03</td>
<td>Hyong-Woo Choi (Andong National University, Korea)</td>
</tr>
<tr>
<td>14:45-15:05</td>
<td>CS04-04</td>
<td>Prakit Somta (Kasetsart University, Thailand)</td>
</tr>
<tr>
<td>15:05-15:25</td>
<td>CS04-05</td>
<td>Cindy Gresyllia PERMADANI (Gadjah Mada University, Indonesia)</td>
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<thead>
<tr>
<th>CS-7. Quality and Function</th>
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<tbody>
<tr>
<td><strong>Chair</strong></td>
<td>Je-Min Lee (Kyungpook National University)</td>
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<tr>
<td>16:00-16:30</td>
<td>CS07-01</td>
<td>Yong-Pyo Lim (Chungnam National University, Korea)</td>
</tr>
<tr>
<td>16:30-17:00</td>
<td>CS07-02</td>
<td>Dae-Ok Kim (Kyung Hee University, Korea)</td>
</tr>
<tr>
<td>17:00-17:20</td>
<td>CS07-03</td>
<td>Gi-Jun Kim (Asiaseed Co., LTD, Korea)</td>
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<tr>
<td>17:20-17:40</td>
<td>CS07-04</td>
<td>Kang-Mo Ku (Chonnam National University, Korea)</td>
</tr>
<tr>
<td>17:40-18:00</td>
<td>CS07-05</td>
<td>Je-Min Lee (Kyungpook National University, Korea)</td>
</tr>
<tr>
<td>18:00-18:15</td>
<td>CS07-06</td>
<td>Kyeonglim MIN (Seoul National University, Korea)</td>
</tr>
<tr>
<td>18:15-18:30</td>
<td>CS07-07</td>
<td>Wening ENGGARINI (Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development, IAARD, Indonesia)</td>
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</table>
### Day 2 (July 3, Wednesday)  
(Convention Hall 2)

#### CS-2. Genomics

**Chair**  
Chang-Soo Kim (Chungnam University)

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
<th>Speaker</th>
<th>Institution</th>
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</thead>
<tbody>
<tr>
<td>09:00-09:20</td>
<td>CS02-01</td>
<td>Yu-Na Kang</td>
<td>Chungnam National University, Korea</td>
</tr>
<tr>
<td>09:20-09:40</td>
<td>CS02-02</td>
<td>Yang-Jae Kang</td>
<td>Gyeongsang National University, Korea</td>
</tr>
<tr>
<td>09:40-10:00</td>
<td>CS02-03</td>
<td>Jung-Min Ha</td>
<td>Seoul National University, Korea</td>
</tr>
<tr>
<td>10:00-10:20</td>
<td>CS02-04</td>
<td>Kyung-Do Kim</td>
<td>LG Chem., Ltd., Korea</td>
</tr>
<tr>
<td>10:20-10:40</td>
<td>CS02-06</td>
<td>Swati TYAGI</td>
<td>National Institute of Agricultural Sciences, Korea</td>
</tr>
<tr>
<td>10:40-11:00</td>
<td>CS02-07</td>
<td>Hyun-Seung PARK</td>
<td>Seoul National University, Korea</td>
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<tr>
<td>11:00-11:20</td>
<td>CS02-08</td>
<td>Hyeono SJI</td>
<td>National Institute of Agricultural Sciences, Korea</td>
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<tr>
<td>11:20-11:40</td>
<td>CS02-09</td>
<td>Byoung-Cheorl Kang</td>
<td>Seoul National University, Korea</td>
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#### CS-5. Biotechnology

**Co-chair**  
Soon-Ki Park (Kyungpook National University)  
Young-Soo Chung (Dong-A University)

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
<th>Speaker</th>
<th>Institution</th>
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<tbody>
<tr>
<td>13:30-14:00</td>
<td>CS05-01</td>
<td>Ryozo Imai</td>
<td>National Agriculture and Food Research Organization, Japan</td>
</tr>
<tr>
<td>14:00-14:30</td>
<td>CS05-02</td>
<td>Young-Soo Chung</td>
<td>Dong-A University, Korea</td>
</tr>
<tr>
<td>14:30-14:50</td>
<td>CS05-03</td>
<td>Eun-Ju Sohn</td>
<td>BioApplications Inc., Korea</td>
</tr>
<tr>
<td>14:50-15:10</td>
<td>CS05-04</td>
<td>Stephen Beungtae Ryu</td>
<td>Korea Research Institute of Biosciences and Biotechnology, Korea</td>
</tr>
<tr>
<td>15:10-15:30</td>
<td>CS05-05</td>
<td>Ok-Ran Lee</td>
<td>Chonnam National University, Korea</td>
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#### CS-8. Genome-Assisted Selection

**Chair**  
Joo-Hyun Lee (Konkuk University)

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
<th>Speaker</th>
<th>Institution</th>
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<tbody>
<tr>
<td>16:00-16:30</td>
<td>CS08-01</td>
<td>B.P. Mallikarjuna Swamy</td>
<td>International Rice Research Institute, Philippines</td>
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<tr>
<td>16:30-16:50</td>
<td>CS08-02</td>
<td>Ik-Young Choi</td>
<td>Kangwon National University, Korea</td>
</tr>
<tr>
<td>16:50-17:10</td>
<td>CS08-03</td>
<td>Jin-Kee Jung</td>
<td>Korea Seed &amp; Variety Service, Korea</td>
</tr>
<tr>
<td>17:10-17:30</td>
<td>CS08-04</td>
<td>Kai-Yi Chen</td>
<td>National Taiwan University, Taiwan</td>
</tr>
<tr>
<td>17:30-17:50</td>
<td>CS08-05</td>
<td>Bjoern TEXTOR</td>
<td>New England Biolabs, Germany</td>
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<tr>
<td>17:50-18:10</td>
<td>CS08-06</td>
<td>Ji-Min Kim</td>
<td>Dankook University, Korea</td>
</tr>
<tr>
<td>18:00-18:30</td>
<td>CS08-07</td>
<td>Jun-Hee Jung</td>
<td>Seoul National University, Korea</td>
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## Day 2 (July 3, Wednesday)  (Convention Hall 3)

### CS-3. Bioinformatics

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
<th>Speaker/Institution</th>
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<tbody>
<tr>
<td>09:00-09:30</td>
<td>CS03-01</td>
<td>Harkamal Walia (University of Nebraska-Lincoln, USA)</td>
</tr>
<tr>
<td>09:30-09:55</td>
<td>CS03-02</td>
<td>Sun-Tae Kim (Pusan National University, Korea)</td>
</tr>
<tr>
<td>10:00-10:25</td>
<td>CS03-03</td>
<td>Hong-Kyu Choi (Dong-A University, Korea)</td>
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<tr>
<td>10:30-10:55</td>
<td>CS03-04</td>
<td>Yeon-Ki Kim (Myongji University, Korea)</td>
</tr>
<tr>
<td>11:00-11:25</td>
<td>CS03-05</td>
<td>Seung-Ill Kim (Seoul National University, Korea)</td>
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<tr>
<td>11:30-12:00</td>
<td>CS03-06</td>
<td>Sook JUNG (Washington State University, USA)</td>
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### CS-6. Phenomics

<table>
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<tr>
<td>13:30-13:50</td>
<td>CS06-01</td>
<td>In-Chan Choi (National Institute of Agricultural Sciences, Korea)</td>
</tr>
<tr>
<td>13:50-14:10</td>
<td>CS06-02</td>
<td>Jae-Hoon Lee (Korea Institute of Science and Technology, Korea)</td>
</tr>
<tr>
<td>14:10-14:30</td>
<td>CS06-03</td>
<td>Hyun-Dong Lee (National Institute of Agricultural Sciences, Korea)</td>
</tr>
<tr>
<td>14:30-14:55</td>
<td>CS06-04</td>
<td>Trevor Garnett (Australian Plant Phenomics Facility, Australia)</td>
</tr>
<tr>
<td>14:55-15:15</td>
<td>CS06-05</td>
<td>Sathiyamoorthy MEYALAGHAN (The New Zealand Inst. for Plant and Food Research Ltd., New Zealand)</td>
</tr>
<tr>
<td>15:15-15:30</td>
<td>CS06-06</td>
<td>Sung-Yul Chang (Korea Atomic Energy Research Institute, Korea)</td>
</tr>
</tbody>
</table>

### CS-9. Seed Company & Marketing

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
<th>Speaker/Institution</th>
</tr>
</thead>
<tbody>
<tr>
<td>16:00-16:25</td>
<td>CS09-01</td>
<td>Darush Struss (East West Seed Co. Ltd, Thailand)</td>
</tr>
<tr>
<td>16:25-16:50</td>
<td>CS09-02</td>
<td>Makoto Endo (Takii Seed Co. Ltd, Japan)</td>
</tr>
<tr>
<td>16:50-17:10</td>
<td>CS09-03</td>
<td>Yong Park (FarmHannong Co., Ltd., Korea)</td>
</tr>
<tr>
<td>17:10-17:30</td>
<td>CS09-04</td>
<td>Jin-Man Lee (Nongwoo Bio Co. Ltd, Korea)</td>
</tr>
<tr>
<td>17:30-17:50</td>
<td>CS09-05</td>
<td>Sang-Ji Byun (Sakado Korea Co. Ltd, Korea)</td>
</tr>
</tbody>
</table>
## Day 3 (July 4, Thursday)

### CS-10. Genetic Resources

**Chair** Haeng-Hun Kim (Sunchon National University)

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
<th>Speaker</th>
<th>Institution</th>
</tr>
</thead>
<tbody>
<tr>
<td>09:00-09:30</td>
<td>CS10-01</td>
<td>Derek W. Barchenger</td>
<td>The World Vegetable Center, Taiwan</td>
</tr>
<tr>
<td>09:30-09:50</td>
<td>CS10-02</td>
<td>Do-Yoon Hyun</td>
<td>National Institute of Agricultural Sciences, Korea</td>
</tr>
<tr>
<td>09:50-10:10</td>
<td>CS10-03</td>
<td>Tae-Ho Han</td>
<td>Chonnam National University, Korea</td>
</tr>
<tr>
<td>10:10-10:30</td>
<td>CS10-04</td>
<td>Hyun Jo</td>
<td>Kyungpook National University, Korea</td>
</tr>
<tr>
<td>10:30-10:45</td>
<td>CS10-05</td>
<td>Abil DERMAIL</td>
<td>Khon Kaen University, Thailand</td>
</tr>
<tr>
<td>10:45-11:00</td>
<td>CS10-06</td>
<td>Desta WIRNAS</td>
<td>IPB University (Bogor Agricultural University), Indonesia</td>
</tr>
<tr>
<td>11:00-11:15</td>
<td>CS10-07</td>
<td>Rosalyn B. Angeles-Shim</td>
<td>Texas Tech University, USA</td>
</tr>
<tr>
<td>11:15-11:30</td>
<td>CS10-08</td>
<td>Ramakrishnan Madhavan Nair</td>
<td>World Vegetable Center South Asia, India</td>
</tr>
<tr>
<td>11:30-11:45</td>
<td>CS10-09</td>
<td>Fahmi Wendra Setiostono</td>
<td>PT. Sampoerna Agro Tbk., Indonesia</td>
</tr>
<tr>
<td>11:45-12:00</td>
<td>CS10-10</td>
<td>Hye-Sung Cho</td>
<td>Fruit Research Institute of Jeollanamdo ARES, Korea</td>
</tr>
</tbody>
</table>

### CS-11. Mutation Breeding

**Chair** Jin-Baek Kim (Korea Atomic Energy Research Institute)

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
<th>Speaker</th>
<th>Institution</th>
</tr>
</thead>
<tbody>
<tr>
<td>09:00-09:30</td>
<td>CS11-01</td>
<td>Qiangyao Shu</td>
<td>Zhejiang University, China</td>
</tr>
<tr>
<td>09:30-10:00</td>
<td>CS11-02</td>
<td>Tomoko Abe</td>
<td>RIKEN Nishina Center for Accelerator-Based Science, Japan</td>
</tr>
<tr>
<td>10:00-10:20</td>
<td>CS11-03</td>
<td>JI-Ung Jeung</td>
<td>National Institute of Crop Science, Korea</td>
</tr>
<tr>
<td>10:20-10:40</td>
<td>CS11-04</td>
<td>Yeong-Deuk Jo</td>
<td>Korea Atomic Energy Research Institute, Korea</td>
</tr>
<tr>
<td>10:40-11:10</td>
<td>CS11-05</td>
<td>Thomas H. Tai</td>
<td>USDA-ARS, Crops Pathology and Genetics Research Unit, USA</td>
</tr>
<tr>
<td>11:10-11:25</td>
<td>CS11-06</td>
<td>Jingbin Chen</td>
<td>Jiangsu Academy of Agricultural Sciences, China</td>
</tr>
<tr>
<td>11:25-11:40</td>
<td>CS11-07</td>
<td>Nurul KHUMAIDA</td>
<td>IPB University (Bogor Agricultural University), Indonesia</td>
</tr>
<tr>
<td>11:40-11:55</td>
<td>CS11-08</td>
<td>SYARIFAH IIS AISYAH</td>
<td>IPB University (Bogor Agricultural University), Indonesia</td>
</tr>
</tbody>
</table>

### CS-12 Genome Editing

**Chair** Jae-Yean Kim (Gyeongsang National University)

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
<th>Speaker</th>
<th>Institution</th>
</tr>
</thead>
<tbody>
<tr>
<td>09:00-09:30</td>
<td>CS12-01</td>
<td>Jae-Yean Kim</td>
<td>Gyeongsang National University, Korea</td>
</tr>
<tr>
<td>09:30-10:10</td>
<td>CS12-02</td>
<td>Seiichi Toki</td>
<td>National Agriculture and Food Research Organization, Japan</td>
</tr>
<tr>
<td>10:10-10:30</td>
<td>CS12-03</td>
<td>Hyun-Uk Kim</td>
<td>Sejong University, Korea</td>
</tr>
<tr>
<td>10:30-10:50</td>
<td>CS12-04</td>
<td>Kwon-Kyoo Kang</td>
<td>Hankyong National University, Korea</td>
</tr>
<tr>
<td>10:50-11:10</td>
<td>CS12-05</td>
<td>Jeong-Hwan Mun</td>
<td>Myongji University, Korea</td>
</tr>
</tbody>
</table>
## Contents

### Plenary Session

<table>
<thead>
<tr>
<th>PS-01</th>
<th>Length Matters: How Might We Narrow the Quality Gap between Cotton and Synthetic Fibers</th>
<th>5</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Andrew H. Paterson</td>
<td></td>
</tr>
<tr>
<td>PS-02</td>
<td>Molecular mechanism of self-incompatibility in Brassicaceae</td>
<td>7</td>
</tr>
<tr>
<td></td>
<td>Masao Watanabe, Seiji Takayama</td>
<td></td>
</tr>
<tr>
<td>PS-03</td>
<td>CRISPR Genome Editing in Plants, Animals, and Human Cells</td>
<td>9</td>
</tr>
<tr>
<td></td>
<td>Jin-Soo Kim</td>
<td></td>
</tr>
<tr>
<td>PS-04</td>
<td>How CRISPR is changing agriculture?</td>
<td>11</td>
</tr>
<tr>
<td></td>
<td>Caixia Gao</td>
<td></td>
</tr>
<tr>
<td>PS-05</td>
<td>The Microbiome and Host Immunity Interplay in Health and Disease</td>
<td>13</td>
</tr>
<tr>
<td></td>
<td>Jihyun F. Kim</td>
<td></td>
</tr>
<tr>
<td>PS-06</td>
<td>Exploring the Genome of Wild Soybean</td>
<td>15</td>
</tr>
<tr>
<td></td>
<td>Hon-Ming Lam</td>
<td></td>
</tr>
<tr>
<td>PS-07</td>
<td>Plant reproduction success: a tale of three -omes</td>
<td>17</td>
</tr>
<tr>
<td></td>
<td>David Honys, Said Hafidh, David Potěšil, Katarina Kulichová, Lenka Steinbachová, Karel Müller, Jan Fila, Christos Michailidis, Till Ischebeck, Zbyněk Zdráhal</td>
<td></td>
</tr>
<tr>
<td>PS-08</td>
<td>Insights into the genetic basis of crop nutritional quality and stress resilience</td>
<td>19</td>
</tr>
<tr>
<td></td>
<td>Michael A. Gore</td>
<td></td>
</tr>
<tr>
<td>PS-09</td>
<td>Identification of a key player on nitrogen use efficiency of rice</td>
<td>21</td>
</tr>
<tr>
<td></td>
<td>Ju-Kon Kim</td>
<td></td>
</tr>
<tr>
<td>PS-10</td>
<td>Towards genetic improvement of root system architecture for developing of climate-resilient rice</td>
<td>23</td>
</tr>
<tr>
<td></td>
<td>Yusaku Uga</td>
<td></td>
</tr>
</tbody>
</table>
Concurrent Session & Oral Session

OCS-01. Abiotic Stress & Yield

OCS01-01 Genome shock, transgressive segregation, and salinity tolerance in rice: Genetics or epigenetics? ................................................................. 27
Benildo G. de los Reyes

OCS01-02 Unlocking the genetic potentials of wild rice species to abiotic stress for rice improvement ................................................................. 27
Sung-Ryul Kim, Kshirod K. Jena, Manas R. Prusty, Sherry Lou Hechanova, Ma. LaRue E. Ballesfin, Eok-Keun Ahn, Pathmasiri Karunarathne

OCS01-03 Rice transcription factors that are involved in abiotic stress tolerance .................................................. 28
Kiyoon Kang, Nam-Chon Paek

OCS01-04 Fine-mapping of the quantitative trait locus qMel-3 controlling mesocotyl length ........................................ 28
Hyun-Sook Lee, Sun Ha Kim, Yu-A Jeon, Woo-Jin Kim, Inkyu Park, Sang-Nag Ahn

OCS01-05 Isozymes analysis in different saline sensitive maize hybrids to identify stress mitigating proteins ................................................................. 29
Md. Motiar Rohman, Sumaiya Haque Omy, Mohammad Amiruzzaman, Md. Aziz Zilani Chowdhury, Masayuki Fujita

OCS01-06 Exploring novel genetic donors of salt tolerance across the tetraploid cultivated cotton germplasm [Gossypium hirsutum] by transcriptome profiling and genetic network modeling ........................................ 29
Junghyun Shim, Kevin Cushman, Naga Bhushana Rao Karampudi, Lori Hinze, Megan Sweeney, Benildo G. de los Reyes

OCS01-07 Pollen germination during heat; Do HSP90s play a role? ................................................................. 30
Christos Michailidis, Zahra Aghcheh Kahrizi, Karel Raabe, David Honys

OCS01-08 Genome-wide Association Study (GWAS) for Ultraviolet-B resistance in soybean ........................................ 30
Taeklim Lee, Kyung-Hye Kim, Ji-Min Kim, Jinho Heo, Jiyeong Jung, Jung-Kyung Moon, Sungtaeg Kang

OCS01-09 Genotype x environment interaction and yield stability analysis of doubled haploid lines of upland rice in multilocation yield trials .................................................................................. 31
N. Kartina, B.S Purwoko, I.S. Dewi, D. Wirmas and Sugiyanta

OCS01-10 Investigating alternative breeding pathways to improve Korean Sesame varieties using the genetic diversity among the World Sesame Collection ................................................ 31
Hae Koo Kim, Seung-up Kim, Yedomon Ange Boyos Zoclanclounon, Ung-Han Yoon, Tae-Ho Kim, Keunpyo Lee
| OCS02-01 | Differential analysis of gluten-associated gene family using RNA-seq in grain and leaves of hexaploid Wheat | Yuna Kang, Chon-Sik Kang, Changsoo Kim |
| OCS02-02 | Soybean-VCF2Genomes: A database to identify the closest accession in soybean germplasm collection | Jungmin Ha, Ho Hwi Jeon, Dong U Woo, Yejin Lee, Halim Park, Joohyeong Lee and Yang Jae Kang |
| OCS02-03 | Genome sequence of *Jatropha curcas* L., a non-edible biodiesel plant, provides a resource to improve seed-related traits | Jungmin Ha, Suk-Ha Lee |
| OCS02-04 | DNA methylation creates diversities in duplicated plant genomes | Kyung Do Kim |
| OCS02-05 | Cancelled |
| OCS02-06 | Complete chloroplast genome sequence of *Chrysanthemum cinerariaefolium*: genome features, comparative analysis and phylogenetic relationships | Swati Tyagi, Jae-A Jung, Jung Sun Kim, Soo-Jin Kwon and So Youn Won |
| OCS02-07 | Chloroplast and mitochondrial genome flux and its impact on DNA barcoding | Hyun-Seung Park, Sae Hyun Lee, Hyun-Oh Lee, Jee Young Park, Byeong Cheol Moon, Chang-Kug Kim, Ho Jun Joh, Woohyeon Cho, Tae-Jin Yang |
| OCS02-08 | Kompetitive allele-specific PCR (KASP) marker development with Korean Japonica rice varieties through genome resequencing and application | Hyeonso Ji, Kyeong-Seong Cheon, Young-Min Jeong, Youn-Young Lee, Jun Oh, Do-Yu Kang, Hyoja Oh, Song Lim Kim, Nyunhee Kim, Eunyeong Lee, Jeongho Baek, Inchan Choi, Kyung-Hwan Kim, Yong Jae Won, In Sun Yoon, Young-il Cho, Jung-Heon Han |
| OCS02-09 | Whole Genome sequencing of *Capsicum annuum* 'Dempsey' Using Pac-bio, Bionano and Hi-C | Siyoung Jang, Jong-Ho Lee, Jinkwan Jo, Hea-Young Lee, Seungill Kim, Yong-Min Kim, Doil Choi, Byoung-Cheol Kang |
**OCS-03. Bioinformatics**

OCS03-01  Heat stress response in rice during seed development .............................................. 36  
Dr. Harkamal Walia

OCS03-02  Next generation proteomics pipelines for agriculture and crop science .................. 37  
Ravi Gupta, Cheol Woo Min, Sun Tae Kim

OCS03-03  TGIL: An integrative bioinformatic platform for genomics-assisted breeding .......... 37  
Jin-Hyun Kim, Joo-Seok Park and Hong-Kyu Choi

OCS03-04  Application of microarray and RNA-Seq to analyze transcriptome network in rice ....... 38  
Yeon-Ki Kim, Jong Sug Kim, Songhwa Chae, Kyong Mi Jun

OCS03-05  Unbiased annotation of target-gene families identifies undiscovered protein-coding genes in plant genomes ................................................................. 38  
Seungill Kim, Doil Choi

OCS03-06  BIMS (Breeding Information Management System) for efficient management of phenotypic and genotypic data ................................................................. 39  
Sook Jung, Taein Lee, Chun-Huai Cheng, Ksenija Gasic, Jing Yu, Jodi Humann, Dorrie Main

---

**OCS-04. Biotic Stress**

OCS04-01  Identification of Genes Involved in Trichome Development and Insect Resistance in Tomato ................................................................. 39  
Jae-In Chun, Won-Ki Hong, Seongmin Kim, Heejin Kim, and Jin-Ho Kang

OCS04-02  Genetic dissection of plant immune gene expression and defense responses .......... 40  
Hyunggon Mang, Libo Shan, Ping He

OCS04-03  How does plant defense-related hormone salicylic acid benefits both plants and humans 40  
Hyong Woo Choi, Daniel F. Klessig

OCS04-04  Genetic and genomic analyses of Cercospora leaf spot resistance in cowpea ............ 41  
Prakit Somta, Usa Duangsong, Timarong Heng, Anochar Kaewwongwal, Kularb Laosatit, Tarika Yiram, Sompong Chankaew, Peerassak Srinives

OCS04-05  Detection of Resistance Gene to Begomovirus in Chili Pepper [Capsicum frutescens L. 'Cempluk'] ................................................................. 41  
Cindy Gresyllia Permadani, Budi Setiadi Daryono
OCS-05. Biotechnology

OCS05-01 The *in planta* Particle Bombardment (iPB) method for crop transformation and genome editing

Ryozo Imai, Haruyasu Hamada, Yuelin Liu, Qianyan Linghu, Yuya Kanagai, Kenji Ida, Yozo Nagira, Naoki Taoka

OCS05-02 Application of soybean transgenesis to improve agricultural or industrial traits

Young Soo Chung

OCS05-03 Approval of recombinant protein-based vaccine against classical swine fever virus in pigs using transgenic *Nicotiana benthamiana* in Korea

Youngmin Park, Dong-Jun An, SeEun Choe, Yongik Lee, Minhee Park, Soohong Park, Sunghun Gu, Kyungmin Min, NamHyung Kim, Sangmin Lee, Jong Kook Kim, Hye-Yeon Kim, Eun-Ju Sohn, and Inhwan Hwang

OCS05-04 Production of Natural Rubber in Dandelion

Sungwoo Bae, Miyoung Kim, Stephen Beungtae Ryu

OCS05-05 Ginsenoside biosynthesis and its regulation in *Panax ginseng* Meyer

Ok Ran Lee, Jin Hoon Jang, Sookwang Yim

OCS-06. Phenomics

OCS06-01 High-throughput phenotyping system (HTPS) for trait analysis of crops in Korea


OCS06-02 Deep digital phenotyping of rosette-type plants and its application for dissecting plant-microbe interaction

Jae Hoon Lee, Unseok Lee, Hyoung Seok Kim

OCS06-03 Development of diagnosis model for the disease and infect symptoms of tomato using AI (Artificial Intelligent)

Hyun Dong Lee, Jae Su Lee, Tae Hyun Kim, Jeong Hyun Baek, Dong Sun Park, Joonwhan Lee, Hyongsuk Kim

OCS06-04 Phenotyping approaches to improve nitrogen use efficiency in wheat

Nicholas Sitlington-Hansen, Brooke Bruning, Huajian Liu, Bettina Berger, Darren Plett, Trevor Garnett

OCS06-05 Enhanced efficiency and precision in potato breeding

Sathiyamoorthy Meiyalaghan, Mark Paget, Stephen Lewthwaite, John Anderson, Samantha Baldwin

OCS06-06 Analysis pipeline for high throughput phenotyping [HTP] data

Sungyul Chang, Unseok Lee, Jin-Beak Kim, and Hyoung-Seok Kim
OCS-07. Quality and Function

OCS07-01 Importance of functional compounds and identification of respective genetic factors in Chinese Cabbage
Yong Pyo Lim, Su Ryun Choi, Jana Jeevan Rameneni

OCS07-02 Bioactive Phytophenols and Vegetable Breeding
Dae-Ok Kim

OCS07-03 Breeding of new green pepper including a-glucosidase inhibitors
Gi Jun Kim, Sanghyeob Lee

OCS07-04 Understanding glucosinolate-myrosinase system to improve quality of Brassica vegetables
Kang-Mo Ku

OCS07-05 Integrative transcriptomic and functional analyses to unveil distinct genetic influences on fruit quality in pepper
Je Min Lee

OCS07-06 Investigation of genetic differences related to fruit quality degradation after harvest in different strawberry cultivars using transcriptome analysis
Kyeonglim Min, Gibum Yi, Hyunsuk Kim, Yoonpyo Hong, and EunJin Lee

OCS07-07 Observation of phenotypic performance, molecular analysis and genetic variability on high yield Ciherang CSSL in the field
Wening Enggarini, Toto Hadiarto, Ma’sumah, Kurniawan Rudi Trijatmiko

OCS-08. Genome-Assisted Selection

OCS08-01 Making rice healthier through genomics-assisted breeding
B.P. MallikarjunaSwamy, Russell Reinke, Mercy Samia, Mary Ann Inabangan-Asilo, Amery Amparado, Chau ThanhNha, Alvin Palanog, Gwen Iris Descalsota-Empleo, Mark Ian Calayugan

OCS08-02 Discovery the different gene expression and whole genome DNA variation in dwarf soybean derived from crossing of cultivar and wild type in soybean
Ik-Young Choi

OCS08-03 Development and Use of Molecular Marker Plant Variety Identification
Jin-Kee Jung, Dong-Min Kim and Eun-Jo Shim
| OCS08-04 | Assessment of genetic differentiation and linkage disequilibrium of tomato germplasm using RADseq-derived SNP markers | Kai-Yi Chen |
| OCS08-05 | High-throughput screening of 2300 genetic markers in *S. lycopersicum* using the NEBNext Direct multiplexed genotyping approach | Björn Textor, Amy B. Emerman, Kruti M. Patel, Sarah K. Bowman, Scott M. Adams, Brendan S. Desmond, Jonathon S. Dunn, Andrew Barry, Susan E. Corbett, Charles D. Elfe, Evan Mauceli, and Cynthia L. Hendrickson |
| OCS08-06 | Novel candidate gene mapping related to insecticide response in soybean | Ji-Min Kim, Kyung-Hye Kim, Taeklim Lee, Jinho Heo, Jiyeong Jung, Jeong-Dong Lee, Sungtaeg Kang |
| OCS08-07 | Mapping of QTLs controlling seed weight using SNP markers in mungbean (*Vigna radiata* [L.]) | Jun Hee Jung, Jae Ah Choi, Jungmin Ha, Moon Young Kim, Suk-Ha Lee |

**OCS-09. Seed Company & Marketing**

| OCS09-01 | Genomics-Enabled Breeding Approaches in Vegetable | Darush Struss, Namfon Chomkao, Amika Yawichai, Maliwan Naconsie, Theeraporn Jiratammakun, Todsapol Kornsri, Roypim Sukkasem and Eliot Cline |
| OCS09-02 | Application of genome information for vegetable breeding in Takii Seed Company | Makoto Endo, Ryohei Arimoto, Hiroyuki Fukuoka |
| OCS09-03 | Development of Kimchi cabbage varieties with high Beta-carotene content | Yong Park, Gyu Dong Oh, Ju Yeon Jung, Jin Hee Shin, Jin Man Park, Kyu Hong Choe |
| OCS09-04 | Introduction - NongwooBio | Jin Man Lee |
| OCS09-05 | Sakata Korea | Sang-Ji Byun |

**OCS-10. Genetic Resources**

| OCS10-01 | Stability of Yield and Yield Components of Chili Pepper in East and Southeast Asia | Derek W. Barchenger, Robert A. Clark, III, Shih-wen Lin, Yen-wei Wang, Tsung-Han Lin, Dolores R. Ledesma, and Paul A. Gniffke |
OCS10-02 Genomics in RDA genebank: its use and perspective for germplasm management

OCS10-03 Use of germplasm resources for Hydrangea breeding
Tae-Ho Han, Seong-Hwa Bak

OCS10-04 Evaluation of agronomic traits and genetic diversity of black soybean with green cotyledon germplasms
Hyun Jo, Jiyoon Lee, Jeong-Dong Lee

OCS10-05 SSR-Genetic Distance and Combining Ability of Sweet and Waxy Corn Lines
Abil Dermail, Bhalang Suriharn, Sompong Chankaew, Jirawat Sanitchon, Kamol Lertrat

OCS10-06 Phenotype analysis for ideotype breeding of sorghum in Indonesia
Desta Wirnas, Neni Oktanti, Hana Nur Rahmi, Siti Marwiyah, Trikoesoemaningtyas, Didy Sopandie

OCS10-07 Draft genome assembly of the wild nightshade species, Solanum lycopersicoides and its pre-breeding applications for tomato (S. lycopersicum) improvement
Puneet Kaur Mangat and Rosalyn B. Angeles-Shim

OCS10-08 Developing mungbeans for the sprout market segment
Ramakrishnan M. Nair, Jo-yi Yen

OCS10-09 Potential Breeding Strategy for Interspecific Crosses of Oleifera x Guineensis as Enrichment Tool to Enhance Oil Palm Genetic Material
Fahmi Wendra S, Francisco Orellana, Olga Leon, Felix Vera, Zulhermana S., Dwi Asmono, Hugo Carvajal, Agry Pradipta and Budi Wahyono

OCS10-10 Characteristics of Subtropical Fruit Genetic Resources and Development of New Varieties in Jeollanamdo of Korea
Hye Sung Cho, Moon Young Park, Hyeon Ju Jeong, Youn Sup Cho, Shin Park, Byeong Sam Kim, Kyung Chul Cho, So Mi Lee, Hye Young Kwon, Hyo joong Gim, and In Tack Hwang

OCS-11. Mutation Breeding

OCS11-01 Induced Mutation versus Genome Editing Facilitated Plant Breeding: Commons and Differences in Genetics, Technology, Regulation and Cost-effectiveness
Qingyao Shu

OCS11-02 Ion-beam radiation mutagenesis and plant mutation breeding
Tomoko Abe, Hiroyuki Ichida, Yoriko Hayashi, Yuki Shirakawa, Kotaro Ishii, Ryouhei Morita
Mutation as a Useful Breeding Utensil to Expand Commercial Value of Korean Japonica Rice

Ji-Ung Jeung, Jong-Min Jeong, Youngjun Mo, Woo-Jae Kim, Su-Kyung Ha, Jinhee Kim, Bo-Kyeong Kim

Characteristics of mutations induced by proton beam-irradiation

Yeong Deuk Jo, Sang Hoon Lee, Sang Woo Lee, Yu-Mi Lee, Sun-Young Kim, Yu Jeong Kwon, Hong-Il Choi, Joon-Woo Ahn, Jin-Back Kim, Si-Yong Kang

Generation and characterization of novel genetic variation in rice for the enhancement of grain quality and agronomic performance

Thomas H. Tai

Potential Mutants for hybrid mungbean

Jingbin Chen, Prakit Somta, Xin Chen, Xiaoyan Cui, Xingxing Yuan, Peerasak Srinives

Diversity and Characterization of Cassava (Manihot esculenta Crantz.) Originated from Open Pollination Seed of M1G4 Gajah Mutant Genotypes Population

Nurul Khumaida, Sintho W. Ardie, Mita Dianasari, Riza A. Putranto

The Morphological and Phytochemical Studies on The Effect of Acute and Recurrent Irradiation in Celosia cristata Seeds

Syarifah Iis Aisyah, Izzatul Muhallilin, Dewi Sukma, Waras Nurcholis

Gene print genome editing in tomato

Vu Van Tien, Dibyajyoti Pramanik, Velu Sivankalyani. Kalyani, Eun-Jung Kim, Tran Thi Mil, Rahul Mahadev Shelake, Jihae Kim, YeonWoo Sung, Duong Thi Hai Doan, Geon Hui Son, Jae-Yean Kim

Precision genome editing in plants via base editing or gene targeting

Katsuya Negishi, Masaki Endo, Ayako Nishizawa-Yokoi, Akira Endo, Hidetaka Kaya, Kiyomi Abe, Namie Ohtsuki, Sakiko Hirose, Hiroaki Saika and Seiichi Toki

Metabolic engineering for the production of hydroxy fatty acid in oil model plant Arabidopsis

Hyun Uk Kim

Improvement of Grain Quality through Application of CRISPR/Cas9 System in Rice

Yu Jin Jung, Sang Su Bae, Yong Gu Cho and Kwon Kyoo Kang

Development and application of genome editing tools in Medicago truncatula

Goon-Bo Kim, Seong-Uk Son, Hee-Ju Yu, Jeong-Hwan Mun
Special Session (50th Anniversary Symposium of the KSBS)
“품종개발 100년, 육종학회 50년 - 주요 성과와 전망”
“100 years of Variety Development and 50 years of KSBS - Main Achievement and Prospects”

<table>
<thead>
<tr>
<th>SS-1 Overview and Food Crops</th>
</tr>
</thead>
<tbody>
<tr>
<td>SS1-01 Brief history and perspectives of crop breeding in Korea</td>
</tr>
<tr>
<td>Hee-Jong Koh</td>
</tr>
<tr>
<td>SS1-02 우리 나라 농번물 품종개발 변천사 및 성과</td>
</tr>
<tr>
<td>SS1-03 Past and Current Status, and Prospect of Barley and Wheat Research</td>
</tr>
<tr>
<td>SS1-04 Development of soybean cultivars in Korea: Current status, challenges and future</td>
</tr>
<tr>
<td>SS1-05 한국의 감자, 고구마 품종개발 변천사 및 전망</td>
</tr>
<tr>
<td>SS1-06 한국 옥수수 품종개발의 변천사와 전망</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>SS-2 Horticultural &amp; Herbal Crops</th>
</tr>
</thead>
<tbody>
<tr>
<td>SS2-01 The Change of Horticultural Seed Industry and the Development of Horticultural Breeding Technology</td>
</tr>
<tr>
<td>Yong Kwon Kim</td>
</tr>
<tr>
<td>SS2-02 한국채소 품종육종 연구의 과거, 현재, 미래</td>
</tr>
<tr>
<td>SS2-03 과수육종 역사, 현황과 전망</td>
</tr>
</tbody>
</table>

xxvi
| SS2-04 | 한국 화훼 육종의 변천과 전망 | 79 |
| SS2-05 | 우리나라 안상, 약용작물 육종의 주요 성과와 전망 | 80 |

### SS-3 Forest Plants

| SS3-01 | 한국의 임목육종 연구 동향: 학술지 논문의 키워드 분석 | 80 |
| SS3-02 | 60 Years of Forest Tree Improvement in Korea - Accomplishments and Prospects | 81 |
| SS3-03 | 산림식물 품종보호제도 현황과 전망 | 82 |

### SS-4 Technology and Policy

| SS4-01 | 인류 만년간의 식물육종 역사를 돌아보면서 내일을 살펴본다 | 83 |
| SS4-02 | Current Statues of GM Crop Development and Commercialization | 83 |
| SS4-03 | Past, Present and Future of Plant Mutation Breeding in Korea | 84 |
| SS4-04 | Achievements and Challenges in Production and Quality Management of Seed | 84 |
| SS4-05 | 우리나라의 식물산품종보호 및 종자관리제도 변천사 | 85 |
| SS4-06 | 종자산업진흥정책과 종자산업 발전 | 85 |
Poster Session

PCS-01. Abiotic Stress & Yield

PCS01-01 Photosynthetic performance in improved lines of rice cv. KDML105 containing salt tolerance gene under salt stress ........................................... 89
Dechudom Pamuta, Piyada Theerakulpisut, Jirawat Sanitchon, Jarunjit Pengrat, Meechai Siangliw, Jonaliza L. Siangliw and Theerayut Toojinda

PCS01-02 Application of Marker- Assisted Selection for Breeding Drought- Tolerant Rice (\textit{Oryza sativa} L.) in Vietnam ............................................................. 89
Pham Thi Thu Ha, Nguyen Thi Lang, Buu Chi Buu and Tran Dang Xuan

PCS01-03 Homology-based cloning of \textit{VfSOC1} of fava bean (\textit{Vicia faba} L.) ......................................................... 90
Jiong Zhang, Chenchen Xue, Jingbin Chen, Xingxing Yuan, Xin Chen

PCS01-04 Seed abundant wheat peptide transporter 2 (TaPTR2) regulates seed germination .......... 90
Choi MG, Jeong SW, Kim EJ, Choi SB, Park CS, Kang CS, and Park Y-I

PCS01-05 Wheat ELL-associated factor (TaEAF) involves in seed germination via regulating storage lipid mobilization .................................................................................. 91
Kim EJ, Choi MG, Jeong SW, Choi SB, Park CS, Kang CS, and Park Y-I

PCS01-06 Drought Stress Evaluation of Agronomic and Resilience-related Traits of Soybean Mutant Lines ............................................................................... 91
Winda Puspitasari, Abdullah Taufiq and Yuliasti Zulhedi

PCS01-07 Study on soil environment improvement for high valuable crop cultivation and field test at the reclaimed tideland ........................................................................ 92
Young-Jun Park, Han-Yong Um, Chan-Sung Oh, Jae-Do Song

PCS01-08 Growth and root characters responses of black gram (\textit{Vigna mungo} L. Hepper) genotypes to waterlogging stress ........................................................................ 92
Sompong Chankaew, Pramint Punglok, Kieatisak Pakdeekaew, Tidarat Monkham and Jirawat Sanitchon

PCS01-09 Effect of diverse drought and phosphorus fertilizer on yield potential and drought response index of rice (\textit{Oryza sativa} L.) genotypes ........................................................................ 93
Tidarat Monkham, Jirawat Sanitchon, Boonrat Jongdee, Grienggrai Pantuwan, Jaquie H. Mitchell, Shu Fukai

PCS01-10 Evaluation of fruit yield and quality in cherry tomato (\textit{Solanum lycopersicum}) varieties under hot and humid condition ................................................................. 93
Nakarin Jeeatid, Yanisa sangsodkaew and Suchila Techawongstien
<table>
<thead>
<tr>
<th>Page</th>
<th>Title</th>
<th>Authors</th>
</tr>
</thead>
<tbody>
<tr>
<td>PCS01-11</td>
<td>Screening of drought-tolerant soybean lines in core populations and EMS-treated population</td>
<td>Thi Cuc Nguyen, Jagadeesh Sundaramoorthy, Gyu Tae Park, Jeong-Dong Lee, Hak Soo Seo, and Jong Tae Song</td>
</tr>
<tr>
<td>PCS01-12</td>
<td>Screening of flood-tolerant soybean lines in EMS-treated 'Pungsannamul' mutant population</td>
<td>Hai Anh Tran, Cuc Thi Nguyen, Jagadeesh Sundaramoorthy, Gyu Tae Park, Jeong-Dong Lee, Hak Soo Seo, and Jong Tae Song</td>
</tr>
<tr>
<td>PCS01-13</td>
<td>Regulation of xylem development by jasmonic acid</td>
<td>Sangyool Lee, Deok Hyun Seo and Geupil Jang</td>
</tr>
<tr>
<td>PCS01-14</td>
<td>Intergenic transformation of <em>PsGPD</em> enhances tolerance to salt stress in rice</td>
<td>So-Young Kim, Min Kang, Seung Uk Ji, Gang-Seob Lee</td>
</tr>
<tr>
<td>PCS01-15</td>
<td>A putatively stress-related gene <em>BrTSR53</em> isolated from Brassica rapa confer salt tolerance in rice</td>
<td>Min Kang, So-Young Kim, Seung Uk Ji, Gang-Seob Lee</td>
</tr>
<tr>
<td>PCS01-16</td>
<td>Salt and Drought Tolerance Evaluation on Foxtail Millet <em>(Setaria italica L. Beauv.)</em> Genotypes</td>
<td>Sintho Wahyuning Ardie, Nurul Khumaida, Nurul Fauziah, Ria Putri</td>
</tr>
<tr>
<td>PCS01-17</td>
<td>Drought tolerance screening for normal maize inbred lines at during growth stage</td>
<td>Bishnu Adhikari, Kyu Jin Sa, Ju Kyong Lee</td>
</tr>
<tr>
<td>PCS01-18</td>
<td>A sesame variety 'KumOk' with high yield and disease resistance</td>
<td>Sungup Kim, Eunyoung Oh, Jung In Kim, Myoung Hee Lee, Suk-Bok Pae, Tae Joung Ha</td>
</tr>
<tr>
<td>PCS01-19</td>
<td>Identification of QTL for Drought Tolerance in RIL Population of Soybean</td>
<td>Beom Kyu Kang, Jae Hyun Oh, Jeong Hyun Seo, Hong Sik Kim, Hyun Tae Kim, Sanjeev Kumar Dhungana, Sang Ouk Shin, In Youl Back, Do Yeon Kwak</td>
</tr>
<tr>
<td>PCS01-20</td>
<td>Comparison of Growth of rice varieties at Maximum tillering stage in the East Coastal Area of Korea</td>
<td>No Bong Park, You Chun Song, Min Hee Nam, Jun Hyeon Cho, Ji Yoon Lee, Dong Soo Park</td>
</tr>
<tr>
<td>PCS01-21</td>
<td>Identification of water use efficient Napier grass accessions using field drought stress</td>
<td>Ermias H. Haile, Meki S. Muktar, Alemayehu T. Negewo, Chris S. Jones and Ki-Won Lee</td>
</tr>
<tr>
<td>PCS01-22</td>
<td>Development of a new <em>japonica</em> rice cultivar 'IS590DS' suitable for direct seeding cultivation</td>
<td>Choon-Song Kim, Man-Kee Baek, Hyun-Su Park, Young-Chan Cho, Jung-Pil Suh, Keon-Mi Lee, Seul-Gi Park, Chang-Min Lee</td>
</tr>
</tbody>
</table>
Calcium-dependent Protein Phosphatase 2A B” Subunits Interact with the bZIP Protein VIP1 and 14-3-3 proteins in *Arabidopsis thaliana*……………………………………………………………………. 100
Hyuk Sung Yoon, Kainen Fujino, Tatsuo Takano, Daisuke Tsugama

Agronomic Traits and Forage Production in a Mixed-planting with Corn for Forage Soybean Cultivars, Chookdu 1 and Chookdu 2……………………………………………………………………. 100
Jin-Dong Seo, Hyun Jo, Minsu Kim, Jong Tae Song, Ali Liakat, Jeong-Dong Lee

Variation of Pre-Harvest Sprouting Rate of Early-Maturing Rice Lines Adaptable to Mid-Alpine Area of Central Northern Region in Korea……………………………………………. 101
Yong Jae Won, Eok Keun Ahn, Ung Jo Hyun, Kuk Hyun Jung, Sung Kook Kim, Eung Gi Jeong, Hyang Mi Park

*Pup1* and *Sub1*, conflict or compatible?…………………………………………………………………. 101
Na-Hyun Shin, Jae-Hyuk Han, Joong Hyoun Chin

The regulation of circadian gene expression is available to improvement of drought stress tolerance ……………………………………………………………………………………………. 102
Jin A Kim, Shipra Kumari, Hyoseon Choi, Soo In Lee, Mi-Jeong Jeong

Important characters in salt tolerant rice based on several methods of screening………102
M.F. Anshori, B.S Purwoko, I.S. Dewi, S.W. Ardie and W.B. Suwarno

Rice OsMYB102 delays leaf senescence by downregulating abscisic acid accumulation and signaling ……………………………………………………………………………………….. 103
Weilan Piao, Suk-Hwan Kim, Nam-Chon Paek

Development of multi-resistant and adaptable for low nitrogen cultivation *japonica* rice cultivar ‘Namchan’…………………………………………………………………………………………. 103
Man-Kee Baek, Hyun-Su Park, Jeong-Kwon Nam, Young-Chan Cho, Jeong-Ju Kim, Woon-Chul Shin, Ki-Young Kim, Cheon-Song Kim, Bo-Kyeong Kim, Woo-Jae Kim, Ji-Ung Jeong, Jong-Min Jeong, Keon-Mi Lee, Seul-Gi Park, Chang-Min Lee, Jeom-Ho Lee

Study of water-logging damage and tolerance of rapeseed (*Brassica napus* L.)………………. 104
Ji-Eun Lee, Kwang-Soo Kim, Da-Eun Kwon, Al-Mahmur Alam, Young-Lok Cha, Youn-Ho Moon, and Yong-Gu Kang

Development of Vertical Cultivation Technology for Standardized Fruits and Mass Production of Small and Medium Sized Watermelon…………………………………………….. 104
Eun Jeong Kim, Sol Ji Noh, Sung-Won Park, Yu-min Jeon, Young Sang Kim, Yoon Sun Huh, Tae Il Kim

Metabololites Profile Analysis of Teosinte in the Flooding Condition………………………….. 105
Jung-Tae Kim, Young-Sam Go, Beom-young Son, Hwan-Hee Bae, Sun-Lim Kim and Sung-Beom Baek
PCS01-34 Identification QTL conferring anaerobic germination and effect confirmation derived from weedy rice PBR

Jong-Min Jeong, Youngjun Mo, Ji-Ung Jeung, Woo-Jae Kim, Su-Kyung Ha, Jinhee Kim, Bo-Kyeong Kim

PCS01-35 Development of SNP-based CAPS makers for AG-tolerant rice cultivars in rice

Jong-Min Jeong, Ji-Ung Jeung, Youngjun Mo, Woo-Jae Kim, Su-Kyung Ha, Jinhee Kim, Bo-Kyeong Kim

PCS01-36 Characterization of grain-related traits of 300 Korean rice varieties

Chang-Min Lee, Hyun-Su Park, Man-Kee Baek, Jung-Pil Suh, Choon-Song Kim, Keon-Mi Lee, Seul-Gi Park, Young-Chan Cho

PCS01-37 Biomass as a major means of affecting methane emissions

Woo Jae Kim, Jong Min Jeong, Jeong Ju Kim, Anna M. McClung, Jin Young Y. Barnaby

PCS01-38 The RING E3 ligase, OsSIRH2-14, positively regulates response to salt stress in rice

Yong Chan Park, Sung Don Lim, Jun-Cheol Moon, Cheol Seong Jang

PCS01-39 Comparative functional analysis of the OsCLR1 gene induced by salt and drought stress and its grass orthologs

Yong Chan Park, Seung Young Choi, Jong Ho Kim, Cheol Seong Jang

PCS01-40 Early Flowering, High Yielding and Multiple Disease-Insect Resistant Forage Rice Cultivar, 'Jowoo' Easy to Cultivate Subsequent with Winter Forage Crops

Eok Keun Ahn, Kuk Hyun Jung, Ung Jo Hyun, Hyang Mi Park, Eung-Gi Jeong, Yong Jae Won, Jeom Ho Lee, Jeong Heui Lee, Ha Cheol Hong, Jae Ki Chang

PCS01-41 Breeding of Whole Crop Silage (WCS) Rice Cultivar for Improving Insect-Disease Resistance, Salt and Herbicide Tolerance

Eok Keun Ahn, Kuk Hyun Jung, Ung Jo Hyun, Hyang Mi Park, Eung-Gi Jeong

PCS01-42 Molecular approach to develop crops with the increased productivity through regulating the shade avoidance syndrome (SAS)

Ora Son, Sunghan Kim, Seul-Ki Jung, and Choong-Il Cheon

PCS01-43 Development of Long Grain Type Aromatic Rice Variety 'Hyangyeol' Adaptable to South-East Tropical Asia

Young-Chan Cho, Man-Kee Baek, Hyun-Su Park, You-Chun Song, Jeong-Kwon Nam, Woo-Jae Kim, Bo-Kyeong Kim, Young-Bok Lee, Chun-Song Kim, Hong-Kyu Park, Jong-Min Jeong, Woon-Chul Shin, Jeom-Ho Lee, Jun-Hyun Cho, Ji-Yoon Lee, Jung-Pil Suh, Jong-Hee Lee

PCS01-44 Genetic analysis of QTL interaction for low-temperature germinability using introgression lines derived from O. rufipogon

Kyu-Chan Shim, Sunha Kim, Hyun-Sook Lee, Yun-A Jeon, Luong Ngoc Ha, Cheryl Adeva, Woo-Jin Kim, Sang-Nag Ahn
PCS01-45  Probable L-ascorbate peroxidase 4 gene regulates flowering time and antioxidant activity in rice.......................................................................................................................... 111
  Yun-A Jeon, Gynheung An, Lae-Hyun Cho, Hyun-Sook Lee, Sun Ha Kim, Won-Yong Song, Sang-Nag Ahn

PCS01-46  Genetic elucidation of North Korean rice varieties for salinity stress tolerance........... 111
  Jung-Woo Lee, Haris Wijaya, Joong Hyoun Chin and Soo-Cheol Yoo

PCS01-47  Selection of Transgressive Segregants in Six Populations of Wheat in Tropical Region... 112
  Nurwanita Ekasari Putri, Yudiwanti Wahyu, Surjono Hadi Sutjahjo, Trikoesoemaningtyas, Amin Nur

PCS01-48  Survival comparison of Larix spp. seedlings under drought stress.............................. 112
  Hye-In Kang, Kyungmi Lee, Yeonju Seo, Jinjoong Kim, Jiah Kim and Insik Kim

PCS01-49  Loose Plant Architecture 1 (LPA1) mutants confers drought tolerant by altering xylem vessel
            enlargement in rice (Oryza sativa)............................................................................................ 113
  Ryza A. Priatama, Jung Heo, Yang Liu, Yuanhu Xuan, Byoung Il Je, Chang-deok Han, Soon Ju Park

PCS01-50  A salt and heat stress moderate resistance and high-yield ginseng 'Eumseong No.9'...... 113
  Jang Uk Kim, Jung Woo Lee, Ick Hyun Jo, Chi Eun Hong, Kyong Hwan Bang

PCS01-51  Identification of QTL for rice pre-harvest sprouting in Korean varieties using a tropical
            condition.................................................................................................................................. 114
  Hyun Ung-Jo, Jeong Guik-Hyun, Ahn Euk-Keun, Park Hyang-Mi, Jeong Eung-Gi, Won Yong-Jae, Jeong O- Yeong

PCS01-52  Mother of FT and TFL1 (MFT) gene is enable to involve Pre-harvest Sprouting (PHS) in Korean
            Wheat (Triticum aestivum)........................................................................................................ 114
  Sang Yong Park, Geon Hee Lee, Tae Kyeum Kim, Chang-Ho Kim, Jae Yoon Kim

PCS01-53  Characteristics of Korean wheat cultivars in terms of Cold intolerance and summer stress
            .............................................................................................................................................. 115
  Ji Hye Heo, Hye Ju Seong, Woo Suk Jung

PCS01-54  Developing gene specific molecular markers of wheat related to flowering and cold tolerance
            .............................................................................................................................................. 115
  Ji Hye Heo, Hye Ju Seong, Woo Suk Jung

PCS01-55  Functional analysis of wheat MAP kinases in response to cold stress......................... 116
  Woo Joo Jung, Yong Weon Seo

PCS01-56  Comparative study on drought stress response in the roots of wheat (Triticum aestivum L.)
            .............................................................................................................................................. 116
  Joseph Noble Amoah and Yong Weon Seo

PCS01-57  Change of gluten profiling under the high temperature during grain-filling............... 117
  Chan Seop Ko, Jin-Baek Kim, Min Jeong Hong, Kyeong Hoon Kim, Yong Weon Seo

  xxxii
| PCS01-58 | Wheat ASR's multiple roles in drought and salt stress | 117 | Jin Seok Yoon, Yong Weon Seo |
| PCS01-59 | Transcriptomic analysis of two Tunisian durum wheat cultivars under salinity stress | 118 | Sang Heon Kim, Dae Yeon Kim, Inés Yacoubi, and Yong Weon Seo |
| PCS01-60 | Traits affecting low temperature tolerance in tomato and their application in breeding program | 118 | Rajametov Sherzod, Myeong Cheoul Cho, Eun Young Yang, Soo Young Chae, Jeong Ho Kim, Chun Woo Nam, Hyeri Lee, Won Byoung Chae |
| PCS01-61 | Improved crop yield and soil properties with rice residue and mineral nitrogen in conservation-agriculture-based cropping systems of eastern Uttar Pradesh, India | 119 | Robin Kumar and Rama Kishan Naresh |
| PCS01-62 | A negative regulator in response to abiotic stress, *Oryza sativa* Drought, Heat, and salt induced RING finger protein 1 | 119 | Ju Hee Kim and Cheol Seong Jang |
| PCS01-63 | MYB96 recruits the HDA15 protein to suppress negative regulators of ABA signaling in *Arabidopsis* | 120 | Hong Gil Lee, Yeong Yeop Jeong & Pil Joon Seo |
| PCS01-64 | Evaluation of salinity tolerance of multiparent advanced generation intercross (MAGIC) population to improve salt-sensitive japonica cultivars | 120 | Suk-Man Kim, Jong-Min Jeong, Bo-Kooyng Kim |
| PCS01-65 | Development Breeding System of Maize Inbred Lines by Doubled Haploid Technology | 121 | Sihwan Ryu, Jaekeun Choi, Min Namgung, Moonjong Kim, Jeongheon Han, Seungchul Choi, Jongyeol Park, Woosik Yong, Gyeongnam Nam, Inseok Seo, and Jinkwan Ham |
| PCS01-66 | Transcriptomic analysis of poplar (*Populus alba* × *P. glandulosa* and *P. euramerica*) in elevated CO2 concentration | 121 | Wonwoo Cho, Hyunseok Lee, Wi-Young Lee, Hyemin Lim |
| PCS01-67 | Characterization of transcription factor genes conferring cold tolerance in rapeseed | 122 | Mukut Sharma, Rahul Ramekar, Ik-Young Choi and Kyong-Cheul Park |
| PCS01-68 | Selection of Cold Tolerance Elite lines Carrying qSCT12UK Using MAS in Tong-il type Rice | 122 | Sumin Jo, Jun-Hyeon Cho, Ji-Yoon Lee, Young-Ho Kwon, Ju-Won Kong, Tae-Heon Kim, Sais-Beul Lee, Jong-Hee Lee, Dong-Soo Park, Jong-Min Ko |
| PCS01-69 | Characterization of stress associated protein 5 to drought stress tolerance in hybrid poplar | 123 | Dan-Be Park, Young-Im Choi, Hyoshin Lee, Eun-Kyung Bae |
Molecular characterization of Oryza sativa arsenic-induced RING finger E3 ligase 3

Jeong Eun Lee, Cheol Seong Jang

Functional Characterization of Drought-Responsive Long Noncoding RNAs (DRIL) in Rice

Nuri Oh, Jimin Lee, Daehoon Jang, Moon-Joo Lee, and Choonkyun Jung

Characteristics of yield and quality as affected by different seedling age among rice varieties in late transplanted rice in southern area

Hyun Kyeng Min, Kyu Nam An, Seo Ho Shin, Dong Kwan Kim

Development of rice varieties enhancing seed weight using Tosl7 mutants

Kyong Mi Jun, Songhwa Chae, Yeon-Ki Kim, Baek Hie Nahm, Joung Sug Kim

Detection of associated gene with Pre-harvest sprouting in rice (Oryza sativa L.)

Seong-Gyu Jang, Mar Lar San, So-Yeon Park, Ja-Hong Lee, Na-Eun Kim, Soon-Wook Kwon

Development of evaluation system and selection genetic resources for resistance to abiotic stresses in soybean

Chuloh Cho, Kyung Hwa Kim, Man-Soo Choi, Jaebuhm Chun, Mi-Suk Seo, Namhee Jeong, Mina Jin, Eok-Keun Ahn, Hyang-Mi Park, Dool-Yi Kim

Comparison analysis of Salttol QTL genes in enhanced salt-tolerant lines from Mogyang/IR64

Chuluunsetsseg Jadamba, Soo Hyeon Nam, Soo In Lee and Soo-Cheul Yoo

Elucidation of salt tolerance mechanism by OsEXPA genes in rice

Chuluuntsetseg Jadamba, Soo Hyeon Nam, Soo In Lee and Soo-Cheul Yoo

Proteome analysis of sesame leaves in response to waterlogging stress at vegetative and flowering stages


In Vitro screening of Soybean Mutant lines using PEG Under Drought Stress and Yield performance under dry Land

Yuliasti and Tifani

Leaf and root proteome analysis of Sorghum in response to lead stress

Swapan Kumar Roy, Soo-Jeong Kwon, Kun Cho, Ju-Young Choi, Sang-Heon Choi, Yong-Hwan Ju, Dong-Gyu Lee, Hyeun-Chung Chun, Hong-Sig Kim, and Sun-Hee Woo

Phenotypic screening of North Korean rice varieties for phosphorus deficiency and drought stress tolerances

Michael Akem Ndizingwan, Hana Ahmed Larbi Idris Hassan Abdulllah and Soo-Cheul Yoo
PCS02-01 Characterization of Complete Chloroplast Genomes of *Artemisia capillaris* and *Artemisia iwayomog*  
Jin-hyuk Kim, Minjung Kim, Sanghee Um, Jong-sung Lim, So-yeon Kang, haerim Park, Hyang Sook Chun, Dongho Lee, and Gyoungju Nah  

PCS02-02 Development of InDel Markers Based on Transcriptome Sequences and Genetic Diversity Analysis of Mungbean Varieties from China  
Qunsan Li, Jingbin Chen, He-ping Gu, Xing-xing Yuan, Xin Chen, Jin Cui  

PCS02-03 Draft genome of a cereal and medicinal crop, *Coix lacryma-jobi*, in the Poaceae family  
Beom-Soon Choi, Nam-Hoon Kim, Hyun Oh Lee, Hye Sik Kim, Myung Ju Shin, Hyo-Won Kim, Kyoung Dae Kang, Tae Seok Park, Chang-Kug Kim, Sang-Choon Lee  

PCS02-04 Nanopore sequencing and its application to genome assembly of various organisms  
Hyun Oh Lee, Myung Ju Shin, Sang-Choon Lee, Beom-Soon Choi, Nam-Hoon Kim, Hye Sik Kim, Hyo-Won Kim, Kyoung Dae Kang, Tae Seok Park  

PCS02-05 Identification of QTLs controlling seed weight and days to flowering in zombi pea (*Vigna vexillata* [L.] A. Rich), an underutilized legume crop  
Kitiya Amkul, Lixia Wang, Kularb Laosatit, Xuzhen Cheng, Peerasak Srinives, Prakit Sontta  

PCS02-06 Development of LOX-3 null near-isogenic *japonica* rice line and characterization of seed longevity and stale flavor  
Hyun-Su Park, Keon-Mi Lee, Man-Kee Baek, Choon-Song Kim, Seul-Gi Park, Chang-Min Lee, Suk-Man Kim, Jung-Pil Suh, Young-Chan Cho  

PCS02-07 Sequencing of the tetraploid *Perilla* (*Perilla frutescens*) genome  
Seon-Hwa Bae, Hong-II Ahn, Myeong-Hee Lee, Jeong-Hee Lee, Keunpyo Lee, Ung-Han Yoon, Ye-Ji Lee, Jundae Lee, Tae-Ho Kim  

PCS02-08 Analysis of the characteristics of transcriptomes in rice by submergence during the ripening stage  
HyeonSeok Lee, Woon-Ha Hwang, Jae-Hyeok Jeong, Seo-Yeong Yang, Yeon-Hwa Lim, Chung-Gen Lee and Kyung-Jin Choi  

PCS02-09 Fine mapping a major QTL associated with seed dormancy in mungbean (*Vigna radiata* [L.] Wilczek)  
Kularb Laosatit, Kitiya Amkul, Prakit Sontta, Tarika Yimram, Jingbin Chen, Xingxing Yuan, Xin Chen, Peerasak Srinives  

PCS02-10 Re-sequenced 235 wild and cultivated soybean accessions reveals genomic signatures for domestication and subsequent improvement  
Jae-Yoon Kim, Seongmun Jeong, Kyoung Hyoun Kim, Jung-Kyung Moon, Namshin Kim
Transcriptome analysis for anthracnose resistance in watermelon reveals insights into the co-expression patterns of changeable expression................................. 134
Yoon Jeong Jang, Minseok Seo, Han Bal-Kum, Cho Hui Joo, Yeo Nan Joo, Huh Jin Hyuck, Gung Pyo Lee

Molecular mapping of the unstable Restorer-of-fertility (Rf) gene in sweet pepper \textit{(Capsicum annuum L.)}................................................................. 135
Moo Chan Kang, Hwa Jeong Kang, Jeong Hhwan Ahn, Byoung Cheorl Kang

Draft genome assembly of the Korean sesame \textit{(Sesamum indicum)} variety Goenbeak................................. 135
Yedomon Ange Bovys Zoclaclounon, Hae Koo Kim, Ung-Han Yoon, Tae-Ho Kim, Keunpyo Lee

Barley RNA viromes in six different geographical regions in Korea............................................. 136
Bong Choon Lee, Sang-Min Kim, Shin Hwa Kim and Sang-Yun Cho

Molecular mechanisms of high-rutin content in tartary buckwheat revealed by whole genome sequencing................................................................. 136
Hwang-Bae Sohn, Su-Jeong Kim, Su-Young Hong, Jung Hwan Nam, Bon-Cheol Koo and Yul-Ho Kim

Improvement of Button Mushroom \textit{(Agaricus bisporus)} Genome Assembly via the Hybrid Assembly with Oxford Nanopore Technology and Illumina MiSeq............................... 137
Ick Hyun Jo, Donghwan Shim, Hyejin An, Tae-Young Heo, Gi Ho Sung, Jong-Wook Chung

Investigation of single nucleotide polymorphism in glucosinolate biosynthesis related genes among subspecies of \textit{brassica rapa}..................................................................................... 137
Sin-Gi Park, Boram Choi, Seung-il Yoo, Dong Jin Lee, Jung Sun Kim

Mutation of TF1 cause the Function Loss of regulating Anthocyanin Biosynthesis in Chrysanthemum ........................................................................... 138
Bo-Ra Park, Da-Hye Kim, Sangkyu Park, Jong-Yeol Lee and Sun-Hyung Lim

Integrative analysis of metabolome and transcriptome of large- and small- nut in Korean chestnut trees \textit{(Castanea crenata)} during nut development......................................................... 138
Min-Jeong Kang, Sang A Lee, Hyo-Ryeon Lee, and Tae-Dong Kim

Whole genome wide sequence variation in dwarf derived from normal growth of F7 RILs of crossing between cultivar and wild type in soybean................................. 139
Neha Samir Roy, Hana Yoo, Rahul Ramekar, Namil-Park, Kyong-Cheul Park, Ik-Young Choi

Genome-wide identification and characterization of bZIP transcription factor gene family in mungbean \textit{(Vigna radiata \textit{(L.) R. Wilczek)}}............................................................. 139
Kang-Heum Cho, Jungmin Ha, Moon Young Kim, Sangrea Shim and Suk-Ha Lee

Identification of microRNAs and their abiotic stress-related target genes in flood-treated soybean Cheongja-3............................................................................. 140
Green Jhang, JinHyuk Kim, Chi-Hwan Kim, Gyoungju Nah, Suk-Ha Lee
<table>
<thead>
<tr>
<th>Page</th>
<th>Title</th>
<th>Authors</th>
</tr>
</thead>
<tbody>
<tr>
<td>PCS02-23</td>
<td>MutMap analysis reveals loci for growth traits in rice</td>
<td>Jun Oh, Kyeong-Seong Cheon, Do-Yu Kang, Hyo Ja Oh, Song Lim Kim, Inchan Choi, Jeongho Baek, Kyung-Hwan Kim, Hyeonso Ji</td>
</tr>
<tr>
<td>PCS02-24</td>
<td>Draft genomes of two medicinal plants, <em>Cynanchum wilfordii</em> and <em>Cynanchum auriculatum</em></td>
<td>Hyun Jo Koo, Chi-hwan Kim, Haerim Park, So Yeon Kang, Jong-Sung Lim, Hyang Sook Chun, Jaeki Chang, Jeonghoon Lee, Youngho Koh, Dongho Lee and Gyoungju Nah</td>
</tr>
<tr>
<td>PCS02-25</td>
<td>Integrated genome structural and functional annotation pipeline for plants</td>
<td>Hoyong Chung, Natarajan Sathishkumar, Kikwang Oh, Sridhar Srinivasan, Mohammed Sameer, Preethiba Gopi, Dawood Dedekule, Junhyung Park</td>
</tr>
<tr>
<td>PCS02-26</td>
<td>Transcriptomic approach of FAD family proteins in <em>Perilla citriodora</em></td>
<td>Hong-Il Ahn, Ye-Ji Lee, Seon-Hwa Bae, Myoung-Hee Lee, Jeong-Hee Lee, Keunpyo Lee, Ung-Han Yoon, Tae-Ho Kim</td>
</tr>
<tr>
<td>PCS02-27</td>
<td>Genome-wide analysis of evolution of the TCP transcription factor family in soybean</td>
<td>Sangrea Shim, Moon Young Kim, Jungmin Ha, Kang-Heum Cho, and Suk-Ha Lee</td>
</tr>
<tr>
<td>PCS02-28</td>
<td>Comparative genomic analysis of three isolates of <em>Phytophthora capsici</em></td>
<td>Muhammad Irfan Siddique, Joung-Ho Lee and Byoung-Cheorl Kang</td>
</tr>
<tr>
<td>PCS02-29</td>
<td>Identification of non-additively expressed genes at early developmental stages in an F&lt;sub&gt;1&lt;/sub&gt; hybrid cultivar of Chinese cabbage</td>
<td>Hasan Mehraj, Kodai Matsuo, Motoki Shimizu, Takeshi Yasuda, Ryo Fujimoto</td>
</tr>
<tr>
<td>PCS02-30</td>
<td>Vernalization alters histone H3 lysine 27 trimethylation at FLC locus in <em>Brassica rapa</em></td>
<td>Ayasha Akter, Satoshi Takahashi, Namiko Nishida, Naomi Miyaji, Takeshi Yasuda, Yutaka Suzuki, Motoaki Seki, Ryo Fujimoto</td>
</tr>
<tr>
<td>PCS02-31</td>
<td>Genome-wide association study for trichome development in the <em>Brassica rapa</em> core collection</td>
<td>Seongmin Hong, Chetan Kaur Bhogal, Su Ryun Choi, Yong Pyo Lim, and Yong-Min Kim</td>
</tr>
<tr>
<td>PCS02-32</td>
<td>The characterization of the gene expression concern to plant growth in the dwarf mutants derived from F7 RILs crossed between cultivar and wild type soybean</td>
<td>Hana Yoo, Neha Samir Roy, Nam-II Park, Kyung-Cheul Park, Ik-Young Choi</td>
</tr>
<tr>
<td>PCS02-33</td>
<td>Transcriptome analysis and characterization of genes associated with leaf development and dimorphic chloroplast differentiation in <em>Bienertia sinuspersici</em></td>
<td>Eun Ju Byeon, Prabakaran Soundrarajan, Yoen-Hee Lee, So Yun Won, Jung Sun Kim</td>
</tr>
<tr>
<td>PCS02-34</td>
<td>QTL Mapping with Stem Related Traits using Recombinant Inbred Lines based on High-Resolution Map in Rice (<em>Oryza sativa</em> L.)</td>
<td>Ye-Ji Lee, Gang-Seob Lee, Hong-II Ahn, Seon-Hwa Bae, Keunpyo Lee, Ung-Han Yoon, Nam-In Hyung, Tae-Ho Kim</td>
</tr>
</tbody>
</table>
PCS02-35 Analysis of glucosinolates content and related-genes expression in 88 Radish (Raphanus sativus L.) ................................................................. 146  
Ji-Nam Kang, Mi-Suk Seo, Jung Sun Kim, So Youn Won, Soo-Jin Kwon

PCS02-36 Construction of A Linkage Map Using Axiom-driven SNPs for Genome Improvement and Molecular Breeding in Octoploid Strawberry ................................................................. 147  
Jungeol Yeum, Jinkwan Jo, Jinhee Kim, Do-Sun Kim, and Byoung-Cheorl Kang

PCS02-37 Genome-wide identification and characterization of high affinity potassium transporter 1 (HKT1) and Na+/H+ antiporters (NHX) family in Bienertia sinuspersici ................................................................. 147  
Prabhakaran Soundararajan, Eun Ju Byeon, So Youn Won, Yeon-Hee Lee, and Jung Sun Kim

PCS02-38 Identification, characterization, and comparative genomics study of YABBY gene family in Bienertia sinuspersici, a single cell C₄ plant ................................................................. 148  
Prabhakaran Soundararajan, So Youn Won, Jung Sun Kim

PCS02-39 The transcriptome identification for anthocyanin biosynthesis in black rice ................................................................. 148  
Chang-Kug Kim, Sang-Ho Kang, Soo-Jin Kwon

PCS02-40 Development and application of KASP marker for high throughput authentication of 7 Panax species ................................................................. 149  
Vo Ngoc Linh Giang, Hyun-Seung Park, Wojong Jang, Hyunjin Koo, Hyeonah Shim, Lee Sae Hyun, Park Young Sang, JinTae Kim and Tae-Jin Yang

PCS02-41 Transcriptome analysis and identification of OsWRKY transcription factor associated with the leaf morphology in rice ................................................................. 149  
Songhwa Chae, Joung Sug Kim, Kyong Mi Jun, Yoonmok Pahk, Duk-Ju Hwang, Gang-Seob Lee, Baek Hie Nahm, and Yeon-Ki Kim

PCS02-42 Application of Korean japonica rice Kompetitive Allele-Specific PCR (KASP) markers in High-Throughput Genotyping system ................................................................. 150  
Youn Young Lee, Youngsil Lee, Hayan Lee, Miyeon Son, Hyeonso Ji, Young-Min Jeong

PCS02-43 Functional Study of PAMP-responsive long noncoding RNAs in Arabidopsis ................................................................. 150  
Jimin Lee, Nuri Oh, Daeheon Jang, Moonjoon Lee and Choonkyun Jung

PCS02-44 Inter- and intra-chloroplast genome diversity and classification of germplasm in Cynanchum species ................................................................. 151  
Sae Hyun Lee, Hyun-Seung Park, Hyeonah Shim, Ho Jun Joh, Hyun-Oh Lee, Jee Young Park, Tae-Jin Yang

PCS02-45 Whole Genome Scan Reveals the Positive Selection in Kohlrabi ................................................................. 151  
Hyun-Jin Koo, Jee Young Park, and Tae-Jin Yang

PCS02-46 Unique features displayed in the chloroplast genomes of the Selaginella genus ................................................................. 152  
Hyeonah Shim, Junki Lee, Nam-Soo Kim, Tae-Jin Yang

xxxviii
PCS02-47 Haplotype analysis of the BADH1 gene and the association with salt tolerance in rice germination stage
Yuan Cao, Lin Cheng, Rungnapa Phitaktansakul, Myeong-Hyun Min, Kyaw Myo Aung, Sang-Ho Chu, Kyu-Won Kim, Jungrye Nam, Yong-Jin Park

PCS02-48 Signatures of differential selection in chloroplast genome between japonica and indica
Lin Cheng, Jungrye Nam, Sang-Ho Chu, Phitaktansakul Rungnapa, Myeong-Hyun Min, Yuan Cao, Ji-Min Yoo, Jee-Su Kang, Kyu-Won Kim & Yong-Jin Park

PCS02-49 Genomic variations and evolutionary studies in diverse varieties of rice
Lin Cheng, Kyu-Won Kim, Jungrye Nam, Yong-Jin Park

PCS02-50 Evidence for selection events during domestication by extensive mitochondrial genome analysis between japonica and indica in cultivated rice
Lin Cheng, Kyu-Won Kim, Yong-Jin Park

PCS02-51 Integration of Genome-Wide/Transcriptome-Wide Studies and eQTL Analysis on Preharvest Sprouting Trait from 378 Asian Cultivated Rice
Myeong-Hyun Min, Rungnapa Phitaktansakul, Kyaw Myo Aung, Lin Cheng, Yuan Cao, Jungrye Nam, Sang-Ho Chu, Kyu-Won Kim, Yong-Jin Park

PCS02-52 Atlas of Omics Information on Badh2 in Rice
Rungnapa Phitaktansakul, Kyu-Won Kim, Ji-Min Yoo, Jee-Su Kang, Kyaw Myo Aung, Myeong-Hyun Min, Lin Cheng, Yuan Cao, Sang-Beom Lee, Seung-Hyun Kim, Joo-hyun Lee, Soon-Wook Kwon, Sang-Ho Chu, Jungrye Nam, Sang-Won Park, Hee-Jong Koh, Young-Sang Lee, Ill-Min Chung, Yong-Jin Park

PCS02-53 Submergence 1 [SUB1] Gene Diversity in 475 accessions of rice genetic resources
Kyaw Myo Aung, Rungnapa Phitaktansakul, Yuan Cao, Lin Cheng, Myeong-Hyun Min, Sang-Ho Chu, Kyu-Won Kim, Jungrye Nam, Yong-Jin Park

PCS02-54 The genetic diversity related to vitamin E biosynthesis pathway using cultivated rice DNA chip data
Kyaw Myo Aung, Sang-Ho Chu, Rungnapa Phitaktansakul, Lin Cheng, Yuan Cao, Myeong-Hyun Min, Jungrye Nam, Kyu-Won Kim, Yong-Jin Park

PCS02-55 Genetic Differentiation Analysis of Ecotype Interactions in Bacterial Leaf Blight Resistance Gene in rice
Jee-Su Kang, Kyaw Myo Aung, Jungrye Nam, Kyu-Won Kim, Yong-Jin Park

PCS02-56 Sequence and Haplotype Variations of Granule-Bound Starch Synthase I and II [GBSS-I, GBSS-II] Genes in Cultivated Rice and Wild Rice Based on Genome Information
Ji-Min Yoo, Rungnapa Phitaktansakul, Kyaw Myo Aung, Lin Cheng, Yuan Cao, Jungrye Nam, Sang-Ho Chu, Kyu-Won Kim, Yong-Jin Park

PCS02-57 Identification of eQTLs of a bacterial leaf blight resistance gene [Xa39] using RNA-Seq data of Korean rice coreset
Jee-Su Kang, Rungnapa Phitaktansakul, Kyaw Myo Aung, Jungrye Nam, Kyu-Won Kim, Yong-Jin Park
| PCS02-59 | Identification of Genetic Diversity in Korean Breeding Lines using Oryza 580K Genotyping Array | Kyu-Won Kim, Jungrye Nam, Yong-Jin Park |
| PCS02-60 | Orthologs Phylogenetic Profile of 18 Plants | Jungrye Nam, Kyu-Won Kim, Yong-Jin Park |
| PCS02-61 | A Strategy that Discovers Conserved Genes from Co-orthologs | Kyu-Won Kim, Jungrye Nam, Yong-Jin Park |
| PCS02-62 | Identification of Indels Causing Frameshift from 3,459 Asian Rice Collection using KNU Axiom Oryza 580K Genotyping Array | Jungrye Nam, Kyu-Won Kim, Yong-Jin Park |

**PCS-03. Bioinformatics**

| PCS03-01 | IT-PCR: a simple web-based integrated tool for picking CRISPR targets to facilitate functional genomics study in rice | Woo-Jong Hong, Yu-Jin Kim, Anil Kumar Nalini Chandran, Myeong-Hyun Yoou, and Ki-Hong Jung |
| PCS03-02 | Repeated Rank-based Marker Selection for Genomic Selection of Low Heritability | Seongmun Jeong, Jae-Yoon Kim, Namshin Kim |
| PCS03-03 | LegExpress: Construction of a translational bioinformatic platform for expression profiling in legume plants | Joo-Seok Park, Jin-Hyun Kim, Yoram Choi, Min-Gyun Jeong, Hong-Kyu Choi |
| PCS03-04 | LegCompara: A real time-responsible DB-linked platform for the translational genome analysis in legumes | Jin-Hyun Kim, Joo-Seok Park, Yoram Choi, Min-Gyun Jeong and Hong-Kyu Choi |
| PCS03-05 | GWAS-based dissection on genes and genomic loci involved in the pigmentation of soybean seeds | Jin-Hyun Kim, Joo-Seok Park, Yoram Choi, Min-Gyun Jeong and Hong-Kyu Choi |
| PCS03-06 | Dynamics of the gene regulatory networks of leaves in *Brassica rapa* | Man-Sun Kim, Han Kyum Choi, Jana Jeevan Rameneni and Yong Pyo Lim |
Transcriptome profiling reveals marker genes for seed dormancy and germination in *Arabidopsis thaliana*... 164
Minsu Park, Taehyeon Park, Jemin Kim, Taewook Kim, Sang-Yoon Shin, Taeyoung Um, Chanseok Shin

Transcriptome analysis in rice irradiated with different types of ionizing radiations... 164
Jae Wan Park, Sung Il Lee, Min Jeong Hong, Jin-Baek Kim, Hong-Il Choi

Web-application for finding the open reading frames (ORF) in diverse sugar cane genomes... 165
Yang Jae Kang

RTFDB: A web-based tool for the prediction of rice transcription factor function... 165
Anil Kumar Nalini Chandran, Sunok Moon, Yo-Han Yoo, Yoon-Shil Gho, Peijian Cao, Rita Sharma, Manoj K. Sharma, Pamela C. Ronald, and Ki-Hong Jung

A comparison of two GBS pipelines to analyze a large onion genome... 166
Tae-Ho Lee, Dong-Jun Lee, Da-Hye Jeon, Seo-Hyeon Ham, Sun-Mi Joung, Su-Yeon Park

Developing a model system to obtain genotype data of a mass of genetic resources... 166

RACSO: Toolkit for random seed orchard design and visualization... 167
Hye Joon Joo, Jae Hyun Park, Byeong Ho Moon

PCS-04. Biotic Stress

Effect of Pinewood Nematode on the Water Content and Early Disease Development of Japanese Black Pine Seedlings... 167
Kwan-Soo Woo, Seung-Beom Chae, II Hwan Lee and Jinjung Kim

Soybean endo-1,3-beta-glucanase interaction with Soybean mosaic virus -encoded P3 protein may contributes the intercellular movement... 168
Cui Xiaoyan, Wang Ying, Yuan Xingxing, Chen Xin

Chutintorn Yundaeng, Prakit Somta, Tarika Yimram, Jingbin Chen, Xingxing Yuan, Peerasak Srinives, Xin Chen

Novel Sources of Resistance to Pepper Yellow Leaf Curl Thailand Virus (*Begomovirus*)... 169
Derek Barchenger, Nakarin Jeetat, Sopana Yule, Shih-wen Lin, Yen-wei Wang, Tsung-han Lin, and Lawrence Kenyon
PCS04-05 Evaluation Phenotypic and Genotyping for Resistance Against Tomato Yellow Leaf Curl Thailand Virus (TYLCTHV) Validated by Ty-2 Ty-3 and Ty-4 Genes in Tomato

Kawin Kruepu, Suchila Techawongstien, and Chanon Lapjit

PCS04-06 Inhibition of fusarium surface rot by sound wave treatment in Arabidopsis thaliana

Ye Eun Kang, Joo Yeol Kim, Soo In Lee, Jin A Kim, Mi-Jeong Jeong

PCS04-07 Sequential double screening method to identify accessions resistant to Fusarium wilt disease in the sesame world collection

Hae Koo Kim, Yedomon Ange Bovys Zoelanclounon, Hyo-Won Choi, Seung-up Kim, Ung-Han Yoon, Tae-Ho Kim, Keunpyo Lee

PCS04-08 Screening of Sclerotinia Rot Resistance in Korean Origin Perilla (Perilla frutescens) Germplasm Using a Detached Leaf Method

Tania Afroz, Ho-Sun Lee, Young-Ah Jeon, Jung-Sook Sung, Ju-Hee Rhee, Awraris Derbie Assefa, Jaejong Noh, Aejin Hwang, On-Sook Hur, Na-Young Ro, and Jae-Eun Lee

PCS04-09 The WY domain in the Phytophthora effector PSR1 is required for infection and RNA silencing suppression activity

Peng Zhang, Yijuan Jia, Jinxia Shi, Chen Chen, and Yongli Qiao

PCS04-10 Gene effects of chili pepper with two different resistant sources to PepYLCV

M. Tanpao, S. Techawongstien, Y. Sangsotkaew, N.Jeeatid, N. Siri, and P. Thummabenjapone

PCS04-11 Discover a new QTL for bakanae disease resistance in rice


PCS04-12 Genetic Mapping of Chili veinal mottle virus Resistant Gene 4 (cvr4) in Pepper

Joung-Ho Lee, Jin-Kyoung Kwon and Byoung-Cheol Kang

PCS04-13 Change of yield by using rootstock in tomatoes

Yul Kyun Ahn, Young Eun Ahn, Kue Hyon Hong, Kwan Ho Lee, Deok Ho Kwon, Myeong Cheoul Cho, Jun Gu Lee, Indeok Hwang

PCS04-14 Discovery of new haplotyped of a soybean cyst nematode resistant gene, GmSNAP18

Prakash Basnet, Neha Samir Roy, Rahul Ramekar, Kyung-Cheul Park, Ik-Young Choi

PCS04-15 Microbial community analysis in cultivation soil with soft-rot disease of Gastrodia elata by metagenomics

Min-Jeong Kang, Hye-Ryeon Lee, Sang A Lee, and Tae-Dong Kim

PCS04-16 Multi-omics approaches reveals co-evolution of microRNAs and disease-resistant genes in pepper

Taehyeon Park, Taewook Kim, Eunyoung Seo, Taeyoung Um, JeongYeon Yoon, Doil Choi, and Chanseok Shin
PCS04-17 Development of multi-resistant japonica rice with a constant extraction of panicle——— 175
Woo Jae Kim, Jong Min Jeong, Young Jun Mo, Su Kyung Ha, Jin Hee Kim, Ji Ung Jeong, Bo Kyeong Kim

PCS04-18 Title: Investigation of the virus infection ratio in different sweet potato \( (Ipomoea batatas) \) generations for mass and quality seed production——— 176
Narayan Chandra Paul, Jung-Wook Yang, Mi Nam Chung, Sang Sik Nam, Gyeong Dan Yu, Seon Kyeong Han, Hyeong-Un Lee, San Goh, Seung-yong Lee, Jin Cheon Park, Im Bin Lee

PCS04-19 Genome-wide SNP discovery and development of molecular markers for bacterial wilt resistance in tomato........................................................................................................ 176
Alebel Mekuriaw Abebe, Jinwoo Choi, Youngjun Kim, Chang-Sik Oh, Inhwa Yeam, and Je Min Lee

PCS04-20 Investigation of the expression level change of phytohormones which induced SAR on sweetpotato by inoculation time of \( Ceratocystis fimbriata \)........................................................................................................ 177
San Goh, Jung-Wook Yang, Sang-Sik Nam, Hyeong-Un Lee, Seung-Yong Lee, Gyeong-Dan Yu

PCS04-21 Phenotypic reactions of soybean differentials following inoculation of \( Phytophthora sojae \) isolates originated in South Korean........................................................................................................ 177
Sunjoo Kang, In Jeong Kang, Sungwoo Lee

PCS04-22 Evaluation of Resistance to Bacterial Stalk Rot Caused by \( Dickeya zeae \) in Maize——— 178
Min Namgung, Moonjong Kim, Jaekeun Choi, Sihwan Ryu, Jongyeol Park, Seungchul Choi, Jeongheon Han, Woosik Yong, Inseok Seo, Gyeongnam Nam, Jinkwan Ham

PCS04-23 A novel resistance gene for bacterial blight in rice, \( Xa43(t) \) identified by GWAS, confirmed by QTL mapping using a bi-parental population........................................................................................................ 178
Suk-Man Kim, Jong-Min Jeong, Bo-Keoyng Kim, Russell Reinke

PCS04-24 Functional characterization of papain-like cysteine proteases genes in rice................. 179
Marjohn Nino, Franz M. Nogoy, Me-Sun Kim, Sothea Ouk, Ju-Young Yang, Yu-Jin Jung, Kwon-Kyoo Kang, Yong-Gu Cho

PCS04-25 Identification of soybean genotypes resistant to \( Phytophthora sojae \) from the Korean cultivated soybean core collection........................................................................................................ 179
Ikhyun Jang, In Jeong Kang, Sungwoo Lee

PCS04-26 Functional analysis of NLR protein from pepper related to enhanced anthracnose resistance in tobacum........................................................................................................ 180
Soohong Kim, Kyong Sil Lee, Yeon-Hee Lee, Eun Jung Suh, Jihee Park, Duk-Ju Hwang, Jae Wahng Do, Jae Bok Yoon, Jungheon Han, Sang Ryeol Park

PCS04-27 \( In vitro \) elimination of Cnidium vein yellowing virus from infected \( Cnidium officinale \) through embryogenesis and shoot-tip culture........................................................................................................ 180
Chanhoon An
Mining tomato leaf proteome in search of potential markers for tomato spotted wilt virus (TSWV) infection using a TMT-based quantitative proteomic approach .......................................................... 181
Ravi Gupta, Cheol Woo Min, Suk Yoon Kwon, Sun Tae Kim

Developing Inbred Line of 'Wonkyo20046ho' SHOWING RESISTANCE FOR THE CLUBROOT GANGNEUNG INOCULUM AND DEEP YELLOW LEAF COLOUR IN Kimchi Cabbage (Brassica rapa L.) ................................................ 181
Suhyoung Park, Suk Woo Jang and Jung-Ho Kwak

Genetic Parameters Analysis and Transgressive Segregants Detection on F2 Population of Peanut (Arachis hypogaea L.) ........................................................................................................ 182
Yudiwanti Wahyu, Andi Sauleka, Acmad

Evaluation of germplasm for development Fusarium resistant freesia cultivar .................. 182
Youn Jung Choi, Jung Nam Suh, Kyung Sook Han, Young Ran Lee, Yun Im Kang

Germplasm Evaluation of Aleurites moluccana based on agro-morphological characteristics ......................................................................................................................... 183
Cici Tresniawati, Syafaruddin and Sakiroh

Evaluation of Rice Tungro Spherical Virus (Rtsv) Resistance from Tropically Adapted Japonica Lines (Oryza sativa L.) Expressing RTSV Resistance Gene eIF4G .............................. 183
O-Young Jeong, Sung-Ryul Kim, Maurene P. Bombay, Gideon V. Torollo, Woong-Jo Hyun, Jeom-Sig Lee

Characterization of a deficient mutant of alpha 1, 3-fucosyltransferase for N-glycan engineering in rice (Oryza sativa) ................................................................. 184
Seon-Kyeong Lee, Chinreddy Subramanyam Reddy, Vimalraj Mani, Soyoung Park, Joon-Soo Sim, Chang-Muk Lee and Bum-Soo Hahn

Characterization of Oryza sativa FLAVONOL SYNTHASE (OsFLS) exhibiting bifunctional catalytic activity ...................................................................................... 184
Sangkyu Park, Da-Hye Kim, Bo-Ra Park, Ju-Hee Yang, Jong-Yeol Lee, Sun-Hyung Lim

Transgenic expression of onion flavonol synthase in tobacco changes flower color .......... 185
Ju-Hee Yang, Sangkyu Park, Da-Hye Kim, Bo-Ra Park, Jong-Yeol Lee, Sun-Hyung Lim

Overexpression of GmIFS1 gene leads to produce the genisteins in tobacco petals .......... 185
Da-Hye Kim, SangKyu Park, Ju-hee Yang, Jong-Yeol Lee, Sun-Hyung Lim
PCS05-05  Analysis of AMT1 (ammonium transporter 1)-Mediated Root Growth in Rice [Oryza Sativa]
Chang-deok Han, Vikranth Kumar, SungHoon Kim, Jinhee Jeong, and Moch Rosyadi Adnan

PCS05-06  Identification and functional analysis of kelch-containing F-box proteins and their expression in wheat grain development
Min Jeong Hong, Dae Yeon Kim, Hong-II Choi, Sungyul Chang, Joon-Woo Ahn, Yong Weon Seo, Jin-Beak Kim

PCS05-07  Isolation of higher crossover rate mutants in Arabidopsis
Juhyun Kim, Jaeil Kim, Jihye Park, Eun-Jun Kim, Eun-Cheon Lim, Yeong Mi Park and Kyuha Choi

PCS05-08  PGR (plant growth regulator) substitution effect on the chrysanthemum transformants of SHI (Short Internodes) related genes
Eun-Jung Suh, Dong Chan Kim, Joon ki Hong, Ji Hee Park, Sang Ryeol Park, Yeon-Hee Lee

PCS05-09  Trait and fertility analyses of F1 and F2 hybrids between genetically modified Brassica napus expressing BrAGL20 and B. rapa
Soo-In Sohn, Young-Ju Oh, Hyeong Joong Kang, Yoonsung Cho

PCS05-10  Optimization of protocol for particle bombardment system in Alstroemeria to produce multiple tolerance against abiotic stresses
Sang-Bong Lee, Ji-Mi Kim, Su-Jin Kim, Jong-Bo Kim

PCS05-11  Overexpression of the alfalfa DNAJ-protein enhances drought tolerance in transgenic plants
Ki-Won Lee, Md. Atikur Rahman, Yowook Song, Hee Chung Ji, Ki-Yong Kim, Gi Jun Choi, Sang-Hoon Lee

PCS05-12  Ginseng-derived PgpPLAIII $\beta$ reduces plant longitudinal growth and lignin content in Arabidopsis and hybrid poplars when overexpressed
Jin Hoon Jang and Ok Ran Lee

PCS05-13  The Utility of Next Generation Sequencing for Single Event Molecular Characterizations and Stacked Event Product Analysis
Andre Silvanovich, Carl Garnaat, Colton Kessenich, Qing Tian, Marianne Malven, Will Urquhart, Jonghyun Kwon and Hye Jung Hyun

PCS05-14  Ginseng-derived two CYP genes functions on plant growth and phenylurea herbicide tolerance
Jin Hoon Jang, Soo Kwang Yim and Ok Ran Lee

PCS05-15  Identification of 'Haryeosaeng' mandarin using multiplex SNP markers
Seong-Beom Jin, Ho Bang Kim, Suk Man Park, Min Ju Kim, Seok-Beom Kang, Gyeong-Rok Yang, Cheol-Woo Choi, Su-Hyun Yun
PCS05-16  Doubled haploid production using two-step regeneration method for shed-microspore culture in pepper [Capsicum spp]........................................................................................................ 191
Eun Young Yang, Eun Joon Park, In Sung Lee, Myeong Cheoul Cho, Chae Soo Young, Chae Won Byoung, Chun Woo Nam

PCS05-17  Development of the analysis and content evaluation technology for allergens in Rice..... 192
Sang-Gu Lee, Si-Myung Lee, Seon-Woo Oh, Soo-Yun Park, Hyeon-Jung Kang

PCS05-18  Characterization of biomass improved gibberellin biosynthesis related gene in rice……192
Won-Tae Yang, Ki-Deuk Bae

PCS05-19  Nutritional comparison of genetically modified tomato............................................ 193
Soo In Sohn, Woo-Suk Cho, Myung-Ho Lim, Taesung Park, Yang Qin, Hyunjung Kang, Younsung Cho

PCS05-20  Phenotypic characteristics of citrus allotetraploids.................................................... 193
Min-Ju Kim, Su-Hyun Yun, Cheol-Woo Choi, Seong-Beom Jin

PCS05-21  Breeding and utilization of hybrid rice and male sterility rice line 134BtA expressing transgene Bacillus thuringiensis........................................................................................................... 194
Bai Jianjiang, Lee Gangseob, Yang Ruifang, Piao Zhongze, Fang Jun, Wan Changzhao

PCS05-22  Production of transgenic overexpression population to discover genes related grain size in rice .............................................................................................................................................. 194
Hye-Jin Yoon, Myeong-Jin Kang, Duk-Ju Hwang, Seung-Bum Lee

PCS06  Phenomics

PCS06-01  Analysis of soybean seed traits using image technology........................................ 195
Eungyeong Lee, JeongHo Baek, Eunsuk Sim, Nyunhee Kim, Song Lim Kim, Inchun Choi, Hyenso Ji, Man Soo Choi, Jung Kyung Moon, Kyung-Hwan Kim

PCS06-02  Measurement of plant growth rate using high throughput phenotyping with soybean core collections .................................................................................................................................. 195
Nyunhee Kim, JeongHo BAEK, Eungyeong Lee, Song Lim Kim, Inchun Choi, Hyeonso Ji, Man Soo Choi, Jung Kyung Moon, Kyung-Hwan Kim

PCS06-03  A trial of image based analysis for determination overgrowth of micro-tome............. 196
Hwang-weon Jeong, Jihee Park, Sang Ryeol Park, Inchun Choi, JungHo BAEK, Young-Joo Seol
PCS-07. Quality and Function

PCS07-01 Evaluation of Red Pepper Growth and Mineral Nutrient of Farm-made Liquid Fertilizers for Sustainable Agriculture ........................................... 196
Yong In Kuk, Se Ji Jang, Young Beom Yun, Dae Seon Kim

PCS07-02 QTL mapping for anthocyanin content in bulb onion (Allium cepa L.) ......................... 197
Yousoo Choi, Hyunwook Ryu, Sunggil Kim, Jundae Lee

PCS07-03 Sound waves affect the total flavonoid and the ascorbic acid contents in sprout vegetables ................................................................. 197
Mi-Jeong Jeong, Joo Yeol Kim, Ye Eun Kang, Soo In Lee, Jin A Kim

PCS07-04 Construction of a linkage map flanking the I locus controlling the dominant white bulb color in onions (Allium cepa L.) .............................................. 198
Inho Seo, Sunggil Kim

PCS07-05 Selection of Suitable Triploid Cultivars for Production of Small-Sized Watermelon using Vertical Cultivation ......................................................... 198
Sol-Ji Noh, Eun-Jeong Kim, Young-Sang Kim, Yu-min Jeon, Sung-Won Park, Tae-II Kim, and Sung-Taek Hong

PCS07-06 Effect of Cultivar and Location on Oil, Fatty Acid, Protein and Tocopherol Content of Peanut (Arachis hypogaea L.) ....................................................... 199
Tae Joung Ha, Myoung-Hee Lee, Eunyoung Oh, Jung In Kim, Seok Bo Song, Kyu-Hwan Choi, Doyeon Kwak

PCS07-07 High Yielding and High Oleate Peanut Cultivar ‘Hae-Ol’ .............................................. 199
Suk-Bok Pae, Eunyoung Oh, Myung Hee Lee, Sung-Up Kim, Jung-In Kim, Tae-Joung Ha

PCS07-08 Evaluation of Natto Processing Qualities and Sensory Properties of Soybean Varieties ..... 200
MinJung Seo, Myoung Ryoul Park, Yu Young Lee, Hye Sun Choi, Dong Sun Shin, Hong Tae Yun

PCS07-09 Genetic Mapping of a Novel Locus Controlling Pungency in Capsicum annuum .......... 200
Seungki Back, Joohyun Lee, Doyeon Hwang, Joung-Ho Lee, Byoung-Cheol Kang

PCS07-10 Perilla cultivar ‘Deulchan’ with high oil content and favorable oil quality ........................ 201
Jung In Kim, Myoung-Hee Lee, Sung-Up Kim, EunYoung Oh, SukBok Pae, Tae Joung Ha

PCS07-11 Evaluation of Lutein and Rosmarinic acid Contents in Perilla Leaves .......................... 201
Jae Eun Park, Myoung-Hee Lee, Jung In Kim, Sung-Up Kim, Eun Young Oh, Suk Bok Pae, Tae-Joung Ha

PCS07-12 A modified colorimetric method for the determination of sucrose content in soybean seeds ....................................................................................... 202
Gyutae Kim, Aron Park, Jooyeong Choi, Bo-Keun Ha
PCS07-13 Phytoene synthase-2 Controls Yellow Fruit Color in Capsicum annuum 'MicroPep Yellow'
Sojeong Jang, Hyo-Bong Jeong, Ayoung Jung, Min-Young Kang, Suna Kim, Sun-Hwa Ha, Jin-Kyung Kwon, and Byoung-Cheorl Kang

PCS07-14 Fibrillin2 is involved in high-light dependent photoprotection and jasmonate dependent senescence inhibition
Inyoung Kim, Hyun Uk Kim

PCS07-15 Development of the nutritional composition database for GM crop risk assessment
Eun-Ha Kim, Soo-Yun Park, Sang-Gu Lee, Seong-Kon Lee, Seon-Woo, Tae-Hun Ryu

PCS07-16 A comparative study on genetic and environmental influence on phenolic acid profiles in Korean red pepper varieties
Gyeong Min Lee, Seonwoo Oh, Sang-Gu Lee, Seong-Kon Lee, Soo-Yun Park

PCS07-17 Enhancing forage yield and nutritive value through maize × legume intercropping systems on paddy fields during the summer season
Yowook Song, Md. Atikur Rahman, Hee Chung Ji, Ji Hye Kim, Eun-A Lim, Won Ho Kim, Ki-Won Lee

PCS07-18 Effect of sound waves treatment on agronomic traits of crops
Mi-Jeong Jeong, Joo Yeol Kim, Soo In Lee, Jin A Kim

PCS07-19 The effect of roasting temperature and time on the rate of oil extraction and functional components in Perilla oil
Jung In Kim, Myoung-Hee Lee, Tae Joung Ha, Jae Eun Park, Eunyoung Oh, Sung-Up Kim, Suk-Bok Pae, Doyeon Kwak

PCS07-20 Expression of Ripening-Related Genes by Calcium Compounds and Chitosan in Trees Extends Shelf-life in Peach Fruits
Guk Jin Lee, Dan Bi Lee, Soon Young Ahn, Seong Jin Choi, Seong Jong Heui Kim, and Hae Keun Yun

PCS07-21 Changes in rutin and quercetin properties of common and tartary buckwheat seeds and groats induced by roasting
Su-Jeong Kim, Hwang-Bae Sohn, Su-Young Hong, Jung-Hwan Nam, Dong-Chil Chang and Yul-Ho Kim

PCS07-22 Multiple Functional Rice “Milyang320” for Complex of Various Protein Property
Jun Hyeon Cho, Ji Yoon Lee, Ju Won Kang, Su Min Jo, Young Ho Kwon, So Myung Lee, You Chun Song, Dong Soo Park, Jong Hee Lee, Jong Min Ko

PCS07-23 Effect of physicochemical characteristics of Korean wheat flour on different types of steamed bread, Korean and Chinese styles
Jin-Hee Park, Kyeong-Hoon Kim, Jin-Woo Yang, Kyeong-Min Kim, Chang-Hyun Choi, Jae-Han Son, Young-Keun Cheong, Kwang-Ho Jeong, Chon-Sik Kang, Chul Soo Park, Seong-Woo Cho
PCS07-24 Correlation of eating quality traits in a RILs population derived from a cross between Hwayeong and Wandoaengmi. Seoul-Gi Park, Hyun-Su Park, Man-Kee Back, Jung-Pil Lee, Chang-Min Lee, Suk-Man Kim, Young-Chan Cho, Choon-Song Kim

PCS07-25 Identification and characterization of MYB-bHLH-WD40 regulatory complexes controlling purple pigmentation biosynthesis in wheat (Triticum aestivum L.). Paulina Calderon Flores, Yong Weon Seo

PCS07-26 Comparison of productivity and functional components for selection of vegetable sweetpotato variety. Gyeong-Dan Yu, Hyeong-Un Lee, San Goh, Sang-Sik Nam, Mi-Nam Jeong, Seung-yong Lee, Jin Cheon Park, Seon-Kyeong Han, Im Bin Lee

PCS07-27 Validation of candidate gene associated with biosynthesis in pericarp using bi-parental population in Capsicum. Do-Gyeong Lee, Minjung Park, Siyoung Jang, ByoungCheorl Kang

PCS07-28 High-Throughput Identification of HMW-GS in Common Wheat Varieties by MALDI-TOF-MS. You-Ran Jang, Sun-Hyung Lim and Jong-Yeol Lee

PCS07-29 Accurate identification of alleles for Wheat Low-Molecular-Weight Glutenin Subunits using Aroona Near-Isogenic Lines and a Set of Standard Cultivars by 2-DGE, MS/MS and RP-HPLC. You-Ran Jang, Susan B. Altenbach, Sun-Hyung Lim and Jong-Yeol Lee

PCS07-30 A MYB Transcription Factor is a Candidate to Control Pungency in Capsicum annuum. Koeun Han, Si young Jang, Joung-Ho Lee, Hea-Young Lee, Do-Gyeong Lee, Byoung-Cheorl Kang

PCS07-31 Effect of Kernel Properties and Storage Temperature Condition on Popping Qualities of Popcorn. Jae-Keun Choi, Jong-Yeol Park, Si-Hwan Ryu, Seung chul Choi, Min Namgung, Moon-jong Kim, Jung Heon Han and Jin Kwan Ham

PCS07-32 QTL mapping for AGI (α-glucosidase inhibitor) activity of pepper leaf extract using genotyping-by-sequencing. Doie Park, Saeyoung Lee, Jundae Lee

PCS07-33 The Effects of Root Pruning on the Growth Characteristics in Quercus acutissima and Q. variabilis. Jinjoong Kim, Hye-In Kang, Kyungmi Lee, In-Sik Kim

PCS07-34 Characterization of ‘GolSam’ lines developed from the cross between Samgwang and 5MT resistant lines in rice. Franz M. Nogoy, Me-Sun Kim, Yu-Jin Jung, Kwon-Kyoo Kang, Yong-Gu Cho
PCS07-35 Identification of SNP marker related to high eating quality using GWAS analysis in rice \textit{(Oryza sativa L.)} .

Me-Sun Kim, Ju-Young Yang, Le Van Trang, Sothea Ouk, Kwon-Kyoo Kang, Yong-Gu Cho

PCS07-36 Genetic and functional analysis of genes related to eating & processing quality of brown rice through GWAS analysis.

Me-Sun Kim, Ju-Young Yang, Le Van Trang, Sothea Ouk, Kwon-Kyoo Kang, Yong-Gu Cho

PCS07-37 Determinations of $\alpha$-glucosidase inhibitory (AGI) activity and flavonoid content from pepper leaves \textit{(Capsicum sp.)}.

Tilahun Assefa Samuel, Eun Young Yang, Myeong Cheoul Cho, Chae Soo Young, Chae Won Byoung, Jundae Lee

PCS07-38 Selection of $\beta$-Carotene High Content Corn Using Molecular Markers.

MoonJong Kim, JongYeo Park, SeungChul Choi, Siwhan Ryu, JaekEun Choi, Min Namgung, WooSik Yong, GyeongNam Nam, Inseok Seo, JungHeon Han, JinKwan Ham

PCS07-39 TMT labeling based proteomics and metabolomics analysis to deciphering the effect of warm water imbibition in soybean seeds.

Cheol Woo Min, Hyejin Hyeon, Ye Eun Cheon, Ravi Gupta, Gi Hyun Lee, Ganesh Kumar Agrawal, Randeep Rakwal, Byong Won Lee, Hyung Won Ryu, Jae Kwang Kim, Sun Tae Kim

PCS07-40 Crucial Role of Sucrose and Sucrose Transporter Genes in Regulating Flowering Time in the Triticeae Tribe.

Depika Prasad, Yong Woon Seo

PCS07-41 \textit{RFS} acts as a flowering inducer independent of photoperiod in rice.

Hyeryung Yoon, Sung-Hwan Cho, Kiyoon Kang, Nam-Chon Paek

PCS07-42 Growth and Profile of fatty acids from \textit{Nigella sativa} L and \textit{Nigella Damascena} Planted in Indonesia.

Ani Kurniawati, Didah Nur Faridah, Nur Cahya Destiawan, Nabila Karimah

---

PCS08-01 QTL mapping and validation of whitefly \textit{(Bemisia tabaci)} resistance derived from \textit{Solanum galapagense} in tomato.

Il Sheob Shin, Mohamed Rhaka, Jung Ching Hsu, Shu Mei Huang, Roland Schafleitner, Peter Hanson

PCS08-02 Construction of single nucleotide polymorphism markers based QTL map and validation of resistance loci to bacterial wilt \textit{(Ralstonia solanacearum)} in tomato.

Il Sheob Shin, Jung Ching Hsu, Shu Mei Huang, Jaw Rong Chen, Roland Schafleitner, Jaw Fen Wang, Peter Hanson
<table>
<thead>
<tr>
<th>PCS08-03</th>
<th>The promise of genomic selection in breaking yield ceiling in rice</th>
<th>218</th>
</tr>
</thead>
<tbody>
<tr>
<td>MK Hossain, MR Hasan, SK Debsharma, MM Rashid, MM Islam, MM Hossain, and MR Islam</td>
<td></td>
<td></td>
</tr>
<tr>
<td>PCS08-04</td>
<td>QTL mapping of powdery mildew resistance in cucumber</td>
<td>219</td>
</tr>
<tr>
<td>Chunying Zhang, Badri Anarjan Mahdi, Sanghyeob Lee</td>
<td></td>
<td></td>
</tr>
<tr>
<td>PCS08-05</td>
<td>Genome-wide association study for seed weight in soybean (<em>Glycine max</em>)</td>
<td>219</td>
</tr>
<tr>
<td>Namhee Jeong, Jaebuhm Chun, Chuloh Cho, Mi-Suk Seo, Dool-Yi Kim, Mina Jin, Man Soo Choi</td>
<td></td>
<td></td>
</tr>
<tr>
<td>PCS08-06</td>
<td>QTL analysis regulating seed α-tocopherol ratio in wild soybean</td>
<td>220</td>
</tr>
<tr>
<td>C. Park, M.S. Dwiyanti, A. J. Nagano, T. Yamada, J. Abe</td>
<td></td>
<td></td>
</tr>
<tr>
<td>PCS08-07</td>
<td>QTL analysis for pod shattering tolerance in soybean (<em>Glycine max</em> Merr [L.]) with RIL populations derived from 'Daewonkong'</td>
<td>220</td>
</tr>
<tr>
<td>Jeong Hyun Seo, Beom Kyu Kang, Hyun Tae Kim, Sang Ouk Shin, Hong Sik Kim, In Youl Baek, Jae Hyeon Oh, Do Yeon Kwak</td>
<td></td>
<td></td>
</tr>
<tr>
<td>PCS08-08</td>
<td>Genome-wide Association, Breeding Signatures and Epistatic interactions among Flowering Time in Korea Soybean</td>
<td>221</td>
</tr>
<tr>
<td>Kyoung Hyoun Kim, Jae-Yoon Kim, Seongmun Jeong, Namshin Kim</td>
<td></td>
<td></td>
</tr>
<tr>
<td>PCS08-09</td>
<td>Functional Analysis of <em>Ruby</em> Alleles Controlling Anthocyanin Pigmentation in <em>Citrus</em></td>
<td>221</td>
</tr>
<tr>
<td>Kyung Uk Yi, Jin-Kyu Woo, Hye-Young Lee, Su Jeong Kim, Young Chul Park, Su-Hyun Yun, Kwan Jeong Song, Ho Bang Kim</td>
<td></td>
<td></td>
</tr>
<tr>
<td>PCS08-10</td>
<td>Study of Quantitative Trait Loci (QTLs) Associated with Allelopathic trait in Rice (<em>Oryza sativa</em> L.)</td>
<td>222</td>
</tr>
<tr>
<td>Ill-Min Chung, Tae-Ho Ham, Gi-Won Cho, Soon-Wook Kwon, Yoonjung Lee, Jeonghwan Seo, Yebin Kwon, JeeHye Kim, Joohyun Lee</td>
<td></td>
<td></td>
</tr>
<tr>
<td>PCS08-11</td>
<td>Assessment of the molecular markers selected for genotyping of soybeans by agricultural traits</td>
<td>222</td>
</tr>
<tr>
<td>Myoung Ryoul Park, Min-Jung Seo, Hong-Tae Yun</td>
<td></td>
<td></td>
</tr>
<tr>
<td>PCS08-12</td>
<td>Assessment and selection of molecular markers for analyzing cross of F1 soybean plants</td>
<td>223</td>
</tr>
<tr>
<td>Myoung Ryoul Park, Min-Jung Seo, Hong-Tae Yun</td>
<td></td>
<td></td>
</tr>
<tr>
<td>PCS08-13</td>
<td>Migration heading date of descendants by selection early maturity lines in oats</td>
<td>223</td>
</tr>
<tr>
<td>Ja-Hwan Ku, Ouk-Kyu Han, Jong-Woong Ahn, Seong-hyu Shin</td>
<td></td>
<td></td>
</tr>
<tr>
<td>PCS08-14</td>
<td>Genotyping 1,969 wheat accessions using SSRs to build a core collection</td>
<td>224</td>
</tr>
<tr>
<td>Kyeong Min Kim, Su Min Seo, Sol Ji Lee, Yu Na kang, Yun Gyeong Lee, Dong Hyun Jeon, Se Hyun Choi, Changsoo Kim</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
PCS08-15  Assessment of Molecular Markers Related to Spike Properties and Tiller Number of Long Spike Korean Wheat Populations
Seong-Woo Cho, Kyung-Suk Jung, Taek-Gyu Kang, Seong-Wook Kang, and Chul Soo Park

PCS08-16  Genome-wide SNP selection associated with protein and oil contents in wild soybean using multi-locus genetic models
Woon Ji Kim, Gu Kang, Hokeun Sun, Tae-Hwan Jun, Man Soo Choi, Sungtaeg Kang, Soon-Chun Jeong, Jung-Kyung Moon, Bo-Keun Ha

PCS08-17  Genome wide association studies for flowering time variation in cowpea (Vigna unguiculata L. Walp)
Eunju Seo, Hokeun Sun, Tae-Hwan Jun, Dong-Kwan Kim, Bo-Keun Ha

PCS08-18  Application of a novel, targeted sequencing-based genotyping approach for cost effective marker assessment in O. Sativa
Kesavan Markkandan, Amy Emerman, Tereza Borba, Aluana Abreu, Bjoern Textor, Evan Mauceli, Kruti Patel, Brendan Desmond, Sarah Bowman, Scott Adams, Jonathon Dunn, Andrew Barry and Cynthia Hendrickson

PCS08-19  Genetic architecture of soybean flowering-time using a variation block analysis
Hwang-Bae Sohn, Su-Jeong Kim, Su-Young Hong, Jung Hwan Nam, Bon-Cheol Koo and Yul-Ho Kim

PCS08-20  Genome-wide association study for seed sucrose content of soybean (Glycine max [L.] Merr.)
Taeyoung Lee, Moon Young Kim, Jungmin Ha, Suk-Ha Lee

PCS08-21  Genom-wide association study of fruit traits and testing genomic selection models in pepper
Ju-Pyo Hong, Hea-Young Lee, Na Young Ro, Jin-Kyung Kwon, Dong-Am Kim and Byoung-Cheorl Kang

PCS08-22  A Maiden Attempt of Genomic Selection in Korean Red Pine (Pinus densiflora) Trees
Donghwan Shim, II Hwan Lee, In-Sik Kim, and Seok Woo Lee

PCS08-23  Tiny Inflorescence controls internode length of inflorescence and shoot in tomato
Jung Heo, Choon-Tak Kwon, Ryza A. Priatama, and Soon-Ju Park

PCS08-24  Functional haplotype and eQTL analyses of genes affecting cadmium content in cultivated rice

PCS08-25  Deciphering the genome of octoploid strawberry (Fragaria × ananassa)
Abinaya Manivannan, Jinhee Kim, Ye Rin Lee, Sun Yi Lee, Dosun Kim, Eun-Su Lee, Hye-Eun Lee, and Byoung-Cheorl Kang
PCS08-26 Integrated bi-parental quantitative trait loci mapping and genome-wide association provides novel candidate genes for plant height and habits in pepper \textit{(Capsicum annuum)} using a superior Dempsey reference genome... 230
Abhinandan S. Patil, Min-Young Kang, Hea-Young Lee, Solomon A. Mekonnen, Muhammad Irfan Siddique, Koeun Han, Jelli Venkatesh, Jin-Kyung Kwon, Byoung-Cheorl Kang

PCS08-27 Development of SNP marker set related to Crown gall disease in Grapevine by GWAS... 230
Dae-Gyu Kim, Hyun A Jang, Mi-Reu Kim, Youn Young Hur and Sang-Keun Oh

PCS08-28 Construction of High Density Linkage Map and QTL Analysis of Plant Height and Height of First Capsule in Sesame... 231
Sungup Kim, Sovetgul Asekova, Eunyoung Oh, Myong Hee Lee, Jung In Kim, Suk-Bok Pae, Tae Joung Ha

PCS08-29 QTL Analysis of Phytophthora blight Disease Resistance in Sesame by Linkage and Association Mapping... 231
Sovetgul Asekova, Eunyoung Oh, Sungup Kim, Myong Hee Lee, Jung In Kim, Suk-Bok Pae, Yoon-Woo Jang, Tae Joung Ha

PCS08-30 A promising multifunctional crop \textit{Miscanthus} and its breeding strategies... 232
Yeon-Ho Park, Jae-Hyoung You, Min-Jung Yook, Do-Soon Kim

PCS08-31 QTL mapping for grain size with Korean \textit{japonica} rice varieties... 232
Kyeong-Seong Cheon, Young-Min Jeong, Youn-Young Lee, Jun Oh, Do-Yu Kang, Hyoja Oh, Song Lim Kim, Nyunhee Kim, Eungyeong Lee, Jeongho Baek, Inchan Choi, Kyung-Hwan Kim, Yong Jae Won, In Sun Yoon, Young-il Cho, Jung-Heon Han, Hyonso Ji

PCS08-32 Genetic analysis of morphological and agronomic traits using progeny between \textit{japonica} rice... 233
Woo Jin Kim, Hyun Sook Lee, Sun Ha Kim, Yun A Jeon, Kyu Chan Shim, Cheryl Adeva, Luong Ngoc Ha, Mirjalol Akhtamov, Sang Nag Ahn

PCS08-33 Identification of Quantitative Trait Locus (QTL) for spikelets per panicle using near isogenic lines derived from an interspecific cross between \textit{Oryza sativa} and \textit{O. minuta}... 233
Luong Ngoc Ha, Hyun-Sook Lee, Sun-Ha Kim, Yun-A Jeon, Kyu-Chan Shim, Woo-Jin Kim, Mirjalol Akhtamov, Cheryl Adeva, Sang-Nag Ahn

PCS08-34 Genome-wide association study of drought tolerance in maize... 234
Rahul Vasudeo Ramekar, Neha Roy, Mukut Sharma, Ik-Young Choi and Kyong-Cheul Park

PCS08-35 Mapping Quantitative Trait Loci related to salinity tolerance at the seedling stage in rice... 234
Le Hung Linh, Khuat Thi Mai Luong, Nguyen Thi Thu, Luong Ngoc Ha, and Sang-Nag Ahn

PCS08-36 QTL mapping for rice grain quality-related traits, nutritional value traits, and heading date using recombinant inbred lines derived from a cross between japonica cultivars... 235
PCS-09. Seed Company & Marketing

PCS09-01 Development of successful technology transfer system based on the systematic assessment of large R&D outcomes of PMBC-----------------------------------------------235
Serry Koh, Hyeon Jung Lee, Kyu Whan Choi

PCS09-02 A study to develop a systematic IP R&D support system to promote technology transfers of SSAC R&D outcomes---------------------------------------------------------236
Serry Koh, Hyeon Jung Lee, Kyu Whan Choi

PCS09-03 ‘AR Tanjeobaksa’, commercial F1 variety resistant to anthracnose in chili pepper----------236
Jae Wahng Do and Jae Bok Yoon

PCS09-04 Effect of soybean moisture contents according to the artificial drying-------------------------237
Won-Young Han, Jin-Woo Bae, Jin-Ki Park, Ok Jae Won, Young Ho Yoon, Gil Soo Han

PCS09-05 조, 기양 기계정식을 위한 모판흡 합설 및 육묘 영향 분석----------------------------------------237
한길수, 박진기, 한원영, 원옥재, 배진우, 류종수, 백인열, 곽강수, 윤영호, 정태욱

PCS-10. Genetic Resources

PCS10-01 Comparative phenotypic and metabolic analysis of Carthamus species----------------------238
Jaeeun Song, Soyoung Park, Chinreddy Subramanyam Reddy, Seon-Kyeong Lee, Joon-Soo Sim, Chang-Muk Lee, Sunyim Bae and Bum-Soo Hahn

PCS10-02 Diversity of flower characters of Jerusalem artichoke germplasm in Thailand------------------238
R. Puttha and S. Jogloy

PCS10-03 Amaranthus cruentus with a low-amylose synthesis phenotype lacks amylose in starch granules in the perisperm-----------------------------------------------239
Young-Jun Park

PCS10-04 Waxy strains of three amaranth grains raised by different mutations in the coding region -----------------------------------------------239
Young-Jun Park

PCS10-05 Cryopreservation of vegetatively propagated crop germplasm: achievements and challenges -----------------------------------------------240
Hyoeun Lee, Haeng-Hoon Kim
PCS10-06 Cryopreservation of *Dysophylla yatabeana* Makino, an endangered wild species, using a droplet-vitrification procedure
Hyeon Lee, Haelim Park, Haeng-Hoon Kim

PCS10-07 Genetic Diversity of Pisifera Elite Parent Using SSR Markers in DxP Sriwijaya Population
Upit Sarimana, Pratiwi Erika, Javier Hererro, Nurcahyono Indarto, Fahmi Wendra, Zulhermana, Dwi Asmono

PCS10-08 Molecular Characterization of 170 New gDNA-SSR Markers for Genetic Diversity in Button Mushroom (*Agaricus bisporus*)
Hyejin An, Ick-Hyun Jo, Youn-Lee Oh, Kab-Yeul Jang, Won-Sik Kong, Jwa-Kyung Sung, Yoon-Sup So and Jong-Wook Chung

PCS10-09 Molecular Characterization of New gDNA SSR Markers for *Glycyrrhiza lepidota* and Cross-Amplification of other *Glycyrrhiza* Species
Jun Hyoung Bang, Ick Hyun Jo, Jong Wook Chung

PCS10-10 Genetic Advance and Evaluation Transgressive Segregant on Two Population Bird Pepper (*Capsicum frutescens* L.)
Abdul Hakim, Muhamad Syukur, Yudiwanti Wahyu

PCS10-11 Recent Progress on the Ornamental Pepper Breeding in Indonesia
Muhamad Syukur, Awang Maharijaya, Sobir, Syarifah Iis Aisyah, Dewi Sukma, Arya Widura Ritonga, Abdul Hakim, Muhammad Ridha Alfirabi Istiqilal, and Sulassih

PCS10-12 Analysis of Glucoraphanin and Sulforaphane Contents in Germinating Broccoli Sprouts
Young-Cheon Kim, Hasui Li, Sanghyeob Lee

PCS10-13 Different Types of Mutation in Pepper Inbreeding Lines Result in a Loss of Pungency
Young-Cheon Kim, Niluphar Akter, Sanghyeob Lee

PCS10-14 Phytochemical and Yield-Related Traits of Winged Bean and Another Substitutive Crops
Muhammad Ridha Alfirabi Istiqilal, Muhamad Syukur, Waras Nurcholis, Sulassih, Kalvin Laia, Dian Rakhmad

PCS10-15 Overexpression of a novel RING-type E3 ubiquitin ligase gene induces formation of coiled branches in Arabidopsis
Gyu Tae Park, Jagadeesh Sundaramoorthy, Hak Soo Seo, Jong Tae Song

PCS10-16 Profiling of agronomic characteristics and phytochemical compounds in sweet sorghum (*Sorghum bicolor* L. Moench) germplasms
Jung Min Kim, Jae Il Ryu, Dong-Gun Kim, Min-kyu Lee, Nguyen Ngoc Hung, Jin-Baek Kim, Bo-Keun Ha, Joon-Woo Ahn, Soon-Jae Kwon

PCS10-17 Genetic variation of Chinese maize inbred lines using morphological character and SSR marker
Yin Vathana, Kyu Jin Sa, Su Eun Lim, Ju Kyong Lee
<table>
<thead>
<tr>
<th>Page</th>
<th>Title</th>
<th>Authors</th>
</tr>
</thead>
<tbody>
<tr>
<td>PCS10-18</td>
<td>Genetic diversity analysis based on SSR Markers in Perilla Crop between Korea and China</td>
<td>Dae Hyun Park, Kyu Jin Sa, and Ju Kyong Lee</td>
</tr>
<tr>
<td>PCS10-19</td>
<td>Morphological variation among accessions of cultivated types of Perilla crop and their weedy types in Korea and China</td>
<td>Kyu Jin Sa, Dae Hyun Park, Su Eun Lim, Ye Ju Ha, Hae Ri Kim, and Ju Kyong Lee</td>
</tr>
<tr>
<td>PCS10-20</td>
<td>Genetic Analysis of Ratooning Ability in Sorghum for Perenial Grain Crop</td>
<td>Trikoesoemaningtyas, Merry Gloria Meliala, Desta Wirnas, Didy Sopandie</td>
</tr>
<tr>
<td>PCS10-21</td>
<td>Heterosis and Combining Ability of F1 Hybrid Grain Sorghum in Korea (Sorghum bicolor L.)</td>
<td>MyeongEun Choe, SeukBo Song, SangIk Han, Jiho Chu</td>
</tr>
<tr>
<td>PCS10-22</td>
<td>Profiling of transcriptome from immature seed after flowering in 50 accessions by RNA-seq. in soybean (Glycine max)</td>
<td>Namhee Jeong, Mi-Suk Seo, Chuloh Cho, Jaebuhm Chun, Dool-Yi Kim, Mina Jin, Man Soo Choi</td>
</tr>
<tr>
<td>PCS10-23</td>
<td>Analysis of Antioxidant Activity in Safflower (Carthamus tinctorius L.) Germplasm Collected from Middle Eastern Region</td>
<td>Yi Jin Jung, Awarris Derbie Assefa, Jae Eun Lee, Ae Jin Hwang, On Sook Hur, Na Young Ro, Young Ah Jeon, Jae Jong Noh, Ho Sun Lee, Ju Hee Rhee, and Jung Sook Sung</td>
</tr>
<tr>
<td>PCS10-24</td>
<td>Genetic diversity in Napier grass (Cenchrus purpureus) collections as revealed by genotyping by sequencing method of the DArTseq platform</td>
<td>Meki S. Muktar, Abel Teshome, Jean Hanson, Alemayehu T. Negawo, Ermias Habte, Jean-Baka Domelevo Entfellner, Ki-Won Lee &amp; Chris S. Jones</td>
</tr>
<tr>
<td>PCS10-25</td>
<td>Early Matured, Pod Shattering Tolerant and Large Seed Soybean cultivar, ‘Nuriol’ for Double Cropping</td>
<td>Beom Kyu Kang, Jeong Hyun Seo, Hyun Tae Kim, Hong Sik Kim, Jae Hyun Oh, Sanjeev Kumar Dhungana, Sang Ouk Shin, In Youl Back, Do Yeon Kwak</td>
</tr>
<tr>
<td>PCS10-26</td>
<td>20-seed Evaluation Method for Sprout Using Perforated Conical tube for Soybeans</td>
<td>Beom Kyu Kang, Jeong Hyun Seo, Hyun Tae Kim, Hong Sik Kim, Sanjeev Kumar Dhungana, Jae Hyun Oh, Sang Ouk Shin, In Youl Back, Do Yeon Kwak</td>
</tr>
<tr>
<td>PCS10-27</td>
<td>Selection of triticale genetic resources with early maturity and good adaptation in the middle-northern area of South Korea</td>
<td>Seonghyu Shin, Ouk-Kyu Han, Ja-Hwan Ku, Jong-Woong Ahn</td>
</tr>
<tr>
<td>PCS10-28</td>
<td>Comparison of FT-IR Spectra for Identifying Functional Extract Differences in Core Segregant Population of Tea Plant</td>
<td>So Jin Lee, Seung Yeob Song, Doo Gyung Moon, Yong Hee Kwon, Chun Hwan Kim, Chan Kyu Lim</td>
</tr>
<tr>
<td>PCS10-30</td>
<td>Evaluation of Fagopyrum esculentum and Fagopyrum tataricum germplasm for sprout growth and rutin and quercetin contents under spring cultivation</td>
<td>252</td>
</tr>
<tr>
<td>PCS10-31</td>
<td>Which Species They Are? - Genetic Resources and Molecular Phylogeny of Ornamental Freshwater Plant Bucephalandra sp, in Trade Market Based on cp DNA Marker</td>
<td>253</td>
</tr>
<tr>
<td>PCS10-32</td>
<td>Male Parents Assignment in F1 Populations of Cacao using SSR Markers</td>
<td>253</td>
</tr>
<tr>
<td>PCS10-33</td>
<td>Development of bacterial blight and rice strip virus resistant, early maturing japonica rice cultivar 'Jodam'</td>
<td>254</td>
</tr>
<tr>
<td>PCS10-34</td>
<td>A New Small Redbean Cultivar 'Honggyeong' with Lodging Resistance and Large Bright Red Seed</td>
<td>254</td>
</tr>
<tr>
<td>PCS10-35</td>
<td>Changes of growth period and cumulative temperature according to seeding times of soybean varieties in the central plain region</td>
<td>255</td>
</tr>
<tr>
<td>PCS10-36</td>
<td>Genotypic variability of major carotenoids and fruit characteristics of 107 tomato wild germplasm</td>
<td>255</td>
</tr>
<tr>
<td>PCS10-37</td>
<td>Selection of soybean varieties highly adapted to high altitudes</td>
<td>256</td>
</tr>
<tr>
<td>PCS10-38</td>
<td>Evaluation of Crop Characteristics of Sweetpotato (Ipomoea batatas L.) Germplasms</td>
<td>256</td>
</tr>
<tr>
<td>PCS10-39</td>
<td>Evaluation on agricultural traits and valuable composition of pigeonpea (Cajanus cajan (L.) Millsp.) genetic resources in Korea</td>
<td>257</td>
</tr>
</tbody>
</table>
PCS10-40 A Study on the Effects of Early Shipment of Cymbidium through Cooling in Plain Land in the High-Temperature Season

Pue Hee Park, Su Young Lee, Hye Ryun An, Pil Man Park

PCS10-41 'Seed Identification Card' a platform using genotype, phenotype and chemotype for managing crop genetic resources and cultivars

Su-Jeong Kim, Hwang-Bae Sohn, Su-Young Hong, Jung-Hwan Nam, Dong-Chil Chang and Yul-Ho Kim

PCS10-42 Discovery and Evaluation of SNP Markers for Downy Mildew Resistance in Maize Population

Kyeong Do Min, Chang-Ho Kim, Hyo Chul Kim, Kyung-Hee Kim, Byung-Moo Lee and Jae Yoon Kim

PCS10-43 Change of Agricultural Characteristics of Core collections of Proso millet of International Crops Research Institute for the semi-Arid Tropics (ICRISAT) in South Korea

Sang-Ik Han, Jee-Yeon Ko, Seuk-Bo Song, Meyong-Eun Choe, Eun-Young Oh, Do-Yeon Kwak, Hyung-Jin Back

PCS10-44 Genetic diversity of fatty acid compositions in brown rice of mini-core collection of Korean rice core set (KRICE_CORE)

Bin Ha, Jae Ung Yang, Sion Noh, Soyeeong Eom, Kyu-Won Kim, Young-Jin Park, Young-Sang Lee

PCS10-45 Breeding of High Productivity Italian Ryegrass Plant in Southern Part of Korea, Breeding Line 'ARX 2'

Ki-Yong Kim, Gi Jun Choi, Jeong Sung Jung, Bo Ram Choi, Sae Young Lee, Ki-Won Lee

PCS10-46 Selection of Breeding Lines for Improving traits in Forage Crop 'Teosinte'

Ki-Yong Kim, Gi Jun Choi, Jeong Sung Jung, Bo Ram Choi, Sae Young Lee, Ki-Won Lee

PCS10-47 Characteristics of inbred lines from octoploid strawberry varieties

Sun Yi Lee, Jinhee Kim, Dae Young Kim, Ji-Hye Moon, Ook Jin Lee, Sang Gyu Kim, Il Rae Rho

PCS10-48 Current Status and Prospects of Rice Breeding in Central Region of Korea for 40 Years after the Development of 'Tongil' rice varieties

Hyang Mi Park, Eung Gi Jeong, Yong Jae Won, Guk Hyun Jeong, Euk Keun Ahn, Ung Jo Hyun, Jeong Jui Kim, Ji Eun Kwak, Jeong Hwa Park, Yong Hee Jeon

PCS10-49 Analysis the genetic diversity of watermelon (Citrullus lanatus L.) germplasm using genotyping by sequencing


PCS10-50 한국 재배중 검정콩의 γ-tocopherol methyltransferase-3 유전자 염기서열에 따른 알파토코페롤 함량

김가희, 이정준, 현도운, 조규택, 이정로
Molecular Diversity and population structure of Korean ginseng (Panax ginseng) germplasm as revealed by microsatellite markers


The Complete Chloroplast Genome Sequence of Japanese Millet Echinochloa esculenta (A. Braun) H. Scholz (Poaceae)


Interspecific hybridization between Capsicum spp. for introgression of alien genome

Jinkwan Jo, Youngin Kim and Byoung-Cheorl Kang

Genetic Diversity and Population Structure of Worldwide Cucumber Germplasm

Hea-Young Lee, Kihwan Song, Jong-Wook Ahn, and Byoung-Cheorl Kang

Genetic parameters estimation of growth trait of Pinus koraiensis in 35-year-old half-sib progeny trial

Kyungmi Lee, Jinjoong Kim, Hyein Kang, Insik Kim, Seokwoo Lee

Characterization of twelve Korean waxy maize (Zea mays L.) landraces by RNA sequencing

Gibum Yi, Hosub Shin, Seung Hwa Yu, Jeong Eun Park, Taegu Kang, and Jin Hoe Huh

Physicochemical Properties of dry-milling flour endosperm elite line

Su-Kyung Ha, Bo-Kyeong Kim, Ji-Ung Jeung, Younghun Mo, Woo-Jae Kim, Jong-Min Jeong, Jinhee Kim

Development of InDel Markers Based on Chloroplast DNA from Korean wild Codonopsis lanceolata for Genetic Diversity Analysis

Enkhtsetseg Yeruult, Jaebok Lee, Hee Jeong Jeong, Jinsu Gil, Serim Kim, Sungcheol Koo, Yi Lee

Screening of FT (FLOWERING LOCUS T) homologs in pepper (Capsicum annuum L.) based on genome database

Yu-Jeong Kwon, Min-Jeong Hong, Sang-Hoon Kim, Dong-Hwan Kim, Jin-Back Kim, Jun-Dae Lee, Yeong-Deuk Jo

The circadian rhythm differences among four Korean soybean cultivars [Glycine max (L.) Merr.] with different flowering time [Glycine max (L.) Merr.]

Da Eun Im, Kun Kim, Kyung Hae-Kim, Sungtaeg Kang, Ju Seok Lee

Intensive selection of wheat world collections for introduction breeding

Yong Jin Lee, Jae Ho Kim, Dae Yeon Kim, Chon-Sik Kang, Kyung-Min Kim, Yu-Mi Choi, Hye-Myeong Yoon, Byeong-Gyu Min, Yong Woon Seo

Genetic Diversity Analysis of Angelica Species Using Chloroplast DNA Markers of Angelica gigas Nakai

Jinsu Gil, Jaebok Lee, Sung Cheol Koo, Ho Bang Kim, Yi Lee
Active Compounds Content of Flower-color Mutants in *Angelica gigas* Nakai

Hong Woo Park, Dae Hui Jeong, Nam Su Kim, Ki Yoon Kim, Hyun Jun Kim, Chung Ryul Jung, Kwon Seok Jeon

---

Genotyping of selected wheat germplasms for grain quality tagging

Jae Ho Kim, Yong Jin Lee, Dae Yeon Kim, Yong Weon Seo

---

Development of InDel Markers Based on Chloroplast DNA for Classification of *Zizyphus jujuba* Mill

Moon Kyo Kim, Ha Kyung Oh, Sang Ik Park, Jae Bok Lee, Jin Su Gil, Enkhtsetseg Yerult, Kyeong Hee Lee, Yi Lee

---

Development of SSR Markers for the Genetic Diversity Analysis of *Schisandra chinensis*

Hee Jeong Jeong, Jaebok Lee, Jinsu Gil, Kyoung Min Lee, Chang Pyo Hong, Sin-Gi Park, Hyo-Jin Kim, Yi Lee

---

Identification of standard type chrysanthemum cultivars using SSR markers

Manjulatha Mekapogu, Oh Keun Kwon, Do Yoon Hyun, Kyung Jun Lee, Myung Suk Ahn, Jong Taek Park, Jae A Jung

---

Selection Efficiency of Chrysanthemum Segregation populations Using White color Related molecular Markers

Jae A Jung, Ga Ram Kim, Oh Keun Kwon, Jong Taek Park, Myong Suk Ahn, and Majulatha Methapogu

---

Breeding of a new cultivar 'Charmgreen' of Hardy *Kiwi* (*Actinidia arguta*)

Hanna Shin, Youngki Park, Mun Seop Kim, Seo Hyun Kim, Jeong Ho Song

---

Proteomic analysis of the life cycle of marine red alga, *Pyropia tenera*

Hyun-Ju Hwang, Jin-Woo Han and Jong Won Han

---

Genetic Diversity and Population Structure to Construct Core Collection from a Large Pumpkin Germplasms

Siyoung Jang, Kihwan Song, Hea-Young Lee, Byoung-Cheorl Kang

---

Evaluation of mutation frequencies induced by gamma-ray irradiation of faba bean seeds using TRAP markers and their application

Soon-Jae Kwon, Min-Kyu Lee, Jae Il Lyu, Dong-Gun Kim, Jung Min Kim, Nguyen Ngoc Hung, Min Jeong Hong, Jin-Baek Kim, Bo-Keun Ha

---

Evaluation of phenolic content and antioxidant activity in two different color chrysanthemum tea cultivars

Ah-Reum Han, Bomi Nam, Bo-Ram Kim, Hyun Mi Kim, Sang Hoon Kim, Jin-Baek Kim, and Chang Hyun Jin
PCS11-03 Characterization of a novel Sg-10 gene responsible for the soyasaponin biosynthesis in soybean
Jagadeesh Sundaramoorthy, Gyu Tae Park, Jeong-Dong Lee, Hak Soo Seo, and Jong Tae Song 

PCS11-04 Characterization and Genetic Analysis of a spotted leaf sheath Mutant Involved in ROS homeostasis in Rice
Dongryung Lee, Backki Kim, Su Jang, Jeonghwan Seo, and Hee-Jong Koh

PCS11-05 Genetic analysis of giant embryo mutants and identification of LARGE EMBRYO(LE) controlling embryo size in rice
Gileung Lee, Yoon Kyung Lee, Eunbyeol Koh and Hee-Jong Koh

PCS11-06 A Novel Allelic Mutation in LPA1 Gene results in Low Phytic Acid in Rice [Oryza Sativa L.]
D. S. Kishor, Choonseok Lee, Zhuo Jin, Ji Hwan Im and Hee-Jong Koh

PCS11-07 Genetic Diversity and Relationship in Soybean MDP [Mutant Diversity Pool] Revealed by TRAP and TE-TRAP Markers
Dong-Gun Kim, Jae-II Lyu, Min-Kyu Lee, Jung Min Kim, Nguyen Ngoc Hung, Min Jeong Hong, Jin-Baek Kim, Chang-Hyu Bae, Soon-Jae Kwon

PCS11-08 Transcriptome Analysis of Differentially Expressed Unigenes Involved in Anthocyanins and Kaempferitrin Biosynthesis in Kenaf [Hibiscus cannabinus L.] Based on De Novo RNA-Seq
Jae Il Lyu, Hong-II Choi, Dong-Gun Kim, Jaihyunk Ryu, Soon-Jae Kwon, Min-Kyu Lee, Jung Min Kim, Nguyen Ngoc Hung, Jin-Baek Kim, Joon-Woo Ahn, Si-Yong Kang

PCS11-09 Development of high linolenic acid soybean mutants and measuring expression of fatty acid related genes in development stages
Nguyen Ngoc Hung, Jae-II Lyu, Dong-Gun Kim, Jung Min Kim, Min-Kyu Lee, Min Jeong Hong, Jin-Baek Kim, Bo-Keun Ha, Soon-Jae Kwon

PCS11-10 Development of EST-SSR markers through de novo RNA seq and application of genetic diversity and relationship in Perilla germplasms
Min-Kyu Lee, Jae Il Lyu, Dong-Gun Kim, Jung Min Kim, Nguyen Ngoc Hung, Jin-Baek Kim, Bo-Keun Ha, Soon-Jae Kwon

PCS11-11 Chemical contents of novel Dendrobium mutants developed by mutation breeding techniques
Jaihyunk Ryu, Yeong Deuk Jo, Sang Hoon Kim, Kyung-Won Kang, Bo-Keun Ha, Si-Yong Kang

PCS11-12 Analysis of Volatile Oil Compositions of Gamma Irradiated Mutant Rose [Rosa hybrid Hortorum] Cultivars
Jaihyunk Ryu, Dong-Gun Kim, Jung Min Kim, Joon-Woo Ahn, Jin-Baek Kim, Sang Hoon Kim
<table>
<thead>
<tr>
<th>Paper Number</th>
<th>Title</th>
<th>Authors</th>
</tr>
</thead>
<tbody>
<tr>
<td>PCS11-13</td>
<td>Variations in Phenolic compounds and chemical fingerprints from the leaves of Roselle [Hibiscus sabdariffa L.] accessions</td>
<td>Jaiyunk Ryu, Jung Min Kim, Dong-Gun Kim, Joon-Woo Ahn, Jin-Back Kim, Soon-Jae Kwon</td>
</tr>
<tr>
<td>PCS11-14</td>
<td>Selection of Mutant with Fatty Acid Compositions in Rapeseed [Brassica napus]</td>
<td>Jaiyunk Ryu, Joon-Woo Ahn, Sang Hoon Kim, Bo-Keun Ha, Si-Yong Kang, Jin-Back Kim</td>
</tr>
<tr>
<td>PCS11-15</td>
<td>Evaluation of sensitivity to DNA methyltransferase inhibitors and gamma rays in rice</td>
<td>Sung Il Lee, Jae Wan Park, Min Jeong Hong, Jin-Back Kim, Hong-Il Choi</td>
</tr>
<tr>
<td>PCS11-16</td>
<td>Studies on Change of Some Agricultural traits of Colored Rice by Gamma-ray Treatment</td>
<td>Tae-Ho Ham, Mi-Young Park, Soon-Wook Kwon, Su-Noh Ryu</td>
</tr>
<tr>
<td>PCS11-17</td>
<td>Identification of genomic region controlling α-linolenic acid concentration for a mutant soybean line 'PE2166'</td>
<td>Minsu Kim, Hyun Jo, Jong Tae Song, Jeong-Dong Lee</td>
</tr>
<tr>
<td>PCS11-18</td>
<td>Response of Embryogenic Calli of Arabica Coffee Var. Kartika against Gamma Irradiation</td>
<td>Meynarti Sari Dewi Ibrahim and Enny Randriani</td>
</tr>
<tr>
<td>PCS11-19</td>
<td>Transcriptome analysis of cowpea in response to gamma-ray and proton-beam irradiation</td>
<td>Ryuuly Kang, Dong-Kwan Kim, Si-Yong Kang, Jeong-Hee Lee, Bo-Keun Ha</td>
</tr>
<tr>
<td>PCS11-20</td>
<td>Characterizing alleles for early maturity at two heading date loci derived from &quot;Baegilmi&quot;, a &quot;Koshihikari&quot; mutant rice cultivar</td>
<td>Youngjun Mo, Ji-Ung Jeung, Woo-Jae Kim, Yong-Min Jeong, Su-Kyung Ha, Jinhee Kim, Bo-Kyeong Kim</td>
</tr>
<tr>
<td>PCS11-21</td>
<td>A Large Sized Sweet Persimmon [Diospyros kaki Thunb.] Cultivar, 'Dannuri' with High Sugar Content</td>
<td>Eun-Gyeong Kim, Ji-Young Son, Gwang-Hwan Ahn, Wan-Kyu Joung, Kwang-Pyo Hong</td>
</tr>
<tr>
<td>PCS11-22</td>
<td>Assessment of Kenaf [Hibiscus cannabinus L.] Mutants Induced by Gamma-Ray</td>
<td>In-Sok Lee, Chan-Ho Kang, Suk-Ju Kwon, Young-Eun Na</td>
</tr>
<tr>
<td>PCS11-23</td>
<td>Breeding efforts to reduce the immunogenic potential of wheat flour: omega gliadins encoded by the D genome of hexaploid wheat may also harbor epitopes for the serious food allergy WDEIA</td>
<td>Jong-Yeol Lee, Sun-Hyung Lim and Susan B. Altenbach</td>
</tr>
<tr>
<td>PCS11-24</td>
<td>Associate analysis for grain size in rice using large grain mutant induced by EMS</td>
<td>Ja-Hong Lee, Mar Lar San, Seong-Gyu Jang, So-Yeon Park, Na-Eun Kim, Soon-Wook Kwon</td>
</tr>
</tbody>
</table>
PCS11-25  Analysis of genetic variations in gamma radiation-induced salt-tolerant silage maize mutants
.................................................................285
Chuloh Cho, Kyung Hwa Kim, Man-Soo Choi, Jaebuhm Chun, Mi-Suk Seo, Namhee Jeong, Mina Jin, Dool-Yi Kim

PCS-12. Genome Editing

PCS12-01  Development of Glucoraphanin-rich Broccoli Inbreeding Lines........................................286
Young-Cheon Kim, Sanghyeob Lee

PCS12-02  Development of Environmental Stress Stable Non-pungent Pepper Inbreeding Lines......286
Young-Cheon Kim, Niluphar Akter, Sanghyeob Lee

PCS12-03  Screening efficient CRISPR-RNPs in protoplasts of two pepper cultivars......................287
Hyeran Kim and Jisun Choi

PCS12-04  Functions and molecular mechanism of NF-Y members with an ERF transcription factor in
developing endosperm and grain filling using CRISPR/Cas9 system..............................................287
Jong Hee Kim, Hyo Ju Lee, Dong Hein Kim, Hee Kyoung Kim, Ki Hong Nam, Yu Jin Jung, Yong-Gu Cho, Kwon Kyoo Kang

PCS12-05  Improvement of grain yield by editing gene related to amino acid transporter using CRISPR
/ cas9 system in rice..................................................288
Dong Hein Kim, Hyo Ju Lee, Hee Kyoung Kim, Jong Hee Kim, Ki Hong Nam, Yu Jin Jung, Yong-Gu Cho, Kwon Kyoo Kang

PCS12-06  Improvement of Grain Quality through Application of CRISPR/Cas9 System in Rice........288
Yu Jin Jung, Sang Su Bae, Yong-Gu Cho and Kwon Kyoo Kang

PCS12-07  Knockout of abscisic acid (ABA)-dependent transcription factor gene OsVP1 using CRISPR/Cas9 system improves germination velocity and pre-harvest sprouting in rice (Oryza sativa L.).................289
Hyo Ju Lee, Dong Hein Kim, Hee Kyoung Kim, Jong Hee Kim, Ki Hong Nam, Yu Jin Jung, Yong-Gu Cho, Kwon Kyoo Kang

PCS12-08  Strategy for Editing Genes Encoding Seed Storage Proteins in Rice via CRISPR-Cas9 System
.........................................................................................289
Kyoungwon Cho, Deepanwita Chandra, Pharm Hue Anh, Oksoo Han

PCS12-09  Homology-directed repair (HDR)-based gene targeting in tomato.................................290
Tien Van Vu, Jihae Kim, Doan Thi Hai Duong, Dibyajyoti Pramanik, Yeon Woo Sung, Sivan V. Kalyani,
Tran Thi Mil, Rahul Mahadev Shelake, Geon Hui Son, Jae-Yean Kim
PCS12-10 *Agrobacterium* and virus-mediated CRISPR/Cas9 genome editing in tomato for viral resistance

Yoo-Jung Yoon, Jelli Venkatesh, Hye-eun Lee, Do-sun Kim, Jin-Kyung Kwon, Byoung-Cheorl Kang

PCS12-11 Construction of Siderophore producing *Agaricus bisporus* transformants

MinSeek Kim, Cheol-Won Yoon and Hyeon-Su Ro

PCS12-12 Genome editing effect of phytoremediation desaturase gene using CRISPR-Cas9 in hybrid poplar

Eun-Kyung Bae, Hyunmo Choi, Hyoshin Lee, Sang-Gyu Kim, Jae-Heong Ko, Young-Im Choi

PCS12-13 The *Arabidopsis* ATXR2 inhibits *de novo* shoot regeneration by controlling cytokinin signaling

Kyounghee Lee, Ok-Sun Park, Sangrea Shim, & Pil Joon Seo

PCS12-14 Systemic gene editing of *AtRabA1* subfamily

Hyeran Kim, Jisun Choi, and Jahee Ryu

PCS12-15 Agrobacterium mediated transformation and genome edition in *Solanum nigrum*

Eun-song Lee, Seung-hye Park, Ryza A. Priatama, Jung Heo, Jae-Cheol Jeong, Woo-Young Bang, Soon Ju Park

---

PCS-13 The Agricultural Genome Center

PCS13-01 Plan for High Throughput Phenotyping Approach to Screen Drought Resistance in Soybean

Jae Young Kim, Sang Hui Lim, Minah Oh, Young June Bae, Minjoo Cho, Kyung-Hwan Kim, Chang Woo Lee, and Yong Suk Chung

PCS13-02 Rice basic Helix-Loop-Helix 79 [OsbHLH079] determines leaf angle and grain shape by upregulating brassinosteroid signaling-associated genes

Hyoseob Seo, Sang-Ji Lee, Byoung-Doo Lee, Nam-Chon Pack

PCS13-03 CONSTUTITIVE PHOTOMORPHOGENIC 1 [COP1] promotes gibberellic acid-mediated seed germination by destabilizing REPRESSOR OF ga1-3-LIKE 2 [RGL2] in *Arabidopsis thaliana*

Byoung-Doo Lee, Yehyun Yim, Nam-Chon Pack

PCS13-04 Ultrafast PCR assays to detect approved genetically modified [GM] cotton

Hyun-Joong Kim, Jin-Young Choi, Ji-Eun Park, Hae-Yeong Kim

PCS13-05 Abiotic stress-specific cis-regulatory element assembling approach to increase response in drought

Kihwan Kim, Hyeonjung Jung, A-hyeon Kang, Jooeun Lee, Kihwan Lim, Won-Chan Kim
PCS13-06  *AtCBX2-OX* decreases lignin content and increases biomass in plants. Yun Young Kim, Won Mi So, and Jeong Sheop Shin

PCS13-07 Identification of OsPAPs responsible for chloroplast development in rice. Sangyool Lee, Deok Hyun Seo, Hoyoong Shin, and Geupil Jang

PCS13-08 Overexpression of two glutathione biosynthesis genes increased productivity via enhanced stress tolerance in rice plants. Jun-Yong Jeong, Jin-Ju Kim, Seong-Im Park, and Ho-Sung Yoon

PCS13-09 A Heat Shock Protein Gene Increases Tolerance to Salinity and High Temperature in *Oryza sativa*. Hee-Jin Kim, Seong-Im Park, Jin-Ju Kim, and Ho-Sung Yoon

PCS13-10 Autophagy interacts with the plant immune receptor. Sung Un Huh

PCS13-11 Pathogen effector PopP2 acetylates the plant autophagy-related protein 8. Sung Un Huh

PCS13-12 Common cis-elements regulated by ABA and JA in *Oryza sativa*. Eun-ji Ga, Jin-Ae Kim, Myung Ki Min, and Beom-Gi Kim

PCS13-13 Overexpression of OsDREB1G gene, a Member of the OsDREB1 Subfamily, increases low temperature tolerance in rice. Eun-ji Ga, Seok-Jun Moon, Myung Ki Min, Jin-Ae Kim, Dool Yi Kim, In Sun Yoon, Taek Ryun Kwon, Myung Ok Byun, and Beom-Gi Kim


PCS13-15 Influence of gene flow from GM to non-GM soybeans by the size of the pollen donor. Youngshin Kwak, Soo-Yun Park, Sang Jae Suh, Bumkyu Lee, Ancheol Chang, Sung-Dug Oh

PCS13-16 Influences of Insect-Resistant Genetically Modified Rice (Bt-T) on the Diversity of Non-Target Insects in an LMO Quarantine Field. Sung-Dug Oh, YoungGeum Shin, Sang Jae Suh, Doh-Won Yun, Ancheol Chang

PCS13-17 Influence of Vitamin A enhanced transgenic soybean cultivation on above-ground arthropods in Korea. Sung-Dug Oh, Soo-Yun Park, Ancheol Chang, Eunji Bae, Minwook Kim, Changwuk Eun, Seong Yun Mun, Yeongjin Son, Young-Kun, Kim, Kihun Ha, and Sang Jae Suh

PCS13-18 Selection of essential genes for ingestion RNA interference against western flower thrips using leaf disc-mediated dsRNA delivery. Seung Hee Han, Ju Hyeon Kim, Kyungmum Kim, and Si Hyeock Lee, Gil Dong Hong, Cheol Soo kim
<table>
<thead>
<tr>
<th>Title</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>PCS13-19</strong> Nutritional composition profiles and natural variation of commercial soybean cultivars cultivated in the different locations during two years**</td>
<td>302</td>
</tr>
<tr>
<td>Seon-Woo Oh, So-Young Lee, Da-Young Bae, Soo-Yun Park, Sang-Gu Lee, Tae-Hoon Ryu, Seong-Gon Lee, Young-Soo Chung, Hyun-Jung Kang</td>
<td></td>
</tr>
<tr>
<td><strong>PCS13-20</strong> <em>GPM1</em> encodes a male gametophyte-specific R2R3 MYB transcription factor required for polarized microspores to undergo pollen mitosis I in Arabidopsis**</td>
<td>303</td>
</tr>
<tr>
<td>Sung-Aeong Oh, Thuong Nguyen Thi Hoai, Hyo-Jin Park, Mingmin Zhao, David Twell, Sang Ju Lee, Jeong Heo Kim, and Soon-Ki Park</td>
<td></td>
</tr>
<tr>
<td><strong>PCS13-21</strong> Increasing resistant starch content in legumes for higher nutritional prospect**</td>
<td>303</td>
</tr>
<tr>
<td>Rupesh Tayade, Hyun Jo, Jeong-Dong Lee</td>
<td></td>
</tr>
<tr>
<td><strong>PCS13-22</strong> Preservation for GMO crops and Bio-Information developed by Agricultural Biotechnology Research Center**</td>
<td>304</td>
</tr>
<tr>
<td>Danim Jo, Hyun Jo, Jeong-Dong Lee</td>
<td></td>
</tr>
<tr>
<td><strong>PCS13-23</strong> Development of useful transgenic Chinese cabbage for the future-proof breeding resources**</td>
<td>304</td>
</tr>
<tr>
<td>Yun Hee Shin, Jee-Soo Park, Na-Ri Shin, Yuri Choi, Kyung-Min Park, Eun-Taeck Woo, and Young-Doo Park</td>
<td></td>
</tr>
<tr>
<td><strong>PCS13-24</strong> Embryo transmission of Alternanthera mosaic potexvirus enables CRISPR editing of GFP-transgenic <em>Nicotiana benthamiana</em> through combined expression of split Cas 9 and guide RNA**</td>
<td>305</td>
</tr>
<tr>
<td>Wen-Xing Hu, Jungkyu Kim, Hanhong Bae, Leslie L Domier, John Hammond, Hyoun-Sub Lim</td>
<td></td>
</tr>
<tr>
<td><strong>PCS13-25</strong> <em>MULTISEEDED1</em> and 2 affects sorghum grain yield regulating at pedicellate spikelet fertility**</td>
<td>305</td>
</tr>
<tr>
<td>Young Koung Lee, Nicholas Gladman, Yinpeng Jiao, Zhanguo Xin and Doreen Ware</td>
<td></td>
</tr>
<tr>
<td><strong>PCS13-26</strong> Epigenetic regulation by microRNA820 in <em>Oryza sativa</em>**</td>
<td>306</td>
</tr>
<tr>
<td>So Young Park, YoungJin Choi, Dong-Hoon Jeong</td>
<td></td>
</tr>
<tr>
<td><strong>PCS13-27</strong> Production of soybean plants with high contents of omega-3***</td>
<td>306</td>
</tr>
<tr>
<td>Hyun Suk Cho, Seon-Woo Oh, Sang-Gu Lee, Jin Young Kim, Hyun Uk Kim, Young-Soo Chung</td>
<td></td>
</tr>
<tr>
<td><strong>PCS13-28</strong> Debunking the Claims that Glyphosate Tolerant GM Crops and the Herbicide are Responsible for Various Modern Diseases**</td>
<td>307</td>
</tr>
<tr>
<td>Donghern Kim, Yumi Choi</td>
<td></td>
</tr>
<tr>
<td><strong>PCS13-29</strong> Understanding of Séralini Affair: Controversy Surrounding the Research Paper Claiming the Causality between Glyphosate tolerant GM Corn and Cancer**</td>
<td>307</td>
</tr>
<tr>
<td>Donghern Kim, Yumi Choi, Kyu-Hang Kyung</td>
<td></td>
</tr>
<tr>
<td><strong>PCS13-30</strong> 국내 개발 우수 생명공학작물의 중국 및 동남아 시장 진출을 위한 국내외 옥종 플랫폼 구축**</td>
<td>308</td>
</tr>
<tr>
<td>이강섭</td>
<td></td>
</tr>
<tr>
<td>PCS13-31</td>
<td>Utilization and stable expressed miraculin protein to <em>in vitro</em> using plant suspension culture system</td>
</tr>
<tr>
<td>-----------</td>
<td>--------------------------------------------------------------------------------------------------</td>
</tr>
<tr>
<td></td>
<td>Hee Kyoung Kim, Ji Yun Ko, Kwon Kyoo Kang, Yu Jin Jung</td>
</tr>
<tr>
<td>PCS13-32</td>
<td>Ubiquitination and decay of NMD factors triggered by pathogen infection fine tunes R transcripts during an early immune response</td>
</tr>
<tr>
<td></td>
<td>Ki Hun Shin, Kyung Man Kim, Sang Hyon Kim</td>
</tr>
<tr>
<td>PCS13-33</td>
<td>Role of a hydrophobic residue in pyrabactin recognition by ABA receptors from Oryza sativa</td>
</tr>
<tr>
<td></td>
<td>Seungsu Han, Yeongmok Lee, Eun Joo Park, Myung Ki Min, Yongsang Lee, Tae-Houn Kim, Beom-Gi Kim and Sangho Lee</td>
</tr>
<tr>
<td>PCS13-34</td>
<td>Investigation of Root Characteristics for Evaluation of Resistance against Waterlogging Stress in Wilde Soybeans</td>
</tr>
<tr>
<td></td>
<td>Se-Hun Kim, Chae-In Na, Jeong-Dong Lee, Yoonha Kim</td>
</tr>
<tr>
<td>PCS13-35</td>
<td>Expression of Resveratrol-Dependent Glucosyltransferase Genes in the Resveratrol Rice DJ526 Germinated Seeds</td>
</tr>
<tr>
<td></td>
<td>Vipada Kantayos, Jin-Suk Kim, Ga-Hyeon Kim, Eui-Shik Rha and So-Hyeon Beak</td>
</tr>
<tr>
<td>PCS13-36</td>
<td>Screening of Candidated Glucosyltransferase Genes in Resveratrol Rice DJ526 Callus</td>
</tr>
<tr>
<td></td>
<td>Vipada Kantayos, Jin-Suk Kim, Ga-Hyeon Kim, Eui-Shik Rha and So-Hyeon Beak</td>
</tr>
<tr>
<td>PCS13-37</td>
<td>Expression of recombinant Miraculin protein in transgenic carrot cell suspension culture</td>
</tr>
<tr>
<td></td>
<td>Yun-Ji Park, Jong-Eun Han, Yoo-Jin Jeong, So-Young Park</td>
</tr>
<tr>
<td>PCS13-38</td>
<td>Agrobacterium-mediated transformation carrot cells for the expression of recombinant Brazzein, a sweet-tasting protein</td>
</tr>
<tr>
<td></td>
<td>Jong-Eun Han, Yun-Ji Park, Yoo-Jin Jeong, and So-Young Park</td>
</tr>
<tr>
<td>PCS13-39</td>
<td>A N molecular sensor system: a breeding technique for development of high NUE rice under low N conditions</td>
</tr>
<tr>
<td></td>
<td>Jae Sung Shim, Dong-Keun Lee, Seowon Choi, Youn Shic Kim &amp; Ju-kon Kim</td>
</tr>
<tr>
<td>PCS13-40</td>
<td>Development of Drought Tolerant Crops using noncoding RNAs</td>
</tr>
<tr>
<td></td>
<td>Seung Woon Bang, Jooyeon Bae, Pil Joong Chung, Joohee Choi, So Yoon Seong and Ju-Kon Kim</td>
</tr>
<tr>
<td>PCS13-41</td>
<td>Genome-wide analysis of radish lincRNAs and partial identification of putative target genes</td>
</tr>
<tr>
<td></td>
<td>Su Hyun Park, Seunghoon Baek, Ara Cho, Jeong-Hwan Mun, Sang-Bong Choi</td>
</tr>
<tr>
<td>PCS13-42</td>
<td>High expression of recombinant proteins in Arabidopsis protoplasts by using Gal4/UAS gene expression system and PTGS suppressor</td>
</tr>
<tr>
<td></td>
<td>Junho Lee, Kyoung Rok Geem and Inhwan Hwang</td>
</tr>
</tbody>
</table>
PCS13-43 Natural variation of anti-nutrient compounds in soybean cultivars grown in different regions
Hwi-Young Park, Sang-Gu Lee, Seon-Woo Oh, Soo-Yun Park, Tae-Hoon Ryu, Young-Soo Chung, Hyeon-Jung Kang

PCS13-44 Analysis of genome evolution of naturally occurring attenuated isolates of *Burkholderia glumae*
Minhee Kang, Eunhye Goo, Jae Yun Lim, Jinwoo Kim, and Ingyu Hwang

PCS13-45 Development of safety assessment methods for transgenic soybeans as cosmeceutical protein production
Jae Kwang Kim, Sung-Dug Oh, Chang-Gi Kim, Ju-Seok Seo, Jung-Ho Park

PCS13-46 Characteristics and efficacy evaluation of transgenic rice for improving glucose metabolism as a medicinal material
Doh-Hoon Kim, Jong-Min Kim, So-Yeon Hong

PCS13-47 A comparative study on metabolic differences of soybean leaves from commercial cultivars and wild species
Soo-Yun Park, Sung-Dug Oh, Sang Jae Suh

PCS13-48 Identification of a synthetic partial ABA agonist, S7
Myung Ki Min, Jin-Ae Kim and Beom-Gi Kim

PCS13-49 Establishment and utilization of scientific information service system for agricultural biotechnology
Bumkyu Lee, Ancheol Chang, Soo Chul Park, Jong Mi Kim

PCS13-50 *Gametic Transfer Defect (GTD2)*, encoding WD40 domain, functions as a positive regulator of pollen tube growth in rice
Yu-Jin Kim, Myung-Hee Kim, Woo-Jong Hong, Sunok Moon, Eui-Jung Kim, Jeniffer Silva, Jin-Won Lee, Soon Ki Park, Ki-Hong Jung

PCS13-51 유전자변형 제조자내성 백간사에 방사선 조사로 육성된 무추대 품종의 항질 안정성 평가
Hong-Gyu Kang, Hyeon-Jin Sun, Yong-Ik, Kwon, Dae-Hwa Yang, Gangsup Lee, Hyo-Yeon Lee

PCS13-52 Overexpression of auxin biosynthetic enzyme YUCCA6 activates glucosinolate biosynthetic pathway in Arabidopsis
Joon-Yung Cha, Jeong Im Kim, Ray A. Bressan, Dae-Jin Yun, Woe-Yeon Kim

PCS13-53 Need for FDA Approval of Transgenic Resveratrol-enriched Rice
Yong-Jae Kim, Hyeon-Jin Kim

PCS13-54 A Study on the Value Increase and Future Application of the Research Team
Jongtaek Kim, Minjin Kim, Byeongrim Ko, Serry Koh, Hyeon Jung Lee, Kyu Whan Choi
Establishment of a system for selecting drought-tolerant plants using image parameters in rice

Development of utilization technology of rice varieties based on Indel big-data
Yo-Han Yoo, Yu-Jin Kim, Anil Kumar Nalini Chandran, Woo-Jong Hong, Hye Ryun Ahn, Yong-Jin Park, Ki-Hong Jung

Transformation of maize immature embryos using Agrobacterium tumefaciens
Joon Ki Hong, Ki Jin Park, Ju-Kon Kim, Gang-Seob Lee, Hee Jeung Jang, Kyung-Hwan Kim, Eun Jung Suh, Yeon-Jee Lee

Construction of Siderophage producing Agaricus bisporus transformants
MinSeek Kim, Sinil Kim, Cheol-Won Yoon and Hyeon-Su Ro

Production of male sterile tomatoes edited by CRISPR/Cas9 system
Jihee Park, Yeon-Hee Lee, Sang Ryeol Park, Eun Jung Suh, Joon Ki Hong, Hwangweon Jeong and Junghoon Han

Agricultural Biotechnology Research Center Development Resources and Life Information Mid to Long Term Preservation
Danim Jo, Hyun Jo, Jeong-Dong Lee

Comparison of Isoflavones in commercial soybean cultivars with different physicochemical characteristics
Da-Young Baek, Seon-Woo Oh, So-Young Lee, Soo-Yun Park, Sang-Gu Lee, Tac-Hoon Ryu, Young-Soo Chung, Hyun-Jung Kang

Analysis and identification of SIHDC-A promoter elements in tomato
Seo Young Park, Se Hee Park, Hyun Min Kim, Sang Hoon Ma, Thanh Dat Mai, Ju Hui Do, Won Choi, Tuan Viet Do, Young Hee Joung

Development of Novel Rice Producing Ginseng Protopanaxadiol
Jin-Suk Kim, Jung Yeon Han, Gahyeon Kim, Vipada Kantayos, Do Won Yun, Yong Eui Choi, So-Hyeon Baek

Study of rubber biosythesis and rubber content increase in Taraxacum kok-saghyz
Seung Baek Hong, Sungwoo Bae, Sang Chul Choi, Stephen Beungtae Ryu

Analysis of sticky germ cell mutant reveals a critical role of a conserved DUF707 family member for the germ cell migration after pollen mitosis I in Arabidopsis
Sung-Aeong Oh, Hye-Jin Park, and Soon-Ki Park

Impaired plastid ribosomal protein L3 and L13 cause an albino seedling lethal phenotype in rice
Jinwon Lee, Seonghoe Jang, Sanghoon Ryu, Seulbi Lee, Joonheum Park, Sichul Lee, Gynheung An, Soon Ki Park
Identification of genes important for male gametophytic development in Arabidopsis
Elmura Torutaeva, Sang Dae Yun, Sung Aeong Oh, Soon Ki Park

Evaluation of heat tolerance using CBF1 and Hsp101 overexpression in Arabidopsis
Sang Dae Yun, Jinwon Lee, Sung Aeong Oh, Moon-Sooh Soh, Soon Ki Park

Optimization of growth rate by regulating chloroplast movement in lettuce
Young Sun Riu, Jeong Wook Heo, Sam-Geun Kong

N-Glycan analysis of glycosylation-modified lines in Rice
Juyoung Choi, Jun-Hye Shin, Sang-Tak Lee, Ju-Hyeon Lee, Han-Bin Oh, Bum-Soo Hahn, Seong-Ryong Kim

THRUMIN1 is the bundling factor of cp-actin filaments for chloroplast photorelocation movement in Arabidopsis
Jeongsu Ahn, Sam-Geun Kong

phot2 as a light switch to regulate CHUP1-CHIP1 interaction for chloroplast photorelocation movement in Arabidopsis
Jae-Woo Han, Gyeong-Hoon Lee, Koji Okajima, Aino Komatsu, Fumio Takahashi, Takayuki Kohchi, Masamitsu Wada, Sam-Geun Kong

Special Session (Green-bio Forum & ILSI Korea)
- Science-based Policy for Gene Edited Crops -

SS5-01 USDA regulatory experience in plant biotechnology, including gene editing
Ibrahim M Shaqir, Associate Deputy Administrator

SS5-02 The regulatory frameworks of genome editing organisms and foods in Japan
Yutaka Tabei

SS5-03 Science-based policies for genome edited crops in Latin American countries
Jin Cha

The Korean Society of Breeding Science Award

Index

lxx
Plenary Session
Plenary Session
Length Matters: How Might We Narrow the Quality Gap between Cotton and Synthetic Fibers

Andrew H. Paterson
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Four members of the *Gossypium* (cotton) genus are cultivated for the production of seedborne epidermal fibers that make possible world cotton commerce. Cotton production has long been pressurized by competition from high quality synthetic fibers, which in the USA alone require more than 200 million barrels of petroleum each year to produce, at a cost exceeding the farm-gate value of the annual cotton crop. Cotton genotypes are known that produce natural fibers rivaling the length, fineness, and strength of synthetic fibers - indicating the genetic potential for dramatic improvement. However, such genotypes are low yielding and suffer other defects that preclude their commercialization. Here, we consider genetic approaches by which cotton might be taken to a new ‘adaptive peak’ of fiber quality, utilizing new genome-based approaches in prudent combination with both naturally occurring and human-induced variations. Insights from cotton’s evolutionary history also shed new light on genetic mechanisms by which cotton may have arrived at its present state of improvement.

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Education
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1985 M.S. Cornell University, Plant Breeding (minor: Agronomy).
1982 B.S. Univ. of Delaware, Agriculture (Summa Cum Laude).

Employment
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Nov 1989 Adjunct Assistant Prof. of Plant Molecular Biology, Univ. Delaware.
1989-1991 Principal investigator, Ag. Biotechnology, E.I. DuPont de Nemours,
1987-1989 Postdoctoral associate, Cornell University (Lab of S. Tanksley).

Recent Main Publications
Molecular mechanism of self-incompatibility in Brassicaceae

Masao Watanabe*, Seiji Takayama

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2Graduate School of Agricultural and Life Sciences, The University of Tokyo, Tokyo, Japan

Self-incompatibility (SI) is an important trait for economical F₁ hybrid seed production in Brassica and allies. The Brassicaceae SI is sporophytically controlled by a large number of haplotypes on the single locus called S, and is also one of the models for cell-cell communication study in higher plants. From our over 30 years’ study, each S haplotype was found to encode the male and female S determinants, which we named SP11 (encoding small cysteine-rich protein) and SRK (encoding receptor-type protein kinase), respectively. Direct and specific molecular interaction between SP11 and SRK from the same S-haplotype induces the incompatibility response in the stigma leading to self-pollen rejection. SP11 is expressed in the anther tapetum, a sporophytic tissue. The self-incompatibility phenotype in pollen is therefore determined by the dominance relationships between the two S-haplotypes carried by the plant. Extensive analyses revealed that these dominance relationships are epigenetically regulated by small RNAs. We will discuss the molecular mechanisms of SI signaling and SI expression. Recently, we identified unique incompatibility phenomenon, unilateral incompatibility (UI) between Japanese and Turkish populations in Brassica rapa. Japanese stigmas are prone to reject Turkish pollen in spite that their S-haplotypes are different, whereas Turkish stigmas accept Japanese pollen in reciprocal crosses. Genetic analysis revealed that this UI was regulated by duplicated S locus genes, PUI1 (Pollen Unilateral Incompatibility 1) and SUI1 (Stigma Unilateral Incompatibility 1), which were similar to SP11 and SRK, respectively. We will also discuss the diversity and similarity of SI and UI in this talk.

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Education  
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1990  M.S. Agronomy, Tohoku University  
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Employment  
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1991-1997  Assistant Professor, Laboratory of Plant Breeding, Faculty of Agriculture, Tohoku University, Sendai, Miyagi, Japan

Recent Main Publications  
CRISPR Genome Editing in Plants, Animals, and Human Cells

Jin-Soo Kim

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Department of Chemistry, Seoul National University, Seoul, South Korea

Genome editing with CRISPR systems is broadly useful in biological research and medicine. Cas9 and Cas9-fused deaminases (a.k.a., Base Editors), however, are limited by off-target mutations. We developed nuclease-digested whole genome sequencing (Digenome-seq) to profile genome-wide specificities of Cas9 nucleases and Cas9-fused deaminases in an unbiased manner. Digenome-seq comprehensively identified off-target sites at which mutations were induced with frequencies below 0.1%. We also showed that these off-target effects could be avoided by using preassembled ribonucleoproteins (RNPs), modified guide RNAs, and Sniper-Cas9, a Cas9 variant isolated via directed evolution in E. coli.

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1987 B.S. Dept. of Chemistry, Seoul National University

Employment
1994-1997 Research Associate, Howard Hughes Medical Institute/MIT
1997-1999 Principal Investigator, Samsung Biomedical Research Institute
1999-2005 CEO and CSO, ToolGen, Inc.
2005-present Assistant/Associate/Full/Adjunct Professor, Seoul National Univ.
2014-present Director, Institute for Basic Science (IBS)

Recent Main Publications
Highly efficient RNA-guided genome editing in human cells via delivery of purified Cas9 ribonucleoproteins. Genome Res. 24, 1012 (2014)
How CRISPR is changing agriculture?

Caixia Gao

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Crop improvement requires the constant creation and use of new allelic variants. Conventional breeding can be limited in providing the genes and alleles required to meet the agricultural challenges. In the past decade, Genome editing can accelerate plant breeding by allowing the introduction of precise and predictable modifications directly in an elite background. The most promising utilization of the CRISPR/Cas9 system can be used to generate targeted genome modifications including mutations, insertions, replacements and chromosome rearrangements. The use of CRISPR in agriculture should be considered as simply a new breeding method that can produce identical results to conventional methods in a much more predictable, faster and even cheaper manner.

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---

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- **2009-present** Professor, Principal investigator, Institute of Genetics & Developmental Biology, CAS, China  
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### Recent Main Publications


The Microbiome and Host Immunity Interplay in Health and Disease

Jihyun F. Kim

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Powered by high-speed high-throughput next-generation genomic technologies, life science and biotechnology are being transformed. In our laboratory, we apply genomic and metagenomic tools to study model microbes and microbial communities. Multi-omics systems-level understanding of the Escherichia coli cell factory may open the door to synthetic biology and next-generation biotechnology. Analysis of genomes sampled from a long-term evolution experiment revealed that the coupling between genomic and adaptive evolution is complex and can be counterintuitive even in a constant environment. The microbiome, comprised of the microbiota and its collective genomes called the metagenome, is an integral part of our body and the ecosystem. Systems understanding of host physiology can be possible only if the microbial counterparts that reside in are fully appreciated and both are considered as a unit, i.e. holobiont. Recent analyses reveal that a myriad of microbial members, mutualistic, commensal, or pathogenic to the host, play pivotal roles in health and disease by producing diverse macromolecules and metabolites. Host-microbiota relationships in the plant rhizosphere and the human gastrointestinal tract, as well as the dynamics of microbial communities, will be presented as examples. In the talk, efforts to develop probiotics or more preferably pharmabiotics for the prevention or treatment of gastrointestinal cancers will also be presented. Synthetic biology concepts and toolkits enable us to modulate the microbiome to maintain (eubiosis) or regain (rebiosis) homeostasis, and even to transform it to become preventive or curative.

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Employment
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2000-2012 Senior/Principal Researcher, Director, Korea Research Institute of Bioscience and Biotechnology
1997-2000 Postdoctoral Associate, Cornell University
1992-1997 Agricultural Researcher, Rural Development Administration

Recent Main Publications
Exploring the Genome of Wild Soybean

Hon-Ming Lam*

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Wild soybeans entrapped important genetic information that may have been lost due to domestication and human selection. Using whole-genome-sequencing approach, we demonstrated that wild soybeans have a much higher genomic diversity than cultivation soybeans. We constructed a recombinant inbred (RI) population using a wild soybean W05 and a cultivated soybean C08. A combination of genetics and genomic studies using this RI population has revealed genomic regions controlling important agronomic traits, such as salt tolerance, nitrogen fixation, anti-oxidation activities, and growth period. To facilitate further mining of unique alleles and genes from wild soybeans, we completed a reference-grade genome of W05, with a final genome assembly of 1013.2 Mb and a contig N50 of 3.3 Mb. To demonstrate the power of the high-quality genome, we used the genomic information to identify major structural changes, including chromosomal translocation and inversion, and copy number variations. For instance, a regional chromosomal inversion was the cause for a change of seed coat color during domestication. [The work is supported by Hong Kong Research Grants Committee AoE Scheme (AoE/M-403/16).]

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Education
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Employment
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2017-present Director, State Kay Laboratory of Agrobiotechnology at The Chinese University of Hong Kong, since August 1, 2017
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Recent Main Publications
Plant reproduction success: a tale of three -omes

David Honyša, David Hafidh, David Potěšil, Katarina Kulichová, Lenka Steinbachová, Karel Müller, Jan Fila, Christos Michailidis, Till Ischebeck, Zbyněk Zdráhal

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The male gametophyte, highly organized haploid flower organ, offers an unique opportunity to analyze development and differentiation of single haploid cells, cell-cell interactions and recognition, cellular polarity and pollen tube tip growth. Transcriptional and posttranscriptional control of gene expression as well as coordinated protein secretion play a vital role during tobacco pollen maturation and tube growth towards an ovule. The need for a high rate of translation during pollen tube growth suggests a demand for a robust storage system that could withstand a long-term storage and transport, ongoing cellular morphogenesis, and yet deliver the message efficiently accompanied with instant translation. A number of pollen genes showed apparent expression discrepancy at mRNA and protein levels and their respective transcripts were shown to be associated with long-term stored ribonucleoprotein particles. Similarly to the role played in growing mammalian neurons, these particles represent pre-loaded complex machinery devoted to mRNA processing, transport, subcellular localization and protein synthesis. Here, we present functional, transcriptomic and proteomic characterisation of pollen storage ribonucleoprotein particles. In particular, we aimed to integrate our knowledge on the categorization of translationally regulated transcripts in developing pollen and to identify the mode of action of the translational repression and de-repression of mRNAs stored in pollen. The selective activation of particular transcripts and their encoding proteins following male-female interaction in semi-in vivo conditions will also be discussed.

The research was financially supported by the Czech Science Foundation (18-02488S and 17-23183S), and the European Regional Development Fund-Project “Centre for Experimental Plant Biology” (No. CZ.02.1.01/0.0/0.0/16_019/0000738).

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Recent Main Publications
Insights into the genetic basis of crop nutritional quality and stress resilience

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Sustainable, resilient food systems are critical to providing food and nutrition security to a burgeoning human population. Maize is an important food staple, particularly in sub-Saharan African countries where it can account for more than half of daily calories. With considerable natural variation in grain tocopherol (vitamin E) and carotenoid (provitamin A) levels, maize could have far-reaching impact in the global South where vitamin deficiencies and insufficiencies are prevalent. A joint linkage-genome wide association study of maize grain tocopherol and carotenoid levels in the 5000-line US nested association mapping panel revealed that the majority of identified quantitative trait loci (QTL) were underpinned by causal genes with a priori roles in tocopherol and carotenoid synthesis and retention. Surprisingly, two homologs encoding a chlorophyll biosynthetic enzyme explained the majority of variation for tocopherol, which are the predominant form of tocopherol in maize embryos. The second part of the talk focuses on northern leaf blight (NLB), a fungal foliar disease of maize that has progressively become more severe in the past 5 years. When evaluating plant response to NLB infection, the visual scoring of gray-brown necrotic NLB lesions at multiple time points throughout the growing season is essential, but this effort is very time-consuming and prone to discrepancies between different human raters. In response to these limitations, an image-based aerial phenotyping system combined with deep learning algorithms was constructed and shown to achieve accurate qualitative and quantitative assessment of NLB lesions under field conditions. The talk will conclude with a summary of ongoing early efforts to develop sentinel plants that respond directly to environmental perturbations by emitting specific, quantifiable signals that communicate the plant’s health status directly.

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2003-2004 Senior Biologist, Lancaster Labs, Lancaster, Pennsylvania, USA
2001-2003 Senior Research Associate, Research Associate, Pioneer Hi-Bred International, Inc., Johnstone, Iowa, USA
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Recent Main Publications
Identification of a key player on nitrogen use efficiency of rice

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Nitrogen (N) is an essential nutrient for plant growth and development. N supply from natural soil is insufficient for crop production and rest of N sources are inevitably supplied by N fertilizer. Although N fertilizer induces great benefits in crop yield, overdose of the fertilizer results in a negative impact on the environment. So, improvement of N-use-efficiency (NUE) of crops aims to reduce N fertilizer usage while maintaining crop yield. To improve rice NUE, we are utilizing two research approaches, forward and reverse genetics. The N sensor system, which can monitor N status in rice, was developed for forward genetics. Two genes for allantoin metabolism, ALLANTOINASE (OsALN) and UREIDE PERMEASE 1 (OsUPS1) are highly responded to N status. OsALN was rapidly up-regulated under a low N condition, whereas OsUPS1 was up-regulated under a high N condition. Taking advantage of their nature in response to N status, we generated N sensors as proALN::ALN-LUC2 and proUPS1::UPS1-LUC2 in rice. Specifically, proUPS1::UPS1-LUC2 sensor showed strong luminescence activity under a high N condition (> 1 mM N source), whereas proALN::ALN-LUC2 sensor showed strong luminescence activity under a low N condition (< 0.1 mM N source). With the N sensor-integrated transgenic rice, we generated an EMS mutant population (10,000 individual lines). We are screening the high NUE rice under low N conditions by activity of the N sensors and trying to identify key players in rice N metabolism based on a MutMap analysis. For reverse genetics, we isolated N sensitive genes by RNAseq analysis. Among them, we are firstly trying to understand roles of OsNFYA3, OsNFYA5, and miR169 in N uptake and senescence utilized by genome editing techniques.

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2010-present Editorial board, Plant Biotechnology Journal
2009-2011 Adjunct professor, China AnHui Rice Research Institute
2008-present Chief editing committee, The Korea Society for Plant Biotechnology
2007-2011 BK21 director, Myongji University
2005-2006 Adjunct professor, University of California Davis
1996-2013 Professor, Myongji University
1993-1999 Program leader, The Rockefeller Foundation

Recent Main Publications


Towards genetic improvement of root system architecture for developing of climate-resilient rice

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Global climatic changes have accelerated drought and soil degradation worldwide in recent years. To produce crops that can be sustainably grown under such unstable and poor environments, it is imperative to develop crops that are robust against various environmental stresses. Adequate root system architecture (RSA) is important for crop growth in soil conditions where water and nutrients are deficient. Because the root system is the only organ for taking up water and nutrients from the ground. Therefore, genetic improvement of the RSA is required to enhance crop production under environmental stresses. Our research group has identified and characterized several quantitative trait loci (QTLs) responsible for RSA in rice so far. The use of such root-related QTLs for molecular breeding based on an ideal RSA may allow us to develop climate-resilient rice. However, to date, identifying the root traits critical for crop production remain a challenge, mostly because of the underground location of the roots. For this, we are developing new technology that will be able to conduct a modelling of ideal RSA that is robust to environmental stress. We launch non-destructive 3D root phenotyping platform using X-ray CT. Using this platform, we try to visualize and digitize the movement of root that are hidden under the ground.

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Recent Main Publications
Concurrent Session & Oral Session
Genome shock, transgressive segregation, and salinity tolerance in rice: Genetics or epigenetics?

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What would be the genetic blueprint for the new generation of crops with minimal penalty to growth and productivity potentials under marginalized environments? Such a profound question pushes even further the frontier of biological complexity that modern plant breeding must conquer beyond the achievements of the Green Revolution. Genomics-enabled plant breeding needs to recognize that such level of complexity cannot be addressed by a reductionist approach, and that any additional physiological gains similar to what has been optimized and achieved by natural selection must involve complex synergies that also require reconciliation with inevitable biological trade-offs. Evolutionary biology supports a theory that genetic recombination under genome shock is an important driver of adaptive speciation, by virtue of the novelities of rare wide-hybrids and recombinants, as also observed among transgressive populations created by plant breeding. Despite the advances in genomic biology and genomics-enabled plant breeding, this classic phenomenon is yet to be fully exploited as potential vehicle to create the stress-adaptive novelities needed in the 21st century, perhaps because it is over-shadowed by the more recent reductionist approaches to genetic manipulation. In this presentation, the author will discuss recent findings on a transgressive population of rice for salinity tolerance, to make a case that stress-adaptive developmental and physiological novelities involve intricate molecular synergies and network rewiring created by genome shock and epigenome confrontation. Modern views on the possible molecular underpinnings of transgressive phenotypes will be presented in context of the recently proposed Omnigenic Theory for quantitative traits, and current understanding of gene regulation by DNA methylation and chromatin remodeling. Perspectives on how genomic and epigenomic modeling could harness a transgressive genome to create the new generation of ecologically resilient crops will be presented as alternative to the more reductionist paradigms of functional genomics and genome editing.

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Unlocking the genetic potentials of wild rice species to abiotic stress for rice improvement

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Abiotic stresses are major obstacles restricting stable production of crops as well as extending cropping land to unfavorable environments. Genetic improvement of the crops is an ideal solution to mitigate crop damages caused by abiotic stress. However, domestication process and repeated use of the elite lines in breeding narrowed down the diversity of genetic variations which is an engine of breeding. Current genetic sources for abiotic stress tolerance originated from cultivated rice are insufficient to cope with abiotic stresses and climate changes. Wild rice species are regarded as a genetic reservoir because they have been surviving at the diverse worldwide geographical locations without any protections. Many genes originated from wild rice species, especially for biotic stress resistance, have been identified and successfully utilized in rice breeding programs. Unlocking novel genetic sources for abiotic stress tolerance from the wild rice species are highly demanded for stable rice production with high yield. We screened two cultivated rice species (Oryza sativa and O. glaberrima) and 22 wild rice species against salinity stress. Three species (O. alta, O. latifolia, and O. coarctata) showed high salt tolerance and four species (O. rhizomatis, O. eichingeri, O. minutula, and O. grandiglumis) exhibited similar level of tolerance compared to the conventional tolerant checks such as Pokkali and FL478. All three CCDD genome species (O. alta, O. latifolia, and O. grandiglumis) exhibited salt tolerance, suggesting that the CCDD genome might possess the common genetic factors for salt tolerance. To reveal the genetic factors for salt tolerance, transfer of the chromosome segments from CCDD genome species into the O. sativa genome (IR64) is under processing using interspecies cross with DNA markers. Efforts for isolation of new germplasm for submergence tolerance found that Loversia perrieri possess rapid internode elongation ability under submergence condition and we developed intergeneric hybrid with O. sativa for further study.

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Rice transcription factors that are involved in abiotic stress tolerance

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Plant-specific transcription factors (TFs) play essential roles in multiple aspects of development, leaf senescence, abiotic and biotic stresses. The rice genome has approximate 2487 genes encoding TF proteins which are classified into 84 families based on their domain composition. Among them, the OsNAC, OsMYB and OsWRKY TFs are largest families consisting of 144, 202, 103 genes, respectively, and more than half the member of their gene exhibits altered gene expression under salt and drought stress conditions. However, the protein functions of rice TFs in abiotic stress and leaf senescence have been revealed in only few reports. To find the rice OsNAC, OsMYB and OsWRKY TFs participating in regulatory mechanisms of abiotic stress and leaf senescence, we constructed an neighbor-joining trees with aligned domain of rice TFs and Arabidopsis TFs of which protein functions are known in abiotic stress and leaf senescence. We found that 60 rice TFs have highly amino acid sequence similarity with Arabidopsis TFs and show altered gene expression under abiotic stress and senescence conditions. To identify the functions of selected TFs in abiotic stress and leaf senescence, we obtained the T-DNA insertion mutants from Kyung Hee University and screened the mutant phenotypes. The results indicated that mutation of three genes encoding OsNAC, OsMYB and OsWRKY proteins, respectively exhibited hypersensitivity to salt stress and/or delayed leaf senescence. In this talk, I will discuss the novel regulatory mechanisms mediated by the rice TFs involved in abiotic stress response and leaf senescence.

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Fine-mapping of the quantitative trait locus qMel-3 controlling mesocotyl length

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Mesocotyl elongation is a key determinant of seedling emergence in the direct-seeding cultivation. Rice cultivars having long mesocotyl show higher seedling emergence after deep seeding. Poor seedling emergence and establishment can lead to yield loss in direct-seeding cultivation by deep-sowing. In previous studies, major quantitative trait loci (QTLs) associated with mesocotyl elongation were detected on chromosomes 1 and 3 using 98 backcross inbred lines derived from a cross between Kasalath and Nipponbare. Two major QTLs, qMel-1 on chromosome 1 and qMel-3 on chromosome 3 were detected both in agar and soil condition. One of them, qMel-3 located in a 6.9-Mb region was targeted for fine-mapping in this study.

To fine map and identify candidate genes of the qMel-3 by substitution mapping, a cross was made between 2 chromosome segment substitution lines (CSSL-6 and CSSL-15), each harboring the Kasalath allele across the qMel-1 and qMel-3 regions. A total of 20 lines having crossing-over in a 6.9-Mb region were selected and used for substitution mapping. Two QTL located in a 6.9-Mb region were separated. The qMel-3.1 was delimited into about 4-Mb region and the other QTL, qMel-3.2 was located within about 1.3-Mb region. Results of association mapping using rice accessions from rice germplasm collection also showed the existence of two QTLs in qMel-3. A number of candidate genes were identified based on microarray analysis displaying differential expressions between NILs and DNA sequence comparisons in qMel-3.1 and qMel-3.2 regions, respectively. RNA expression analysis of candidate genes were carried out and the results will be discussed. This research was supported by "Cooperative Research Program for Agriculture Science and Technology Development (Project No. PJ0132142019)"

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Isozymes analysis in different saline sensitive maize hybrids to identify stress mitigating proteins

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Four prescreened hybrids, BIL214·BIL218 as tolerant, BHM-7 and BHM-9 as moderate tolerant and BHM-5 as susceptible based on phenotype and biochemical parameters like NADPH-oxidase (NOX) activity, histochemical detection of superoxide radical (O2•-) and H2O2, methylglyoxal (MG), proline and K+/Na+, were studied to identify saline stress inducible isozymes for understanding oxidative stress tolerance in maize. To examine the probable causes of different salinity sensitivity, five days old seedlings were transferred on hydroponic culture containing 12 dSm NaCl induced salinity in Hoagland nutrient solution, and ROS, MG and their metabolizing antioxidants and glyoxalases were analyzed on 0th (control), 3rd, 6th and 9th day of stress. Fully expanded leaves. Then the seedlings were allowed to grow in saline free Hoagland solution, and after 3 days recovery data were recorded. As stress progressed, the susceptible hybrid exhibited significantly higher O2•-, H2O2 and MG than the tolerant hybrid. Native gel isozymes showed that both Mn-SOD and Cu/Zn-SOD increased with stress period in BIL214·BIL218 while they decreased after 6th day in other hybrids. The drastic decrease of catalase (CAT3) under salinity in susceptible hybrids might be crucial to show higher H2O2 contents. Similarly, presence of ascorbate peroxidase (APX1 and APX2) under salinity played important roles in H2O2 metabolism. For other enzymatic antioxidants like guaiacol peroxidase (POD) and glutathione peroxidase (GPX) had almost similar induction pattern in all the hybrids. Better homeostasis of glutathione (GSH) and ascorbate (AsA) under salinity was observed in tolerant hybrids probably due to higher glutathione reductase (GR), although monodehydroascorbate reductase (MDHAR) and dehydroascorbate reductase (DHAR) activities were comparatively higher in susceptible hybrid. Comparatively lower MG under salinity in tolerant hybrid was due to higher activities of glyoxalases. Importantly, activities of all the enzymes decreased in recovery. Therefore, highly expressed isozymes like CAT3, APX1 and APX2 thrust new research.

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Exploring novel genetic donors of salt tolerance across the tetraploid cultivated cotton germplasm (Gossypium hirsutum) by transcriptome profiling and genetic network modeling

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The paradigm for the identification of genes involved in abiotic stress tolerance mechanisms in plants has mostly been based on with differential expression. Such an approach has been fruitful in terms of revealing critical mechanisms that can be correlated with biochemical and physiological responses. In this study we performed a comparative analysis of the salt stress response transcriptomes of a minimal comparative panel representing an extreme contrast for salt tolerance across the Gossypium Diversity Reference Set. RNA-Seq libraries were constructed from the roots and shoots of highly salt-tolerant and highly salt-sensitive cultivars at 0h, 24h, 72h, 96h, 144h after mild to moderate levels of salt stress. From these datasets, we identified 1,179 differentially expressed genes (DEGs) with high stringency of over 2 folds difference, including 597 genes in the shoot and 582 genes in root. Among 1,179 DEGs, a subset of 814 were upregulated in both tolerant and sensitive genotypes. Interestingly the expression increased exponentially across the entire duration of the stress experiment in the susceptible genotype, but only gradual increases were observed in the tolerant genotype with 2-fold to 200-fold difference between genotypes. Another subset of 123 DEGs were upregulated in the sensitive genotype but downregulated in the tolerant genotype. On the other hand, the expression of a subset of 152 DEGs increased exponentially in the tolerant genotype and gradually increased in the sensitive genotype and another subset of 42 DEGs were upregulated in the tolerant genotype but downregulated in the sensitive genotype. Extreme upregulation of a subset of 937 genes were associated with susceptibility. Gene ontology analysis classified the 1179 DEGs to 17 functional categories including 142 genes of transcription factors. We propose that under salinity stress, the susceptible genotype expends maximum effort to escape the abiotic challenge. This is expressed in terms of over expression of genes conferring tolerance.

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Pollon germination during heat: Do HSP90s play a role?

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HSP90 proteins have been shown to be required for the promotion and maintenance of protein complexes that have critical roles in signal transduction, cellular trafficking, chromatin remodelling, cell growth and differentiation. In A. thaliana, seven members of the HSP90 family have been identified. Amongst them, four are found in the cytoplasm and nucleus (AtHsp90-1 to 90-4), and one in mitochondria (AtHsp90-6), ER (AtHsp90-7), and chloroplasts (AtHsp90-5). Among the AtHSP90s, AtHsp90-1 is stress-inducible and shares comparatively low sequence identity with the constitutively expressed AtHsp90-2 to -4. Sequence identities between cytosolic and other subcellular localized AtHSP90s are at an average of 50%. Application of heat stress on flowering A. thaliana plants identified severe loss of fertilization ability on buds harboring unicellular to bicellular stage pollen. Analysis of the HSP90 family T-DNA lines identified a 25% pollen defect at the mature pollen stage for the AtHsp90-1 and AtHsp90-5 lines. To dissect the role of the HSP90 members in pollen development, RNAi was utilized to downregulate the cytoplasmic HSP90 members. The RNAi cassette was spatiotemporally regulated to act upon different stages of pollen development. Overexpression lines for the HSP90-1 and HSP90-5 members with a C-terminal fluorophore fusion were also analysed. These lines, driven by the Lat52 promoter, active during mature pollen stage and throughout the proagamic phase of pollen development were utilized for analysing the role of these specific HSP90 members in pollen tube germination and growth.

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Genome-wide Association Study (GWAS) for Ultraviolet-B resistance in soybean

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The depletion of the ozone layer in the stratosphere is one of the major environmental issues and has led to increasing the intensity of ultraviolet-B (UV-B) radiation reaching Earth’s surface. Organisms are damaged on their DNA by enhanced UV-B radiation, which is harmful even if it is such a small part in solar spectrum. It could cause serious yield losses in plants because of the biochemical damage. Soybean [Glycine max(L.) Merr.], a major legume crop, is sensitive to UV-B radiation. Therefore, its needed to breed the new UV-B resistant soybean cultivar.

In this study, 690 soybean landrace germplasms were genotyped by Axiom 180K Soya SNP array chip and phenotyped after 14 days under UV-B radiation condition. Three categories of phenotypic traits were scored: Degree of leaf chlorosis damage (DLC), Degree of leaf shapedamage (DLS) and Degree of total plant damage (DTP). Genome-wide association study (GWAS) was conducted to identify SNPs significantly associated with the three traits. Based on a threshold of -log(P) ≥ 5.0, 2 SNP markers were identified on 6 and 11 chromosomes respectively. We could select positional 20 candidate genes on 11 chromosome.

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**OCS01-09**

**Genotype × environment interaction and yield stability analysis of doubled haploid lines of upland rice in multilocation yield trials**

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The aims of this research was to determine the effect of genotype-by-environment interaction on yield among doubled haploid lines (DH) of upland rice to obtain stable and high yielding lines through multilocation yield trials. Fourteen lines and two upland varieties i.e. Inpago 10 and Limboto were planted at 6 different locations in Indonesia, i.e. Bogor, Indramayu, Sukabumi, Malang, Blitar, and East Lampung. In each location, the experimental design was randomized complete block design with three replications. Stability was analyzed using linear regression model. Combined analysis of variance showed that the effects of location, genotype and interaction of genotype×location were highly significant (P<0.01) for grain yield. There was considerable variation for grain mean yield among both genotypes (DH lines) and environments (locations) which made it difficult to select stable lines in response to environmental change. ST6 and ST9 were classified as stable DH lines and widely adapted in all locations based on Finlay-Wilkinson, Eberhart-Russel and AMMI stability analysis. ST13 was classified as stable only by Finlay and Wilkinson's analysis, but achieved the highest average yield of six locations (5.00 tons.ha⁻¹), higher than check variety Inpago 10 (4.03 tons.ha⁻¹), and similar to Limboto (4.98 tons.ha⁻¹). ST6, ST9, and ST13 DH lines also had high yield potential (6.26-7.18 tons.ha⁻¹). In addition, AMMI analysis also showed that ST1 was DH lines specifically adapted to Malang, while ST7 was specifically adapted to Blitar.

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**OCS01-10**

**Investigating alternative breeding pathways to improve Korean Sesame varieties using the genetic diversity among the World Sesame Collection**

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Sesame is one of the oldest oil crop cultivated in the world. The genus *Sesamum*, has numerous wild relatives which are native to sub-Saharan Africa but the cultivated type, *Sesamum indicum*, probably originated in India. Extracted as oil or directly consumed as a healthy ingredient, its cultivation has recently expanded to new agroeocologies. Although the domestication of sesame is quite old, the genetic diversity in the currently available released varieties in Eastern Asia seems very narrow (relatively recent introduction in China, Korea and Japan). Even though there were major changes in plant morphotype between wild and cultivated sesame, there remains a great potential to design new ideotypes of sesame better adapted to each agroeocology. Here, we investigated the phenotypic diversity of over 400 accessions among the Sesame World Collection (including 300 African accessions) in comparison with the most recently released Korean varieties. The analyses highlight the lack of correlation between the different yield components (i.e. capsule number and size, branch number, height related traits, seed size and number). In the meantime, it also reveals the great potential of using a proper combination of those traits could lead to newly adapted varieties taking into account of G×E×M interactions. As an example, we demonstrate that a contrasting combination of yield related traits can lead to similar final yields. In a high input system (high density/fertilization), a uniculum plant type with multiple capsules per leaf axil [HI ideotype] appears advantageous. In a low input system (low density/fertilization), a multiple branching plant type with one capsule per leaf axil [LI ideotype] could provide higher plasticity. In addition, a higher diversity is observed in the LI ideotype group. In all cases, we suggest that there should be more effort to introduce novel combinations of traits from the genetic diversity available among the Sesame World Collection.

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**OCS02-01**

**Differential analysis of gluten-associated genefamily using RNA-seq in grain and leaves of hexaploid Wheat**

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Wheat is an important food resource in the world, but it causes a variety of allergic reactions such as WDEIA (Wheat-dependent exercise-induced anaphylaxis), Celiac disease, and food allergy. Gluten in the wheat endosperm is an important protein that determines some traits related to flour quality such as viscosity and elongation, but it also causes various allergic reactions. Among such malfunctioning reactions, WDEIA is a disease that occurs after physical exercise after the consumption of wheat products, and it causes symptoms such as rash, asthma and stunning. It has been known that omega-5 gliadin and high molecular weight glutenin subunits act as the main allergens for the WDEIA. We performed the comparative analysis of omega-5 gliadin deleted O-free and two parent lines (Keumkang and Ogseuru). In order to analyze the transcriptome of three lines, DEG analysis was performed by RNA sequencing of each grain and leaves. The differentially expressed genes related to the gluten gene family were distinguished and functionally annotated through gene ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG). In addition, SNP data for each variety were used to identify genesto which the nonsynonymous substitution occurred. Through this comparative analysis, we found some significant differences in allergen-inducing gluten-associated genes among the three lines.

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**OCS02-02**

**Soybean-VCF2Genomes: A database to identify the closest accession in soybean germplasm collection**

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The development of next generation sequencer (NGS) and the analytical methods allowed the researchers to profile their samples more precisely and easier than before. Especially for agriculture, the certification of the genomic background of their plant materials would be important for the reliability of seed market and stable yield as well as for quarantine procedure. However, the analysis of NGS data is still difficult for non-computational researchers or breeders to verify their samples because majority of current softwares for NGS analysis require users to access unfamiliar Linux environment. Here, we developed a web-application, “Soybean-VCF2Genomes”, http://pgl.gnu.ac.kr/soy_vcf2genome/ to map single sample variant call format (VCF) file against known soybean germplasm collection for identification of the closest soybean accession. Based on principal component analysis (PCA), we simplified genotype matrix for lowering computational burden while maintaining accurate clustering. With our web-application, users can simply upload single sample VCF file created by more than 10x resequencing strategy to find the closest samples along with linkage dendrogram of the reference genotype matrix. The information of the closest soybean cultivar will allow breeders to estimate relative germplasmic position of their query sample to determine soybean breeding strategies. Moreover, our VCF2Genomes scheme can be extended to other plant species where the whole genome sequences of core collection are publicly available.

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**OCS02-03**

**Genome sequence of *Jatropha curcas* L., a non-edible biodiesel plant, provides a resource to improve seed-related traits**

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*Jatropha curcas* ( physic nut), a non-edible oilseed crop, represents one of the most promising alternative energy sources due to its high seed oil content, rapid growth, and adaptability to various environments. We report ~339 Mb draft whole genome sequence of *J. curcas* var. Chai Nat using both the PacBio and Illumina sequencing platforms. We identified and categorized differentially expressed genes related to biosynthesis of lipid and toxic compound among four stages of seed development. Triacylglycerol (TAG), the major component of seed storage oil, is mainly synthesized by phospholipid:diacylglycerol acyltransferase in Jatropha, and continuous high expression of homologs of oleosin over seed development contributes to accumulation of high level of oil in kernels by preventing the breakdown of TAG. A physical cluster of genes for diterpenoid biosynthetic enzymes, including cashene synthases highly responsible for a toxic compound, phorbol ester, in seed cake, was syntetically highly conserved between Jatropha and castor bean. Transcriptomic analysis of female and male flowers revealed the up-regulation of a dozen family of TFs in female flower. Additionally, we constructed a robust species tree enabling estimation of divergence times among nine *Jatropha* species and five commercial crops in Malpighiales order. Our results will help researchers and breeders increase energy efficiency of this important oil seed crop by improving yield and oil content, and eliminating toxic compound in seed cake for animal feed.

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**OCS02-04**

**DNA methylation creates diversities in duplicated plant genomes**

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Most plants are polyploid due to whole-genome duplications (WGD) and can thus have duplicated genes. Although a majority of duplicated genes are lost through non-functionalization or pseudogenization, many can be retained through balancing gene dosage or functional divergence. DNA methylation can contribute to the regulation of gene expression in plants, yet little attention has been paid to the role of DNA methylation in the functional divergence of paralogous genes. Using high-resolution methylation maps of accessions of domesticated and wild soybean, we show that in soybean, a recent paleopolyploid with many paralogs, DNA methylation likely contributed to the elimination of genetic redundancy of polyploidy-derived gene paralogs. Transcriptionally silenced paralogs exhibit particular genomic features as they are often associated with proximal transposable elements (TEs) and are preferentially located in pericentromeres, likely due to gene movement during evolution. In addition to soybean, the genome sequence and DNA methylome of cultivated peanut (*Arachis hypogaea* L.), an allopolyploid genome that contains two sets of chromosomes originated from the ancestral species, will be presented.

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Complete chloroplast genomesequence of *Chrysanthemum cinerariaefolium*: genome features, comparativeanalysis and phylogeneticrelationships

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Chrysanthemum (family Asteraceae) is genus of economic significance and valuable properties and member of this genus used around the world as cut flower or pot plants as well as have important role in oriental medicine. The cp genome size is 150,158 bp with a typical quadriparti structure and consisting of a pair of inverted repeat regions (24,502 bp) separated by large singlecopy region (82,729 bp) and small single copy region (18,435 bp). Sequencing analyses indicated that the cp genome encodes 124 genes, including 86 protein-coding genes, 35 tRNA genes and 8 rRNA genes. The genome structure, gene order and codon usage are typical of angiosperm cp genomes. We also identified 52 simple sequence repeats (SSR) loci, fewer of them are distributed in the protein-coding sequences compared to the noncoding regions. Comparison of *C. cinerariaefolium* cp genome to other Asteraceae cp genomes indicated the inverted repeats (IRs) and coding regions were more conserved than single copy and noncoding regions, and several variation hotspots were detected. Phylogenetic analysis based on cp genomes indicated a close relationship among the species. In summary, the complete cp genome sequence of *C. cinerariaefolium* reported in this study will provide useful plastid genomic resources for population genetics and pave the way for resolving phylogenetic relationships of Asteraceae family.

**Keywords:** Chrysanthemum, Asteraceae, Chloroplast genome, Phylogenetic, Sequence divergence, SSRs
Chloroplast and mitochondrial genome flux and its impact on DNA barcoding

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DNA barcoding technology is used to classify and authenticate herbal plants and also contributes to prevent economically motivated adulteration (EMA) of those products. However, underestimating the genomic complexity mediated by horizontal plastid genome transfer can cause undiscovered shortcomings in DNA barcoding and molecular taxonomy. We assembled organelle genomes of Cynanchum wilfordii, an herb used as a functional food in the treatment of menopausal disorders, and C. auriculatum, which is found in EMA of C. wilfordii in Korea. In both species, the mitochondrial genome contained sequences related to ~35% of the plastid genome, termed mitochondrial plastid DNAs (MTPTs). Mitochondrial genome show dynamic rearrangement but gene sequence were identical and plastid genomes were structurally identical but genes showed sequence variation which was estimated to diverged approximately 2 million years ago (mya) between two species. MTPT pseudogenes was estimated to be horizontally transferred 10 mya and also more conserved than plastid genes of two species. Co-amplification of MTPTs and intraspecies diversity of plastid genomes could cause a plastid DNA barcoding paradox resulting in mis-authentication of herbal productor taxonomical mis-positioning. We identified dynamic and lineage-specific MTPTs up to 75 kb that contributed to diversifying mitochondrial genome structure complexity across diverse plant species.

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Kompetitive allele-specific PCR (KASP) marker development with Korean Japonica rice varieties through genome resequencing and application

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Plentiful variations in the important agronomic traits such as disease resistance and pre-harvest sprouting exist within Korean japonica rice varieties. Therefore, it is possible to do mapping useful genes with populations derived from crosses between them. But, deficiency of molecular markers discriminating Korean japonica rice varieties has made these efforts difficult. However, abundant SNPs can be revealed between closely related crop varieties by genome sequencing enabling development of sufficient DNA markers. We analyzed genome sequence data from 13 Korean japonica rice varieties and discovered 740,566 SNPs. Of the discovered SNPs, 1,014 SNP sites were selected on the basis of polymorphism information content (PIC) value higher than 0.4 per 200-kbp interval, and were converted to Kompetitive Allele-Specific PCR (KASP) markers. We are testing these KASP by genotyping 13 sequenced Korean japonica rice varieties using them. About 500 KASP markers have been developed up to the present, and more markers are being developed. We performed mapping QTLs for rice bakanae disease (BD) resistance using the developed KASP markers. A major QTL, qJFR9, was found at 30.1 centimorgan (cM) on chromosome 9 with a logarithm of the odds (LOD) score of 60.3 with an F2:F3 population derived from a cross between Sanggwang, BD-resistant Korean japonica variety, and Junam, BD-susceptible Korean japonica variety. Also, a major QTL, qJFR1-1, was found at 98.9 centimorgan (cM) on chromosome 1 with LOD score of 21.4 with an F2:F3 population derived from a cross between Nampyeong, BD-resistant Korean japonica variety, and Junam. These results demonstrate that the developed KASP markers are very useful in mapping genes for important traits in Korean japonica rice varieties. The KASP markers developed in this study will accelerate molecular breeding in Korean japonica rice varieties, and the detected QTLs for BD-resistance will be helpful for breeding BD-resistant varieties.

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Whole Genome sequencing of *Capsicum annuum* ‘Dempsey’ Using Pac-bio, Bionano and Hi-C

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Peppers including pungent and non-pungent varieties are an important vegetable crop worldwide. During the past two decades, there has been a great progress in molecular breeding and genomics in pepper. Genome sequence assemblies for three *Capsicum* species including *C. annuum*, *C. chinense*, and *C. baccatum* have developed by the short-read sequencing, and are available for genetic study and molecular breeding. Here, we report an improved *C. annuum* genome assembly of a non-pungent line ‘Dempsey’ at the chromosomal scale using single-molecule sequencing (Pac-Bio), optical mapping (Bionano) and chromosome conformation capture technologies (Hi-C). Our assembly featured contig N50 sizes of 18.3Mb and 257 Mb after Pac-Bio sequencing and Hi-C scaffolding, respectively. The genome size of Dempsey was estimated to be 3.03 Mb. Top 12 contig lengths were ranged from 332 Mb to 173 Mb with total length of 3.0 Mb demonstrating that 99.9% of sequenced reads were assembled. The validity of the assembly was further demonstrated using a genetic map with skim sequencing of 120 ‘Perennial’ x ‘Dempsey’ RILs. The order of all 1,911 bin markers in each linkage groups were mostly matched with the nucleotide sequence order of pseudomolecules. ‘Dempsey’ is more contiguous than other previous *Capsicum annuum* assemblies. Several gaps in the previous assemblies were continuous in ‘Dempsey’. To predict gap size and repeat position, Pac-Bio sequence will be anchored to Bionano optical map and hybridize with Pac-Bio + Hi-C scaffolds. This assembly can be used as golden standard genome for comparative analysis with other *Capsicum* species and genome wide association study.

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Heat Stress Response in Rice During Seed Development

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Early seed development in rice is very sensitive to high temperature stress. Even a transient heat stress during this stage results in decreased seed size at maturity and impacts seed quality. The genetic and molecular processes impacted by high temperature stress, especially in the endosperm need to be explored to gain a better understanding for developing rice that is more resilient to high temperature. Our research focus is to elucidate the molecular basis of seed developmental responses to heat stress using a suite of omics strategies. We have used transcriptomics and methylome analysis to identify the pathways and genes involved in response of developing rice seeds to higher temperatures. We will present these findings with special focus on stress responsive transcription factors. On-going work on natural variation in rice germplasm for heat stress will also be presented.

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36
Next generation proteomics pipelines for agriculture and crop science

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Proteomics technology aims to map the protein landscapes of biological samples, and it can be applied to a variety of samples including cells and tissues. Because the proteins are the main functional molecules in the cells, their levels reflect much more accurately the cellular phenotype and the regulatory processes within them than gene levels, mutations, and even mRNA levels. With the advancement in the technology, it is possible now to obtain comprehensive views of the biological systems and to study large proteome overview. Here, we discuss the technological advancements in mass spectrometry-based proteomics called as next generation proteomics, which allow analysis of tissue samples for agriculture and food science, leading to the large-scale plant proteomics studies. Furthermore, we discuss the technological developments in plant proteomics studies, which provide the basis for biological clues to understanding protein function. So far, using an in-house developed method for protein isolation, combined with the Q-Exactive Hybrid Quadrupole-Orbitrap Mass Spectrometer, more than 5000 proteins were identified in plant tissues as a case study. The acquired MS data to quantify protein abundance were analyzed with MaxQuant (ver. 1.5.3.30). As a case study, we like to introduce MSP1 induced-signalling components in rice leaves by integrated proteomic and phosphoproteomic analysis. MSP1 is a Magnaporthe oryzae secreted protein that elicits defense responses in rice. However, the molecular mechanism of MSP1 action is currently elusive. Moreover, it is also not clear whether MSP1 functions as a pathogen-associated molecular pattern (PAMP) or an effector. Here we report that transient expression of extracellular MSP1 in Nicotiana benthamiana leaves results in accumulation of reactive oxygen species (ROS) while intracellular MSP1 has no effect. Co-infiltration of extracellular MSP1 with salicylic acid (SA), abscisic acid (ABA) and methyl jasmonate (MeJA) markedly enhanced ROS production, indicating a cross-talk between MSP1 induced signaling and these phytohormones signaling pathways. A TMT-based quantitative proteomic analysis led to the identification of 6691 proteins of which 3049 were identified in the plasma membrane while 3642 were identified in the cytoplasmic fraction. A parallel phosphoproteome analysis led to the identification of 1906 phosphopeptides and integration of proteome and phosphoproteome data showed activation of proteins related to the proteolysis, jasmonic acid biosynthesis, redox metabolism and MAP kinase signaling pathways in response to MSP1 treatment. Further, MSP1 induced phosphorylation of some of the key proteins including RBOHB, MEKK1, MPK3/6, CDPK and CaM suggest activation of PAMP-triggered immunity (PTI) in response to MSP1 treatment. In essence, our results strongly support the functioning of MSP1 as a PAMP and provide an overview of the MSP1 induced signaling in rice leaves.

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TGIL: An integrative bioinformatic platform for genomics-assisted breeding

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Innovation and advancement of NGS technology, in recent years, have played a key role in acceleration of genomic data production and fast accumulation of related omics information. Literally, It is certain that biology is moving towards ‘big data era’ of omics. Such big data should be useful for molecular breeding and will open a new venue for omics-driven breeding programs. Towards this direction, we are developing and constructing an integrative bioinformatic platform for legume genomics-assisted breeding (named as TGIL: translational genomics interface for the legumes, http://tgil.donga.ac.kr). To build up the platform, a wide array of genome data, including seven fully sequenced legume species (G. max, M. truncatula, L. japonicus, P. vulgaris, C. arietinum, Cajanus cajan and V. radiata) and two non-legume models (A. thaliana and O. sativa), were employed as the fundamental information resources. The platform consists of three major modules, i.e., databases, analytical module and user interface. Including basic genome DB, the database contains gene functional information, orthologous gene DB, transcriptome DB and gene network DB. Analysis platform is equipped with interactive comparative genome analysis module and CSGM (cross-species genomic marker) designer program (http://tgil.donga.ac.kr/CSGMdesigner), as well as other general tools for genome data processing. User interface is being developed with the intention of providing breeder-friendly platform on which they can readily obtain data and/or information associated with traits of interest and design molecular markers. We anticipate that the integration of these bioinformatic modules and tools will contribute to accomplishing a modern concept of genomics-driven breeding, so called ‘reverse breeding’ or ‘breeding-by-design’.

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Application of Microarray and RNA-Seq to Analyze Transcriptome Network in Rice

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Microarray has been applied to various areas in the transcriptome analysis. To determine the cis-elements of transcription factors, a protein-binding microarray (PBM) has been applied. In an analysis of OsSMF1, which is a basic leucine zipper transcription factor that is involved in the regulation of rice seed maturation. OsSMF1 (previously called RISBZ1) is known to interact with GCN4 motifs (TGA(G/C)TCA) to regulate seed storage proteins. OsSMF1 (also known as OsbZIP58) functions as a key regulator of starch synthesis. Quadruple 9-mer-based PBM and electrophoretic mobility shift assay experiments revealed that OsSMF1 binds to the ACGT (CCACGT(C/G)), GCN4 (TGA(G/C)TCA), and GCN4-like (GGA(T)GAC) motifs. We also identified 60 putative OsSMF1 target genes using a combination of data from expression microarrays and RiceArrayNet. Of these OsSMF1 target genes, 20, 22, and 17 genes contained ACGT, GCN4, and GCN4-like motifs within the 2-kb promoter region, respectively. We confirmed that OsSMF1 regulates Os03g0168500 (thioredoxin), RPBF, NAC6, and hypothetical proteins (Os12g0626100 and Os11g0882400) and directly binds to Os03g0168500 promoter vivo. This study suggests that OsSMF1 functions in a wide range of seed development processes with specific binding affinities for three DNA binding motifs.

We also developed rice alternatively spliced transcript microarray (ASDM) and applied to differentiate the transcriptome of 4 representative organs of Oryza sativa L. cv. Ilmi: leaves, roots, 1-cm-stage panicles and young seeds at 21 days after pollination. Comparison of data obtained by microarray and RNA-Seq showed a bell-shaped distribution and a strong co-lineation for highly expressed genes. Transcripts were classified according to the degree of organ enrichment using a coefficient value (CV, the ratio of the standard deviation to the mean values): highly variable (CVI), variable (CVII), and constitutive (CVIII) groups. A higher index of the portion of loci with alternatively spliced transcripts in a group (IAST) value was observed for the constitutive group. Genes of the highly variable group showed the characteristics of the examined organs, and alternatively spliced transcripts tended to exhibit the same organ specificity or less organ preferences, with avoidance of ‘organ distinctness’. In addition, within a locus, a tendency of higher expression was found for transcripts with a longer coding sequence (CDS), and a spliced intron was the most commonly found type of alternative splicing for an extended CDS. pre-mRNA splicing might have evolved to retain maximum functionality in terms of organ preference and multiplicity.

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Unbiased annotation of target-gene families identifies undiscovered protein-coding genes in plant genomes

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Whole-genome annotation error that omits essential protein-coding genes hinders further research. We developed Target Gene Family Finder (TG Fam-Finder), an optimal tool for the structural annotation of protein-coding genes containing target domain(s) of interest in eukaryotic genomes. Large-scale re-annotation of 50 plant genomes identified an average of 149, 166, and 86 additional far-red-impaired response 1, nucleotide-binding and leucine-rich-repeats, and cytochrome P450 genes that were missed in previous annotations. We detected significantly higher number of translated genes in the new annotations using mass spectrometry data from seven plant species compared to previous annotations. TG Fam-Finder took strikingly reduced annotation run-time and improved accuracy compared to a conventional annotation tool. Furthermore, we demonstrated utility of TG Fam-Finder beyond plant genomes via re-annotation of gene families in 47 animal genomes. TG Fam-Finder along with the new gene models can provide an optimized platform for unbiased functional, comparative, and evolutionary studies in eukaryotes.

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BIMS (Breeding Information Management System) for efficient management of phenotypic and genotypic data

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Breeding programs produce large amount of data that require efficient management systems to keep track of performance, pedigree, geographical and image-based data as well as genotyping data. The integration of breeding data with publicly available genomic and genetic data, as well as the integration of each breeder’s own genotypic and phenotypic data in a database enhances genetic understanding of important traits and maximizes the marker-assisted breeding utility by breeders and allied scientists. We report the progress on BIMS, Breeding Information Management System, which we have implemented in in Genome Database for Rosaceae, CottonGEN, Citrus Genome Database, Cool Season Food Legume Database and Genome Database for Vaccinium. BIMS allows individual breeders to integrate their phenotypic and genotypic data with public genomic and genetic data and at the same time have complete control of their own breeding data and access to tools such as data import/export, search/download, statistical data analysis and a data archive. BIMS incorporates the use of an Android App called Field Book, an open-source software for phones and tablets, which will allow breeders to replace hard-copy field books, thus alleviating the possibility of transcription errors while providing faster access to the collected data. The use of Field Book and BIMS promotes the use and development of standard trait descriptors and metadata as well. We will report current functionality and future development.

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Identification of Genes Involved in Trichome Development and Insect Resistance in Tomato

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Trichomes are specialized epidermal structures that protect plants from abiotic and biotic stresses. In depth knowledge of the molecular mechanisms that control trichome development in Arabidopsis, which produces unicellular nonglandular trichomes, has provided significant insight into the genetic basis of variation in trichome habit. Solanaceous plants including tomato produce several different types of multicellular nonglandular and glandular trichomes on aerial tissues. In contrast to our understanding of unicellular nonglandular trichomes, much less is known about the development and ecological function of multicellular trichomes. Here, we report identification of several genes involved in trichome development and examine their roles in plant defense against insect attack in tomato.

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Genetic dissection of plant immune gene expression and defense responses

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To ward off pathogen invasion, plants have developed at least two innate immune systems in addition to constitutive physical barriers. Plants recognize invading microorganisms by detection of conserved signatures, termed microbe-associated molecular patterns (MAMPs) through pattern recognition receptors (PRR) and mount pattern-triggered immunity (PTI). Pathogens have evolved mechanisms to evade PTI and deliver effector proteins recognized by intracellular nucleotide-binding eucine-rich repeat (NLR) proteins to activate effector-triggered immunity (ETI). However, the signaling regulators downstream of plant NLR resistance proteins remain elusive. To elucidate additional ETI signaling components, we establish a sensitive genetic screen with an ethyl methanesulfonate (EMS)-mutagenized population of Arabidopsis transgenic plants harboring a luciferase reporter gene under the control of the WRKY46 promoter (pWRKY46::LUC). As an early marker gene, WRKY46 is quickly and strongly expressed by bacterial effectors triggering ETI, but not by MAMPs triggering PTI. A series of mutants with altered pWRKY46::LUC activity after avrRpt2 infiltration were identified and named as Arabidopsis genes governing immune gene expression (aggie). Molecular and biochemical analysis of aggie101 led to discovery of ANX1-mediated regulation in both ETI and PTI.

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How does plant defense-related hormone salicylic acid benefits both plants and humans

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Salicylic acid (SA) plays a key role in plants, including plant development, stomatal closure, thermogenesis, and response to abiotic and biotic stresses. Its role in plant immunity is the most extensively studied, but it is still only partially understood. In plants, more than two dozens of SA-binding proteins (SABPs) are identified based on the classical biochemical approaches and genome-wide high-throughput screens. Interestingly some of these proteins exhibited high affinity against SA, while the others showed low affinity, in vitro. Presence of SABPs exhibiting a wide range of affinities for SA may provide great flexibility and multiple mechanisms through which SA can act. Importantly, similar screening of human proteome identified several target proteins of SA and its natural and synthetic derivatives (Salicylates). Many of these human proteins, like their plant counterparts, are associated with immunity or disease development. High Mobility Group Box protein (HMGB) and Glyceraldehyde 3-Phosphate Dehydrogenase (GAPDH) were identified as SABPs and play important roles in disease responses in both plants and humans.

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Genetic and genomic analyses of Cercospora leaf spot resistance in cowpea

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Cercospora leaf spot (CLS) caused by Cercospora canescens and Pseudocercospora axillaria is an important disease of cowpea (Vigna unguiculata) grown in tropical regions. Initially, we determined mode of inheritance of resistance to CLS and estimated broad-sense heritability (H2) and genetic effects of the resistance using six basic populations (P1, P2, F1, F2, BC1P1, BC1P2) generated from the cross between ‘CSR12906’ (P1: susceptible) and ‘IT90K-59-120’ (P2: resistant). Mendelian segregation analyses suggested that the resistance to both fungi is controlled by a single gene or two genes. Quantitative analysis by generation mean analysis revealed that the resistance is controlled by a single gene. By using variance of the basic populations, average number of major genes estimated for the resistance caused by C. canescens was 1.05 and by P. axillaria 0.92. H2 estimated for resistance to both fungi was very high (>90%). Altogether, these results indicated that the resistance is controlled by a single recessive gene. Subsequently, we identified QTL controlling the resistance by bulked segregant analysis (BSA) using an F2 population (P1 F2) of 190 individuals. BSA analysis demonstrated that simple sequence repeat (SSR) marker CEDG304 located on linkage group 9 (LG) associated with the resistance. Quantitative trait locus (QTL) mapping detected a single major QTL, qCLS9.1, on LG9 controls the resistance. The QTL accounted for up to 90% of the disease score variation. Lastly, we conducted fine mapping of the QTL for the resistance using a larger size F2 population of the cross P1 F2 and newly developed SSR markers. Results revealed qCLS9.1 is consisted of two tightly linked genes known for their involvement in plant disease resistance. In conclusion, the CLS resistance in IT90K-59-120 is a simple and highly heritable trait being under the control by two tightly genes.

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Detection of Resistance Gene to Begomovirus in Chili Pepper (Capsicum frutescens L. 'Cempluk')

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Chili pepper is a primary need for Indonesian food, which known as its rich taste of spicy food. Consumption of chili pepper average 4.6 kg/capita/year. However, chili pepper very susceptible to various diseases and viral infections, especially Begomovirus infection. Chili pepper infected with Begomovirus has low fruit productivity, and tends to fail crops. Solution to reduce outbreak of Begomovirus infection is through plant breeding used superior seed selection, and testing Begomovirus resistance gene in selected samples. Cempluk selection in field resulted F1, which expected as superior character resistance to Begomovirus gene. This study aim to analyze Begomovirus resistance gene in Cempluk which grown in 2 locations, on field and in Greenhouse located at Mutihan, Bokoharjo Village, Kalasan, Yogyakarta. Observation on plant height and scale of Begomovirus infection used SPSS 16.0 software. 1-Way Anova test and Kruskal-Wallis test. DNA extraction from leaves, amplification of Begomovirus gene linked SCAR primer 1198 bp at Faculty of Agriculture and Breeding, Faculty of Biology UGM. 1-Way Anova test on plant population differed in 6 scale, 1-Way Anova test shown difference of height rate at each scale, and Kruskal-Wallis test shown p-value sig. 0.00 <of α = 0.05, differences in plant height per scale accepted. Kruskal-Wallis test shown that data on plant population in field have valid differences in plant height categories based on 6 scales. Whereas in Greenhouse population, 1-Way Anova test shown homogeneous plant height rate in Greenhouse population even though there were varies scale on Begomovirus infection. Gene character showed positive resistance to Begomovirus in presence of 1198 bp band DNA of 6 samples on 0 scale, obtained both from field and Greenhouse. While 6 samples on scale 5, which infected with Begomovirus in both locations neither presence of band DNA and resistance gene.

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The \textit{in planta} Particle Bombardment (iPB) method for crop transformation and genome editing

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Transformation is a key element for new breeding technology including genome editing. In many crop species, requirement of \textit{in vitro} culture and regeneration hampers application of transformation technology to varieties of commercial importance. It is desirable to develop a novel non-culture-based transformation methodology. To this end, we have developed a simple, reproducible, \textit{in planta} transformation method in wheat, using biolistic DNA delivery. Shoot apical meristems (SAMs) contain a subepidermal cell layer, L2, from which germ cells later develop during floral organogenesis. Therefore, the L2 cells can be an excellent target for the introduction of heritable genome modifications. SAM-exposed embryos from imibed mature seeds were bombarded with the GFP gene and grown to fifth leaf stage where DNA integration was tested by PCR. Out of 577 bombarded plants, five showed transgene integration and one showed inheritance to T1 generation. We successfully transformed the model wheat cultivar ‘Fielder’, as well as the recalcitrant Japanese elite cultivar ‘Haruyokoi’. The biolistic delivery of gold particles coated with plasmids expressing CRISPR/Cas9 components designed to target \textit{TgGASR7} were bombarded into SAM-exposed embryos of imibed mature seeds. Mutations in the target gene were assessed in fifth-leaf tissue by cleaved amplified polymorphic sequence (CAPS) analysis. Eleven (5.2%) of the 210 bombarded plants carried mutant alleles, and the mutations of three (1.4%) of these were inherited in the next generation (T1). Genotype analysis of T1 plants identified plants homozygous for the three homologous genes. These plants showed no detectable integration of the Cas9 and guide RNA genes, indicating that transient expression of CRISPR/Cas9 introduced the mutations. Together, our current method can be used to achieve \textit{in planta} genome editing in wheat using CRISPR/Cas9 and suggests possible applications of genome editing to other recalcitrant plant species and variations.

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Application of soybean transgenesis to improve agricultural or industrial traits

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Soybean [\textit{Glycine max} (L.)] is one of the most significant sources of vegetable oil and protein for food. Transformation is an optimal technique for developing soybean varieties with desired traits that are difficult to obtain from traditional breeding. \textit{Agrobacterium}-mediated transformation has been efficiently used to introduce foreign genes into soybeans in my lab for las several years. First target was to improve agricultural traits, such as yield increase, viral resistance, drought and salt tolerance.The results from those trials for agricultural purpose will be introduced in the presentation. More and more information on genes is available thanks to rapidly developing genome research. The accumulating new findings of gene provide us an opportunity to genetically engineer soybean by modifying its physiological pathways or adding new genes into soybean genome. Second part of my presentation will cover addition of new value or function for industrial use of soybean via genetic transformation. Especially, engineering of soybean lipid pathway will be discussed. Finally, brief prospect of transgenesis in plant cell culture will be introduced and compared with industrial LMO application in animal cell culture.

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Approval of recombinant protein-based vaccine against classical swine fever virus in pigs using transgenic Nicotiana benthamiana in Korea

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Classical swine fever virus (CSFV) is highly contagious, and fatal to infected pigs. Vaccines against CSFV have been developed from attenuated or modified live viruses. These vaccines are effective for immunization of animals, but they are associated with problems such as the accidental spreading of viruses to animals in the field, and with barriers to trade following vaccination. Here, we report the generation of transgenic Nicotiana benthamiana plants for large-scale, cost-effective production of E2 fusion protein for use as a recombinant vaccine against CSFV in pigs. Transgenic N. benthamiana plants harboring an intergenic, single-copy insertion of a chimeric gene encoding E2 fusion protein had high levels of transgene expression. For large-scale production of E2 fusion protein from leaf tissues, we developed a protein-purification protocol consisting of cellulose-binding domain (CBD)-cellulose-based affinity purification and size-exclusion gel-filtration chromatography. E2 fusion proteins showed high immunogenicity in piglets and provided protection against CSFV challenge. The CBD in the E2 fusion protein was also highly immunogenic. These results suggest that plant-produced recombinant E2 fusion proteins can be developed into cost-effective vaccines against CSFV, with the CBD as a marker antigen to differentiate between vaccination and natural infection. Based on the results, HERBAVAC™-CSF Green Marker vaccine won approval in April, 2019.

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Production of Natural Rubber in Dandelion

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The Hevea brasiliensis tree is currently the only commercial rubber producing Crop. Because of the poor genetic variations, there is always a potential danger of crop failure with diseases. Hevea also has another fundamental problem of life-threatening allergy caused by the proteins in the latex. It is, therefore, highly desirable to develop alternative rubber crops that produce a high quality rubber without allergy. Most candidates for the alternative rubber crops have some drawbacks as relatively shorter length of rubber polymer and/or lower rubber production compared to the Hevea. In order to make them commercially viable rubber crops, it is required to either increase the size of rubber polymer and improve rubber production. We propose to genetically manipulate the pathway of rubber biosynthesis by introducing functional genes and/or by blocking the expression of certain genes. We are investigating the gene(s) that determine the rubber polymer size or rubber production. At the same time, we have tried to develop non-GM lines of Russian dandelion that is significantly improved rubber content and root biomass compared to wild type. Ultimately we aim to apply the basic technology to an alternative target crop and produce high quality natural rubber without allergy.

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**OCS05-05**

Ginsenoside biosynthesis and its regulation in *Panax ginseng* Meyer

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Ginsenosides, glycosylated triterpenes (saponins), are considered to be the major pharmaceutically active ingredients of ginseng. Various medicinal efficacies have been ascribed to ginseng saponins, including anti-inflammatory, antitumor, neuroprotective, and immunoprotective effects. Diverse plant isoprenoids are synthesized in the plastids, mitochondria, endoplasmic reticulum, and cytoplasm. The enzyme 3-hydroxy-3-methylglutaryl-coenzyme A reductase (HMGR) catalyzes the first committed step, and isoprene synthase (IS) is proposed to be the second rate-limiting enzyme of ginsenoside biosynthesis in the central isoprenoid pathway. Ginsenoside backbones, categorized as protopanaxadiols, protopanaxatriols, and oleanane saponins, are synthesized by dammarenediol synthase or beta-amyrin synthase from 2,3-oxidosqualene. These triterpene backbones then undergo various modifications, such as oxidation, substitution, and glycosylation. To understand where different types of ginsenosides are synthesized, tissue/organ-specific gene expression patterns and the functional characterization of HMGR, IS, and cytochrome P450 with the corresponding regulated ginsenoside content were analyzed. Protein-protein interaction partners and putative regulatory gene studies on ginsenoside biosynthesis were searched using the protein expression library of *Panax ginseng* Meyer. Ongoing genome-editing technology using CRISPR-Cas9 in tetraploid ginseng root will also be addressed.

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**OCS06-01**

High-throughput phenotyping system (HTPS) for trait analysis of crops in Korea

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Recently, most advanced countries are building platforms to study plant phenotypes using image sensors. The National Institute of Agriculture Sciences in Korea has constructed an in-door plant phenotyping system including conveyors and image sensor chambers in a smart greenhouse. As an application of this system, we conducted QTL analysis for seedling stage growth rate with a recombinant inbred population derived from a cross between Milyang23 and Gihobyco. We collected image and manual data for shoot length and leaf area etc. Correlation coefficients between image and manual data was very high (> 0.93) showing high accuracy of image data. Two major QTLs were found on rice chromosome 1 and 12, which could be helpful in breeding high seedling vigor and yield varieties. Also, we conducted experiments to establish methods for selecting drought-tolerant plants using image parameters with drought-tolerant rice phytochrome B mutants (osphyb). The values of image parameters from RGB camera such as plant area were increased in osphyb plants compared to wild type (WT) plants under drought condition. Near-infrared (NIR) intensities from NIR camera, leaf temperature from infrared (IR) camera, and fluorescence parameters such as Fv/Fm from fluorescence camera also showed significant differences between osphyb plants and WT plants. In addition, soybean seed trait analysis was performed with 400 cultivars from soybean core germplasm population using RGB camera images. Eight traits including area, width etc. were measured. Based on these seed phenotype data and soybean genome-wide SNP genotype data, GWAS was conducted revealing three significant loci on soybean chromosome 6, 14, and 15 for seed weight. The HTPS system set up in this study will be actively used in various studies on QTL mapping, GWAS, gene function and so on. We are conducting further studies to set up more HTPS methods applicable to wider range of crops and traits.

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Deep digital phenotyping of rosette-type plants and its application for dissecting plant-microbe interaction

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Technological advances over the past decade have expanded our ability to perform rapid, precise and non-destructive analysis of plants at the phenome level. Here, we present recent developments of our automated plant-imaging-analysis system that can be adapted to both high-throughput plant phenotyping hardware and hand-held devices, such as smartphone camera. A U-Net-based deep learning network was trained on the publicly available and our accumulated dataset of the rosette-type model plant, Arabidopsis thaliana, allowing precise segmentation and tracking of plant. The segmented images were used to assess various morphological parameters and greenness of the whole plant and/or individual leaf depending on the purpose of use. We successfully utilized the digital phenotyping system in the classification of different accessions of A. thaliana and the detection of diseased plants. In particular, leaf-tracking technique enabled a time-course analysis of diseased leaves with two different symptoms (necrosis and yellowing) and healthy leaves after bacterial infection. Digital phenotyping was also used to analyze images acquired from Arabidopsis seedling flood-inoculation assay for the study of plant-microbe interactions. We showed accurate quantification of changes in plant growth and color under varied infection conditions. This study provides insight for potential utilization of digital plant phenotyping not only in breeding but also plant protection against pathogens.

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Development of diagnosis model for the disease and infect symptoms of tomato using AI (Artificial Intelligent)

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In protected farming, diagnosis of plant diseases and symptoms of infection is an important issue. This research is aiming to develop a method for the detection of diseases/infestations using AI (Artificial Intelligent) technology. The collected damaged plants RGB photographs, which have disease and infection symptoms by insect, are sorted according to its labels by deep learning meta-architectures. We combined each of these meta-architectures and developed the model using artificial neural network learning such as convolutional neural network (CNN) method. We developed the web-based software to diagnose tomato disease by applying the developed model. As a result of the test for the tomato diseases (powdery mildew, gray mold, miner etc.) in the laboratory environment, it showed more than 90% accuracy. In order to apply to the actual greenhouse environment, the image information collected in various conditions such as the light effect, the size of the symptoms, and the color of the disease symptoms are required, and a more accurate diagnosis model should be developed by the additional learning through the collected data. In the future, we will carry out advanced research and provide unapplicable tomato disease diagnosis system to the greenhouse.

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OCS06-04

Phenotyping approaches to improve nitrogen use efficiency in wheat

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Improved nitrogen use efficiency (NUE) in crop plants has the potential to significantly reduce fertilizer application costs and increase crop yield. NUE is a complex, multi-component trait and screening for NUE in field trials poses the challenges of low heritability and high environmental interaction. High resolution image based phenotyping technologies allow for non-destructive measurement of plant growth and are a useful tool for determining nitrogen (N) responses. However, growth response by itself does not tell us anything about the dynamics of uptake, allocation and remobilisation. Here we present results from using a high throughput phenotyping platform to investigate the nitrogen response of wheat varieties combined with hyperspectral based non-destructive measurement of leaf N content to determine N dynamics. Treatments incorporated N additions during growth to reflect common farmer practice. High resolution biomass estimates based on image analysis easily determine differences in N response between high and low N treatments, including those with supplemented N. Hyperspectral based N measurements revealed that leaf N showed a general pattern of increase then decrease during the life of a leaf but overall levels differed between treatments and varieties. The N addition treatments showed dramatic increases in leaf N in a short time frame. Being able to measure the dynamics of plant responses to N over time, combined with imaged based growth analysis may greatly enhance our chances to develop high NUE cereals. The results are promising and the next step is the take these technologies to the field.

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OCS06-05

Enhanced efficiency and precision in potato breeding

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Disease resistance, improved yield and quality are important objectives of global potato breeding programmes. Selecting parental plants with the desired characteristics, crossing them and then identifying offspring that combine beneficial attributes from both parents are key steps to achieve these objectives. New specialised technologies and techniques may help to improve the selection efficiencies and precision of these steps; these have been investigated and implemented within the PFR potato breeding programme. The technologies we have investigated are: 1: Pollen preservation, to improve inter-clonal nicking and crossing efficiency; 2: Marker-assisted selection, with allelic dosage data to optimise parental and progeny selection; 3: Imaging technologies for phenotyping: Disease screening in plant breeders’ field trials is often characterised by repeated observations of symptoms over time. A common (univariate) approach is to summarise the repeated disease scores by a single value (e.g. the sum) for each variety/plot and analyse the summarised data. This does not take account of variance heterogeneity or correlated information that may be present in longitudinal data. However, repeated measures data (potentially collected routinely with imaging technology) could be modelled using smoothing splines and the area under the disease progress curve for genetic evaluation of quantitative resistance, as demonstrated for potato late blight (\textit{Phytophthora infestans}). Furthermore, to identify high-yielding, early-maturing potato varieties (rapid early growth and maturation, then senescence), we used a reflectance measurement approach to model canopy growth development, followed by determination of how the area under the growth curve relates to total plot yield. This approach provides a more objective measure for maturity date and canopy duration than subjective scoring methods. An overview of these approaches will be summarised in this presentation.

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**OCS06-06**

### Analysis pipeline for high throughput phenotyping (HTP) data

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High throughput phenotyping (HTP) sensor data (images) provide enrich information of plant physical description at any time point. Since there are many challenges utilized sensor data to biological meaningful data, we came up with three parts (prepare, data analysis, and data interpretation & visualization) analysis pipeline for HTP data. First, data preparation (feature extraction) with deep learning algorithms. Second, phenotyping data merged with genomics data and the data analysis with machine learning algorithms. Third, data interpretation from previous step and visualized outputs. In this study, we applied geometry morphometrics (GM) as phenotypic markers (features) to characterized different population structures. In result showed that effectiveness overall pipeline and GM markers to study population in the post-genomics era.

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**OCS07-01**

### Importance of functional compounds and identification of respective genetic factors in Chinese Cabbage

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The functional genomics and molecular breeding researches have been rapidly expanded to understand metabolic pathways and related gene functions on important functional compounds in Chinese cabbage (*B. rapa*). We analyzed and identified the accessions which are enriched with health promoting functional compounds such as glucosinolates, anthocyanins, vitamins, β-carotene, total sugars, lutein, flavonol, Fe, Ca, etc. Further, we have generated double haploid (DH) lines through microspore culture to investigate various aspects of nutriogenetics and nutrimics of these inbred lines. For glucosinolates, we have performed a conventional QTL analysis using F2/3 mapping population of *B. rapa* combined with genome-wide association approach by using natural population to identify the genomic region and genes regulating glucosinolate biosynthesis in *B. rapa* crops. Similarly anthocyanin, the predominant flavonoids in red/purple crops, were tested for its inhibitory effects in cultured endothelial cells and hyperlipidemic apolipoprotein E-deficient mice using anthocyanin-rich extract from red Chinese cabbage and found to reduce the risk of vascular inflammatory diseases. Furthermore, we generated biparental mapping population from red and green Chinese cabbage and QTL mapping coupled with genotyping by sequencing (GBS) approach was used to identify genomic loci associated for anthocyanin biosynthesis. The transcriptome sequencing of both parents along with QTL mapping revealed 703 differentially expressed genes regulating anthocyanin biosynthesis. Among these, 211 positively associated genes are identified in leaf tissues of red Chinese cabbage samples. Our overall results will be additive resource for future studies on nutritional breeding of enriched varieties of *B. rapa* and their subspecies for human health.

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Bioactive Phytophenols and Vegetable Breeding

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Phytophenols, also known as phenolic phytochemicals, are plant secondary metabolites and a broad spectrum of chemical compounds with a hydroxyl (—OH) group attached to an aromatic ring. Phytophenols are not yet established as essential nutrients and can be categorized into different subgroups, such as phenolic acids, flavonoids, tannins, lignans, and stilbenes. Over 10,000 of phytophenols have been identified in plants. Although phytophenol influences color, taste, and texture in vegetables and their processed products, it acts as physiologically active substance. Researchers have paid much attention to phytophenols due to their beneficial health effects such as antioxidative, anti-cancerous, anti-inflammatory, and neuroprotective effects. Epidemiological studies suggest that dietary intake of plant-based foods rich in phytophenols is associated with lower risk of neurodegenerative and cardiovascular diseases. Overwhelming free radicals and reactive oxygen species (ROS) can result in oxidative stress to proteins, lipids, RNA, and DNA in cells, causing cell damage, diseases, and aging. Due to the phenolic structure in phytophenols, they act as effective antioxidants. Exogenous antioxidants from plants such as vegetables may neutralize excessive free radicals and ROS. Vegetables rich in a wide range of 2 phytophenols can supply considerable amounts of antioxidants in our daily diets. There has been a demand for phytophenol-rich vegetables. Development of new cultivars of vegetables with elevated levels of phytophenols is one of the major reasons for breeding. Consumption of vegetables newly bred for high phytophenol concentrations can provide more antioxidants in the diet. Therefore, breeding of new vegetable cultivars with increased amounts of bioactive phytophenols will serve as a good strategy to efficiently provide a good source of antioxidants to consumers.

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Breeding of new green pepper including α-glucosidase inhibitors

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Pepper (Capsicum annuum L.) is a very economically important vegetable. Nowadays, the fourth industrial revolution has improved the quality of life, people have begun to be interested in health as well as functional foods. This study, was focused on development new green chili including functional components. It had been collected pepper genetic resources from Korea and overseas and carried out characterization of them since 2008. Finally, it had been selected and cultivated several males and females strains till 2013. The breeding lines were set up the combination plan in the first half of 2013. Those were completed the combination test and selection in the second half of 2013. In 2014, it was conducted a regional adaptability test through the farmer-house test. It was registered production and sales to the Mi-in green pepper in the second half of 2015. Pepper contains many nutrients such as vitamins A, B, C, flavonoids and antioxidants. Especially, AGI (Alpha glucosidase inhibitor) in pepper is known to have higher content of leaf than fruit. But most of consumers are hard to use the these leaves. For this study, it was progressed AGI component analysis with cooperation of Department of Bioindustry and Bioresource Engineering in Sejong University. For functional component comparing, 14 green peppers including Mi-in green pepper were analyzed for AGI content in this study. It was used distilled water and 70% Ethanol for extraction of AGI, and analyzed for HPLC analysis to confirm before AGI extraction. In the result, it was demonstrated Mi-in green pepper contains the highest content of AGI out of 14 varieties. Further, it will have to conduct more studies like clinical trials and demonstrate superiority as the health functional food. This study was supported and carried out by GSP.

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**OCS07-04**

**Understanding glucosinolate-myrosinase system to improve quality of Brassica vegetables**

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Glucosinolates are sulfur and nitrogen-containing plant secondary compounds that originally made by plants for their defense to insect herbivores. These glucosinolates are hydrolyzed by endogenous myrosinase and produce various hydrolysis compounds based on the reaction conditions. Other reaction conditions including Mg ions, co-factor enzymes, and pH also regulate this glucosinolate and myrosinase enzyme reaction. Different hydrolysis compounds from the same glucosinolate have different bioactivity. Isothiocyanates have anti-insect activity although nitriles form of hydrolysis compounds has ovipositional activity. Interestingly, these insects or pathogens defense compounds also have health-promoting activities. Sulforaphane is a well-known anti-cancer compound in broccoli floret. However, a certain portion of glucosinolate is converted to sulforaphane due to epithiospecifier protein (ESP). The ESP activity is crucial when it comes to health-promoting activity of broccoli or other Brassica vegetable. ESP is one of myrosinase co-factors that inhibits formation of isothiocyanate, resulting in nitrile formation. When glucosinolin converts to sulforaphane nitrile, the quione reductase, anti-cancer biomarker, activity is 100 times lower than sulforaphane. Thus, ESP enzyme activity is a vital component for health promoting activity. Many people know broccoli is good for human health. However, not many breeders spend effort and time to manipulate ESP activity. Another example of importance of ESP is the flavor of mustard or wasabi. The active compound of wasabi for flavor is allyl isothiocyanate from sinigrin. When ESP converts sinigrin to nitrile form of hydrolysis, the flavor intensity is significantly weaker than allyl isothiocyanate. Other importance of the glucosinolate-myrosinase system including response to insect damage and sensorial quality will be discussed during this seminar.

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**OCS07-05**

**Integrative transcriptomic and functional analyses to unveil distinct genetic influences on fruit quality in pepper**

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Pepper and tomato provide suitable model for comparative analysis of fruit quality. We present distinct molecular patterns of ripening and metabolisms between pepper and tomato by transcriptomic analysis. Our analyses unveil potential mechanisms of fruit quality due to defect of regulators and ethylene synthesis. In order to pursue functional analysis of fruit quality regulators, virus induced gene silencing (VIGS) in pepper fruits are newly developed. VIGS with tandem constructs harboring An2 as a visible reporter in anthocyanin-rich pepper plants canfacilitate the application of functional genomics in the study of metabolic pathways and fruit biology. Among the fruit quality regulators, Golden-like 2 transcription factor (GLK2) is shown to distinct expression pattern rationalizing differential ripening pattern. Allelic variations within GLK2 show large natural variation in chlorophyll content and immature fruit color. The gene silencing of GLK2 caused light green immature and peach ripe fruits due to ~10-fold reduction of chlorophyll and carotenoid levels. The expression level of the chlorophyll and carotenoid biosynthetic genes in GLK2-silenced fruits was much lower than that of control. The integrated analysis allows us to better understand genetic factors of fruit quality in pepper.

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Investigation of genetic differences related to fruit quality degradation after harvest in different strawberry cultivars using transcriptome analysis

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Strawberry (Fragaria × ananassa Duch.) is one of the economically important horticultural crops, but has a short postharvest life due to quick softening, rapid metabolism, and decay. To analyze the genetic components related to the postharvest senescence of strawberry fruit, we performed transcriptome analysis using five Korean strawberry cultivars (Seolhyang, Danhyang, Kingsberry, Sunnyberry, and Mudhyang). Fruit was harvested according to the size and coloration (small-green, medium-green, and large-red). Large-red fruit for each cultivar was stored at 10°C for 10 d to evaluate postharvest storability. Both firmness and decay rate were used as postharvest storability factors in our study. The fruit firmness was the highest in Sunnyberry (11 N) during storage period, while Kingsberry was the lowest (7 N). Also, the decay rate of Kingsberry was the highest (33%) and 6.6 times higher than Sunnyberry (5%). These results showed that among the five cultivars, the postharvest storability of Sunnyberry and Kingsberry was the best and worst, respectively. Thus, we used the two cultivars for transcriptome analysis. Because changes in mRNA levels during fruit maturation and ripening could affect the postharvest senescence of strawberry fruit, fruit in the green and red stages for each cultivar was used for transcriptome analysis. In Kingsberry, expression of cell wall degrading genes was higher than that of Sunnyberry during ripening. The metabolism of carbohydrates and organic acids was not clearly different between the two cultivars, but lipid metabolism related genes were differentially expressed. Fatty acid synthesis related genes was more upregulated in Sunnyberry compared to Kingsberry. In addition, diverse transcription factors belonging to WRKY, NAC, and AP2/EREBP family were differentially expressed during ripening between the two cultivars. Therefore, our results suggest that postharvest senescence is not only affected from different ripening patterns, such as cell wall degradation and fatty acid biosynthesis, but also genetically regulated by various transcription factors.

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Observation of phenotypic performance, molecular analysis and genetic variability on high yield Ciharang CSSL in the field

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Ciherang is the most famous rice variety in Indonesia. More than 60% of the total rice-planting area in Indonesia is planted with Ciherang. The advantages of Ciherang are high number of productive tillers that reach 15.5, faster harvest time, also sufficient resistance to pests and diseases. Therefore, Ciherang is considered as a good candidate to contribute to food security in Indonesia by means of increasing its productivity. Improvement of Ciherang productivity might be done by crossing with an Indonesian new plant type rice line, B11143D to form the population of Chromosome Segment Substitution Lines (CSSL). B11143D line has the advantages of fewer unproductive tiller and higher grain number per panicle. This research was aimed to obtain CSSL that have a higher yield potential compared to Ciherang, as well as to conduct molecular and genetic variability analysis in the CSSL. The results showed that there were CSSL with longer panicle and higher filled grain number compared to Ciherang and Inpari31, namely no 1, 3 and 19. Molecular analysis using the SSR markers resulted in graphical genotypes for CSSL and in general the chromosomal segments outside of the target chromosome are back to the recurrent parents, Ciherang. The uniformity value for yield potential characters has a range of 30 - 64%. This indicates that the selection of CSSL strains needs to be continued in the next planting season. The panicle length, the number of filled grain, and the weight of 100 grains had the high heritability value with the range of 69.16 - 90.12%, while the number of panicle and grain weight per panicle had a low heritability value. This indicates that the panicle length, the number of filled grain, and the weight of 100 grains are determined by the work of additive genes and can be used as selection criteria in this study.

Keywords: Ciherang, high yield, Chromosome Segment Substitution Lines

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Making rice healthier through genomics-assisted breeding

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Worldwide more than two billion people, particularly children and women suffer from Iron, Zinc and Vitamin A deficiency related diseases. Micronutrient deficiencies or hidden hunger is highly prevalent in South and South East Asia, where rice is the major staple food and supplies 50 to 80% of the daily caloric intake, but polished rice is low in essential micronutrients (Fe, 2-3 ppm; Zn, 12-14 ppm; β-Carotene, 0 ppm). Zinc deficiency causes stunting, diarrhea, impaired immune function and infertility, iron deficiency causes anemia and poor cognitive development; while, vitamin A deficiency causes blindness and reduced immunity, resulting in serious global health problems. Biofortification of rice with micronutrients has been suggested to be one of the most sustainable, targeted, food-based and cost effective approaches to combat micronutrient malnutrition. Rice genetic resources especially *A. sativa* accessions have huge genetic variation for grain zinc which can be efficiently used in breeding programs to develop high zinc rice varieties; similarly genetically modified high iron rice and golden rice can supply iron and provitamin A respectively. Development of healthier rice varieties with micronutrients and vitamin A will contribute significantly to improve the health of human populations and resulting in inclusive growth. We are implementing genomics assisted breeding programs to develop healthier rice varieties at International Rice Research Institute. Recent progress in development of healthier rice varieties will be discussed in the presentation.

Keywords: Rice, genomics, nutrition, Fe, Zn, Vitamin A

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Discovery the different gene expression and whole genome DNA variation in dwarf soybean derived from crossing of cultivar and wild type in soybean

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The understanding regulation of plant growth type is an important element to breeding for high yield product. We discovered 6 dwarf mutant soybeans in the populations derived from crossing of G. max and G. soja. Also, we found a hetero recessive mutant from soybean crossing. We tried to find differently expressed genes to classify and understand the regulation of genes related to plant growth in a mutant, dwarf soybean which are happened in F5 derived from crossing of G. max var. Peking and G. soja var. IT182936. We found that the expressed genes relationship are complexed to the plant growth. There are highly significantly up- or down-regulated genes in the comparing of gene expression in normal and dwarf soybeans. There are classified that the genes related to disease and stress responsive showed with the up-regulation in dwarf soybean. Such over-expression of disease resistance and other immune responsive genes could be targeted to understand the gene regulation in dwarf soybean. Such over-expression of disease resistance and other immune responsive genes could be targeted to understand the gene regulation in dwarf soybean. Otherwise, photosynthesis related genes are very low expression in dwarf lines. We also compared the whole genome DNA sequence between 2 dwarf and 2 normal growth soybean derived from F6 of the crossing population. The each 2 dwarf lines were derived from each normal growth soybean plant in each F6 recombinant inbred lines (RILs). We identified a total of 458,209 and 337,001 SNPs in each dwarf and normal sets. We discovered a total of 33 homogenous non-synonymous SNPs that are happen at the same loci in each 2 sets of dwarf and normal soybean derived from normal growth soybean. Our results provide important information for improving our understanding of the genetics of soybean plant height and crop breeding. These could be useful genetic resource for plant breeders, geneticists and biologists.

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Development and Use of Molecular Marker Plant Variety Identification

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The lettuce (*Lactuca sativa* L.) is annual salad plant in the *Asteraceae* family. In particular, lettuce is the most commonly cultivated leaf vegetables, and it is one of the most popular vegetables in the world. Genome-wide association mapping offers higher resolution for locating quantitative trait loci (QTLs) than QTL mapping in biparental populations. The lettuce varieties can be classified into many types such as a leaf shape, size, rosette and head. Recently, it has been classified as crisp head, butter head, cos or romaine, leaf, stern, latin and oil-seed lettuce. Here, we performed an association mapping study for 7 agronomic traits (Leaf: anthocyanin coloration, Leaf blade: lobed, Leaf blade: vein, Leaf: leaf attitude, Leaf: blistering, Leaf: blistering size, Leaf blade: shape in longitudinal section) using a panel of 96 varieties. The panel was genotyped at an average density of one marker per 156.6 kb using genotyping by sequencing technology. A total of 276,462 raw SNPs were discovered, which after stringent filtering revealed 17,877 high quality SNPs of which 6.4% were present in genic regions. These filtered 17,877 SNPs were used to perform an association analysis for 8 agronomic traits using a mixed linear model as implemented in the TASSEL software. A total of twenty three QTLs were detected on chromosome 1, 3, 4, 5, 7, 8 and 9 and the phenotypic variance explained by each QTL ranged from 26.7 to 61.8%. These markers will be useful in marker-assisted selection after further validation with assessment whether these markers are relevant in other backgrounds and segregating populations.

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Assessment of genetic differentiation and linkage disequilibrium of tomato germplasm using RADseq-derived SNP markers

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To mine new favorable alleles for tomato breeding, we investigated the feasibility of utilizing *Solanum pimpinellifolium* as a diverse panel of genome-wide association study through the restriction site-associated DNA sequencing technique. Previous attempts to conduct genome-wide association studies using *S. pimpinellifolium* were impeded by an inability to correct for population stratification and by lack of high-density markers to address the issue of rapid linkage disequilibrium decay. In the current study, a set of 24,330 SNPs was identified using 99 *S. pimpinellifolium* accessions from the Tomato Genetic Resource Center. Approximately 84% of *PstI* site-associated DNA sequencing regions were located in the euchromatic regions, resulting in the tagging of most SNPs on or near genes. Our genotypic data suggested that *S. pimpinellifolium* were divided into three single-ancestry subpopulations and four mixed-ancestry subpopulations. Additionally, our SNP genotypic data consistently confirmed the genetic differentiation, achieving a relatively reliable correction of population stratification. Previous studies utilized the 8K tomato SNP array, SoliCAP, to investigate the genetic variation of *S. pimpinellifolium* and we performed a meta-analysis of these genotypes. The result suggested SoliCAP array was less appropriate to profile the genetic differentiation of *S. pimpinellifolium* when more accessions were involved because the samples belonging to the same accession demonstrated different genome patterns. Moreover, as expected, rapid linkage disequilibrium decay was observed in *S. pimpinellifolium*, especially in euchromatic regions. Approximately two-thirds of the flanking SNP markers did not display linkage disequilibrium based on \( r^2 = 0.1 \). However, the 18-Kb linkage disequilibrium decay indeed reveals the potential of single-gene resolution in GWAS when markers are saturated.

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High-throughput screening of 2300 genetic markers in *S. lycopersicum* using the NEBNext Direct multiplexed genotyping approach

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Targeted DNA sequencing is rapidly being adopted for the molecular screening of markers during selective crop breeding. For these applications, the need for cost-effective and high-throughput technologies to process large numbers of samples is imperative. Here we describe a novel capture-by-hybridization method for targeted genotyping of crops. This simple workflow allows processing of up to 9216 samples in a single 96-well plate within 7 hours and is easily automated. The NEBNext Direct multiplexed genotyping approach can target 100 to 5000 markers from up to 96 samples within a single hybridization. Here we developed a panel targeting 2300 SNPs in the tomato crop, *S. lycopersicum*. Baits were placed within 75 nucleotides of the targeted SNPs, allowing for an efficient sequencing run of 75 bases of target sequencing, 8 bases of sample barcode, 8 bases of hybridization barcode, and 12 bases of a unique molecular identifier for filtering PCR duplicates. After an initial screening of the panel, the bait concentrations were adjusted by performance to ensure uniform coverage of the targets. The optimized panel resulted in greater than 90% of the sequencing reads mapping to targeted regions and highly uniform coverage, with a minimum SNP coverage of at least 20 unique reads. As a result, this approach reduced the cost and increased the throughput of crop sequencing while generating robust data to reliably genotype multiple varieties of *S. lycopersicum*.

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Novel candidate gene mapping related to insecticide response in soybean

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Insect damage is one of themajor limiting factors for soybean (*Glycinemax* (L.) Merr.) productionas insects vector viruses and cause damage by feeding on foliage, vascular sap, stems, roots, pods, and seeds (Steffey, 2015). Tornamag yield losses, application of insecticides or genetic resistance has often beenthe tools in management. For example, insecticide usage increased in response to soybean aphid dissemination in the north central region of the USA (Coupe and Capel, 2015), where 80% of soybean production occurs. Bean bugs, *Riptortusclavatus* (Hemiptera: Alydidae), are key to control yield loss in soybean of South Korea. Etofenprox insecticides, derivative of pyrethroid, are frequently applied to managebean bugs. We found interesting response to insecticide of etofenprox in soybean breeding field trial. Only two varieties, which have common ancestor, show a plant damage response to insecticides. For genetic studies, two recombinant inbred lines (RILs) were used. To construct genetic map, Illumina GoldenGate SoyOPA-4 6K Assay and Axiom® 180K SoySNP Assay were used for genotyping. After construction of 1.3 Mbp genetic map, we identified a 548 Kbp candidate region with fine mapping. Candidate region was narrowed down to 148 Kbp with association analysis between markers and phenotype of RILs. Novel 16 candidate genes were investigated in this region with SoybaseWm82.a4.v1 genome browser.

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Mapping of QTLs controlling seed weight using SNP markers in mungbean (*Vignaradiata (L.) Wilczek*)

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Mungbean (*Vignaradiata (L.) Wilczek*) is an important legume crop as it provides protein and other micronutrients. Despite seed weight being one of the most important yield determining traits, seed weight remains to be yield limiting factor. To date, there has been no study using high resolution SNP based genetic map for quantitative trait locus (QTL) analysis in mungbean. In this study, we used 187 F11 recombinant inbred lines (RIL) population derived from cross between VC1973A and V2984 to identify QTLs controlling seed weight. We carried out QTL analysis using four sets of hundred seed weight data measured in 2013, 2014, 2016 and 2018. Out of total 19 QTLs, we identified six recurring QTLs between same marker intervals over the repeats and fiveyear specific QTLs. We carried out synten analysis of the recurring mungbean QTLs against the soybean genome. We were able to support locus with at least two soybean QTLs. Afterward, we checked the genes within the QTL region contained Arabidopsis orthologue known to control the seed weight. We were able to identify three potential candidate genes Vradi07g10680 (AP2 homologue), Vradi07g11480 (ANT homologue), and Vradi05g20690 (AHP4 homologue). Fine mapping approach or construction of new ultra-high density genetic map is required to determine precise candidate genes. Nonetheless, this is the first time SNP based genetic map has been used to identify QTLs controlling seed weight. In future, these loci can assist in breeding mungbean genotype with appropriate seed weight.

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Genomics-Enabled Breeding Approaches in Vegetable

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The technical advances in genome sequencing and genomics have a great impact on plant breeding and provide high potential for accelerated breeding with high accuracy and efficiency. The utilization of molecular markers is still one of the efficient tools for integrated breeding, but the methods for developing trait markers has changed drastically. Several methods based on sequencing of small fragments have emerged with great potential for marker discovery and exploring genetic diversity in plant genomes. Genotyping by sequencing (GBS) is one of these methods which can be used for marker discovery and rapid, high-throughput genotyping in a cost effective manner. Sequencing methods such as GBS enable the development of thousands of markers in a very short time. We used GBS for SNP calling, gene discovery and genetic diversity analysis in 96 accessions of tomato and lettuce each. In tomato 99% of the GBS reads could be mapped in the reference genome. Furthermore, we could call around 300K high quality SNPs. Further In most of the major resistance genes, such as TYLCV, Bacterial wilt, Fusarium and late blight, haplotypes have been identified which can be used as molecular markers for marker assisted selection. Approximately 25% of SNPs are located in more than 14,000 genes of tomato. In lettuce around 4,500 SNPs used to study the genetic relationship of 96 mostly commercial lettuce varieties. The varieties could be clustered in 5 groups with relatively narrow genetic variation. Conventional breeding induces mutations randomly throughout the genome. In recent years inducing Targeted mutations has become a powerful tool for generating new variations and new traits in a timely and cost effective manner. New traits which do not exist in the wild types can be generated by genome editing. Through genome editing DNA can be modified precisely. We used Crispr/cas 9 to generate Doubled Haploid (DH) inducer lines in tomato and Watermelon. There is high similarity between the CenH3 gene in tomato and watermelon. We used the sequence information of tomato to identify the CenH3 gene in watermelon. The goal of our project was to determine whether inducing point mutations in the CenH3 gene of watermelon and tomato leads to disrupting the function of CenH3 and whether the mutated lines can serve as inducers for double haploid lines.

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Application of genome information for vegetable breeding in Takii Seed Company

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Takii Seed Company was founded in 1835 in Japan; it is one of the oldest vegetable and flower breeding companies in the world. At present, we mainly breed F1 hybrid varieties of various vegetables and flowers using conventional breeding technologies. In the current plant breeding activities, DNA markers, which are linked with some desired traits such as disease resistance, are crucial for efficient breeding processes. Recent progress in Next Generation Sequencing (NGS) and other concomitant technologies could provide us with a great amount of genome sequence information to facilitate the generation of abundant DNA markers. Abundant DNA markers also accelerate the rate of identification of the positions and/or sequences of the genes that regulate the traits. In addition, NGS technologies facilitate efficient screening of mutants and germplasm collections for allelic variants in the target genes.

To facilitate the application of genomic information in breeding activities, we have collaborated with KeyGene, a biotechnology company in the Netherlands, since 2005. As a result of the collaboration, the number of DNA markers that are used for selecting desired traits has considerably increased over the last decade. Currently, in the case of tomato, approximately 50 loci can be selected with DNA markers in our company. The most common method of DNA marker selection is using only one DNA marker that is linked to a trait. However, Marker Assisted Back-Cross, in which a large number of DNA markers that are distributed in the entire chromosomes are used, has also been attempted in several crops, with the aim of shortening the backcross breeding cycle. We have also screened mutations in specific genes using NGS from mutant populations of tomato and pepper, and could obtain mutants that exhibited the expected phenotypes. In this session, our activities mentioned above will be presented in detail.

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베타카로틴 고함량 가을배추 품종개발
Development of Kimchi cabbage varieties with high Beta-carotene content

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건강에 대한 관심 증가로 세계 가정용 농식품 시장과 국내 건강기능식품 시장의 연평균 성장률이 각각 7.9%, 8.4%로 추정하고 있으며 기능성 채소에 대한 관심 또한 높아지고 있다. 국내외 다수업체에서 고기능성 향량에 초점을 맞추어 기능성 농산물 및 개발에 노력을 하고 있다. 봄물(주)에서도 황설화 작물 및 노화방지에 효능이 있는 베타카로틴 고함량 배추 품종인 ‘베타후레쉬’와 ‘CCAB682’를 출시하였다. 베타카로틴 함량이 높은 가을배추로 내외부 특성이 일반배추와 확연히 구별성이 있는 고당도 품종이다. 인공배제를 활용하는 등 차별화 마케팅 활동을 통해 ‘베타후레쉬’배추의 브랜드가 확립되었고 배추 소비확대에도 기여하고 있다. 베타카로틴 고함량 배추의 효율적 육성을 위해 Co-dominant 마커를 개발하였고, 이를 통해 계통 육성을 진행하고 있다. 우량계통의 신속 정확한 선발 및 베타카로틴 고함량 배추 품종의 전적형화로 연중재배와 소비를 촉진시키고자 한다.

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Introduction - NongwooBio

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NongwooBio is the leading vegetable seed company in Korea. NongwooBio was founded in 1967. In 1997, Korea’s major vegetable seed companies - Hungnong, Chungang and Seoul seed were into bankrupt due to the global economic crisis. NongwooBio was survived under serious business environment and take the leader position in 2000’s. The active investment on R&D and global expansion was the strong back up the company to overcome the economic crisis.

Today, NongwooBio has 6 subsidiaries in different countries which has sales, R&D and production. NongwooBio plan to expend it’s global business network to Europe, Russian and South America step by step. We believe that we can grow to be one of top 10 global vegetable seed company with such a assertive investment.

NongwooBio have never forget our mission “Contribution to the growth of farmer’s income with excellent variety”.

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Stability of Yield and Yield Components of Chili Pepper in East and Southeast Asia

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Multilocation trials are important for breeding programs to identify high- yielding, adapted lines for a wide range of environments. In this study, we evaluated yield and yield components (fruit weight, fruit length, and fruit width) as well as days to 50% anthesis and fruit maturity of the 10 chili pepper lines in the International Chili Pepper Nursery 15 (ICPN15). Performance data of the ICPN15 entries were collected in seven different environments in five countries (Indonesia, South Korea, Thailand, Taiwan, and Vietnam). Significant genotype-by-environment (G x E) interactions were detected for all traits evaluated. Additive main effect and multiplicative interaction analyses indicated high environmental influence on yield, days to 50% anthesis, and maturity, whereas genotype was the greatest contributor to variability in the market-driven yield components of fruit length, width, and weight. Four lines (ICPN15-4, -5, -7, and -10) were identified as highly stable and could serve as sources of yield and yield component stability in either short fruit market segments (ICPN15-4) or long fruit market segments (ICPN15-5, -7, and -10). We used publicly available weather data to help in explaining the source of the environmental variability; however, differences between analyzed and observed weather were too pronounced to be useful. This is evidence that weather data should be collected at each testing environment. This study provides a basis for future studies in the stability of important horticultural traits in pepper and highlights the need for further work in this area.

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Genomics in RDA genebank: its use and perspective for germplasm management


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National Agrobiodiversity Center (NAC, RDA Genebank) has been conserving about 226,000 plant genetic resources from 1,593 species of diverse crops. They are conserved in the form of seeds in genebank as potential reservoir representing various combinations of genes and alleles for future use. Recent genomics researches allow genebank to develop markers for diversity analysis, evaluation of characters and detection of genes of interest. RDA genebank has developed and applied SSR markers for the analysis of population structure and genetic diversity in various crops, and these results helped to establish strategies for the introduction and collection of new resources. More recently, we have performed the chloroplast genome sequencing for Capsicum species and some grain crops, which led to detect cpSSR and SNP markers. These markers are used for analyzing genetic diversity and discriminating species. In the analysis of sweet potato germplasm collected from worldwide, cpSSR markers were also found to be useful for diversity analysis of clonal plants with maternal inheritance. In addition to diversity analysis, accurate identification of species plays an important role in terms of germplasm management and expansion of diversity. For discriminating the difference between species, chloroplast barcode genes were applied to wheat and legume and combination of them increased the discrimination power. Genotyping-by-sequencing (GBS) data for melon germplasm produced SNP markers for discrimination of melon and Korea melon; they have same scientific names but different characters of fruit. Association study between genotype from GBS and phenotype from germplasm helped us to identify the significant markers. Candidate markers detected from GBS in various crops will be applied to germplasm management including diversity analysis, species identification and evaluation. In the near future, there will be an era in which these markers are integrated and easily analyzed on the chip.

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Use of germplasm resources for Hydrangea breeding

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The popularity of hydrangea is steadily growing in Korea, including deciduous or evergreen shrubs, and small trees or climbers. It attracts attention as a garden plant as well as cut flowers. Their popularity as a garden plant has risen radically because gardeners recognized their positive attributes, especially the long period of blooming combined with ease of maintenance. Six kind of hydrangeas are being under study. H. macrophylla is commonly known as cut flowers. H. paniculata popular in today’s landscape bloom in middle to late summer. They have colder hardy. H. quercifolia giving the cinnamon- colored peeling bark in the winter provides soft powdery leaves in the spring, large creamy white flowers in the summer and vivid burgundy leaves in the fall of the year. H. arborescens grow on slopes and in ravines. It is hardy species that will survive the snowy winters and the hot summers. H. anomala climbs up a tree or the side of a building. H. serrata are found on the Je-ju island of Korean. They are colder hardy than H. macrophylla. We are studying hydrangea breeding for cold hardy garden hydrangea. Previously, we performed interspecific hybridization using H. macrophylla, H. paniculata, H. arborescens and H. serrata. As a result, various interspecific hydrangea seeds were obtained. At present, two more distant species were being under study in order to create unique breeding lines using H. quercifolia and H. anomala. Thereby, the study of the impact of genetic distance is being underway by using interspecific hybridization, seed formation and seed germination. Self-pollination and genetically remote-related cross pollination resulted low rate of seed formation and germination. Various crosses within H. macrophylla species showed wide range of seed formation rate. It warranted further genetic study regarding the genetics of seed formation and germination.

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Evaluation of agronomic traits and genetic diversity of black soybean with green cotyledon germplasms

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Soybean (Glycine max [L.] Merr) is not only economically one of important crops in the world, but is also widely used for human consumption in East Asia. Black soybean with green cotyledon, especially has been used as medicinal material and food like soybean cooked with rice in Korea since ancient times. The characteristic of a green cotyledon trait in plant is associated with STAY-GREEN genes. Soybean cotyledon color has been identified to be controlled from nuclear genes (D1 and D2) and a cytoplasmic gene (cytG). Since Korea is one of central regions of genetic diversity for soybean, genetic diversity of black soybean with green cotyledon has been distributed in Korea. Evaluation of collected genetic resources of black soybean with green cotyledon play an important role in food-grade breeding program in Korea. The objective of this study was to assess genetic diversity of 467 black soybean with green cotyledon accessions by using a 6K SNP array. In addition, Black soybean with green cotyledon accessions were to evaluate the agronomic and biochemical traits. The results showed the phenotypic variation of agronomic traits such as stem length, flower color, 100-seed weight, number of branches, flowering and maturity date among the 467 accessions. Although they are black soybean, the anthocyanin content ranged from 3.5mg/g to 167.6mg/g. Through the measurement of chlorophyll content and genotyping with D1, D2 and cytG, another research supported the results accessions with cytG had significantly lower amount of total chlorophyll content than one with mutant alleles of D1 and D2. This significance was due to the accumulation of chlorophyll b content. By using 6K genotype data and phenotypic data, core subset with sixty-nine accessions were established from 467 accessions by PowerCore software. Core subset of black soybean with green cotyledon accessions can be utilized as genetic resources in breeding program.

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SSR–Genetic Distance and Combining Ability of Sweet and Waxy Corn Lines

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Limited labor, cost, and time regarding hybrid formation and expanded yield trials encourages breeders to identify potential F1 hybrids without crossing all possible combinations by line screening based SSR-genetic distance. Therefore, this study aimed to (i) determine combining ability of 24 hybrids, (ii) assess the genetic distance of 11 parental lines employing SSR markers, and (iii) study the association between SSR-based genetic distance and hybrid performance for yields characters. 11 parental lines, 3 waxy and 8 sweet corns, originated from diverse climatic zones (tropical Thailand, subtropical China, and temperate USA) were crossed following North Carolina Design II and were genotyped applying 30 polymorphic SSR markers. 24 hybrids, 11 parents, and 3 check varieties were evaluated in two seasons (2017/2018) at Khon Kaen University, Thailand. Among eleven lines, 101LBW (6.8 ton ha⁻¹; 1.10**) and Y.18 (6.9 ton ha⁻¹; 1.08**) were good combiners focusing on high-yielding performance. Minor contribution of SCA effects on yields revealed an essential role of parental adaptation. SSR-based genetic distance between sweet and waxy lines was wide enough ranging from 0.67 to 0.92. Contrasting dendrogram pattern and insignificantly poor correlation between SSR and phenotypic based-genetic distances indicated that agreement between SSR and phenotypic markers was lacking. SSR-based genetic distance failed to predict hybrid performance, heterosis, and SCA as poor correlation was revealed. Absence of dominance effect and high genetic distance among parental lines were suspected being plausible factors for poor prediction.

Keywords: Biodiversity, dissimilarity matrix, microsatellite marker, parental selection, hybrid breeding

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OCS10-06

Phenotype analysis for ideotype breeding of sorghum in Indonesia

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Sorghum is an alternative source of carbohydrate due to its attractive nutrients content which is relevant to prevent non-infectious diseases. The study was aimed to develop an ideotype of sorghum to obtain high yielding lines by combining morphological, physiological, and biochemical traits into single genotypes. A total of 65 fix lines consisted of 51 F5 lines of sorghum derived from three populations of PI-10-90A × Nambu, PI-150-20A × Nambu, and PI-150-20A × Kawali with five check varieties and some others breeding lines were tested by Augmented experimental design. Traits observed were plant height, stem diameter, leaf related traits, days to flowering and harvesting, panicle height and diameter, and seed weight. Data analysis was done for variance analysis and correlation analysis. The analysis of variance revealed a significant difference between the lines tested. All characters observed were highly influenced by genetic factors with high broad sense heritability in the range of 51.5 (days to flowering) to 93.8 (plant height). Low heritability of 14.7 was observed for green leaf percentage. A morphological character such as stem diameter, flag leaf area, leaf greenness, and green leaf percentage was positively correlated with seed weight per plant. Panicle diameter and 100-grain weight were also indicated a positive correlation with seed weight. Among the traits contributed to seed weight, stem diameter, flag leaf area, leaf greenness, and panicle diameter can be combined into single genotype by independent culling selecting the genotype with phenotypic value of more or the same as 18 mm of stem diameter, 200 cm² of flag leaf area, 45 CCI of leaf greenness, and 50 mm of panicle diameter. The best ten lines selected from this ideotype breeding showed a higher yield of 70.5 g per panicle compared to the check varieties with a yield average of 48.2 g per panicle.

Keywords: attractive nutrients content, ideotype, sorghum

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Draft genome assembly of the wild nightshade species, *Solanum lycopersicoides* and its pre-breeding applications for tomato (*S. lycopersicum*) improvement

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*Solanum lycopersicoides* is a wild nightshade relative of tomato with known resistance to a wide range of pests and pathogens, as well as tolerance to cold, drought and salt stress. To efficiently utilize the potential of *S. lycopersicoides* as a genetic resource for cultivated tomato improvement, we sequenced its whole genome using the Illumina HiSeq 3000 platform and assembled a draft sequence based on a tomato reference genome using ABySS and PAGIT. Analysis of the 10X *S. lycopersicoides* draft genome was conducted using publicly available software including QUAST, AUGUSTUS, RepeatModeler, RepeatMasker, tRNAscan-SE and GMATA. The consensus sequence of *S. lycopersicoides* spanned 1.45 Gb, with an estimated 34.27% GC content and 39,918 genes distributed across thirteen pseudomolecules. Transposable elements in the form of LINES, SINES, LTRs and RCs comprised 19.85% of the whole genome. Based on microsatellite mining of the *S. lycopersicoides* sequence assembly and genomic alignment between *S. lycopersicoides* and tomato, SSR and indel-based markers were designed and used to map the genomic landscape of diploid introgression lines segregating from monosomic alien additional lines (MAALs) of *S. lycopersicoides* in the genetic background of cultivated tomato. Genotyping using 310 polymorphic markers that are distributed across the tomato genome identified a total of 32 unique alien introgressions spanning 3.22-27.16 Mb in chromosomes 1, 2, 4, 5, 6, 7, 8, 9, 10 and 12 of twenty-five diploid derivatives of the MAALs. A high degree of non-parental and/or heterozygous alien chromosome transmission was observed, with 60% of the diploid derivatives having the same non-parental introgression in chromosome 5. Phenotypic and agronomic evaluation of the lines associated the alien chromosome introgressions with putative QTLs controlling fruit and leaf shape and size, locule number and drought tolerance. Results of this study will leverage research on the use of *S. lycopersicoides* as a genetic resource for tomato improvement.

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Developing mungbeans for the sprout market segment

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Sprouts produced from mungbean (*Vigna radiata* (L.) R. Wilczek var. *radiata*) is popular in Southeast Asia. The demand for mungbean sprouts has been growing not only in Asia, but also in other parts of the world. The higher vitamin C content in mungbean sprouts compared to grains make it a healthier option. Due to the higher vitamin C content in sprouts, the bioavailability of important micronutrients like iron and zinc is enhanced. In countries like Vietnam, domestic production of sprouts is common, while mungbeans are exported to other countries including Europe for commercial sprout production from Myanmar. Consumer preference is for mungbean sprouts that are bright white and crisp, with short roots and small cotyledons, a shelf life of at least seven days and free of bacterial or chemical contaminants. The screening of the mungbean mini-core collection (296 accessions) developed at the World Vegetable Center revealed significant variation for key traits required by the sprout market segment. Uniformity of grain products would enable the farmers to get better value for money and also cater to high value markets such as the sprouting industry. One of the major constraints for improving pulses productivity is the non-availability of quality seed of improved varieties to farmers, at the right time. Varietal admixture leads to non-realization of the unique traits for which a particular variety has been developed and results in poor yield for farmers. This also leads to poor adoption of improved varieties. Improvements and innovations should be first targeted to the seed production sector and later on to the grain sector. We envisage that this would help the farmers involved in grain production to have access to quality seed of improved varieties, leading to higher adoption rates and thereby improve the pulses production and productivity and also have a uniform product.

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Potential Breeding Strategy for Interspecific Crosses of Oleifera x Guineensis as Enrichment Tool to Enhance Oil Palm Genetic Material

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The genetic resources are the basic materials required by plant breeders to improve the current and future planting material developed by the planters. Meanwhile, the breeding program of many perennial crops such as oil palm started with narrow genetic base, so it needs new efforts to improve existing oil palm resources through breeding strategies. *Elaeis oleifera* (Kunth, Cortés) is known as the American oil palm, native to and broadly developed naturally along the riverbanks in Central America and northern regions of South America, tolerating many kinds of environmental stresses, resulting a broader environmental adaptability compared to the African oil palm. While African oil palm (*Elaeis guineensis*, Jacq.) is by far the most productive oil crop and now become one of the world most widely consumed edible oils. The general objective of the research is to observe the performance of interspecific hybrid OxG from some Oleifera and Guineensis origins combination in two different locations, both in Ecuador and Indonesia. For initiating the activities, determine the precise and connected crossing designs of OxG was the first step, continued with arranging and conducted field trial of OxG based on the experimental designs to obtain performance data of OxG from different locations across the countries. Twenty accessions of Oleifera from two different origins and fourteen families of Guineensis Pisifera from four origins used for interspecific crosses. Preliminary observation indicates that not all of Oleifera had compatibility cross with Guineensis, several of crosses even did not develop pollinated bunches after repeated controlled pollination done. Interim result, fifty progenies of interspecific hybrid OxG planted in field in year 2017 shows normal vegetative development. Further observation related to productivity and oil quality is needed for completing this research.

**Keywords:** *E. oleifera*, *E. guineensis*, interspecific cross, genetic material.

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Characteristics of Subtropical Fruit Genetic Resources and Development of New Varieties in Jeollanamdo of Korea

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Because of global warming, the average temperature on the Korean peninsula is expected to rise 2°C by 2040. The cultivation areas of late harvesting citrus, which were grown on Jeju Island, are moving northward not only in South Jeolla province and south Gyeongsang province, but also in Chungcheong province. In addition, various subtropical crops have been introduced to korea, which is being attempted to grow all over the country, and the amount of imports is gradually increasing.

In this study, we introduce the main characteristics of genetic resources collected from home and abroad and the status of nurturing new varieties for the excavation of subtropical fruits suitable for the climate of our country.

Since the 1990s, fruit research institute at Jeollanamdo Agricultural Research and Extension Services has been collecting the genetic resources of subtropical fruits such as kiwifruit, loquat, and pomegranate at home and abroad, and used them for breeding. Among the collected plant resources, the total 301 accessions comprising kiwifruit, loquat, pomegranate, fig and Yuzu, have been registered as national resources of Agricultural Genetic Resources Center of Rural Development Administration.

Most kiwifruit are green and yellow in color, some resources are red, which are mostly originated from China. On the other hand, most of the resources collected in Korea are wild collections of Actinidia arguta, which are small fruits (less than 15g), contains high soluble solids (over 16%) and have no hair on fruit surface. Loquat has been also introduced from China, Japan and Spain, which are yellow-white juicy fruits (30 to 40g), maturing in June. The pomegranate petals are mostly red but there are some resources with white, pink, and mixed color as well. Fruit shapes of fig resources are conical and western pear shape. The fruit surface color is light green to dark purple and the color of the pulp was all purple.

There are differences in fig fruit size. Big fruits are Seungjeong Doughpin, Banane, and some Japanese collections. Druri, Brunswick and Daeel contain high sugar. Most yuzu fruits are round obate. The yuzu fruits have 30 and 39 seeds per fruit but Daejeongeum has very few or no seed.

Up to now, 16 kiwifruits, 3 loquats, 1 pomegranate have been selected from our long-term breeding program and registered as new variety. Among new kiwifruit selections, Haewon (kiwifruit) are big fruit (average 140g) with green flesh and high sugar, Haeguem (kiwifruit) is yellow pulp with high soluble solids (over 15%), Bidan contains extraordinary high vitamin C content (over 500mg/100 fresh weight). Mihwang loquat yellow-white fruit pulp, Jinwang is big and late maturing fruit and Joabi is early maturing fruit. Dannahnong pomegranates is the first own selection in Korea, which has low acidity. By now, these new varieties have been distributed to growers (about 224 hectares)

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Induced Mutation \textit{versus} Genome Editing Facilitated Plant Breeding: Commons and Differences in Genetics, Technology, Regulation and Cost-effectiveness

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Genome editing has emerged as a powerful tool in plant breeding in recent years, with a trend to replace the “old” technique of mutation induction. However, genome editing and induced mutation facilitated plant breeding share a lot in genetics and many breeding objectives could be achieved by either approach. In the present presentation, the molecular genetic features of mutations generated through classical (chemical and physical) and random mutagenesis and (genome editing based) targeted mutagenesis will be reviewed and compared, together with the procedures and applicability of these two approaches, using rice as an exemplary crop. Then, based on these findings, the comparative advantages of the two approaches will be discussed in the context of both techniques and regulation related cost-effectiveness for their commercial use. While genome editing has its technical advantages in plant breeding, mutation induction using physical and chemical mutagens still has its own uniqueness (and thus irreplaceable by genome editing) and even has advantages over genome editing for certain traits, in addition to its zero regulation cost. Hence, classical mutagenesis can still be a useful tool for plant breeding and genetics, particularly when it is applied properly and together with other molecular techniques.

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Ion-beam radiation mutagenesis and plant mutation breeding

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We have developed a unique technology for mutation induction using ion beams from particle accelerators at the RI Beam Factory. Ion beams provide a high linear energy transfer (LET) to break the both DNA strands and the histones. The DNA damage is clustered and difficult to be repaired completely by the cells. At relatively low doses, heavy-ion beams induce mutations at a high rate without severely inhibiting growth. We have collaborated with companies and agricultural experiment stations on plant breeding using ion beams. As a result, 30 new cultivars were generated from irradiated materials including Japanese barnyard millet with short culm and low amylose content ‘Nehariko2’ and tearless onion ‘Smile ball’. LET is an important parameter to be considered in ion beam mutagenesis. We investigated the effect of LETs ranging from 23 to 650 keV/μm on mutation induction in rice. The most effective LET (LETmax) was 30 keV/μm. Subsequently, we analyzed gene mutations using whole genome sequencing. The major mutations were single-nucleotide variants and small insertions and deletions. Irradiation at LETmax is effective for plant mutation breeding because of its very high mutation rate and sufficient energy to disrupt a single gene. LETmax mutants have become increasingly useful and important in modern genetic studies, enabling the discovery of genes that control important traits. The discovery of genes using mutants and genome technology may lead to the emergence of a new field in biology, “mutagenomics”. In the future, we would like to contribute to advances in these fields, examine the effects of physical factors (e.g., nuclear species, LET, and dose) on DNA-mutated regions, and elucidate the mechanism of mutagenesis with ion beams.

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**Mutation as a Useful Breeding Utensil to Expand Commercial Value of Korean Japonica Rice**

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Rice breeding is an endless procedure of creating desirable haplotype expressing improved performances of agronomic traits. Narrow genetic diversity of Korean Japonica rice cultivars have been a major limit factor not only in developing resistant tolerant lines against stresses, but also in expanding genetic availability in terms of widening end-use properties. Although introducing novel allele types might be possible via crosses with wild relatives, it demands additional tedious efforts to restore the unique genetic background of the recurrent parents. Our study is preliminary based on the mutation breeding, by which desired traits could be acquired with the least impact on the unique haplotype of the current market leading rice cultivars. Under assumptions of 1) screenings to find new favorable alleles would be conducted under the current cultivation circumstances, 2) identified useful alleles are supposed to be introduced into the current japonica elite lines promptly, and 3) the alleles could be potential resources for functional genomics accompanied with DNA marker systems and Rice Pseudomolecules, three japonica cultivars (Namil, Samkwang, and Koshihikari) were treated with Sodium Azide (SA) or Ethyl methanesulfonate (EMS) to establish mutant stocks. Through screening and evaluating the mutant lines, several mutant lines were selected for their improved performances in terms of important agronomic traits such as resistance and tolerance against biotic and abiotic stresses, and modified endosperm characteristics. To localize favorable mutated allele types, mapping populations were constructed by using the progenies from the crosses between the mutant lines and Milyang23, or their wild type cultivars. Association analyses, between DNA marker genotype and evaluated phenotype of each progeny line, were adopted to localize the putative chromosomes locations involved to favorable traits. Simultaneously, breeding programs have being conducted, by using favorable mutant lines as donor parents, to transfer the favorable alleles into other elite Korean Japonica cultivars.

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**OCS11-04**

**Characteristics of mutations induced by proton beam-irradiation**

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In radiation mutation breeding, type of ionizing radiation is one of the important factors that affect frequency and spectrum of mutations. Although gamma-rays have long been widely used for mutation breeding, particle beams such as heavy ion beams have been characterized by recent genomics studies and shown to have various mutagenic effects according to their types. We characterized the mutagenic effects of proton beams that are categorized as particle beams, but have much lower LET (linear energy transfer) compared to those of heavy ion beams. First, DNA breaks and oxidative damages by irradiation were investigated in cymbidium by comet and MDA (malondialdehyde) assays, respectively. Compared to gamma-rays, proton beams were expected to induce more frequent DNA breaks or more severe oxidative damages according to their energies. We further characterized the mutation frequency and spectrum using Arabidopsis mutant populations. Screening of mutant phenotypes showed that proton beam-irradiation caused mutations in higher frequency and wider spectrum. In addition, whole genome sequences of mutant lines indicated that proton beams may induce large-scale DNA mutations (e.g. large deletions and translocations) more frequently compared to gamma-rays although frequency of single base substitutions was similar between two types of radiation. Therefore, we expect that proton beams can be used for mutation breeding to enhance mutation frequency and spectrum. We are now constructing database on the effects of proton beam-irradiation in diverse crops to use it for practical mutation breeding.

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**OCS11-05**

**Generation and characterization of novel genetic variation in rice for the enhancement of grain quality and agronomic performance**

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Induced plant mutants are important resources for the breeding of improved varieties to provide food, feed and fiber to an ever-increasing global population. While mutagenesis has long been a key tool for plant breeders, the more recent development of powerful, high throughput sequencing-based strategies for mutation detection has increased the value of mutant resources, enabling functional genomics of agriculturally important traits. The major goals of my research program during the past 15 years have been the identification of novel mutations and traits to further the understanding of agronomic performance and grain quality in rice and the development of novel genetic resources for breeding improved varieties. Towards these ends, chemical mutagenesis has been employed to generate mutant populations in the japonica rice varieties Nipponbare, Kitaake, and Sabine. Using the reverse genetics approach Targeting of Induced Local Lesions in Genomes (TILLING) by sequencing, mutations in genes involved in seed phytic acid content, starch biosynthesis, and silicon/arsenic uptake and accumulation have been identified over the years. Forward genetics has also been employed to complement the TILLING by sequencing approach and to identify morphological and developmental mutants of rice. Characterization of the phenotypic effects of mutations identified via TILLING and progress towards isolating the genes underlying mutant phenotypes obtained by forward genetics screens will be presented using examples involving grain quality, the uptake of silicon and arsenic, and the biosynthesis and accumulation of cuticular waxes.

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**Potential Mutants for hybrid mungbean**

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Mungbean (*Vigna radiata* L.) is a cleistogamous plant in which flowers are pollinated before they open, which prevents yield improvements through heterosis. We generated a chasmogamous mutant (*cm*) mungbean in which open flowers are pollinated. An *F₂* population derived from a cross between *cm* and Sulu-1 was used for gene mapping. Segregation analyses revealed that a single recessive gene regulates the production of chasmogamous flowers. Using newly developed InDel and simple sequence repeat markers, the *cha* gene responsible for the chasmogamous flower trait was mapped to a 277.1-kb segment on chromosome 6. Twelve candidate genes were detected in this segment, including *Vradi06g12650*, which encodes a YUCCA family protein associated with floral development. A single base pair deletion producing a frame-shift mutation and a premature stop codon in *Vradi06g12650* was detected only in *cm* plants. This suggested that *Vradi06g12650* is a *cha* candidate gene. Besides, we developed a sterile mungbean, which shows no pollen emitted from anthers. BSA-Seq was performed and the mutant gene responsible for sterility was mapped on chromosome 9 of mungbean genome. These mutants are important genetic resources for developing hybrid mungbean, however, it is still long way to go and more effort should be done for the target of increasing the yield of mungbean by using heterosis.

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Diversity and Characterization of Cassava (*Manihot esculenta* Crantz.) Originated from Open Pollination Seed of M1G4 Gajah Mutant Genotypes Population

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Cassava (*Manihot esculenta* Crantz.) is a starchy root crop and potential future crop for food, feed, bio fuel also for industrial use such as bio-plastics material. Cassava breeding program goals nowadays not only focusing on tuber yield but also the starch content that can be harvested especially for industrial demand. Low cassava genetic source due to vegetative propagation, expect can be increased by utilizing another genetic source from open pollination (OP) seeds. Present research was carried out to evaluate the diversity and characterize qualitative and quantitative characters on cassava plant originated from OP seeds population of Gajah genotypes putative mutant M1G4 generation. More than 1500 OP seeds were germinated in nursery and vigorous seedlings being selected to be transplanted in field. Cassava OP population observed on 9 months after planting (MAP) including plant qualitative and quantitative characters before harvesting phase and tubers in harvesting phase. One simple method to identify the starch content on tuber parenchyma using coloring treatment by spraying 1% iodine to 1 cm thick of middle tuber flesh slice. Grouping based on qualitative characters forms a dendrogram with three large groups. Distribution of 214 OP genotypes based on tuber weight per plant and stem diameters, plant height, level of branching, number of tubers, and tuber cortex thickness shows that 8 genotypes are potential to be developed in the next testing stage by vegetative propagation. Furthermore, all of the cassava tuber genotypes used have higher amylose content with the color transformation into blue-purple color. The color analysis shows the color changes to blue-purple color around 30-95% of the flesh. This percentage are expected can tested cassava tuber and can be used as rapid method to measures cassava starch content.

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The Morphological and Phytochemical Studies on The Effect of Acute and Recurrent Irradiation in *Celosia cristata* Seeds

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The present work investigated the morphological and phytochemical changes in *Celosia cristata* L. seeds exposed to gamma irradiations. *C. cristata* seeds were irradiated with acute radiation at doses of 470, 480, and 490 Gy and were planted until M4 generation. Recurrent irradiation was done on M4 seeds at a dose of 250 Gy. The morphological and phytochemical diversity was performed in M6 generation. The highest difference in recurrent irradiated plants were found on plant height, plant diameter, number of branches, and flower width, while the number of flower and flower length were found highest diversity in acute irradiation. Morphological changes in recurrent irradiated and acute radiation plants showed at the shape and color of flowers. The qualitative phytochemical showed not different between acute and recurrent irradiated plants. It can be concluded that the acute and recurrent irradiated changes the morphological of *C. cristata*, but not in phytochemicals contents.

Keywords: morphological, phytochemical, *Celosia cristata*, mutation, gamma radiation, acute radiation, recurrent irradiation

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Gene print genome editing in tomato

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Genome editing (GE) based on CRISPR technology, one of the new plant breeding techniques coined as plant breeding innovation (PBI), is expected to open a new era of crop breeding. GE takes place usually through the DNA repair pathways. DNA double strand breaks (DSBs) occurred in cells are a serious threat to survival and all living organisms have developed mechanisms to treat and repair DSB rapidly. Among them, cells rapidly ligate the ends of the truncated DNA through the non-homologous end joining (NHEJ) repair pathway, where some nucleotides can be deleted or inserted, resulting in mutations. On the other hand, homology-directed repair (HDR) pathway can occur when homologous DNA templates are present, which is very inefficient compared to the NHEJ pathway in plant somatic cells and is not well utilized as a tool in plant GE. I coin HDR-mediated genome editing as ‘gene print genome editing (GPGE)’, because this process copies genetic information from provided gene fragment. Unlike the NHEJ repair pathway, which mainly produces knock-out, the GPGE pathway can replace long DNA fragments as well as SNP mutations, allowing replacement of alleles or pyramidal integration of multiple genes in a specific locus of a chromosome. The GPGE is very advantageous to crop breeding and I believe, will provide ultimate means to edit genome freely. We report our approaches and results to improve HDR efficiency through various approaches using geminivirus - based plant replication in tomato model crops.

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Precision genome editing in plants via base editing or gene targeting

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CRISPR/Cas9-mediated genome editing systems require an appropriate protospacer adjacent motif (PAM) sequence at the target site. SpCas9 recognizes the shortest known PAM, NGG, but we showed that an engineered SpCas9 (SpCas9-NGv1) recognizing only NG as the PAM sequence can efficiently mutagenize the rice and Arabidopsis genomes. SpCas9-NGv1 nickase fused to the cytidine deaminase enabled C to T substitutions near 5’ end of the 20-nt target sequence (Endo et al., 2019 Nature Plants). Furthermore, we reported that SpCas9-NGv1 nickase fused to the adenosine deaminase enabled A to G substitutions at a position -16 to -13 upstream from the PAM (Negishi et al. 2019, Plant Biotech J).

However, desirable substitutions are not always introduced into a target gene by these base editing systems. Gene targeting (GT), enables to modify targeted sequences as expected via homologous recombination (HR) using a donor DNA as a template. In rice, precise modification of the targeted sequence via GT using the positive-negative selection system and subsequent removal of the positive selection marker has been developed (Nishizawa-Yokoi et al. 2015, Plant J). Here, we would like to compare base editing system and GT system and discuss about future trends of precision genome editing in rice and other plants.

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Metabolic engineering for the production of hydroxy fatty acid in oil model plant Arabidopsis

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Fatty acids of most plants are composed of common fatty acids such as saturated and unsaturated fatty acids. However, castor produces a unique fatty acid, hydroxy fatty acid (HFA) in seeds. Because HFA is used as chemical raw material including soap, lubricant and plastic, it is industrially important to produce and accumulate in HFA in oil crop. Many researchers have tried to produce and increase HFA accumulation in Arabidopsis as a model oil plant using transformation of genes that are related to HFA synthesis from castor, but have not yet reached the level of castor production. So we made a vector that coexpressed five HFA biosynthesis-related genes from castor. This vector consists of the following five genes. FAH12 directly synthesizes HFA. Acyl-CoA lysophosphatidylcholine acyltransferase (LPCAT) can transfer HFA-CoA from phosphatidylcholine (PC) into the acyl-CoA pool. Phospholipid:DAG acyltransferase1-2 (PDAT1-2) synthesize the TAG by transacylation of the sn-2 HFA from PC-HFA to diacylglycerol (DAG). PC: DAGphosphocholine transferase (PDCT) generates PC-derived DAG by removing the head group of PC. Diacylglycerol acyltransferase 2 (DGAT2) can transfer HFA from acyl-CoA pool to DAG and make triacylglycerol (TAG). Currently, we have reached the coexpression level of five genes related to HFA synthesis and accumulation of HFA in TAG isolated from castor and mutation of Arabidopsis endogenous gene fatty acid elongation 1 (FAE1) with CRISPR/ Cas9 to produce 30% of HFA in Arabidopsis seeds. This technology will be applied to the oil crop Camelina.

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Improvement of Grain Quality through Application of CRISPR/Cas9 System in Rice

YuJin Jung, SangSu Bae, YongGu Cho and KwonKyoo Kang

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Grain quality improvement is a key target for rice breeders, along with yield. It is a multigenic trait that is simultaneously influenced by many factors. Over the past several years, breeding for semi dwarf cultivars and hybrids has significantly contributed to the attainment of high yield. However, grain quality tends to decline somewhat, requiring research attention. Since the rice genome sequence has been decoded, it has been easy to discover useful genes and to induce target mutations, and has succeeded in revealing the function of quality related genes. In recent years, with the development of gene editing technology, knockout techniques of target genes have been developed and succeeded in many crops. Genome modification using CRISPR/Cas9 not only improves the quality of rice but also enables new research in various life science fields. In this presentation, we would like to discuss the successful compilation of many genes related to various aspects of rice grain quality through CRISPR/Cas9 technology. Especially, we analyzed 23 starch synthesis related genes such as Wx, SBEI, SBEIIb, ISA1, FLO2, FLO5/ALK and PHO1, and transcription factors regulating Waxy genes. Currently, T2 and T3 generations of null segregants selected from T1 generation are being cultivated and analyzed. Interestingly, studies on functional genomics at larger scales have become possible because of the availability of gene editing technology. Therefore we discuss the progress made in rice by employing the CRISPR/Cas9 editing system and its eminent applications. We also elaborate possible future avenues of research with this system, and our understanding regarding the biological mechanism of rice grain quality improvement. The rapid shift of research toward the utilization of CRISPR/Cas9 systems for targeted mutagenesis could be a promising approach for overcome barriers to breeding improved quality rice.

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Development and application of genome editing tools in *Medicago truncatula*

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The legume-rhizobium symbiosis is initiated through the activation of the Nodulation (Nod) factor-signaling cascade, leading to a rapid reprogramming of host cell developmental pathways. In the previous study, we identified thousands of novel candidate genes undergoing Nod factor-dependent, ethylene-regulated expression in *Medicago truncatula* Jemalong A17. In this work, we combine stable transformation with CRISPR/Cas9-mediated genome editing tools to characterize the molecular function of MtGA2ox10 encoding the C20-GA2-oxidase, a candidate regulator of early symbiosis in *M. truncatula*. RNA sequencing analysis and quantitative polymerase chain reaction revealed that MtGA2ox10 was induced as early as 6 h post-inoculation (hpi) of rhizobia and reached peak transcript abundance at 12 hpi. Promoter::β-glucuronidase fusion showed that the promoter activity was intensively localized in the root infection/differentiation zone during the early stage of rhizobial infection and in the vascular bundle of the mature nodule. The CRISPR/Cas9-mediated deletion mutation of MtGA2ox10 suppressed infection thread formation, which resulted in reduced development and retarded growth of nodules on the *Agrobacterium rhizogenes*-transformed roots. Over-expression of MtGA2ox10 in the stable transgenic plants caused dwarfism, which was rescued by GA₃ application, and increased infection thread formation but inhibition of nodule development. These findings suggest that MtGA2ox10 plays an important role in the rhizobial infection and the development of root nodules through fine catabolic tuning of GA in *M. truncatula*. Additionally, the genome editing tools developed in this study will be novel biotechnology tools for biological studies as well as crop improvement in legumes.

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Special Session
(50th Anniversary Symposium of the KSBS)
Special Session (50th Anniversary Symposium of the KSBS)
“품종개발 100년, 육종학회 50년 - 주요 성과와 전망”
“100 years of Variety Development and 50 years of KSBS : Main Achievement and Prospects”

- 주제: “품종개발 100년, 육종학회 50년 - 주요 성과와 전망”
- 일시: 2019.7.3.(수) 09:00 - 7.4(목) 12:00
- 장소: 광주 김대중컨벤션센터 C3 세미나실
- 주관: 한국육종학회  ○ 후원: 국립식량과학원, 국립원예특작과학원, 국립산림과학원, 국립종자원

<table>
<thead>
<tr>
<th>SS-01, 총괄 및 식량작물 (Overview and Food Crops)</th>
<th>SS-2 원예 . 특작용 (Horticultural &amp;Herbal Crops)</th>
</tr>
</thead>
<tbody>
<tr>
<td>09:00-09:10 인사말</td>
<td>13:30-14:00 김용권 (신경대학교)</td>
</tr>
<tr>
<td></td>
<td>The Change of Horticultural Seed Industry and the Development of Horticultural Breeding Technology</td>
</tr>
<tr>
<td>09:10-09:40 고희종 (서울대학교)</td>
<td>14:00-14:30 조명철 (국립원예특작과학원)</td>
</tr>
<tr>
<td></td>
<td>Brief History and Perspectives of Crop Breeding in Korea</td>
</tr>
<tr>
<td>09:40-10:10 조영찬 (국립식량과학원)</td>
<td>14:30-15:00 정경호 (국립원예특작과학원)</td>
</tr>
<tr>
<td></td>
<td>우리나라 벼 품종개발 변천사 및 성과 (History and Result of Rice Variety Development in Korea)</td>
</tr>
<tr>
<td>09:40-10:10 Coffee break</td>
<td>15:00-15:30 김원희 (국립원예특작과학원)</td>
</tr>
<tr>
<td></td>
<td>한국 옥수수 품종개발의 변천과 전망 (Changes and Prospects in the Development of Corn Varieties in Korea)</td>
</tr>
<tr>
<td>10:10-10:40 박태일 (국립식량과학원)</td>
<td>15:30-16:00 현동윤 (국립원예특작과학원)</td>
</tr>
<tr>
<td></td>
<td>Past and Current Status, and Prospect of Barley and Wheat Research</td>
</tr>
<tr>
<td>10:40-11:10 김홍식 (국립식량과학원)</td>
<td>16:00-16:30 현동윤 (국립원예특작과학원)</td>
</tr>
<tr>
<td></td>
<td>Development of soybean cultivars in Korea: Current status, challenges and future</td>
</tr>
<tr>
<td>11:10-11:40 남상식 (국립식량과학원)</td>
<td>16:00-16:30 Coffee break</td>
</tr>
<tr>
<td></td>
<td>한국의 감자·고구마 품종개발 변천사 및 전망 (History and Prospect in the Development of Potato and Sweet potato Varieties in Korea)</td>
</tr>
<tr>
<td>11:40-12:10 백성범 (국립식량과학원)</td>
<td></td>
</tr>
</tbody>
</table>
SS-3 임목, 산림 (Forest Plants)

좌장 이석우(국립산림과학원)

16:30-17:00 이수형 (국립공주대학교)
한국의 임목육종 연구 동향: 학술지 논문의 키워드 분석
(Research Trends in Tree Breeding and Improvement in Korea: keyword analysis of research papers)

17:00-17:30 이석우 (국립산림과학원)
임목육종 60년 - 성과와 전망
(60 Years of Forest Tree Improvement in Korea - Accomplishments and Prospects)

17:30-18:00 장용석 (국립산림품종관리센터)
산림식물 품종보호제도 현황과 전망
(Prospect and Status of Plant Variety Protection of Forest-sector in KOREA)

2019년 7월 4일, 목요일

SS-4 육종기술 및 정책 (Technology and Policy)

좌장 조용구(충북대학교)

09:00-09:30 박효근 (서울대 명예교수)
인류 만여년간의 식물육종 역사를 돌아보면서 내일을 살펴본다.

09:30-10:00 박수철 (서울대학교)
Current Statues of GM Crop Development and Commercialization

10:00-10:30 강시용 (한국원자력연구원)
Past, Present and Future of Plant Mutation Breeding in Korea

10:30-11:00 윤진영 (한국종자연구회, 과문)
Achievements and Challenges in Production and Quality Management of Seed

11:00-11:30 방문진 (국립종자원)
우리나라는 식물신품종보호 및 종자관리제도 변천사
(History of New Plant Variety Protection and Seed Management in Korea)

11:30-12:00 양미희 (농림축산식품부)
종자산업진흥정책과 종자산업 발전
(Policy on the Fostering of Seed Industry in Korea)
Brief history and perspectives of crop breeding in Korea

Hee-Jong Koh
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Crop breeding is the genetic improvement of crops for human benefit. In Korea, crop breeding initiated from the early 20th century since the agricultural development station was set up in 1906. First improved rice varieties through hybridization ‘Namsoon 13’ was released in 1932. After a series of restructuring, Rural Development Administration, a centralized national organization for agricultural research and development, was established in 1962, and crop breeding researches have been performed in a large scale at affiliated breeding institutes. With the development and release of ‘Tongil-type’ rice varieties from 1972, ‘Korean Green Revolution’ was achieved, which led the self-sufficiency of staple food crop in Korea. ‘Tongil-type’ rice varieties out-yielded most of the rice varieties bred so far in the world and recorded the highest yield on a national scale. Thereafter, traditional breeding technologies of Korean breeders were leveled up, and lots of crop varieties have been developed under various breeding objectives including yield, disease and insect resistances, improved and diversified quality, and functional crops. Breeding vegetable crops have been carried out mostly at the private companies. The first F1 hybrids of vegetables were Wonye #1 and #2 of ‘Kimchi’ cabbage developed in 1960 at Horticultural station. Breeding technologies in Korea for ‘Kimchi’ vegetable crops are the world highest level, which have been proved by the seed exports. Recent progress in biotechnology and genomics has expanded the breeders’ horizon providing a molecular platform on the traditional plant breeding, which was figured as ‘plant molecular breeding’. MAS techniques have been routinely incorporated in most of crop breeding programs, and novel variations have been created through GM and NBT techniques. Crop breeding in Korea has been partly supported by the government in terms of research and development projects and is expected to be one of the poles sustaining the agricultural industry for the future.

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Past and Current Status, and Prospect of Barley and Wheat Research

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Barley is a major food crop of human, cultivated 1,000 years before rice. A systematic breeding program for Korean barley began in 1906 with the selection and introduction breeding. In 1908, landrace barley was collected and focused on selection and introduction breeding for high yielding variety. In 1980s and 1990s, the breeding was carried out for diversity, thereafter we aim to improve quality, productivity and lodging tolerance varieties that can be applied to the paddy field in Korea. And the efficiency of breeding also improved through mutation and bulbusum method.

Wheat cultivars have been cultivated 40 varieties in Korea. In the early stage, we developed domestic wheat variety aim to early maturing and high yielding. Since 2000, the cultivar ‘Keumkang’ have been distributed and cultivated by most of the farmers. Now we are developing stable cultivation techniques and disease resistant varieties in response to climate change. Recently, we developed ‘Ofree’, it is reduced allergy substance wheat in the world and the black wheat ‘Arheuk’, is containing the highest anthocyanin contents.

Now it is time to take aggressive action to support the strategic survival of Korean wheat and barley industry. Barley is a health food that requires a multifaceted effort to improve breeding efficiency as well as working on developing varieties containing large amounts of functional components and more resistant to stronger biotic and abiotic stresses in response to climate change. It is necessary to recognize the role of wheat and barley as the second main crop after rice and to improve the self-sufficiency rate of these crops for the health and food industry crisis of Korean.

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Development of soybean cultivars in Korea: Current status, challenges and future

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Soybean is the raw material of traditional foods such as tofu and soy-paste, and is the next important food crop after rice in Korea. Domestic production of soybean has varied depending on cultivation area and productivity. The decline of soybean production has been intensifying since 2013, and its self-sufficiency rate for food has fallen to 22% in 2017. The proportion of domestic soybean as raw materials for processing has reduced through replacement with the cheap imported ones. A few number of soybean cultivars with high yield and desirable agricultural performance have been developed for various end-uses since the first cross-bred cultivar, ‘Kwangkyo’ in 1969. More efforts are needed to develop elite cultivars contributing to the expansion of the domestic production and consumption. Improvement of high quality and functionality of Korean soybean is the first criteria to be differentiated from the imports. Aiming at the development of high yielding varieties for ensuring productivity and economic profitability, the ability to improve agricultural stability against environmental challenges should be considered by securing valuable traits such as abiotic and biotic resistance, and adaptation to paddy cultivation and mechanization. In terms of consumption, it is important to improve the quality and processing characteristics for end-uses that can meet the needs of soyfood industry and consumers, such as chemical constituent, physical traits, and processing quality so that the use of Korean soybeans in soy-products should be increased. To cope with the trends of wellbeing and health functional food-based consumption, and to create new demands, it is required to identify functionalities of soybean-containing ingredients and to cultivate various functional soybean cultivars as new sources for specific industrial purposes. Limitation of productivity and value-added quality of soybean could be overcome through innovation of breeding programs into new breeding paradigm using the omics-based bioinformatics and molecular breeding systems.

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한국은 감자·고구마 품종개발 변천사 및 전망

남성식*, 박영문, 이형윤, 조지훈, 정미남, 한선경, 유종현, 황영지, 고산, 이승용

1농촌진흥청 국립식량과학원 바이오에너지작물연구소
2농촌진흥청 국립식량과학원 고기능농업연구소


고구마는 우리나라에서 자연 개화가 어렵기 때문에 인위적으로 접목을 하여 개화를 유도하고 인공교배를 통해 종자를 얻는다. 고구마는 동질 6배체로 인체체가 90개 존재하여 유전적으로 다양하기 때문에 교배에 의해 많은 변이체가 만들어질 가능성이 높다. 그러나 고구마는 자가 교잡불가능성, 그리고 교배 불임균이 존재하여 목적하는 변이나을 후세에서 쉽게 얻기 어렵다. 시대의 흐름에 따라 고구마의 역할도 변화하였는데 1970년대 이전에는 부식의 재배 대체를 위한 구형작물의 역할을 수행하였으나 1980년대부터 2000년까지는 그의 자급 역할로 고구마 소비가 감소함으로써 생산량도 감소하였다. 그러나 2000년부터는 감론 가능성 식품으로서 소비 증가와 함께 재배의 도약기를 맞이하고 있다. 그에 따라 품종의 개발도 90년대 이전에는 최대생산을 위한 다수화 품종 육종(속정승, 수원 147호, 신미, 진미 등), 90년대 이후에는 식미가 우수한 분질 고구마(율미, 신평미, 중미 등)의 품종 개발을 진행하였으며, 2000년대부터는 식미가 우수한 모든 품종(자색고구마(자미), 자색고구마(자미), 자색고구마(자미) 등)이 개발되었으며, 2000년대부터는 음료 및 건강식품에 이용되는 품종(Ugmi, 낙미, 신미이 등)이 개발되었다. 앞으로는 현재의 교배육종 시스템에 부속작품 기술을 접목하여 단계별 육종계통 선양 강화 및 비파괴 품질 분석기 정립을 통해 수요가 요구하는 품종 조이육종 기술이 요구된다. 고구마는 마이오식품산업과 연계하여 다양한 산업화를 통해 고부가가치 시장을 창출함으로써 고구마 산업은 지속적으로 발전할 것으로 전망된다.

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한국 옥수수 품종개발의 변천과 전망

백성복, 손병영, 김정태, 배현희, 고영삼, 김성림
농촌진흥청 국립식량과학원

국내에서 1960년 이전에는 육종적으로 개량이 되지 않은 재배종 또는 방임 수분 품종들이 재배되었다. 1960년대는 품종개발 기반을 조성하는 단계로, 1989년 미국에서 합성품종을 도입하여 적응력 높은 황옥2호를 선발하였고 1982년부터 농가에 보급하면서 체계적인 옥수수 개량이 시작되었다. 1990년대는 합성품종에서 교감잡종으로 진화한 시대였으며 교감잡종 중에서도 단교잡종 옥수수에 차별화하였다. 단교잡종 수입호는 1976년에 내병 내독성 다수성 품종으로 육성되어 10a당 780kg으로 황옥2호보다 52%가 증가하여 단수량을 선진국 수준으로 근접시킬 위기적인 품종이었다. 1980년대는 1970년대의 종실 주요의 육종에서 정부의 축산진흥사책과 함께 재배면적이 급격히 증가하였던 사임자용 옥수수로 육종목표가 선정되는 시기였으며 단교잡종 보급이 정착되었다. 이 때에 경제작물로서 개발된 단수성수와 참수성수로 대응한 품종개발이 이루어지기 시작하여 대응으로 단수성수인 단육1호와 참수성수인 참육1호가 개발하여 선보였고, 사료용을 포함하여 10개의 품종이 개발되었다. 1990년대는 국외화 및 농산물 수입 개방화 시대를 맞아 소비자의 생활수준이 고급화 되면서 소비자의 요구가 다양화 되었고 이 때에 비로소 옥수평품종 품종개발 체계가 정착되어 종실 및 사임자용 2, 찰옥수 2, 단육 및 참수성수 2품종이 개발 되었다. 2000년대에 들어서면서 FTA 등 외부 농업 환경변화, 기후변화에 따른 품종개발의 방향전환 등 현도 대응 연구가 활발해져서 육종별로 품질 다양화 되고 재배 안정성이 뛰어난 품종이 29개나 육성되는 등, 옥수수 품종 개발의 전성기를 맞이하였다. 사임자용으로 후기녹색성이 좋은 건강수수만 높은 평양육, 도복에 강하고 상품성이 우수한 참수성수 미백호가 개발되었는데, 광대용과 미백2호는 인기가 높아 지금도 가장 많이 재배되는 품종으로 국내 옥수수 자급률 향상에 크게 공헌하였다. 그 외에도 자색찰옥수, 박암옥수, 흔한 전용 찰옥수, 참과 초당옥수를 이어 참여한 참찰조상수 등이 이 시기에 개발되었다. 1980년대에는 사계절 여건이 더욱 다양화 되면서 품종개발이 관 또는 대학 기우체에서 종묘회사 등의 민간영역으로 확대되었고 수요자가 직접 참여하여 품종을 개발하는 수요자 참여형 품종개발 시스템 도입과 종자 수출을 위한 품종 개발로 육종의 범위가 더욱 확대되었다. 수요자가 직접 참가하고 육종한 지역특유한 참수성수 황금맛찰, 인도시장에서 판매되고 있는 종자수출용 단육수수 Mithas 등 수양 품종들이 자속적으로 개발되었다. 참수수는 수입산 보다는 품종과 계화한정성이 뛰어난 것으로 평가 받고 있으며, 종실 및 사임자용도 수입 품종을 대체할 수 있는 수준(당초품 종실량 1,000kg/10a, 다수품 종실량 2,369/10a)으로 발전하였다. 이와 같이 옥수수 품종 개발은 사계절 영향에 대응하여 변화. 발전하게 현대 국립종자원에 등록된 옥수수 품종은 110개가 달한다. 옥수수 품종 개발 성과와 연구가치가 확대됨에 따라 향후 옥수수 품종은 더욱 다양해질 전망이다. 참살이류와 환경에 따른 안심먹거리 및 기능성 식품에 대한 관심 증가로 사용 품종수수는 비타민 및 미량요소 강화, 간اهر 나무성 강화 등 고농도의 가능성을 보유한 품종이 자속적으로 개발될 전망이다. 단, 참과 초당옥수료 지연형종에서 매우 선호하여 현재의 참수성수 소비 위주의 사감조상과 단, 초당옥수료로 전환될 것으로 보인다. 종실성옥수수는 부가가치가 향상 위하여 라이선스, 말도자연 등을 특수성분이 강화된 품종이 개발되어 사용하는 것으로 사임자용수수는 생산성 증대를 위해 20기적과 2기적 등 작물체계에 적합한 수가가 110일 이하인 조속 및 맞춤형품종 조성, 사감조상 가는 고소성 및 고양장 품종, 손에 적응하는 내습성 고폴오래 품종이 출현할 것으로 보인다. 수출용 품종개발 분야에도 담보가, 종실, 아프리카 등에 잘 적응하는 옥수수 품종이 자속적으로 개발되어 우리나라의 식량종자 방어가 높아질 것으로 기대된다.

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The Change of Horticultural Seed Industry and the Development of Horticultural Breeding Technology

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The change of horticultural seed industry and the development of horticultural breeding technology

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한국채소 품종육종 연구의 과거, 현재, 미래

조병철*, 경광호, 양은영, 재원범, 남춘우, 장석우, 권영석, 문지해, 김도선, 전희, 하윤찬

1전북 완주군 이서면 농생명 100, 국립원예특작과학원 재소과


현재는 채소 품종육종이 대부분 민간 종자회사를 중심으로 이루어지고 있지만 조장기 채소 품종육종의 기반 마련은 원예시험장의 역할이 있다. 우리나라 주요 채소 품종들은 대부분이 일대잡종 기술을 이용해 품종을 육성하여 판매하고 있고, 해외로 수출되는 세계 최고 수준의 채소 품종육종 기술과 만위를 보유하고 있다. 우리나라 채소 산업은 농업생산량 48조 2천억원 중 21%를 차지하고 있다. 이러한 우리나라 채소 종자 산업의 동부발전은 품종 구성을 변화, 재소의 주요공급 체계 확립, 채소 수출 산업의 결과이다. 재소품종 구성의 변화에는 일대잡종을 생산하여 판매함으로 생산성, 균일성, 내병성 등이 고고장 보다 우수하고, 반복해서 종자를 생산하여 교육받으므로 종묘회사의 경제적 성장에도 크게 기여하게 되었다. 재소는 진화하거나 가공하여 소비하는 것이라는 신선한 상태로 소비하는 형태다. 우리나라의 재소계는 분명한 각 재소마다 생산기술이 제한되어 있는데 농업 소비자들에게 신선채소를 공급 할 수 있는 것은 다양한 농가재의 개발, 재배기술의 발전뿐만 아니라 재소품종 개량의 역할이 크게 기여한다. 채소 종자 수출량 또한 목탄드로프세트 등 국가가 지원하는 R&D 사업이 단�반처되어 무, 양배추, 고추 등을 중심으로 지속적으로 증가하고 있다.

앞으로 우리나라 채소 산업의 발전을 위해서는 지속적인 새로운 품종의 개발과 소비자들의 요구에 맞는 신선 재소의 안정적인 공급이 요구된다. 과거 한국의 재소 품종 개발이 생산성과 재배 안정성에 중점을 두었다면 미래에는 고부가가치 가능성, 안전성, 고급품 재소 품종 개발에 대한 요구가 늘어날 것으로 예상된다. 이에 부응하기 위해서는 산학관련이 협력하여 새로운 육종기술의 지속적인 개발과 고급품 재배를 통해 채소 품종 개발에 노력해야 할 것으로 생각된다.

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한국 화훼 용도의 변천과 전망

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1전라남도 농촌진흥청 태안농업기술센터, 전라남도 농촌진흥청
2전라남도 농촌진흥청 총무과, 전라남도 농촌진흥청

국내 국립농업기술원에 출원 및 등록된 화훼 품종 수는 매년 300여건 정도로 급속도로 증가된 것으로 5,638건 중 화훼류가 3,722건으로 58.6%를 차지한다. 이는 화훼 특성상 다양한 화형, 화색을 필요로 하며 품종변화가 빠르게 반영될 것으로 보인다. 화훼 품종특성의 태도기로 봐야 한다. 화훼 품종특성의 태도기로 봐야 한다. 화훼 품종특성의 태도기로 봐야 한다. 화훼 품종특성의 태도기로 봐야 한다.

1980년대에는 화훼 품종특성의 태도기로 봐야 한다. 화훼 품종특성의 태도기로 봐야 한다. 화훼 품종특성의 태도기로 봐야 한다. 화훼 품종특성의 태도기로 봐야 한다. 화훼 품종특성의 태도기로 봐야 한다.


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한국화훼의 변천과 전망

김현희*, 박희희, 정재영, 박기영, 서정남, 김오근, 유봉식, 이수영, 박진환, 최은정, 안해런, 이영란, 강윤규

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우리나라 인삼, 약작물 육중의 주요 성과와 전망

현동운

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지향은 조선왕조실록에 재배, 수확, 재배조, 재배지역 등이 기록된 것으로 보아 조선시대 또는 그 이전부터 중국에서 도입된 인삼종이 국내에서 재배 및 이용되었을 것으로 추정된다. 지향은 현재까지 12품종이 개발되었으며, 1995년 작물시험장에서 중국의 '복정호'를 도입한 후 집단화하여 '지향호'를 육성한 것이 국내 최초 품종이다. 이후 이로써 재배품종은 갤럭시(주)에서 개발한 '고기능성품종과', 현재 국내의 지향재배종은 토강이 약 75%를 차지하며, '다강', '고강' 등 일부 품종이 재배되고 있다. 현재까지 지향의 품종육성은 수량증 증대 외부의 산발움 육종 수준이었으나, 최근 임무리(장), 류리무공생 등 내생성 품종 및 유휴양분 과정으로 품종육성을 목표로 유전자원간 교배를 통하여 우량품종을 육성하고 있다. 특히 수태물의 직접 이용하기 이론적 자원들의 특성상 지향개경작업체와 재배농가가 요구하는 재배가 용이하고 가공적상이 뛰어난 품종개발에 그 목표를 두고 있다. 다가오는 작업자 지향은 현재 영양변식을 통한 종자 보급을 하고 있으나 순계육성을 통한 종자변식 적용으로는 품종개발을 장기적으로 추진 중이며, 이를 위하여 순계 육성을 위한 반수체 배양 등의 육종기술 개발이 필요할 것으로 생각된다.

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한국의 임목육종 연구 동향: 학술지 논문의 키워드 분석

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전체 육종면적의 31%를 차지하는 산림은 인간의 의료, 수산업의 원산, 수목용량의 주요 재료를 제공할 뿐 만 아니라 산소 생산, 수원, 토양회복, 생물다양성 유지 등 다양한 생태계서비스 기능을 제공한다. 우리나라의 산림은 일제강점기와 한국전쟁을 겪으면서 상당 부분이 약화되었으나, 1970년대 치산녹화 사업을 시작하면서 산림 복구에 성공하여 현재는 산림의 공익적 가치가 126조원 이상을 차지할 만큼이 되었다. 재배품종은 주요 재배품종의 생산 배경에서 1950년대부터 시작한 국내 임목육종 연구가 큰 몫이라는 평가가 지배적이다. 본 연구에서는 우리나라의 임목육종 연구 성과를 1) 임목육종 방식, 2) 임목육종 목적과 주제, 3) 임목육종 대상 수종별로 간단히 소개한다. 또한, 자극에서 국내외의 다양한 산림과학자들에서 발표한 임목육종 연구논문들의 내용을 바탕에 관련 연구 키워드를 수집하여, 이 분야의 세계적 연구동향과 국내 연구동향을 객관적으로 비교 분석한다. 이를 통해 우리나라 임목육종 연구의 과거와 현재 위치를 평가하고, 나아가 임목육종 분야를 예측하고 계획하는 데 도움이 되고자 한다.

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60 Years of Forest Tree Improvement in Korea – Accomplishments and Prospects

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Forest tree improvement is relatively a young science and its purpose is to provide guidance for the conservation, management and sustainable utilization of genetic resources of the natural and managed forests. In South Korea, forest tree improvement programs started in 1956. The programs had two main aims: to guarantee the genetic origin of the forest reproductive materials used in afforestation and reforestation and to develop genetically improved individuals and varieties of some commercially important trees. Since the launch of the forest tree improvement programs, biomass production has been the major improvement target, together with overall adaptability to different sites. Further improvement targets have recently been added, including wood quality traits and more specific targets linked to adaptation to abiotic and biotic factors in response to new socioeconomic needs and global changes. Additionally, since the early of 1970s, forest genetic resource conservation and forest fruit and nut tree breeding have been in progress in South Korea. Molecular breeding techniques based on omics information are being developed to enhance the efficacy of selection and to accelerate forest tree breeding cycles. Genetic engineering including gene editing has also been applied, but is currently limited to research purposes. Forest tree improvement will be an integral part of bioeconomy in securing the production of good quality raw materials in large quantities and will play a significant role in sequestering carbon dioxide and slowing climate change in the long term.

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산업식물 품종보호제도 현황과 전망

장용석

중앙 충주지 수안보면 수화리로 72 삼림청 국가산림품종관리센터 품종심사과


사람들은 음식과 생활을 "생물자원 진행사"라고 알고 있다. 산림부와 농림자원전략상 사례로도 재고해 보고 있다. 산림관보의 바꾸소나이나 한국과의 식물자원에 속해 복용 들어 산림업과 연결시키는 "생명산업"육종에 집중적으로 투자하고 있다. 또한, 2017년에는 유전자원을 활용한 정방품의 익시공유를 규정한 새로운 국제규범인 "생명산업자원"이 국가에 보급되면서 식물자원을 이용한 비료산생제가 여러개에 반영하고 있다. 이러한 혁신적인 기술로, 식물에 대한 지식재산권으로서의 품종보호제도가 아닌 산림화와 산림산업 정책으로 연결되어야 한다가기 때문에 육식물을 활용한 우리나라의 생명산업 발전에 일조할 수 있도록 지속적인 정책들을 펼쳐나가야 할 것으로 생각된다.

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Current Statues of GM Crop Development and Commercialization

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Global area of genetically modified crops (GM crops) continued to grow and reached 189.8 million hectares in 2017. Recently, a total of 24 countries approved GM crops for planting and an additional 43 countries formally imported biotech crops for food, feed, and processing, meaning that biotech crops are now commonly accepted in those countries. The first-generation GM crops have been first developed and commercialized by global agricultural companies belonging to advanced countries such as the United States and Europe. The fact that more than 90 percent of first-generation GM crops, which have been commercialized for 20 years, are both insect resistance and herbicide-resistant proves that they continue to have an effect on improving agricultural productivity and increasing farmers’ income. As the effectiveness of GM crops has been proven and technology has been developed, the trend of GM crop development has recently changed. In other words, it is moving from farmer-oriented to benefiting both farmers and consumers. In Korea, National Program for GM Crops (NCGC), one of the Next-Generation BioGreen 21 Programs organized by Rural Development Administration (RDA) was established in 2011 to develop biotech crops that will be used in the future to solve our agricultural problems. To accomplish this mission, the NCGC carried out the exploration of useful functional genes, development of qualified events, and the safety assessment of developed events. We will introduce the current statuses of global and domestic GM crop development and commercialization.

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Past, Present and Future of Plant Mutation Breeding in Korea

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In Korea, study of mutation breeding was started in early 1960s by some researchers at the Atomic Energy Research Institute, Rural Development Administration (RDA) and several universities, using seeds irradiated by gamma rays in the United States. In 1966, when the Radiation Agriculture Research Institute (RARI) was established, mutation breeding using radiation was actively conducted for a while. But the RARI was merged into the Korea Atomic Energy Research Institute (KAERI) and RDA in 1973, and radiation agricultural research was neglected by the two agencies. In the 1980s, the relevant research department was lost, which resulted in a recession period of radiation breeding research. The Advanced Radiation Research Institute (ARTI) under the KAERI was established to promote the radiation research and industry in the 2005, which led to activation of radiation breeding research. In addition, Radiation Breeding Research Center (RBRC) at the ARTI was established with support of the Ministry of Agriculture, Food and Rural Affairs in 2013. In recent, importance of seed and genetic resources has been emphasized in Korea, and many institutes, companies and private breeders are also interested in mutation breeding. The RBRC is trying to develop advanced radiation breeding techniques and new genetic resources using mutation techniques combined with bio-tech to deal with loss of biodiversity due to global climate change and environmental degradation, growing global demand for food and bio-energy, and strengthened protection for new plant varieties. New mutant varieties more than 150 were developed and registered officially in Korea. In recent, new mutant varieties are quickly increasing and commercializing mainly developed by private company and breeders especially on flowers and landscape plants.

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Achievements and Challenges in Production and Quality Management of Seed

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Government-led system for seed production and distribution of major crops was constructed by enforcement of the Major Crops Seed Law in 1962. Korea Variety and Seed Service has been playing the key role in operating the system, in cooperation with breeding institutes under the Rural Development Administration and provincial Basic Seed Centers. In case of the most important crop, rice, quality of certified seed has been continuously improved from simply cleaned seed in the 1960s to graded, disinfected, coated seed of the present. Its coverage to the total planted area was increased from 13% in 1990 to 60% in 2015. The Foundation of Agricultural Technology Commercialization and Transfer, since its inception in 2010, has involved in production/distribution of certified seed of rather minor crops/varieties, which had not been properly cared for by the system mentioned above.

Vegetable seed has been produced and marketed by the private sector. In the latter half of 1950s, it became possible to replace the smuggled seed with domestically produced seed in major vegetables. Vegetable seed market was opened in 1991 and since then seed companies explored overseas production sites suitable for quality and cost to meet the needs from local as well as export markets. Acquisition of major local seed companies by multinational majors in late the 1990s has brought chances for the Korean vegetable seed firms to upgrade their operational plant production and quality assurance practices to the global standards.

Small and ever-decreasing size of local seed market has been and will be a serious factor limiting the seed business in Korea. It is necessary to develop technologies to overcome the adverse weather in domestic as well as overseas production areas, which is being worsened and more frequent by the climatic change. Production system has to be improved to reduce labor and other costs. Non-destructive methods for quality assessment need to be developed especially for seed health test against diseases requiring large number of expensive seeds. Seed enhancement technology such as biological treatment is becoming an essential part for holistic farm solutions, where seed is not only a carrier of the genetic constitution of a plant variety, but also plays the complementary role to make up for limitations of the varieties bred and/or cultural managements practiced.

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우리나라의 식물신품종보호 및 종자관리제도 변천사

방문전

경상북도 김천시 혁신8로, 국립종자원 품종보호과

우리나라의 식물신품종보호 및 종자관리제도의 변천사를 보면, 오랜 기간 동안 식량주권의 확보를 위해 노력한 결과, 음식물자원의 보호와 활용을 위한 제도가 시작되었다. 1970년대 중반에 시작된 식물신품종보호법으로, 식물신품종보호제도는 그간의 역사를 바탕으로 제정되어 왔다.

이후 1997년 종자산업법을 제정하면서 식물신품종보호제도 및 국가종자품목등재제도를 도입하였고, 우리나라의 종자산업은 더욱 발전하게 되었다. 우리나라의 종자산업은 식량주권 확보를 위해 우선적으로 정책을 추진하면서 크게 정책종자를 제조, 재소종자로 만드는 민간이 담당하는 구조로 형성되었다. 주요 식물종자인 벼, 붓나무, 콩, 감자, 옥수수 등은 정부보급종으로 생산 공급이 관리되어 오다 가 현재 감자, 옥수수는 지자체 및 민간으로 이행되었다. 민간부분의 종자산업은 IMF 외무위기로 우량 토종종자회사가 외국적 종자회사에 합병되어서 크게 위축되었으나 이후 민간학연의 노력으로 급상승하였다.


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종자산업진흥정책과 종자산업 발전

연구회

농림축산식품부 종자생명산업과

종자산업이 생명공학 등 참담기술을 접목하여 가습적기와 부가가치가 높은 산업으로 발전함에 따라 모산토 등 클로벌 농업화사업 등은 종자 산업뿐만 아니라 직결 참여해 왔다. 산림작물은 미래의 국가생산력의 좌초가 중요한 분야로 인식하여 다양한 육성방법을 수행하여 추천하고 있으며 미래형식태변화를 저지하는 측면까지 고려하고 있다. 우리나라도 종자산업의 중요성을 인식하고 2000년대 전후부터 지속적으로 산업육성정책을 추진해 왔다.


그러나 근본적으로 국내 종자산업의 구조가 취약하여 유전자원, 유통기술, 마케팅 등 각 분야에서 해결해야 할 과제가 신책에 있는 실정으로, 종자산업의 구조화, 품종개발 주제간 역할분담과 협력 방안 등의 필요성도 지속적으로 제기되어 왔다.

이에 종자산업은 미래농업을 선도하는 식량산업으로 성장시키기 위해 2011년 종자산업법 개정을 통해 지원근거를 마련하고, 이후 2012년 주거의 "종자산업 육성 종합계획", 을 수립하여 추진하고 있다. 1차 종합계획에서는 기초 인프라 구축에 집중하였고, 2차 종합계획은 수출확대 및 업계 규모와 지원에 주력하고 있다.

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Poster Session
Photosynthetic performance in improved lines of rice cv. KDML105 containing salt tolerance gene under salt stress

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Rice cv. Khao Dawk Mali 105 (KDML105) is the most aromatic rice originating in Thailand. This cultivar is highly susceptible to abiotic stresses, especially salt stress at seedling stage. The objective of this study was to investigate the photosynthetic performance in response to salt stress in two improved KDML105 lines (containing salt tolerance genes from Pokkali; the salt tolerance donor) namely RGD14376 and RGD12-150-B-21-3 compared to KDML105. Rice seedlings were grown for 21 days in hydroponic solutions and then exposed to salt-stress (150 mM NaCl) for 0, 3, 6 and 10 days and recovered from stress for 3 and 5 days. The results indicated that when subjected to salt stress all plant cultivars/lines exhibited significant reductions in net photosynthesis rate ($P_n$), stomatal conductance ($g_s$), Transpiration rate ($E$), maximal quantum yield of PSII photochemistry ($F_{v}/F_{m}$), effective quantum yield of PSII photochemistry ($F_{v'}/F_{m'}$) and SPAD reading while water use efficiency (WUE) were increased. Compared to KDML105, the improved line RGD12-150-B-21-3 showed less injury under salt stress and significantly higher $P_n$, $g_s$, $E$, WUE, $F_{v}/F_{m}$, $F_{v'}/F_{m'}$ and SPAD readings.

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Application of Marker-Assisted Selection for Breeding Drought-Tolerant Rice (Oryza sativa L.) in Vietnam

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Development of high yield and abiotic-stress tolerance rice varieties is one of the urgent and essential demands for people living in the areas of Mekong Delta, Vietnam, where being seriously affected by climate changes, especially long-day drought and hot-temperature situations. This experiment used IR75499-73-1-B as a drought-tolerant donor and OMCS2000 as a recipient parent for breeding new rice lines with good drought-tolerant capacity and high yield. Seven SSR markers (RM219, RM201 RM105, RM23602, RM23877, RM24103, and RM328) were used for identifying drought-tolerant target genes in breeding populations, including backcrossing populations (BC1F2). As a result, primer RM23877 showed the highest number of homozygous allele bands (11 lines), corresponding to donor line. Followed by RM105 and RM201 appeared 9 lines. Drought screening in BC1F2 generation indicated that BC1F2-45 and BC1F2-54 lines resulted in strong drought-stress resistance and high productivity. Outputs of this study suggested that application of marker-assisted (MAS) method might be a new approach for Vietnamese scientist to develop new agricultural crops possessing good agronomic traits as well as adapting to climate changed regions in Vietnam.

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Homology-based cloning of VfSOC1 of faba bean (*Vicia faba* L.)

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Faba bean (*Vicia faba* L.), as a legume crop planted in winter, is of benefit to the land use capability, thus it is more and more popular in the world. The procedure of vernalization is important for flowering of winter plants, and *SOC1* is an important gene in the pathway of vernalization of *Arabidopsis*. In our research, *VfSOC1* of faba bean was obtained using homology-based cloning, and the result shows that *VfSOC1* encodes a 26.004 kDa protein with 226 amino acid residues. Phylogenetic analysis revealed that *VfSOC1* is closely related with MsSOC1 of *Medicago truncatula*. The result of subcellular localization showed that VfSOC1 was detected in the cell membrane and nucleus. qPCR was performed, and the result showed that the expression level of *VfSOC1* of leaves was higher than other tissues. Expression level of *VfSOC1* was increasing as the time of vernalization treatment (4°C) extended (0 d, 7 d, 14 d and 21 d), and the gene still keep higher expressed after transferring the plants into room temperature (21°C). Our results provided preliminary evidence of that *VfSOC1* is a vernalization related gene in faba bean.

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Seed abundant wheat peptide transporter 2 (TaPTR2) regulates seed germination

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RNA seq. analysis of wheat line Iksan with long spike showed that expression of peptide transporter 2 (TaPTR2) involved in hormone responses as well as dipeptide uptake increased 2.5 times compare to maternal line Keumkang. Therefore, in the present study, we characterized molecular physiological function of TaPTR2, via heterologous expression into *Arabidopsis thaliana* PTR2 (AtPTR2; At2G02040) mutant, overexpression and complementary expression plants. Among the PTR groups, the expression level of AtPTR2 was almost three times higher than that of the control group until 18 hours after vernalization and then decreased. This indicates that PTR2 transcription is most significantly affected at the early germination stage and may play an important role in seed germination via increased transcriptional level. In order to investigate which factor correlates with TaPTR2 during germination, germination rate was measured under ABA-, GA- and glucose-fed conditions, respectively. Germination inhibition observed in *Arabidopsis* PTR2 mutant (ptr2) under 1/2 MS media was significantly increased by 2% glucose feeding compared to wild type (Col-0), whilst *TaPTR2* expression transgenic lines are similar to wild type. In the medium containing both 2% glucose and ABA, the germination rate of *ptr2* showed an additive effect or a summation effect which is significantly lower than that of ABA and glucose alone. In addition, ABA biosynthesis inhibitor (nordihydroguaiaretic acid; NDGA) did not affect germination. In contrast, ABA catabolism inhibitor (dioniazole; Dini) and glucose inhibited germination of *ptr2* more than wild type. This suggests that *ptr2* does not promote the biosynthesis of ABA but inhibits degradation, resulting in maintaining ABA content high has the effect of inhibiting germination.

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Wheat ELL-associated factor (TaEAF) involves in seed germination via regulating storage lipid mobilization

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RNA seq. analysis of long-spike-wheat Iksan and maternal Keumkang showed that expression of extensins are more abundant in long-spike-wheat. On the database, Arabidopsis EAF (AtEAF) is predicted as a hydroxyproline-rich glycoprotein forming a major extenin family, containing extenin motif SP₁ and SP₃ and an ELL-associated factor (EAF) in Camelina sativa, an RNA polymerase subunit adjusting rate of mRNA synthesis. AtEAF is mainly expressed on seed and seed-germinating stage but also expressed slightly on vegetative stage. Subcellular localization of AtEAF is nucleus. Germination rate of Arabidopsis eaf mutant was delayed significantly compared to wild-type and exogenous GA (gibberellic acid) rescued this delayed germination. Seedling growth was also severely inhibited in terms of hypocotyl length and fresh weight. Exogenous sugars rescued these phenotypes. FAME analysis with gas chromatography revealed that EAF is related to breakdown of seed storage lipid (TAG) for germination and seedling establishment before photosynthesis. Triticum aestivum also has 7 EAF (TaEAF) on 2⁵ chromosome, 4⁴ chromosome and 5⁶ chromosome. Among these, TaEAF on 5⁶ D chromosome is close to AtEAF with well-conserved motifs. To characterize its biological role, we introduced TaEAF driven by CaMV 35S promoter to Arabidopsis eaf mutant. TaEAF rescued hypocotyl length, fresh weight and also helped breakdown of seed storage lipid of aef mutant. These results suggest that TaEAF has a role in lipid mobilization during seed germination.

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Drought Stress Evaluation of Agronomic and Resilience-related Traits of Soybean Mutant Lines

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Drought-tolerant soybean variety has an important role in maintaining the yield stability. The objective of this research was to evaluate the tolerance of soybean mutant lines to drought stress. A total of ten soybean mutant lines, and two check varieties (Panderman and Dering-1) were evaluated at two levels of soil water availability (100% and 40%). Treatment combinations were arranged in a randomized complete block design, replicated four times. Observations consisted of plant height, chlorophyll content index, days to flowering, days to physiological maturity, plant biomass at R5 stage (roots, stems, and leaves), number of branches, number of pods, number of empty pods, seed weight, 100 seeds weight, evapotranspiration and stress tolerance index. The results showed that drought stress treatment (40% of available water) during the period of crop growth provided a very high drought stress to all genotypes tested thus reducing variables of plant growth, variables of yield and yield components, delaying the time of flowering and physiological maturity. Five out of ten lines indicated tolerant to drought stress which level of tolerance higher than both check varieties. Potential yield, seed size and water use efficiency of the five selected lines were better than Panderman and Dering-1. Physiological maturity of selected lines were two days, except G6K which was five days, longer than Panderman, but nine days shorter than Dering-1. These lines could be proposed as candidate of new variety tolerant to drought stress.

Keywords: Drought stress evaluation, Mutant lines, Soybean

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Study on soil environment improvement for high valuable crop cultivation and field test at the reclaimed tideland

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This study is one of “Agri-Bio Industry Technology Development Program, Ministry of Agriculture, Food and Rural Affairs(MAFRA)” and aims to develop high value added agricultural technology through cultivation environment standardization and field scale study for upland cultivations in reclaimed tidelands. The main contents of this study is evaluate the water management method, the low-cost/high-efficiency soil management method and the optimal cultivation management model for the crops at reclaimed land. Therefore, in this study, we will develop the technology of high value added agricultural land based on reclaimed tidelands through exploration and demonstration of optimal environmental condition.

Major contents and characteristics in this study were as follows:

1. Development of water management method for high value crop cultivation at reclaimed tidelands
   - Setting on soil salinity criteria and desalination point
2. Development of low-cost/high-efficiency soil management method at reclaimed tidelands
   - Development of low-cost/high-efficiency culvert drainage system
3. Development of optimal cultivation management model for high value crops at reclaimed land
   - Development cropping system manual and performance analysis
4. Development of optimized smart water management/control system at reclaimed tidelands
   - Developing optimized soil moisture measurement system and algorithm

These results will provide the standardization of a high value crop cultivation system at reclaimed tidelands.

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Growth and root characters responses of black gram (Vigna mungo L. Hepper) genotypes to waterlogging stress

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The fluctuation of rainfall is a serious situation in Thailand, causing drought and waterlogging during crop production. Waterlogging causes serious problem for black gram [Vigna mungo (L.) Hepper] production, especially during the early rainy season where crop production is often affected by more precipitations. Waterlogging also affects plant growth and grain yield production of black gram. The information of crop responds to stress such as plant growth and root characters are important especially for black gram waterlogging tolerance improvement.

In this study, six black gram accessions including, 4 cultivated and 2 wild related species were evaluated under three water regimes (control, at 7 days waterlogging and 14 days waterlogging). The results found that cultivated black gram varieties including, Pitsanulok 2, Mash 8-5(B), Blackgram (68/71) and JP109668 demonstrated high ability of waterlogging tolerance by maintaining excellent growth rate, good leaf score, more adventitial root formations and well recovery after stress. While, JP107874 and NPGRL Acc. 130 (R), the wild related varieties, were susceptible to waterlogging due to slow growth and low value of root traits as compared with cultivated varieties. The results suggested that these cultivated black gram varieties have been selected for waterlogging during crop domestication. Future study is recommended in order to elucidate for waterlogging genetics domestication of black gram.

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PCS01-09

Effect of diverse drought and phosphorus fertilizer on yield potential and drought response index of rice (*Oryza sativa* L.) genotypes

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Drought is the major obstacle for rice production especially under rainfed area. The fluctuation of rainfall induces the different drought types throughout growing stage of rice. Moreover, the nutrition availability is the main factor under limiting of water. The objectives of this study was evaluated of rice yield and yield potential under different drought conditions and identified of drought response index of rice genotypes for selection criteria. The study was conducted under three conditions as flooded condition, aerobic or rainfed which alternative wet and dry and late season drought condition which water was decreases at panicle initiation stage. The result showed that drought was affected to the 68.4% decreasing under severe drought and only 1.4% decreasing under fluctuation of rainfall (aerobic condition). High rate of phosphorus fertilizer applying was provided to highest grain yield under severe drought condition and phosphorus accumulation in leaf and seed of rice under these conditions was significantly higher than under flood and aerobic conditions. The genotypes by phosphorus integration were found under all conditions in grain yield but genotype number 2 (IRUBN030051-2-181), 6 (IRUBN030062-1-54) and 7 (IRUBN030062-1-64) were good response especially under water deficiency condition. The drought response index could use as a selection criteria due to high correlation between drought and aerobic condition that genotypes number 2 was greatest under both conditions. The further research will use the drought response index as a selection criteria and the response of genotypes was different under diverse drought condition. So, the screening and selection should be done under both drought and aerobic and rainfed condition for confirm the potential of genotypes.

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PCS01-10

Evaluation of fruit yield and quality in cherry tomato (*Solanum lycopersicum*) varieties under hot and humid condition

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High temperature and relative humidity strongly affected flower and fruit yield of tomato (*Solanum lycopersicum* L.). Processing tomato cultivars with heat tolerance have been reported, however heat tolerance in cherry tomato cultivars are limited. This study was to investigate performance of heat tolerance in cherry tomato lines under hot and humid condition. This experiment was conducted under plastic-net house in the rainy season during the period from May to October 2017. Randomize complete block design with three replications was used in this experiment. The results show that maximum air temperature and relative humidity was 38.9 °C and 89.6 % respectively that should be a good condition for evaluating heat tolerance in cherry tomato. V207 and V108 showed the highest fruit yield (578.3 and 568.5 g/plant, respectively) and high fruit setting (31.5 %, respectively) but V207 couldn’t produce seed (0 seed). G5 showed the highest TSS (11.2 °brix) and lycopene (39.62 mg/100g FW), however it had low fruit yield (117.1 g/plant) and fruit setting (10.5 %). In conclusion, V108 should be used as a good genetic resource for heat tolerance in cherry tomato breeding program.

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Screening of drought-tolerant soybean lines in core populations and EMS-treated population

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Drought is one of the major abiotic stresses that strongly limits crop productivity and yield. Soybean (Glycine max (L.) Merr.) is an important leguminous plant which is popularly known as drought-sensitive crop. The purpose of the present study is to screen of drought-tolerant accessions and utilize them as genetic resources for the development of high yielding drought-tolerant varieties. In the present study, index of leaf wilting score was used to isolate tolerant accessions. A total of 771 accessions (386 accessions of G. max and 385 accessions of G. soja) of soybean core populations in Korea and 1362 lines of EMS-treated Pungsannamul population were screened for drought tolerance in greenhouse condition. Out of them, 6 very tolerant and 21 tolerant accessions were identified from G. soja core population, whereas only a single tolerant line was isolated from the G. max EMS population. Further, genome-wide association study was carried out to detect genome region that controls the quantitative trait loci (QTL) for drought tolerance by using 131,620 SNP markers in genetically diverse sets of the 377 G.max and 318 G. soja soybean core population accessions. Association analysis identified 8 SNPs in G. max and 2 SNPs in G. soja that are associated with canopy wilting at the significance level of -Log10 (P) > 5. A chromosomal region associated with the canopy wilting was mapped by six significant SNPs on Gm17, which correspond with the previously reported QTLs. The chromosomal regions defined in this study can be further investigated to identify the causal gene(s) responsible for the drought tolerance in soybean. This work was carried out with the support of “Cooperative Research Program for Agricultural Science & Technology Development (Project No. PJ014168032019)” by the Rural Development Administration, Republic of Korea.

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Screening of flood-tolerant soybean lines in EMS-treated 'Pungsannamul' mutant population

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Flooding is one of the most serious abiotic stress that reduces the productivity of crops in many important agricultural regions of the world. Soybean (Glycine max (L.) Merr.) is the important legume crop, which is generally sensitive to flooding stress. The present study is aimed to screen and identify the flood-tolerant soybean lines in EMS-treated 'Pungsannamul' mutant population. In this study, soybean plants at the V2 stage were submerged in water for 5-7 days and foliar damage after the removal of water was used to evaluate the level of flood tolerance. A total of 1100 mutant lines were screened for flood tolerance in greenhouse condition. Out of them, two lines were identified with no foliar damage in two replications at greenhouse condition. In further studies, the tolerant lines isolated will be utilized for the breeding program to identify the genetic resources involved in flood tolerance.

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Regulation of xylem development by jasmonic acid

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Xylem development is affected by environmental stresses such as drought and oxidative stress, and recent findings showed that jasmonic acid (JA) is involved in this process. In this study, we showed that polar auxin transport regulated by PIN3 and PIN7 is involved in the JA-mediated xylem development. PIN3 and PIN7 encoding auxin efflux carriers are responsible for polar auxin transport. The mutant plants that lack the activity of PIN3 and PIN7 developed extra xylems in vascular tissues like the JA-treated wild-type plants. Visualization of auxin response and xylem development in the roots treated with NPA, an inhibitor of polar auxin transport showed that disruption of polar auxin transport is involved in the xylem phenotype of pin3 pin7 double mutants. We also found that cytokinin increases expressions of PIN3 and PIN7 while JA decrease. Together with the previous finding that JA and cytokinin act antagonistically, these indicated that PIN7-mediated polar auxin transport system modulates xylem development in response to JA. Collectively, these suggest that JA promotes xylem development by disrupting auxin transport in vascular tissues, and the auxin efflux genes, more especially PIN7 whose expression is suppressed by JA mediate this process.

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Intergenic transformation of *PsGPD* enhances tolerance to salt stress in rice

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Climate change caused by global warming is expected to cause serious damage to agricultural productivity and movement of cultivated land. Salt stress is particularly an important abiotic stress that seriously affects plant growth and development. Transgenic potatoes expressing glyceraldehyde-3-phosphate dehydrogenase (GPD), isolated from *Pleurotus sajor-caju*, had increased tolerance to salt stress. We transformed rice with *PsGPD* using Agrobacterium-mediated transformation. We determined the transgene copy number by quantitative real-time PCR method. Intergenic genomic locations of the inserted T-DNA were confirmed by adaptor-ligation polymerase chain reaction and analysis using FSTVAL (http://bioinfo.mju.ac.kr/fstval/).

To elucidate the role of *PsGPD* in stress tolerance, responses of *PsGPD-OX* transgenic rice plants to salt stress conditions were examined. *PsGPD-OX* #5, #6, and #17 lines were treated with salt stress on MS medium containing 100 mM or 200 mM of NaCl for 5 and 14 days. Morphological analysis revealed differences between the three transgenic *PsGPD-OX* rice and the wild-type rice. The germination rates of the three transgenic *PsGPD-OX* lines of rice were significantly higher than that of the wild type rice, indicating that they were more tolerant to 200 mM NaCl than the wild type rice. In addition, the three transgenic *PsGPD-OX* rice lines had significantly longer length of root and shoot compared to the wild type rice. These results suggested that overexpression of *PsGPD* improve more tolerance to salt in rice.

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A putatively stress-related gene *BrTSR53* isolated from *Brassica rapa* confer salt tolerance in rice

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Plants often face a variety of biotic and abiotic stresses that influence their development, growth and productivity. *BrTSR53* gene, a putative stress-related gene isolated from *Brassica rapa*, was used to generate overexpression transgenic rice. We confirmed the over-expression of *BrTSR53* was by quantitative RT-PCR and western blot analysis. To elucidate the role of *BrTSR53* in stress tolerance, we examined responses of *BrTSR53*-OX transgenic rice plants to salt stress conditions. We treated *BrTSR53*-OX #12, #28, and #32 lines with salt stress on MS medium containing 100 mM or 200 mM of NaCl for 5 and 14 days. Morphological analysis revealed differences between the three transgenic *BrTSR53*-OX rice and the wild-type rice. The germination rates of the three transgenic *BrTSR53*-OX lines of rice were significantly higher than that of the wild type rice, indicating that they were more tolerant to 200 mM NaCl than the wild type rice. In addition, the three transgenic *BrTSR53*-OX rice lines had significantly longer length of root and shoot compared to the wild type rice. These results suggest that the *BrTSR53* gene played an important role in the tolerance of rice to salt stress. Therefore, it might be a potential target for the purpose of improving salt tolerance of rice and other crops.

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Salt and Drought Tolerance Evaluation on Foxtail Millet (*Setaria italica* L. Beauv.) Genotypes

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Salinity and drought are two of the major abiotic stresses limiting global crops production. Foxtail millet is a relatively tolerant crop to salt and drought stress, thus studying the tolerance mechanism of this species is of great importance. In this study, the salt and drought tolerance level of foxtail millet genotypes were evaluated on seedling stage using nutrient culture system. Four foxtail millet genotypes, ICERI-4, ICERI-5, ICERI-6, and ICERI-10 were grown hydroponically in nutrient solution containing salt (0, 60 and 120 mM NaCl) or osmoticum (0 and 20% PEG) for 2 weeks. Observations were made on the malondialdehyde (MDA) content at 3 days-after-treatment (DAT), root anatomy variables at 5 DAT, root system architecture at 5, 10 and 15 DAT, and on growth variables at 15 DAT. Based on the stress tolerance index (STI), ICERI-5 and ICERI-6 genotypes were more tolerant to salinity or drought compared to ICERI-4 and ICERI-10 genotypes. The tolerant genotypes (ICERI-5 and ICERI-6) had higher root diameter and cortex thickness compared to the sensitive genotypes (ICERI-4 and ICERI-10) under salinity. Root stele diameter and the number of metaxylem remained unchanged under drought stress (20% PEG) in ICERI-5 genotype (tolerant), while those variables were significantly decreased in ICERI-10 genotype (sensitive). ICERI-5 genotype (tolerant) also showed longer- and more-seminal roots compared to ICERI-10 genotype (sensitive) under drought stress (20%/PEG). An increase in MDA content due to salinity or drought was observed in all genotypes tested. The different root-anatomical and -architectural changes under salinity or drought stress between the tolerant- and sensitive genotypes indicate that those attributes of the roots might determine the salinity or drought tolerance level of foxtail millet.

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Drought tolerance screening for normal maize inbred lines at during growth stage

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Drought is one of the major abiotic factors that seriously affect the production of cereals crops including maize which is widely grown in the world. Screening on drought facilitates on selecting genotypes and understanding the drought tolerant traits. Drought stress and rescue after stress on maize inbred lines were carried out in this study. The different plant growth attributes such as plant height, leaf area and weight, stem weight, root length, shoot and root fresh and dry weight, and the total leaf chlorophyll content were measured. Six flint inbred lines (FLD12, FLD23, FLD24, FLD33, FLD35, and FLD37) were screened as drought tolerant lines whereas six flint inbred lines (FLD01, FLD13, FLD16, FLD18, FLD29, and FLD31) were screened as drought susceptible lines. Growth attributes on different drought conditions were subjected to correlation test and analysis of variance which showed the highly significant relationship with each other. As drought effect differed from inbred lines indicating wide variability of drought response at early growth stage of maize plants. The results obtained from the present study would be useful on selecting maize genotypes on future breeding programs for enhancing drought tolerance.

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A sesame variety ‘KumOk’ with high yield and disease resistance

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A sesame variety ‘KumOk’(Sesamum indicum L) with fusarium wilt disease resistance and high yield was developed in 2017. It was crossed between ‘HS762-9-2-2’ and SI971241 in 2004. ‘KumOk’ has few branch and triple capsule per node and white seed coat color. And maturing date of ‘KumOk’ is 21st August and height is 143cm and capsule number is 76. Especially ‘KumOk’ showed fusarium wilt disease resistance in the field. And the yield of ‘KumOk’ was about 1.23ton per hectare, 34% higher than ‘Kopoom’. ‘KumOk’ showed crude fat content with 49.1% and crude protein content with 28.7% and lignan content with 6.1mg/g

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Identification of QTL for Drought Tolerance in RIL Population of Soybean

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Drought is one of the major abiotic stresses to reduce seed yield in soybean. To improve the breeding efficiency for drought tolerance of soybean, QTL for drought tolerance was identified using 147 F2 recombinant inbred lines (RILs) developed from a cross between a tolerant parent ‘PI416937’ and a susceptible parent ‘Cheonsang’. The parents and RILs were genotyped using 180K Axiom Soy SNP array and linkage map was developed by using Ici Mapping 4.1. The RILs along with the parents were cultivated in drought and normal conditions with two blocks in rain shelter in 2017 and 2018. Plant height (PH), number of nodes (ND), number of branches (BC), number of pods (PD), biomass (BM), leaf area (LA), 100-seed weight (SW), and seed yield (YD) were evaluated for each line. Weighted drought coefficient (WDC) was calculated with those traits for QTL analysis. The PH, ND, BC, PD, BM, LA, SW and YD were significantly different for genotypes and treatments. The WDC for ‘PI416937’ and ‘Cheonsang’ was 0.76 and 0.65 in 2017 and 0.76 and 0.45 in 2017, respectively. The mean and range of WDC for RIL population were 0.87 and 0.22-3.01 in 2017, and 0.67 and 0.40-1.00 in 2018, respectively. QTL for drought tolerance were identified on chromosomes 6, 7, 10 and 19. The QTL on chromosome 7 showed 3.3-4.1 of logarithm of odds (LOD) and explained 9.6-12.1% of phenotypic variance (PVE). The QTL on chromosome 10 showed 2.2-2.5 of LOD and 5.9-7.3% of PVE. Similarly, the QTL on chromosome 19 showed 3.6-4.0 of LOD and 10.8-11.6% of PVE. Identified QTL showed 1.0-11.0 of confidence interval (CI). Since WDC shows a combined value of variations for various agronomic traits rather than a single trait affected by drought treatment, it can be used as a criterion of measuring drought tolerance.

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Comparison of Growth of rice varieties at Maximum tillering stage in the East Coastal Area of Korea

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This study was designed to identify selection japonica rice varieties with good growth its early stage, adaptable to east costral area of Korea. Plant height and tiller numbers were investigated 1km and 2km distance from sea at the maximum tillering stage (2016-2018). Twenty varieties including ‘Yeongdeongbyeo’ Japonica rice varieties were used to transplanting May 25, 3 plants/hill. Growth of rice varieties in early stage were decreased at 1km distance from the sea than that of the 2 km. Plant height of each varieties at 1km distance from the sea was 0.2 to 26.8 % shorter to those of the 2 km. Tiller number of each varieties at 1km distance from the sea was 2.0 to 29.5 % lower to those of the 2 km. New varieties including ‘Sangbo’ and ‘Saechilbo’ were less influenced by distance from the sea among the varieties tested.

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Identification of water use efficient Napier grass accessions using field drought stress

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Napier grass (\textit{Conyza purpureasc Schumach} L.) is an important perennial forage native to Africa and now introduced and grown in many tropical and subtropical countries. It is considered as a short-term drought tolerant forage which is a useful trait in areas with low soil moisture during the dry season. In order to exploit the potential of this grass species for improved water use efficiency (WUE), a field drought stress experiment was conducted with the objective to identify traits that underlie enhanced water use efficiency and to select best performing genotypes that can thrive in low soil moisture areas. Eighty-four Napier grass accessions from the International Livestock Research Institute (ILRI) and Brazilian Agricultural Research Corporation (EMBRAPA) were planted following a \textit{r} by \textit{r} design in four replications at Bishoftu, Ethiopia. During the dry season, the established plants were subjected to drought stress in such a way that two blocks were irrigated to a volumetric soil water content (VWC) of 20% i.e. optimal water (OW) and the other two blocks were irrigated with a reduced amount of water which corresponds to a VWC of 10% i.e. water stress (WS). The accessions were evaluated for physiological, morphological and agronomic performances. Generally, there was significant variation between treatments OW/WS for traits evaluated indicating the potential of the field drought stress study for performance testing of genotypes in respective environments. Accordingly, the stress tolerance index (STI) and WUE analysis in WS showed significant performance variation of Napier grass accessions implying genotypes differ in their economic use of water for increased biomass production under water limited condition. Accessions that showed consistent enhanced WUE and biomass productivity across harvests are promising for future verification and utilization.

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Development of a new \textit{japonica} rice cultivar ‘IS590DS’ suitable for direct seeding cultivation

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Although direct seeding has the advantages of saving labor and reducing costs for farmers, the cultivation areas of direct seeding have not been increased in South Korea. One way to overcome this problem is to develop direct-seeding-only varieties under flooding condition. Rice variety for wet-direct seeding should have excellent germination ability and seedling growth under submergence. We developed a rice new cultivar ‘IS590DS’ with high emergence rate (50.3\%) and survival rate (42.6\%) under flooding condition compared with check variety ‘Dongan’ (37.2\%, 33.3\% respectively). Moreover, it showed 74\% of germination rate under low temperature condition (13°C). ‘IS590DS’ was developed from a cross between ‘Hopum’ having a good eating quality and high yield in direct seeding cultivation and ‘HR24787-26-5-2’ having good properties related to direct seeding by the rice breeding team of NICS, RDA in 2018. It is a mid-late maturing \textit{japonica} rice variety with high grain quality and also has good milling characteristics, good palatability of cooked rice, and resistance to multiple diseases, especially bacterial blight and stripe virus disease. It has 75 cm culm length and 23 cm panicle length. Brown rice of ‘IS590DS’ with 1,000 grain weight of 24.2 g was heavier than that (20.9 g) of check variety (‘Nampyeong’). The milled rice yield of this variety is about 5.41 MT/ha, 9\% higher than that of check variety (‘Dongan’), under wet-direct seeding during four-year local adaptability trials (2015-2018). ‘IS590DS’ could be utilized in the breeding programs for developing new variety suitable for direct seeding under flooding condition.

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**Calcium-dependent Protein Phosphatase 2A B” Subunits Interact with the bZIP Protein VIP1 and 14-3-3 proteins in Arabidopsis thaliana**

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VIP1 (VIRE2-INTERACTING PROTEIN1) is a bZIP protein in Arabidopsis thaliana. VIP1 changes its subcellular localization from the cytoplasm to the nucleus when cells are exposed to mechanical or hypo-osmotic stress. The nuclear accumulation of VIP1 requires VIP1 de-phosphorylation and Ca" signaling. The VIP1 de-phosphorylation causes dissociation of 14-3-3 proteins, which prevent VIP1 nuclear localization. The VIP1 de-phosphorylation is mediated by protein phosphatase 2A (PP2A), which consists of the scaffold A subunit, the regulatory B subunit, and the catalytic C subunit. The substrate specificity of PP2A is determined by the regulatory B subunits, which are classified into B, B', B" and B" families based on their structures. However it is unclear how PP2A B subunits mediate the interactions with VIP1 and 14-3-3 proteins. Here, we show that PP2A B"-family subunits can physically interact with VIP1 and 14-3-3 homologs. PP2A B" subunits have putative 14-3-3 protein-binding sites and EF-hand motifs, which can bind Ca". Yeast two-hybrid assays, in-vitro pull-down assays, and bimolecular fluorescence complementation (BiFC) assays all showed that VIP1 physically interacts with PP2A B"-family subunits. Similar experiments showed that all of these PP2A B"-family subunits more strongly interact with VIP1 C-terminal region than with VIP1 N-terminal region. The pull-down assay also revealed that the divalent cation chelators EDTA and EGTA both inhibit interactions between VIP1 and PP2A subunits, and that the phosphorylation states of VIP1 do not affect the interactions between VIP1 and PP2A subunits. Yeast two-hybrid assays showed that PP2A B"-family subunits physically interact with 14-3-3 homologs in yeast cells. These results support the idea that PP2A B"-family subunits recruit VIP1 to the PP2A holoenzyme and induce the VIP1 de-phosphorylation followed by the dissociation of 14-3-3 proteins. Further analysis is required to elucidate how PP2A holoenzyme modulates VIP1 and 14-3-3 proteins under mechanically stressed conditions.

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**PCS01-24**

**Agronomic Traits and Forage Production in a Mixed-planting with Corn for Forage Soybean Cultivars, Chookdu 1 and Chookdu 2**

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Soybean [Glycine max (L.) Merr.] cultivar ‘Chookdu 1’ (registration number: No. 7159) and ‘Chookdu 2’ (registration number: No. 6758) were developed as forage soybean cultivars at Kyungpook National University, Republic of Korea. They were grown in tests over three years and compared with a commercial seed cultivar for seed yield and forage productivity planted in the same row in mixed plantings with corn. Chookdu 1 and Chookdu 2 are tall, indeterminate growth habit selections from a cross between wild soybean (Glycine soja Sieb. & Zucc.), ‘PI 483463’, and cultivated soybean, ‘Hutcheson’ (PI 518664). The plant height of Chookdu 1 and Chookdu 2 were 80.9 cm and 81.4 cm, respectively, compared to 54.7 cm for the ‘Pungsanammul’ commercial seed check. The three-year seed yield of Chookdu 1 and Chookdu 2 were 2.0 and 2.2 t/ha, respectively, and not significantly different from Pungsanammul at 2.4 t/ha. Of the two cultivars Chookdu 2 averaged the most total forage fresh weight (65.0 t/ha). The three year mean forage yield of mixed-planting of corn and Chookdu 2 and Chookdu 1 was 10.4% and 3.8% greater, respectively, than corn monoculture. Results show Chookdu 1 and Chookdu 2 are suitable soybean cultivars for mixed planting in the same row with corn to improve forage yield. They should be useful as parents to use in breeding to develop forage-type soybeans of high quality and yield for use in livestock feed.

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**Variation of Pre–Harvest Sprouting Rate of Early–Maturing Rice Lines Adaptable to Mid–Alpine Area of Central Northern Region in Korea**

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In terms of the physiological and genetic variations, environmental factors such as migration of rainy season, frequent typhoon occurrence and locally heavy rains make the pre-harvest sprouting (PHS) phenomena increase. Recently, these have been taken into consideration as the important agricultural trait because of loss of grain production and declining grain quality after PHS. For the selection of pre-harvest sprouting tolerant lines adaptable to mid-alpine area of central northern region, yield trial lines including check varieties have been tested every year. From 2011 to 2018, PHS rate (mean±standard error) of check varieties, Odae, Joun, Jinbu and Unkwang showed 3.3±0.75, 0.1±0.11, 8.6±2.47 and 16.7±4.83, respectively. From the above results, we could ascertain degree of PHS of check varieties following as Joun>Odae>Jinbu>Unkwang. The coefficient of variation of the above varieties were 56.6%, 48.2%, 70.6% and 70.9% respectively. These tested lines for each year was 33 ~ 157. The year of 2011, 2013 and 2017, where the overall average was less than 10%, appear to be low due to the tested lines’ traits and the weather conditions. The ratio of strong responding lines showing PHS rate of less than 5% was decreased from 61.9% in 2011 to 30.3% in 2018, while an average of less than 10% was 62.3%. The average of less than 20%, which is practically unproblematic, was 77% (63.0 ~ 88.4%), indicating that most lines had been tolerant to PHS. Considering recent worsening meteorological disasters, it would be expected a promising result for the production of high quality rice in mid-alpine area, where cultivates early maturing varieties. However, considering yearly variation of the varieties showing moderate and weak response, it will be possible to develop varieties that are high quality and tolerant to the PHS, by further increasing the accuracy of the test.

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**Pup1 and Sub1, conflict or compatible?**

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Rice is one of the major staple crops in Asia, and the rice consumption is increasing globally. Recently, rice cultivation areas in rain-fed system are suffering from various abiotic stresses, which is leading to decrease of yield. Because different abiotic stresses occur simultaneously or sequentially under unfavorable conditions, the breeding multiple-stress tolerant rice should be developed. We have focused on phosphorus deficiency, which is caused by drainage after submergence and tested functional compatibility of two major QTLs in rice: Sub1 (Sub1A) for submergence tolerance; Pup1 (PSTOL1) for phosphorus uptake tolerance. Sub1 and Pup1 were introgressed into IR64, which has high yielding and high quality indica rice. IR64, IR64-Pup1 (Pup1), IR64-Sub1 (Sub1) and IR64-Pup1-Sub1 (IPS) were used to test compatibility of two QTLs. Screening results under stress conditions 1) Submergence conditions: Phenotypic analysis revealed that IPS showed significant tolerance, and the expression levels of Sub1A and PSTOL1 were not different between Sub1 and IPS, and Pup1 and IPS. 2) Phosphorus deficient (P-def) conditions: Tolerance of IPS to P-def. showed inconsistent results on 2-types of soils. While Pup1 showed strong tolerance, IPS showed weakest phenotype on artificial soils system by mixing of seaweed and vermiculite (Pup1 and IPS didn’t showed any difference on natural soils). Compared IPS to Pup1, the expression levels of Sub1A were increased in IPS root, but PSTOL1 expression levels were not altered. These results suggest that co-existence of Pup1 and Sub1 with functions is feasible under submergence conditions, but not in P-def. conditions. Further analyses are being conducted to figure out how do Pup1 and Sub1 work in different kinds of stress conditions.

**Key words:** phosphorus-deficiency tolerance, submergence tolerance, Sub1, Pup1, interaction, rice

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The regulation of circadian gene expression is available to improvement of drought stress tolerance

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Circadian clocks integrate environmental signals with internal cues to coordinate diverse physiological outputs. They are involved in numerous processes such as internal metabolic and hormonal signals, ranging from the control of metabolism, growth, development, and stomatal opening to metabolic processes. The polyploid species Brassica rapa includes a variety of vegetable crops, such as Chinese cabbage, bokchoy, turnip, and broccolietto, as well as oilseed crops, such as turnip rape and sanson. Many of these varieties are agriculturally important worldwide. GIGANTEA is known as clock gene and related to various processes in plant. The GIGANTEA (GI) gene was first discovered due to its important contribution to photoperiodic flowering and has since been shown to be a critical component of the plant circadian clock and to contribute to multiple environmental stress responses. We identified and cloned a GI homolog from the B. rapa Chinese cabbage genome. We showed that the GI gene in B. rapa (BGI) was similar to Arabidopsis GI in terms of both expression pattern and function. We developed GIGANTEA reduced Chinese cabbage. RNAi-mediated suppression of GI expression in the Chinese cabbage, B. rapa DH03, increased tolerance to drought stress. We also wanted to know if some circadian clock genes directly affect abiotic stress response and tolerance in Brassica rapa. We confirmed to change the expression in transgenic plants under drought stress condition. Our results suggest manipulation of gene expression through RNAi and transgenic expression could enhance tolerance to abiotic stresses and thus improve agricultural crop production.

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Important characters in salt tolerant rice based on several methods of screening

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The objectives of the study were to determine the important characters of rice tolerant to salinity stress based on morphology and physiology and the relationships among several methods of salinity tolerance screening. The study consisted of 4 experiments representing all critical stages of rice growth, namely germination, seedling-vegetative, and reproductive stage. Screening at germination stage by floating the seeds on top of 200 ml plastic tray filled with sterile distilled non-saline and saline water (saline EC 8.1 dS/m) was carried out at the Plant Physiology and Molecular Laboratory, Biology Department, IPB University. Screening at seedling stage using hydroponic system (EC 0.8 vs 13.4 dS/m) and vegetative and reproductive stages using pot (EC 0.46 vs 5.6 dS/m) were carried out at ICABIOGRAD greenhouses. The field experiments were carried out in two places: Darmaga, Bogor (normal, 2 dS/m) and Eretan, Indramayu (saline, 8.4 dS/m). Floating, hydroponic and pot experiments used a split-plot randomized complete block design (RCBD) where the main plots were environments and subplots were genotypes. The field experiment used nested RCBD design where replications nested in the environment. All experiments were repeated three times. The results showed that chlorophyll (total, a and b) and carotenoids were the important physiological characters in all critical stages of rice plants exposed to salinity stress. The important morphological character in screening at germination stage was shoot height, while at seedling stage were fresh weight and dry weight of shoot, and at reproductive stage were the number of filled grains, the weight of 1000 grains and productivity. The best method for early detection of rice lines sensitive to salinity stress was hydroponics screening method. In this research, the pot screening method in the greenhouse was highly related to the adaptability of rice lines to salinity stress in the field.

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Rice OsMYB102 delays leaf senescence by downregulating abscisic acid accumulation and signaling

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MYB-type transcription factors (TFs) play important roles in plant growth and development, and in the responses to several abiotic stresses. In rice (Oryza sativa), the roles of MYB-related TFs in leaf senescence are not well documented. Here, we examined the rice MYB TF gene OsMYB102 and found that an OsMYB102 T-DNA activation-tagged line (termed osmyb102-D), which constitutively expresses OsMYB102 under the control of four tandem repeats of the 3SS promoter, and OsMYB102-overexpressing transgenic lines (3SS:OsMYB102 and 3SS:GFP-OsMYB102) maintain green leaves much longer than the wild type under natural, dark-induced, and abscisic acid (ABA)-induced senescence conditions. Moreover, an osmyb102 knockout mutant showed an accelerated senescence phenotype under dark-induced and ABA-induced leaf senescence conditions. Microarray analysis showed that a variety of senescence-associated genes (SAGs) were downregulated in the osmyb102-D line. Further studies demonstrated that overexpression of OsMYB102 regulates the expression of SAGs, including genes associated with ABA degradation and ABA signaling (OsABF4, OsNAP, and OsCYP707A6), under dark-induced senescence conditions. OsMYB102 inhibits ABA accumulation by directly activating the transcription of OsCYP707A6, which encodes the ABA catabolic enzyme ABSCISIC ACID 8'-HYDROXYLASE. OsMYB102 also indirectly represses ABA-responsive genes, such as OsABF4 and OsNAP. Collectively, these results demonstrate that OsMYB102 plays a critical role in leaf senescence by downregulating ABA accumulation and ABA signaling responses.

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Development of multi-resistant and adaptable for low nitrogen cultivation japonica rice cultivar 'Namchan'

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Recently, climate change threat rice cultivation stability and require multi-resistance about main disease. Breeding research on rice was focused on the development high quality, stability and labor-saving cultivation technologies for the stable production of rice that meets producers and consumer preferences. Rice cultivars adaptable to low nitrogen cultivation while maintaining relatively high yield and high quality rice in low nitrogen cultivation.

'Namchan' is a mid-late maturing cultivar adapting to the Honam, Yeongnam and Middle Plain area in Korea. It has multiple resistant to leaf blast(BL), bacterial blight (BB) and rice strip virus (RSV). And it is a stable variety against climatic condition and a low nitrogen cultivation adaptable variety.

The agricultural traits of 'Namchan' are 79cm in height, 14 in panicle number per hill, 112 in number of grains per panicle, 88.1% in percentage ripened grain and 21.5g in 1,000 grain weight of brown rice. The milled rice exhibits translucent, relatively clear non-glutinous endosperm and head rice milling recovery ratio is 71.6%. During 3 years of local adaptability trials (9kg/10a for N), the yield potential of 'Namchan' was estimated as 634kg/10a in milled rice, which was 18% higher than that of 'Nampyeong' and 545kg/10a in low nitrogen cultivation which was 19% higher. 'Namchan' is expected to be utilized as a stable variety against climatic change and environment-friendly cultivation strengthen the resistance to main disease and adaptable to low nitrogen cultivation.

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PCS01-31

Study of water-logging damage and tolerance of rapeseed (*Brassica napus* L.)

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Rapeseed (*Brassica napus* L.) is one of the most important oil-producing crop in the world and is mainly grown in fields. Recently, it grown with paddy in Republic of Korea and China. In order to cultivate the optimal rapeseed breeding for paddy cultivation, we observed the water-logging damage of 44 rapeseed lines during seedling stage and flowering period. After 6 days of water-logging treatment during seedling stage, the total chlorophyll content of rapeseed accessions decreased to 78% (Total chlorophyll content of water-logging treatment in 6 days / them of water-logging treatment in 0 day) on average. There were 21 lines with lower than average total chlorophyll content reduction and the lowest accession was 25%. However, there were no differences in the rapeseed accessions growth characteristics such as dry weight, leaf length and leaf width. Based on the reduction of total chlorophyll content by water-logging treatment, we selected 20 rapeseed lines showing water-logging tolerance. Water-logging stress was applied to selected rapeseed lines for 6days during flowering period. Due to water-logging treatment, rapeseed showed broken-flowering shoots and then secondary branch was growing and which causes the delaying flowering period. The mean broken-flowering shoots rate of rapeseed lines by water-logging treatment was 52.4% ‘J8634-B-30’ which has been reported to have cold tolerance, showed the lowest damage rate of 21.9%, followed by ‘F6-80’ (23.1%). The current study showed that damage of 44 rapeseed lines by water-logging during seedling stage and flowering period was confirmed and two accessions showing water-logging tolerance were identified. These lines can be used as a genetic resource to improve the water-logging tolerance.

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PCS01-32

Development of Vertical Cultivation Technology for Standardized Fruits and Mass Production of Small and Medium Sized Watermelon

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The consumption pattern of watermelons in Korea is changing from large size to small and medium size. Consumers also want a variety of watermelon varieties, such as seedless watermelons and color watermelons. To respond to these consumer needs, we have developed a vinyl house safe vertical cultivation method that can mass produce small and medium sized watermelons. The watermelon varieties used in the test were 'Black Boy', a triploid small black watermelon, and 'Lyofresh No.2', a large doubled watermelon. In conclusion, the I-type vertical cultivation was superior to the creeping or arched cultivation in terms of fruit setting ratio, yield and quality. The vertical cultivation shape is I-type, and the planting distance is 20cm. The stem is cultivated in two stalks using an induction net. Fertilize the third female flower and pinch off the shoot apex at the end of the stem. In this way watermelons fruit setting rate is improved. I-type vertical cultivation method increases the planting number four times more than the creeping cultivation. As a result, the quantity of fruit per 10a of 'Lyofresh No.2' increased 2.6 times and that of 'Black Boy' increased 2.9 times. The medium and small watermelons showed higher yields and yields than the mini watermelon cultivation method (arched cultivation). Large-size watermelons have a small fruit size, medium quality, improved quality, increased number of fruits and improved productivity. When watermelon was cultivated by I type vertical cultivation method, small fruit intensive production was possible and work efficiency was improved. After developing the standard fruit production technology of watermelon, it is expected to be able to export high quality watermelon seeds to farmers.

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Metabololites Profile Analysis of Teosinte in the Flooding Condition

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In a lot of meteorological disasters, flooding can drastically affect upland crop production loss. Especially in the development of corn varieties, there is a need for the development of corn varieties that are resistant to flooding. Teosinte contains genes for resistance to flooding because of the climatic characteristics of the collected countries. Therefore, development of corn varieties to cope with climate change and the growing corn at paddy field in Korea are required to introduce the characteristics of teosinte. In this study, we investigated to the change of metabolites related to flooding resistance after flooding conditions. In order to detect the metabolites, we analyzed metabolites using GC/MS. And then using the AMDIS program and NIST database, we created a corn metabolites library of the data obtained GC/MS. Between the treatment and non-treatment, corn leaves showed significant differences 44 metabolites out of a total of 173 substances (known 22, unknown 22). In corn root, a total of 160 metabolites were detected, with significant differences among 70 metabolites, 37 of which were known and 33 of which were unknown. Thirty-five metabolites representing significant differences between treatment and non-treatment were thought to be related to the flooding. In common with corn leaves and roots, d-fructose(Coefficient=0.893), myo-inositol(Coefficient=0.71) and L-threonine(Coefficien=0.74) were greatly increased and erythronic acid(Coefficien=0.89), galactaric acid(Coefficien=0.89) and D(+)-Trehalose (Coefficien=0.56) were greatly decreased. Therefore, although glucose may be considered a flooding resistance indicator, a more detailed study is needed. These results are thought to be available as a selection indicator for genetic resources and may be useful for the development of flooding resistance varieties.

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Identification QTL conferring anaerobic germination and effect confirmation derived from weedy rice PBR

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Direct seeding of rice is a very useful cultivation method, in particular, as means of saving labor and reducing cost. However, poor germination and unstable seedling establishment at field after seeding are major problems face in expansion of direct seeding. Korean japonica-type landrace PBR was assessed as an AG tolerance donor through low-temperature germination and germination rate under submergence in different temperature conditions. The donor was crossed with Nampyeong, and the F₁ plants were selfed to develop F₂ recombinant inbreds lines. Three QTLs, qAG1, qAG3, and qAG11, were identified by composite interval mapping on chromosomes 1, 3, and 11, respectively. The percentage of phenotypic variance explained by each QTL ranged from 6.71 to 14.52%, and the QTLs (qAG1, qAG11, and qAG3) were mapped within 0.5, 0.6 and 0.8 cM intervals between the flanking markers, respectively. In an evaluation of the most effective QTL combination under submergence, two QTL combinations (qAG1+qAG3+qAG11 and qAG1+qAG11) showed stable survival rates under all submergence conditions. Based on the results, we will characterize the candidate genes within the detected target regions in further research, and the lines with advantageous alleles will be used to develop reliable cultivars to support the wide adoption of direct seeding practices in japonica rice.

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Development of SNP-based CAPS makers for AG-tolerant rice cultivars in rice

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Anaerobic germination (AG) tolerance has been considered as one of the important factors determining the stable seedling establishment in rice wet direct cultivation. Therefore, the development of rice varieties with AG tolerance is necessary for expanding direct-seeding of rice. To increase the selection efficiency of AG tolerant line in rice breeding program, we have developed two sets of AG-resistant Caps markers (CAP1/XhoI, CAP2/DraI) detecting qAG1 and qAG11 based on re-sequencing data of the QTL regions. 188 recombinant inbred lines (RILs) and 58 BC1F2 plants were used for the validation of the markers. The results showed that two maker sets were able to accurately detect qAG1 and qAG11 locus, CAP1/XhoI could digest specifically the allele qAG1 and CAP2/DraI was able to digest specifically the qAG11. RILs and BC1F2 plants carrying qAG1 and qAG11 showed high survival rate under flooding condition, indicating a detection of the target locus by the CAPS markers. CAP1/XhoI and CAP2/DraI would be a useful in breeding programs for developing AG-tolerant japonica rice cultivars adapted to the wet-direct seeding in Korea.

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Characterization of grain-related traits of 300 Korean rice varieties

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To elucidate the characteristics of grain-related traits of Korean rice varieties bred at National Institute of Crop Science(NICS) in 1979 to 2017, we evaluated grain-related traits (grain length, width, thickness, ratio of length to width, 1,000-grain weight) using the brown rice harvested in 2018. The average of grain length ranged from 4.62 to 6.74 mm, width ranged from 2.15 to 3.45 mm, thickness ranged from 1.32 to 2.38 mm were 5.3 mm, 2.8 mm and 2.0 mm, respectively. The japonica varieties had longer grain width, thickness than Tongil-type varieties but other traits (grain length, ratio of length to width) of japonica varieties is shorter than those of Tongil-type varieties. In correlation analysis divided into japonica and Tongil-type varieties, grain length showed high correlation with ratio of length to width(0.774, 0.538) and grain width and thickness showed high correlation with 1,000-grain weight(0.725, 0.636; 0.710, 0.770). According to cluster analysis based on 4 grain-related traits except to 1,000-grain weight, 300 varieties were divided into three main groups. Group A had japonica 240 varieties and was characterized by relatively short grain length, ratio of length to width than other groups. Group B was composed of 36 Tongil-type varieties and 12 japonica black rice varieties and characterized by longer grain length, ratio of length to width shorter grain width, thickness than Group A. Group C was composed of 11 japonica varieties Sindongjin, Sobi, Huimangcham, Dumi, etc. and 1 Tongil-type varieties Mokyang and was characterized by relatively longer all traits except to ratio of length to width than other group. In further study we will perform genotype analysis of traits regarding grain characteristics the specific DNA markers.

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Biomass as a major means of affecting methane emissions

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Climate change is causing global warming and greenhouse gases are known to be one of the main causes. Most of the greenhouse gases are carbon dioxide, but the effect of keeping heat of methane is 25 times higher than carbon dioxide. Methane emissions were highest in livestock (37%), followed by rice cultivation (15%). More than 90% of methane generated in the rice paddy is released into the atmosphere through the aerenchyma, which is estimated to produce 20 to 150 Tg per year. Rice cultivation area continues to expand with population growth, and methane emissions are expected to increase accordingly. Thus, the methane-reducing technology in the rice fields is a key study to minimize climate change and keep the atmosphere. The purpose of the study was to investigate genetic variation in methane emissions; therefore, five rice cultivars were examined to relate seasonal methane profiles with anatomical and/or physiological characteristics i.e. root and shoot biomass, tiller number, aerenchyma density, plant height, developmental stage and etc. The results showed that root biomass was a major driver that affected total methane emissions. Further quantification of methane emissions was performed with ten recombinant inbred lines of a bi-parental mapping population segregating for root biomass, and verified root biomass as a trait affecting methane emissions. Soil microbiome analysis associated with root biomass is under investigation and will be assessed temporal and spatial profile of soil microbial composition using 8 RILs and 2 parents (Francis and Rondo) by 16S rDNA sequencing at four developmental stages and three root compartments.

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The RING E3 ligase, OsSIRH2-14, positively regulates response to salt stress in rice

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Salinity is major abiotic stress limiting growth, productivity, and physiology of crop plants in many areas of the world. Strategies for improving salinity tolerance in plants are critical for crop breeding programs, by modulating Na⁺ uptake from the soil. Here, we found that a rice gene, OsSIRH2-14, encoding the RING Ub E3 ligase plays an important role in salinity tolerance. The transcript level of OsSIRH2-14 were highly expressed in root tissues treated with NaCl. Subcellular localization results showed that OsSIRH2-14 was localized in the cytoplasm, Golgi, and plasma membrane. OsSIRH2-14 Physically interacted with salt-related proteins including an HKT-type Na⁺ transporter (OsHKT2;1), and then led to protein degradation via ubiquitin/26S proteasome system. Compared to wild-type plants, OsSIRH2-14-overexpressing rice plants showed significantly enhanced salinity tolerance and reduced Na⁺ accumulation in the aerial shoot and root tissues. These results suggest that the OsSIRH2-14 E3 ligase positively regulates the salinity stress response by modulating the expression of salt-related proteins.

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Comparative functional analysis of the *OsCLR1* gene induced by salt and drought stress and its grass orthologs

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Abiotic stresses such as salt and drought significantly reduce the grain yield and productivity of cereal crop. As sessile organisms, plants have evolved mechanisms that allow them to adapt and survive periods of abiotic stresses. Among these, the ubiquitin-proteasome system (UPS) has been studied as a key mechanism to understand the post-translational modification of target proteins via the attachment of molecules such as ubiquitin mediates a variety of cellular functions. Here, a rice gene, *OsCLR1*, encoding the RING-H2 type E3 ligase and its other grass orthologs were examined to determine the evolution of their molecular functions during speciation. The *OsCLR1* gene showed high expression levels under salt and drought stress. By contrast, the three grass orthologs, *SiCLR1* from *Sorghum bicolor*, *ZtCLR1* from *Zea mays*, and *TaCLR1* from *Triticum aestivum*, showed different responses to these stresses. Subcellular localization and *in vitro* ubiquitination assay showed that all four orthologs harbor E3 ligase activity with cytosol-targeted localization, demonstrating their conserved molecular functions. Heterogeneous overexpression of *OsCLR1* in *Arabidopsis* showed higher survival rates under both salt and drought stress than the control plants (WT). However, this pattern was not observed in those of the other orthologs overexpressing plants. In addition, *OsCLR1*-overexpressing plants exhibited lower germination rates in ABA than WT, while the three ortholog *CLR1*-overexpressing plants showed rates similar to the WT. These results indicate the positive regulation of *OsCLR1* in response to salt and drought in an ABA-dependent manner. Despite the molecular functions of the three *CLR1* orthologs remain largely unknown; these results provide an insight into the evolutionary fate of *CLR1* grass orthologs during speciation after the divergence from a common ancestor.

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Early Flowering, High Yielding and Multiple Disease–Insect Resistant Forage Rice Cultivar, ‘Jowoo’ Easy to Cultivate Subsequent with Winter Forage Crops

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In 2018, annual domestic rice production was amount to 386 million tons but rice consumption has constantly been decreasing, so that per capita rice consumption dropped to 61.0kg, that result in excess supply of rice. Therefore, the government is promoting "paddy field-use alternative crops cultivation support project" for a limited period of two years from 2018 to control rice supply and demand. Though forage rice is a good way to resolve that instability between supply and demand while keeping features and function of paddy field, at this point, the farmers tend to avoid to plant it without subsidies, as compared to eating rice, due to low income. And so we need to raise economic value and cultivation stability through increasing yielding capacity, disease-insect resistance and yearly production of high quality forage linked with winter forage crops, etc.. To save working on disease and insect control and to produce the ‘green’ safety forage, ‘Jowoo’ which is resistance to blast, bacterial blight(race K1, K2, K3 and K3a), rice stripe virus, brown planthopper and small brown planthopper was bred. Its average dry matter yield for three years reached 18.2 MT/ha, 19% higher than of ‘Nokyang’, that means to be able to raise economic value. Furthermore, its feed value is judged high, because its total digestible nutrients(TDN), 72.2% is equivalent to or more as compared to general forage crops. Due to those usability, ‘Jowoo’ will play an important role in controlling supply and demand through the adjustment of rice production, which is a government policy task.

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Breeding of Whole Crop Silage (WCS) Rice Cultivar for Improving Insect–Disease Resistance, Salt and Herbicide Tolerance

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To control rice over-production and increase domestic forage self-sufficiency, rice cultivars for WCS use in Korea have been bred since 2000s. Rice varieties for feed are mainly needed to have high-biomass, multiple resistance to diseases and insects, direct seeding suitability and easy weed control for cost saving and high feeding value. To develop those rice cultivars, high yielding genetic resources, Tongil-type and New Plant Type rice germplasm have been mainly used to breed. As results, rice varieties and elite lines developed for forage are resistant to lodging, despite their long leaf and culm, and have high biomass, that is, high total dry matter yield ranged from 14.7 t/ha of a ‘Jonong’ variety to 20.6 t/ha of a ‘Cheongwoo’. Moreover, some of these varieties, ‘Yeongwoo’, ‘Cheongwoo’, ‘Miwoo’ and ‘Jowoo’ are multiple-resistant to diseases and insects such as blast, bacterial blight (race K1, K2, K3, K3a), rice stripe virus and (small) brown planthopper to facilitate eco-friendly cultivation and production. Furthermore, total digestible nutrients important to evaluate feeding value are pulling up to 72.2% level of a ‘Jowoo’ variety from 59.5% of ‘Mogyang’. Most recently, to use them versatility, we are also developing salt tolerant SaltTol QTL introgression elite WCS rice line using marker assisted selection for reclaimed area utilization and imidazolone tolerant WCS rice cultivar from Yeongwoo-EMS mutant lines to cultivate easily. These useful rice varieties and promising lines are expected to contribute in control of rice over-production and self-sufficient feed supply in Korea.

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Molecular approach to develop crops with the increased productivity through regulating the shade avoidance syndrome (SAS)

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Plants absorb photosynthetically active radiation (PAR, 400-700 nm) to produce carbohydrates for the energy source. Red light:Far-red light (R:FR) ratio is reduced in the dense vegetation. To obtain the unfiltered light, plants in the shade promote the hyponastic growth, hypocotyl elongation and petiole elongation, a response known as the shade avoidance syndrome (SAS). As shade promotes the immature and rapid elongation of leaf-bearing organs and early flowering, SAS reduces the vegetable crop yield significantly. In shade-avoiding plants such as Arabidopsis, rice, tomato etc., changes in light quality and quantity are sensed by phytochrome (phy) photoreceptors. Under normal vegetation, active phytochromes (P_{A}) interact with phytochrome-interacting factors (PIFs). We have sought ways to regulate SAS for modulating the plant response, so that crop yield can be maintained with compromised responses to shade condition. Expression of some transcription factors known and unknown, have been regulated by transgenics overexpressing them or expressing amiRNAs against them. Transgenic Arabidopsis harboring TCP13-GFP displayed shade avoidance response. On the other hand, suppressed shade avoidance phenotypes were found in transgenic Arabidopsis expressing an amiRNA against TCP13, TCP5, and TCP17 (amiR-3TCP), as well as in triple mutant tcp3tcp13tcp17. AmIR-3TCP showed also compromised expression of SAS marker genes, PIL1, PIL2 and YUC9, corroborating the role of TCP13 in the shade avoidance response. Arabidopsis expressing an amiRNA against ATHB2 and its two close homologs, HAT3 and ATHB4 (amiR-3ATHB) showed elongation of root length, corresponding to diminished SAS. For further analysis, transgenic tomato will be generated with orthologs of above SAS-related transcription factors. These approach should give us insights on how we can modulate crop plants for preventing significant yield loss due to SAS.

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Development of Long Grain Type Aromatic Rice Variety ‘Hyangyeol’ Adaptable to South-East Tropical Asia

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Hyangyeol (KGIR1) as indica long grain aromatic rice variety adaptable to south-east tropical Asia was developed from the cross combination between Senpidao and SAG4. A line KR52-443-2-1 that developed in Cambodia based on pedigree selection method had good phenotype, and high grain quality and yield potential. This line has an average of 108 days in growth duration and 96 cm in plant height in tropical regions. This line showed rough rice yield of 6.05~7.21 MT/ha in Mekong delta, Vietnam and 3.40~4.85 MT/ha in Yangon region, Myanmar. This line was designated to KGIR1. In the test of value of cultivation and utility (VCU) of five Mekong delta regions, KGIR1 showed 5.86 MT/ha in dry season and 4.24 MT/ha in wet season, 2018. These yield were 97.7% and 86.7 % of the yield of Mekong delta standard variety OM5451(common non-gutinous). In regional adaptability test of heavy nitrogen fertilizer of 180 kg/ha in normal season culture in Jeonju, Miliyang and Suwon, Korea, the milled rice yield of KGIR1 was an average of 6.84 MT/ha in the range of 6.76~6.99 MT/ha. These yield means 102% of those of standard variety Dasan. KGIR1 has 6.95 mm in length and 3.19 in the ratio of length/width, and 18.3g of 1000-grain weight in brown rice. The contents of amylase and protein are 19.1% and 7.0%, respectively. In the experiment of processing in the commercial RPC, Myanmar, the percentage of whole grain was 53.3% in 12 % milling. KGIR1 has translucent and clear milled rice kernel without white core and belly. This variety has susceptible to bacterial blight and brown plant hopper, but showed resistance to blast, stripe virus and dwarf virus. KGIR1 was given the name ‘Hyangyeol’ for releasing in south-east Asia countries, Cambodia, Myanmar and Vietnam.

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Genetic analysis of QTL interaction for low-temperature germinability using introgression lines derived from O. rufipogon

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Low-temperature germinability (LTG) is one of the essential factors in direct seeding method for rice cultivation. In our previous study, five QTLs controlling the LTG were identified using BC2F2 population derived from an interspecific cross between a Korean elite line Hwaseong and Oriza rufipogon (IRGC 105491). Among this population, one introgression line, CR1022, harbors qLTG1 and qLTG3 loci derived from O. rufipogon. In this study, we examined QTL interaction between qLTG1 and qLTG3. CR1022 was crossed with Hwaseong and 769 F2 plants were generated and 60 plants which were classified as six genotype groups were selected based on the genotype of qLTG1 and qLTG3. For LTG evaluation, healthy 20 seeds of six genotype groups were incubated at 13℃ in the growth chamber and germinated seeds number was counted from 4 to 8 days after incubation. Phenotyping results showed that the O. rufipogon alleles at qLTG1 and qLTG3 increased the LTG, respectively. Moreover, plants containing both qLTG1 and qLTG3 from O. rufipogon showed the highest LTG score. A two-way ANOVA indicated significant interaction between qLTG1 and qLTG3, indicating that the two QTLs possibly have genetic interaction in regulating LTG. The qLTG3 locus was closely located with the known qLTG3-1 (Os03g0103300) gene. In addition, the sequence variation of qLTG3-1 gene was found between Hwaseong and O. rufipogon. To compare the effect of O. rufipogon haplotype in LTG, haplotype analysis of qLTG3-1 was conducted using 106 rice accessions. Understanding the genetic interaction of these QTLs will be useful in rice research and breeding especially in the development of better direct seeding varieties with LTG.

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Probable L-ascorbate peroxidase 4 gene regulates flowering time and antioxidant activity in rice

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Ascorbate peroxidase (APX) gene is one of the major members of the ROS scavenging system that plays an important role in the metabolism of hydrogen peroxide (H$_{2}$O$_{2}$) in higher plants. In this study, we characterized probable L-ascorbate peroxidase gene 4 (LOC_Os09g36750) in near isogenic line (NIL) derived from an interspecific cross between Hwaseong and Oryza rufipogon. The NIL plants showed delayed flowering compared to Hwaseong under the natural long-day condition. Flowering time (called as heading date in rice) is an important agronomic trait that determines yield in rice and is precisely controlled by various exogenous and endogenous factors. To study how ascorbate peroxidase gene is involved in the mechanism of flowering, we examined the expression levels for flowering time regulators under short-day (12h light/12h dark), long-day (14h light/10h dark), and natural long-day conditions. Also, to investigate the antioxidant activity in Hwaseong and NIL, the 3,3-diaminobenzidin (DAB) staining and 2,2-diphenyl-1-picrylhydrazyl (DPPH) assay were both conducted. The DAB staining and DPPH assay were performed to understand whether target gene plays role in scavenging H$_{2}$O$_{2}$ in rice. In addition to, we measured the APX activity from Hwaseong and NIL leaves. The oxidation of ascorbate was determined by the decrease in the absorbance at 290nm. Taken together, the probable L-ascorbate peroxidase 4 plays an important role in rice related flowering time and antioxidant activity.

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Genetic elucidation of North Korean rice varieties for salinity stress tolerance

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Rice is considered sensitive to salinity, particularly during the early vegetative and late reproductive stages. Most of the QTLs for salt tolerance were identified in bi-parental populations derived from indica varieties. North Korean (NK) rice varieties consisting of japonica germplasm have not yet largely been assessed for salinity stress tolerance. In this study, we investigated genetic composition of NK rice varieties for salinity stress tolerance by phenotyping at the seedling stage and genotyping with previously identified six DNA markers for salinity stress tolerance. Phenotypic response of rice genotypes to salinity stress at seedling stage were varied with a few strong tolerant varieties. The number of alleles for each marker were ranged from 3 to 10, and a total of 30 alleles were detected for six markers distributed on chromosome 1, 2, 3, 6, and 11. The markers for salinity tolerance derived from indica background were not significantly correlated to the salt tolerance phenotype. However, the AMT1.3 marker derived from japonica background showed significant correlation with the phenotype, indicating that this marker would be used for marker-assisted selection (MAS) for salinity stress tolerance in the NK varieties. Furthermore, these results indicate that sub-species should be taken into consideration to select DNA markers for MAS.

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Selection of Transgressive Segregants in Six Populations of Wheat in Tropical Region

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The development of tropical wheat in Indonesia needs to be done by utilizing the transgressive segregation phenomenon. The research aimed to identify transgressive segregants among F2 generation of wheat. The study was carried out from September 2017 - January 2018, at the Balithi Experimental Station, Cipanas, Cianjur regency, West Java province with 1100 m above sea level altitude. Six populations of F2 generation of wheat (Guri1/Selayar, Guri2/Selayar, Guri3/Selayar, HP1744/Selayar, Jarissa/Selayar, Vee/Selayar) and seven parent genotypes (Guri 1, Guri 2, Guri 3, HP1744, Jarissa, Vee, and Selayar) were planted in a randomized complete block design (RCBD) with three replications. Each replication was in a plot measuring 1 m x 5 m with 30 cm x 20 cm spacings so that each F2 population had 225 individuals. Observations were made on the number and seed weight per plant. The results showed that the seed number and seed weight per plant have high broad sense heritability in the six populations of F2 generation. ‘Putative’ transgressive segregants were identified as F2 individuals which perform better than the best parent. It showed that, in all populations, the best individuals have far higher number and weight of seeds than the best parent. The F2 phenotypic segregation formed a curve with positive skewness. The further the curve extending from the position of the parent indicates there would be more transgressive segregants. The rank of F2 population with the percentage of transgressive segregants for seed weight per plant from the highest is as follows: Guri3/Selayar (67.86%), Jarissa/Selayar (63.12%), HP1744/Selayar (55.88%), Vee/Selayar (44.95%), Guri2/Selayar (28.39%) and Guri1/Selayar (25.77%).

Key words: broad sense heritability, genetic variability, positive skewness, seed weight per plant

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Survival comparison of Larix spp. seedlings under drought stress

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Drought has been considered to be one of the main factors affecting forest tree survival, growth and species distribution in response to climate change. The purpose of the study is to compare drought resistance among species, families or clonal lines of Larix, the major timber trees in temperate forest. The samples were consisted of 1) open-pollinated (OP) progenies of five mother trees of L. kaempferi, 2) clonal emblings (SE-propagated plants) of 3 OP seeds of L. kaempferi, 3) clonal emblings of 3 hybrid seeds of L. kaempferi×L. decidua, 4) seedlings of L. gmelini. Drought stress was given in a way that does not water to treatment group. Wilting stage was observed and survival rate was measured every 3-4 days. As the result of survival analysis, there was significant difference in survival among sample groups (p<0.0001), but clone or family effects within groups were not observed. Among sample groups, hybrid emblings showed the highest survival rate and seedlings of L. kaempferi showed fast wilting to drought stress. The survival probabilities were higher in emblings than seedlings in L. kaempferi (p<0.0001). Hybrid emblings showed higher survival probability than L. kaempferi emblings (p<0.0001).

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**Loose Plant Architecture 1 (LPA1) mutants confers drought tolerant by altering xylem vessel enlargement in rice (Oryza sativa)**

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Loose Plant Architecture 1 (LPA1) is an INDETERMINATE domain transcription factor domain that regulates tiller angle, leaf angle, and shoot gravitropism in rice. In this study, we found that LPA1 mutants have morphological changes that confer drought resistance in rice. lpa1-2 exhibit rolled leaf phenotype that normally present in plant under drought stress. Analomical analysis showed the enlarged metaxylem vessels were absent in the vascular bundles of lpa1-2 mutant leaf blades whereas wild type and revertant have metaxylem vessels normally enlarged in the bundles. Further, we tested drought stress and water uptake efficiency revealed that lpa1-2 is more resistant to drought and used less water compared to wild type and revertant. LPA1 transcripts extracted by Laser Capture Microdissection (LCM) were expressed in the pre-vascular cells not in parenchyma cells of leaf primordium. Microarray analysis showed that differentially expressed genes related to cell wall were highly affected in the mutant. Further analysis showed that LPA1 may regulates xylem-development and Pectin degradation genes which affect the secondary cell wall formations. The result suggests that LPA1 have a crucial role in metaxylem development and the ability of drought tolerant may potential for rice breeding.

**Keyword:** drought stress, metaxylem, vascular development, water uptake

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**A salt and heat stress moderate resistance and high-yield ginseng ‘Eumseong No.9’**

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Ginseng is a perennial and low temperature crop, so it is vulnerable to physiological disorders caused by salt and heat. Therefore, it was required to develop ginseng cultivars which are resistant to salt and heat stress and have high-yield. A new ginseng 'Eumseong No. 9 (ES9)' with high-yield and salt and heat stress moderate resistance was developed in the National Institute of Horticultural & Herbal Science. ES9 seeds were collected from the farmer field in 2003. Physiological investigation and propagation were conducted from 2008 to 2010. It was given the name ES9 through the observed yield trial from 2011 to 2013 and local adaptability was carried out from 2014 to 2018. All phenotypes including agronomic characteristics, seed yield, and physiological response to biotic/abiotic stresses were investigated according to the ginseng GAP and Test guidelines. The stem color is dark-purple and distribution of anthocyanin coloration is along the whole stem. Leaflet shape in cross section is flat. Red leaf and red berry at maturing stage were observed. Inflorescence type is simple, and attitude of lower florets is horizontal. The time of emergence, flowering and berry maturity of the ES9 were similar to 'Chunpoong(CP)'. Stem length of ‘ES9’ was longer than that of CP, whereas stem diameter was thicker than that of CP. Main root length was shorter than but main root diameter is thicker than that of CP. The yield performance of ES9 was 596 kg/10 a in local adaptability test for two years, which is 10% higher than that of CP. ES9 showed moderate resistance at high temperatures and salt stress. Our study demonstrated that ES9 is an ideal variety with heavier root weight and enhanced stress resistance and contribute will enhance biotic/abiotic stress resistance and increase the farmers' income.

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Identification of QTL for rice pre-harvest sprouting in Korean varieties using a tropical condition

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Recently, in Korea, the rate of rice ripening has been accelerated year by year, due to the influence of global warming. In accordance with that, the risk of pre-harvest sprouting usually triggered by autumn rainfall is also increasing in harvest season. Pre-harvest sprouting leads to a negative effect in agronomic traits. Specially it affects rice yield, quality and processing performance. To prevent pre-harvest sprouting damage, there are strategies of escaping and resistance. The former is to adjust sowing date to avoid panicles to meet high temperature ripening and rainy season. However it has a limitation to expect exact environmental conditions during the ripening stage. The latter is to practically develop pre-harvest sprouting tolerant cultivars. To identify the QTLs related to pre-harvest sprouting, we made the 126 recombinant inbred lines (RILs) derived from a cross between tolerant Tongil type cultivar, ‘Milyang 23’, and sensitive japonica cultivar, ‘Hwayeong’. For genotyping, 816 SNP markers were evenly distributed on the twelve chromosomes. For phenotyping, one set of RILs was transplanted in a tropical region to induce rapid ripening condition. 3 panicles from 3 individuals were tagged at the early heading stage. After 40days, tagged panicles were rolled using wet paper towel and incubated at 30°C with 100% humidity for 7days. Then germination percent of each panicle was used for pre-harvest sprouting QTL analysis. We identified several significant QTLs located in 11th and 12th chromosome. And one of the detected QTLs had a high LOD score and explained over 10% of total phenotypic variation. This QTL would provide valuable information regarding development of pre-harvest sprouting tolerant cultivar.

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Mother of FT and TFL1 (MFT) gene is enable to involve Pre-harvest Sprouting (PHS) in Korean Wheat (Triticum aestivum)

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Pre-harvest sprouting (PHS) is the precocious germination condition of grains while the spike is still in the mother plant. Because PHS in wheat drastically reduced the quality and economic value of wheat grain, the improving PHS wheat is one of the most important breeding goal in Korean wheat breeding program. Mother of FT and TFL1 (MFT) gene is known to be a very important gene for seed dormancy and has been shown to be highly expressed in mature wheat seeds placed in low temperature environment. A total of 22 Korean cultivar of common wheat including ‘Keumgang’ (accession no. IT213100) and ‘Woori’ (accession no. IT175538) were used in this study. The germination experiment was conducted using the sandburry method. Phylogenetic analysis was performed for MFT gene and created the neighbor-joining tree (NJ method). Quantitative real-time PCR was carried out with DAF (Day After Flowering) wheat grain and variety germination experiment using Rotor-Gene Q (QIAGEN Hilden, Germany). The highest germination rate (>70%) was observed in most cultivar. There is no significant difference in the dormancy breaking, germination among cultivar. However, PHS by mist analysis, which did not overcome the dormancy breaking, showed that there was a difference in germination among cultivar. We isolated MFT genes from 22 Korean wheat cultivar and identified an InDel sequence (TATG) in the exon region. After phylogenetic analysis, 22 Korean wheat cultivar were classified two groups according to possess of InDel sequence. Above all, quantitative RT-PCR was performed using Korean encouraging cultivar ‘Keumgang’ and PHS resistance cultivar ‘Woori’. In particular, moisture treatment and germination experiments using ‘Keumgang’ and ‘Woori’. As a result, MFT transcript from Woori in the PHS resistant group has been confirmed to have a higher level gene expression than Keumgang in the PHS susceptible group. Further experimental results will be discussed.

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114
Characteristics of Korean wheat cultivars in terms of Cold tolerance and summer stress

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In general wheat is planted in the autumn, and harvested in the summer. But if missing the appropriate time to plant due to the overlap of another crop’s harvest season (e.g. rice), it is able to sow at the following spring. In Korea, the seasonal types of wheat are divided into I-VII types, and generally I-II types are spring type, III type is alternative, and above IV types are winter type. The domestic cultivars of wheat are mostly II-III type. In this study, we planted 44 wheat cultivars that have various seasonal types. We compared the characteristics of wheat growth, heading dates with the time of the sowing, and identified the threshold of sowing date. The results of this could be resources for selecting wheat cultivars suitable for spring and autumn sowing. Twenty seven domestic wheat cultivars, and 17 foreign wheat cultivars are sowed in spring and autumn periodically from early October of 2019 to early April of 2019. Overall, the growth characteristics of foreign cultivars were superior to those of domestic cultivars, but the heading dates weren’t earlier than domestic cultivars. The earliest heading date is 22th April 2019, and the cultivars are Kyungwang (North Korea wheat), Jonong wheat sown on 11th October 2018. In case of the spring sowing, the first heading date is 7th May 2019. Out of these cultivars, Jonong, which is known as alternative seasonal type, had earlier heading dates compared to other cultivars in both spring and autumn sowing. Jonong was the only cultivar that was shown the 7th May heading date among the cultivars sown on 14th March 2019. These results could be used as basic data for selection of wheat germplasm suitable for spring or autumn sowing. Characteristic growth traits of those cultivars including cold tolerance and behavior against heat stress will be discussed.

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Developing gene specific molecular markers of wheat related to flowering and cold tolerance

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The seasonal types of wheat are related to heading dates. The seasonal type assessment of wheat is determined by biological analysis such as cotyledon unfolding after treatment or no-treatment at low temperature. This method has the disadvantage that relatively difficult and laborious. We have tried to develop molecular markers that show different unique patterns depending on the species based on genetic diversity using genes related to the cold tolerance and flowering behavior. It is possible to use them as markers to determine the characteristics of each species. In this experiment, we extracted DNA of 8 wheat cultivars including Jokyung and Seol. We designed the gene-specific primer in gene specific genomic sequences to identify polymorphism among the wheat cultivars. Representative genes associated with seasonal type and flowering such as vernalization and photoperiod, (e.g. DREB, CBF) that were found to be related to cold stress response were selected. We will present polymorphic diversities of genomic DNA sequences of key regulatory genes related with flowering and cold tolerance.

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Functional analysis of wheat MAP kinases in response to cold stress

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MAP kinase plays diverse roles in plant growth and development and also in tolerance to biotic and abiotic stresses. MAPK cascades (MAPK, MPKK, MPKKK) control their target protein’s activity by phosphorylating its serine/threonine residues. Although MAPK family has been extensively studied in many plants, its functional characterization in wheats has been lagged due to huge and complex wheat genomes. Cold is one of the most devastating stresses in winter wheat growth. Wheats overcome freezing temperature through the process called ‘cold acclimation’, in which diverse genetic and phenotypic changes occur to minimize the stress. In this study, we first analyzed RNAseq data and screened certain wheat MAP kinases showing gene expression changes against both short and long time cold treatment. To identify their mode of actions in cold tolerance, their interacting proteins were screened using yeast-two hybrid assay. Many known stress tolerance-related proteins were identified and their gene expressions to cold treatment were observed. The interaction of the MAP kinase and its interacting protein was verified by Bimolecular fluorescence complementation assay and their subcellular location was detected using GFP-tagged fusion proteins. Our study will help to understand molecular mechanisms of cold acclimation and especially MAP kinase in wheats.

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Comparative study on drought stress response in the roots of wheat (Triticum aestivum L.)

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Drought is a major environmental stress limiting plant growth, development, and resulting in a drastic decline in the yield of crops, globally. Plant’s roots play a crucial role in water uptake, signal transduction and perception of shoots to the effect of drought. Although the response of wheat shoots to drought has been well documented, knowledge on the wheat roots response to drought stress is marginally limited. The study was, therefore, designed to comparatively evaluate the response of the roots of four wheat (Triticum aestivum L.) genotypes, differing in their response to drought stress on the basis of their genotypic variations, at the physiological, biochemical, and transcriptional regulation level. To identify the drought response of the wheat genotypes, the total biomass of plants was initially assayed. Further characterization was performed at the physiological and biochemical level by the determination of the malondialdehyde (MDA) and proline content after episodic drought treatment. Furthermore, the reverse transcription-polymerase chain reaction (RT-PCR) was performed to ascertain the changes in the expression pattern of antioxidant enzymes, expansin, osmolyte biosynthesis, and drought stress-responsive genes. Conclusively, wheat genotypes showed a differential response to drought, in relation to physiological and biochemical drought parameters evaluated, similar to differential gene expression pattern observed for drought-responsive genes used in the study. The results of the study will be valuable for identifying useful candidate genes, and for launching a breeding program for developing a novel wheat cultivar with enhanced tolerance against drought and various environmental stresses.

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Change of gluten profiling under the high temperature during grain-filling

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Hexaploid common wheat (Triticum aestivum L.) represents about 30% of the world’s cereal numbers, with over 220 million ha cultivated worldwide. Heat stress is one of the major environmental factors that gives detrimental effects on crop yield as well as quality. The increased temperature during reproductive phase of plant growth has emerged as a serious problem all over the world. To study the effect of high temperature stress on wheat grain development, especially on wheat storage protein synthesis, numerous physico-, biochemical studies were conducted. Gluten composition changes during grain-filling period under the heat stress were evaluated via 1D SDS-PAGE and 2D gel electrophoresis (2DE). Gluten proteins that were present as 2DE spots were monitored as stress period elapsed. The spot profiling was measured by intensity was grouped as 7 patterns. Among the analyzed patterns, significant spots (2 HMW glutenin, 3 LMW-glutenin, 11 Alpha-, Beta- gliadin) showing the pattern of decrease under heat stress treatment were selected. The selected gluten spots might explain rapid decrease of wheat grain and flour quality derived from the wheat grown under adverse heat temperature.

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Wheat ASR’s multiple roles in drought and salt stress

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Abiotic stresses such as drought, high salinity, cold, extreme temperatures directly affect plant growth and reducing crop productivity. Wheat is one of the staple crops in the world. Recently, wheat production is adversely affected by abiotic stresses. In this study, we identified ASR gene family from wheat using database collection with HMMER2 program in Ensembl Plants. The sequence alignment and phylogenetic analysis were performed compare with ASR sequences of other crops. Transcripts of wheat ASR genes were examined in respond to abiotic stresses and hormones. To investigate the functions of wheat ASR gene respond to abiotic stress, we generated over-expression ASR gene in Brachypodium distachyon L. Over-expression ASR gene was examined phenotypic analysis as well as physiological analysis under drought stress. Transgenic plants of wheat ASR affected expression levels of stress-related and ABA biosynthesis genes under drought stress condition. Moreover, we examined stomatal aperture in transgenic plants and WT plants under drought stress condition. In addition, we performed interaction study of wheat ASR using yeast two hybrid and BiFC assay. These results may be helpful for study of the molecular mechanisms of plant response against abiotic stresses.

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Transcriptomic analysis of two Tunisian durum wheat cultivars under salinity stress

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Durum wheat (Triticum turgidum ssp. durum) is a mainly cultivated crop for human food around the globe. As a result of worldwide climate change, durum wheat production would be more threatened by abiotic stresses such as soil salinity, drought, heat, and cold in many countries. Salinity stress is a major problem to inhibit crop production in Tunisia. To reduce this occurrence, two Tunisian durum wheat cultivars, ‘Om Rabia’ (salt-tolerant cultivar) and ‘Mahmoudi’ (salt-susceptible cultivar), were exploited to transcriptome analysis under salinity stress. Salinity stress was treated for 48 hours of 150 mM NaCl at the fully expanded 3rd leaf stage. Physiological responses in leaf blade were classified. RNA was extracted from leaf blades and RNA sequencing was performed using Illumina Hi Seq 2500. Function of differentially expressed genes (DEG) were categorized with Gene Ontology (GO) analysis. Cation binding in molecular function, macromolecule metabolic process in biological process, and nucleus in cellular component showed the highest values, respectively. Also, EuKaryotic Orthologous Groups (KOOG) analysis and Kyoto Encyclopedia of Genes and Genomes (KEGG) analysis were performed for analyzing detailed metabolic pathway. As a result, the most identified transcriptomes were involved in carbohydrate metabolism. These results would be rewarding to prospective breeding project for salinity tolerant tetraploid durum wheat.

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Traits affecting low temperature tolerance in tomato and their application in breeding program

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It is essential to develop tomato (Solanum lycopersicum L.) cultivars with tolerance to low temperature for reducing production cost and increasing fruit quality in winter. This study was conducted to investigate the effect of low temperature during the night on vegetative and reproductive growth among 40 different tomato breeding lines. Seeds were sown in October 10 of 2018 and seedlings with 5-6 true leaf transplanted on 8 November 2018 into two polyethylene film greenhouses whose night temperatures were maintained at 10°C (low temperature, LT) and 15°C (normal temperature, NT). There was significant difference in plant height between plants grown in LT and NT. The largest difference in plant height between LT and NT was observed in ‘TabtimdaengT2021’ and the smallest was ‘B-blocking’. Leaf length and width was also significantly lower in LT than NT. For stem diameter, however, differences between LT and NT were generally not significant and some lines in LT showed ticker stem diameters than those in NT. Flowering was significantly delayed among tomato lines in LTac but some lines such as ‘Power Guard’ and ‘TOMATE RASTEIRO RIO GRANDE’ showed smallest difference in days to flower between LT and NT. Most of breeding lines did not show significant difference in the number of flowers per cluster between LT and NT but in fruit set ratio per cluster. These results suggest that low temperature during the night cause retarded growth and days to flowering, which delay the harvest time. Moreover, it did not affect the number of flowers but the number of fruits per cluster, implying fertilization has more critical roles in low temperature tolerance than pollination. Breeding lines with fast growth and flower development as well as high fruit set ratio were selected for breeding cultivars with low temperature tolerance.

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Improved crop yield and soil properties with rice residue and mineral nitrogen in conservation–agriculture–based cropping systems of eastern Uttar Pradesh, India

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Heavy tillage residues in rice-wheat system have been traditionally burned or removed; that is often criticized for soil organic and nutrient losses, reducing soil microbial activity and increasing CO2 emission. Minimum tillage and appropriate management of rice-wheat residue has widely been promoted as a practice to maintain or improve soil quality and enhance crop productivity for sustainable agriculture. Field experiments were conducted in rice-wheat rotation under conservation management to determine the effects of rice residue and mineral nitrogen on crop yield and soil properties. Increasing rice residue (6 t ha−1) rates increased soil organic carbon in upper depth (0-15 cm) and decreased the soil water evaporation by 25% in comparison to no-till bare soil and reduced the soil water infiltration by 13% and soil loss by 11%. Number of spike per plant, grains per spike, grains per plant and grain weight was significantly increased with increased N and residue. The lowest grain yield was obtained from 1 t ha−1 residue incorporation without N application showing the soil N imbalance. Soil nutrient supply (N, P and K) was also influenced by rice residue and average annual SOC gain was increased with increasing amounts of residues, with a mean of 0.28 t ha−1 year−1 to ~5 t ha−1 year−1. The optimum crop growth and the highest grain yield was achieved from the highest crop residues and N rates, indicating that the most reliable system for dryland wheat production. Our results indicated that rice residue along with nitrogen fertilizers have the potential to increase crop yield, improve soil aggregation and decrease soil water evaporation.

Keywords: Conservation agriculture, rice residue management, Nitrogen, soil organic carbon, conservation tillage, productivity

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A negative regulator in response to abiotic stress, Oryza sativa Drought, Heat, and salt induced RING finger protein 1

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Environmental stresses such as drought, high temperature, and soil salinity, negatively affect germination, vegetative growth, and reproductive development of plants. Here, we reported on molecular function of a RING finger E3 ligase, Oryza sativa Drought, Heat and Salt-induced RING finger protein 1 (OsDHSRP1). Transcripts of the OsDHSRP1 gene was highly expressed at various abiotic stresses and hormone treatment, such as NaCl (200 mM), drought, and heat (45 °C) as well as such as ABA (0.1 μM). In addition, in vitro ubiquitination assays demonstrated that OsDHSRP1 with RING C3HC4 type domain harbored E3 ligase activity. The results of yeast-two hybridization, in vitro pull down assay, and bimolecular fluorescence complementation supported that OsHORP1 is able to regulate two substrates, O. sativa glyoxalase and O. sativa cysteine proteinase 1 in the cytosol. Heterogeneous overexpression of OsDHSRP1 exhibited sensitive phenotypes in compared to control plant under heat (acquired thermo-tolerance), NaCl (150, 200 mM), mannitol (100, 200 mM), and PEG (-0.5 MPa) treatment. However, OsDHSRP1-overexpressing plants showed no significant different under ABA treatment as compared to that of wild type. These results suggest that OsDHSRP1 plays a negative regulator in plant responses to abiotic stresses such as heat, salt, and drought.

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MYB96 recruits the HDA15 protein to suppress negative regulators of ABA signaling in *Arabidopsis*

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Abscisic acid (ABA) is an important phytohormone that stimulates plant responses to various environmental stresses. The R2R3-type MYB96 transcription factor is a key mediator that activates target genes involved in drought tolerance, hormone metabolism, lateral root development, and cuticular wax biosynthesis in response to ABA. The MYB96 transcription factor also represses some ABA-repressible genes to further enhance ABA responses, but the mechanism of how the transcriptional activator represses gene expression remains unknown. Here, we report that MYB96 interacts with the histone modifier HDA15 to suppress negative regulators of early ABA signaling. The MYB96-HDA15 complex co-binds to the promoters of a subset of RHO GTPASE OF PLANTS (ROP) genes, ROP6, ROP10, and ROP11, and represses their expression by removing acetyl groups of histone H3 and H4 from the cognate regions, particularly in the presence of ABA. In support, HDA15-deficient mutants display reduced ABA sensitivity and are susceptible to drought stress with derepression of the ROP genes, as observed in the myb96-1 mutant. Biochemical and genetic analyses provide further support that MYB96 and HDA15 are interdependent in the regulation of ROP suppression. Our study demonstrates that MYB96 confers maximal ABA sensitivity by regulating both positive and negative regulators of ABA signaling through distinctive molecular mechanisms.

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Evaluation of salinity tolerance of multiparent advanced generation intercross (MAGIC) population to improve salt-sensitive japonica cultivars

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Abiotic stress breeding is essential ways to prevent yield loss under stress-affected environments. Especially for damage caused by salt in soils about 6.5% of the world’s total area is affected by the stress, resulting in an abundant yield reduction every single year. However it is difficult to find resistant cultivar to the stress in *japonica* type rice due to absence of tolerant source and difficulty of excluding accompanying linkage drag. In this study, we evaluated the salt stress of *Japonica* type MAGIC population in their seedling and booting stages when are the most sensitive to the stress. 20 out of a total 380 lines showed tolerant reaction in seedling stage Based on tolerant degree of Pookali, which is salt tolerant variety. Another 30 lines present tolerant reaction in booting stage comparing reaction of salt tolerant variety, FL 478. Tolerant reaction between seedling and booting stage indicated a weak positive correlation in this population. While the tolerance in booting stage showed a strong negative correlation resulting in delaying days to heading and decline of culm and panicle length in the population. In present we are developing hydride population using the selected lines based on this study. Through further genetic analysis and QTL mapping will be performed to improve salt-sensitive *Japonica* cultivars.

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Development Breeding System of Maize Inbred Lines by Doubled Haploid Technology

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Line development and hybrid selection are the main procedures for maize breeding. Line development in South Korea is largely dependent on conventional breeding methods. This conventional line development system is tedious, labor-intensive, and time-consuming procedure. Currently, doubled haploid technology was introduced and settled in Korea by Maize Research Institute. Doubled haploid technology in maize is a rapid line development system and many foreign maize research institutes have been actively using this technology. In this study, we wanted to set up doubled haploid technology in South Korea. It is a temperate area, so we can do only one breeding cycle in a year and the yellowing time of maize is usually overlapped with rainy season in South Korea. In order to overcome this weather condition, we settled a special greenhouse for doubled haploid breeding. Line development system by doubled haploid technology considering domestic environmental conditions has three steps: haploid induction, chromosome doubling and line production in the greenhouse, and line assessment and seed multiplication. Haploid induction rate for field and waxy maize were 5.4 to 7.4 and 4.1 to 9.4 %, respectively. The number of inbred lines developed by doubled haploid technology in 2016, 2017 and 2018 were 255, 176 and 278, respectively. Using developed DH lines, we made various crosses and several hybrids such as JK185 were selected. When we compare with foreign institutes, it was not the mass line production, but it can be a reasonable settlement of doubled haploid technology in South Korea. We expect the number of annual developing lines will be increased and our breeding efficiency will be greatly progressed by this technology.

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Transcriptomic analysis of poplar (Populus alba × P. glandulosa and Populus eurameriana) in elevated CO₂ concentration

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Poplar is a significant model species for studying the effects of abiotic stresses on trees. Here, we analyzed the differences in the transcriptomes of P. alba × P. glandulosa hybrid poplar clone (Clivus) and Populus eurameriana clone I-476 using high-throughput transcriptome sequencing techniques and elucidated the functions of the differentially expressed genes using various functional annotation methods. Plants were grown at ambient (400 ppm) and elevated CO₂ concentrations (ambient × 1.4, 560 ppm and ambient × 1.8, 680 ppm) during 16 weeks in Open-Top Chambers (OTCs). We obtained 272,355 contigs raw data and identified 207,063 unigenes by Trinity transcript assembly. Transcriptomics results revealed a differential expression of 2,477 induced genes and 1,285 repressed on the leaves by elevated CO₂. Elevated CO₂ decreased the expression of genes related to Golgi membrane, zinc ion binding and lipid localization, but enhanced heat shock protein, oxidative stress related genes and starch synthase. We also detected 49,467 and 41,826 potential specific simple sequence repeats (SSRs) from the transcriptomic data for Clivus and I-476, respectively. These data should be useful for future gene discovery, molecular studies and tree improvement.

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Characterization of transcription factor genes conferring cold tolerance in rapeseed

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Brassica napus are the third most important oilseed crop in the world; however, in Korea, it is greatly affected by cold stress, especially in the winter season, limiting the growth and production of seeds. The Plant Kingdom have developed a peculiar stress response mechanism generally divided into three stages; cold stress signaling, transcriptional/post-transcriptional regulation, and stress-response mechanism. Massive no. of proteins are involved in this process, which is regulated by Transcription factors (TF). It has been reported that around 5-7% of plant genome code for more than 1500 TFs governed by multiple families, making it a suitable candidate for modification to improve cold tolerance in B. napus. Our objective here is to study different TFs involved in cold stress in B. napus. To achieve this, we performed in silico analysis to download 900 cold response genes and functionally annotate them. We then shortlisted 90 genes related to TF governed by different families and performed expression analysis. A total of 20 genes were finally identified after analyzing their expression under cold stress. The most significant members among these TF genes were comprised by Zinc finger protein, followed by heat shock proteins, and Mth TF genes. Our future prospect will be to select appropriate genes to construct a cold tolerant transgenic plant.

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Selection of Cold Tolerance Elite lines Carrying qSCT12 using MAS in Tong-il type Rice

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Extreme temperature represents a key factor limiting global rice plant distribution. Super yield rice cultivars, Tong-il rice varieties, produce high yields in temperate climates but are frequently harmed by chilling stress. Especially rice is a highly sensitive to low temperature below 15-20°C because of originating from tropical or subtropical climates. Seedling of rice is easily damaged to low temperature and result in yellowing, growth retardation, reduced tiller, which can cause severe yield losses. So, this study was developed cold tolerance elite lines by the advanced backcross and MAS in rice breeding programs. We used Hanareaum2/Unkwang F1 RILs and BC2F2 BILs population to select elite line harboring qSCT12. We observed cold phenotype of 384 RILs population in the growth chamber conditions. We selected the strongest cold tolerance line, HU165, and then advanced backcross twice. We are fine mapping by using hetero in BC2F3 generation. And then, chlorophyll content of this population was measured from these rice seedlings. For observation of cold tolerant phenotype of RIL population in the growth chamber, we treated cold stress (5-13°C) 9, 11, 13°C for 14 days and recovery for 4 days. QTL analysis was performed with QTL IciMapping program. We named QTLs as Seedling Cold Tolerant (SCT) in growth chamber. Three QTLs for SCT was detected on chromosome 11-1, 11-2, and 12. Among these QTLs, qSCT12 on chromosome 12 showed 26.3 LOD score with 25.5% of phenotypic variation. We identified a gene pyramiding effect of three QTLs when qSCT11.1, qSCT11.2 and qSCT12 were combined, cold tolerant was the strongest in our experimental conditions. We developed 20 Indel marker for finding hidden cold tolerance gene. At the same time, we selected 48 cold tolerance elite lines carrying qSCT12 using MAS 686 BC2F3 BILs population. After that we observed 48 lines in treated cold stress. The major QTL that designated qSCT12 was been mapping in 82kb region between InDel12-29 and InDel12-30. And after phenotyping, we can select 3 lines more strong cold tolerance than Hanareaum2 and very similar to Hanareaum2. Chlorophyll Content is over 160(mg/m²) and a phenotypic scale is 1 to 3. This results support that this elite line will be useful genetic resource developing for the adaptation of Tong-il type rice in the temperate regions.

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Characterization of stress associated protein 5 to drought stress tolerance in hybrid poplar

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Abiotic stresses pose a major threat to the forestry production. Stress associated protein (SAP) genes have been related to the biotic or abiotic stress response in poplars such as Populus euramatica and P. trichocarpa. However, there are few reports about the specific functions of SAP genes in trees. In this study, we isolated and characterized the molecular and physiological responses of PagSAP5 gene from hybrid poplar (P. alba x P. glandulosa). The PagSAP5 protein with AN1 and A20 Zn-finger domains were classified into the group I of SAP family. PagSAP5 showed differential regulation in response to various abiotic stresses such as drought, salt and cold. This gene was localized in the nucleus. PagSAP5 overexpression in transgenic poplar plants increased tolerance to drought stresses. Compared with wild type lines, PagSAP5 overexpression lines lead to a significant increased the expression levels of a abscisic acid (ABA) signaling related gene (ABCG22), and that of the drought inducible genes (RAB18, RD29B and RD22) under drought stress. These results suggest that PagSAP5 gene could be a valuable candidate for improving drought stress tolerance in forest trees.

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Molecular characterization of Oryza sativa arsenic-induced RING finger E3 ligase 3

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Abiotic stresses, such as high salinity, extreme temperature, drought, and heavy metals, are known to be limiting factors of agricultural productivity. In particular, high level of arsenic (As) is the most devastating environmental stress that affects plants in several ways, inhibiting growth, affecting nutrient uptake and altering plant metabolic processes. Plants have evolved diverse biological defense mechanisms against the damage or injury caused by adverse environmental conditions. One of the pathways to protect from the environment is believed to be post transitional modification through ubiquitination-mediated protein degradation. In our previous study, expression levels of 24 genes encoding Oryza Sativa RING finger protein, which were selected based on the domain analysis, were examined under arsenic stress. Among them, we further examined the expression patterns of some rice RING finger proteins in response to arsenic stress through qRT-PCR. Expression of OsAIR3 (Oryza sativa arsenic-induced RING finger E3 ligase 3, Os08g31930) was highly induced under only arsenic stress but not in other abiotic stress conditions such as drought, salt, and ABA. In vitro ubiquitination assay to examine whether OsAIR3 exhibits E3 ligase activity, showed that the OsAIR3 protein formed poly-ubiquitin products; however, a single amino acid mutation (OsAIR3C197A) of the RING domain in OsAIR3 did not form poly-ubiquitination chain. Within the cell, the expression of OsAIR3-EYFP fusion protein was found to be localized to the nucleus under AsV treatment (1,900um). For further study, phenotypical experiments with overexpressing transgenic plants and investigating proteins are interacting with OsAIR3 would be demanded.

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Functional Characterization of Drought-Responsive Long Noncoding RNAs (DRIL) in Rice

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Long noncoding RNAs (lncRNAs) have appeared as critical regulatory factors of various biological processes in both plants and animals. In Rice (Oryza sativa L.), it has been known that several lncRNAs regulate key biological processes such as phosphate homeostasis, flowering and fertility. However, systematic examination of rice lncRNAs involved in abiotic stress responses has not been reported. Here, we re-analyzed the expression profile of lncRNAs in publicly available rice transcriptome datasets derived from abiotic stress treatments to unveil the potential roles of rice lncRNAs in abiotic stress responses. Overall, we identified 10,831 rice lncRNAs that were significantly altered in shoot and/or root tissues under four different abiotic stresses. Based on Venn diagram analysis, we observed strong cross-talks between different stress signaling pathways, showing transcriptional regulatory networks underlying lncRNA expression changes in response to abiotic stresses. In addition, we identified novel drought-induced lncRNAs (DRIL) through transcriptome analysis of drought-treated rice. Real-time RT-PCR analysis confirmed the differential expression patterns of these lncRNAs under various stress conditions. To determine the regulatory role of lncRNAs in abiotic stress signaling, lncRNAs were transiently overexpressed in rice protoplasts. As a result, LNC_Os08g32065 (DRIL) overexpression increased the expression levels of stress marker genes such as Wsi18, glutamate dehydrogenase, and GEM-like protein. Our results show the first comprehensive identification and functional characterization of a group of abiotic stress-responsive lncRNAs in rice.

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Characteristics of yield and quality as affected by different seedling age among rice varieties in late transplanted rice in southern area

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Many parts of South Korea experience frequent and severe droughts due to the recent climate change. Spring drought has been repeatedly occurred water shortage region, which caused late transplanting. This study aimed to investigate the yield and quality characteristics of rice varieties by varying seedling age and transplanting time for stable late transplanted rice cultivation in southern area. We treated the days of seedling age as 25, 35, 45 and the transplanting time were on July 10th, 30th and the planting density was 92 hills/3.3 m² with early-maturing rice variety “Jomyung1” and mid-maturing rice variety “Ilmi”. As a control, we transplanted 2 type of rice varieties on June 15th with 25-days old seedlings. Each experimental group was divided into vegetative growth period and reproductive period based on heading date. At the vegetative growth period, Jomyung1 showed higher average, maximum, minimum temperature and sunshine hours and lower precipitation than that of control and Ilmi showed higher temperatures and the amount of precipitation and sunshine hours were less. At the reproductive period, both varieties showed lower temperature, sunshine hours and higher precipitation than that of control. The accumulative temperature for 40 days after heading date was 612 ~ 793 °C, which didn’t reach 840 ~ 920 °C of the optimal temperature during the ripening period. The panicle number per m² of Jomyung1 was 75 ~ 100 fewer than that of the control and Ilmi was 36 ~ 84 fewer. Grain filling ratio of Jomyung1 decreased 7.5-28.6% in each transplanting time compared to that of control, while that of Ilmi increased by 1.0-5.1%. On the 10th of July, the protein contents of the two varieties was similar to that of the control, but was higher 7.1 ~ 7.9% on July 30. The head rice ratio was similar for both varieties on July 10, but dropped to 48 ~ 81% on July 30. Head rice yield were different in seedlings with different nursery periods depending on the variety. On the 10th July, the head rice yield were 84-93% of the control at 25, 35-day old seedling for Jomyung1, 25, 35, 45-day old seedling for Ilmi. It is considered that the late transplanted rice will be possible until July 10th in southern area.

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Development of rice varieties enhancing seed weight using *Tos17* mutants

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Rice is one of the major crops in the world and provides the staple food for over half of the world's population. It is important to develop rice varieties with higher yield and stress tolerant to cope with climate change, depletion of natural resources and population growth. In the previous study, we generated 2,500 mutants via insertion of *Tos17*, a mobile endogenous retrotransposon that is active during tissue culture, using the Korean domestic rice cultivars *Oryza sativa* L. japonica Limibyeo (IM) and Baegjinju1ho (BJJ1). Here, of the 1,000 lines of *Tos17* insertion mutants, we selected 6 mutants with a 16–36% increase in the 1000-grain weight compared with that of the wild type. In the 877, 878, and 884 mutant lines, *Tos17* was inserted into the exon of phosphate transporter, the 5' UTR of *Ammonium transporter*, and the exon of *retrotransposon*, respectively. This study demonstrates the potential utility of *Tos17* mutants via an efficient tissue culture method in various rice cultivars for the improvement of agronomic traits including seed weight.

*Tos17* has been a useful tool for insertional mutagenesis and the functional analysis of genes, but it can cause somaclonal variation by alterations in gene expression during callus induction. For deletion of *Tos17* from the genome of rice, we designed CRISPR/Cas9 vector for the long terminal repeat sequences of *Tos17*. We succeeded in producing rice plants lacking the *Tos17*. This variety could be used as original seeds in rice transformation.

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Detection of associated gene with Pre–harvest sprouting in rice (*Oryza sativa* L.)

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Preharvest sprouting (PHS) is one of the most important traits considered in rice breeding program, as it reduces grain yields and grain quality under unpredictable moisture conditions. PHS resistant line (R-PHS) and PHS susceptible line (S-PHS) were selected from same F1 recombinant inbred lines(RILs). Comparing whole genome sequences of two lines, polymorphic region were explored in only four chromosomes (chromosome 1, 5, 7 and 8).

For association analysis, 89 F1 lines were developed from a cross R-PHS and S-PHS. Almost agricultural traits such as plant height, culm length, and heading date showed uniform in F1 lines. In field condition, PHS rates of R-PHS and S-PHS were 1.29% and 36.10%, respectively. PHS rates of F1 population showed from 0.0% to 77.0%. For R-PHS and S-PHS, germination rate of the panicles 45 days after heading were 7.46% and 15.48%, respectively. The germination rate of F1 population showed from 0.60% to 77.89%. After genotype analysis of segregation population, we will carry out QTL analysis that related PHS resistance gene.

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Development of evaluation system and selection genetic resources for resistance to abiotic stresses in soybean

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Drought and flooding are one of the major abiotic stresses for crop production. Soybean (Glycine max [L.] Merr.) is generally sensitive to drought and flooding stresses. It is necessary to develop drought and flood stress-tolerant cultivars to prevent yield losses in drought and heavy rainfalls worldwide. In this project, a total of 1000 soybean germplasms provided from National Agrobiodiversity Center of Rural Development Administration (RDA) will be evaluated for drought and flooding tolerance in next 5 years. This project is necessary to develop the evaluation system with 1000 soybean germplasms for drought and flooding stress and to select the stress-tolerant soybean germplasms under drought and flooding stresses. Rainout shelter and flooding canal is underway to be developed in the field to evaluate soybean accessions. The field based high-throughput phenotyping are required to understand the abiotic stresses and to monitor phenotype variation among soybean germplasms under a controlled condition in the field. The root architectures and shoot parameters under drought and flooding conditions will be analyzed to improve the accuracy and efficiency of phenotyping. Through this project, the selected soybean lines will be suitable for use as breeding materials for the development of stress tolerant-soybean varieties under drought and flooding condition. Development of mapping populations can be used for the detection of QTL regions for drought and flooding stresses. Finally, markers will be developed to select the tolerant-soybean in breeding program.

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Comparison analysis of Saltol QTL genes in enhanced salt-tolerant lines from Mogyang/IR64

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Salinity is one of the major abiotic stress that inhibit growth and decrease yield of crop plants. Therefore, it is necessary to develop a silage rice (Oryza sativa L.) with increased salt tolerance for the cultivation in saline soil such as reclaimed land. In order to develop a salt tolerant silage rice, we carried out to transfer Saltol, a major QTL associated with salt tolerance, from IR64 into Mogyang. To determine the effect of salt stress, Dongjin, Mogyang, IR64, and FL478 cultivars were grown on medium containing 0, 0.1, 0.2, 0.3, or 0.4% sodium chloride (NaCl). The shoot length was decreased with increasing salt concentration and roots growth was almost arrested at over 0.3% NaCl concentration. In addition, we observed phenotype of fifty-eight lines derived from the cross of Mogyang x IR64 (Mogyang/IR64) lines after growing on 0.3% NaCl medium for two weeks and selected 11 Saltol introgression lines showing a better growth than wild-type. The introgression type of the Saltol was by PCR using 6 QTL markers, AP3206, SKC1, PECT4, RM10793, SaT1, and RM562 from 11 Saltol introgression lines. The PCR results showed that two cross lines (767913 and 767921) were inserted with the Saltol of Mogyang type and the other cross lines were mixed with Mogyang and IR64 type. To confirm the PCR results, we conducted direct sequencing and that results showed consistent with the PCR results. The salt tolerant lines identified in this study will be further evaluated in saline soil and will be analyze the correlations of increased salt tolerance with Mogyang or IR64 Saltol.

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Elucidation of salt tolerance mechanism by OsEXPA genes in rice

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Excessive amounts of salts, especially sodium chloride, in the soil induce osmotic and ionic effects, leading to changes in plant metabolism and reduced plant growth and development in rice. Expansins are cell wall proteins that are key regulators of cell wall extension during plant growth. Overexpression of OsEXPA remarkably enhanced the salt stress tolerance with greener leaves, higher levels of chlorophylls, longer root and shoot lengths, survival rate and number of tillers under hydroponic salt stress conditions (150 mM NaCl) compared with the wild type (WT). Transcript analysis revealed that OsEXPA is spatially expressed in stem base, root and panicle, and highly induced two hours after salt treatment. Analysis with transgenic rice plants with OsEXPA:GUS represented that promoter activity was mainly observed in vascular tissue of roots and leaves, suggesting that OsEXPA is working in the vascular tissues of either root and shoot. The overexpression of OsEXPA (OX) accumulated less Na+ in the leaf and root tissues and considerably more K+ in both the leaf and root, with Na+/K+ ratio significantly lower in OX lines compared to WT. The OX lines also displayed greater antioxidant competence as indicated by their lower EC and reactive oxygen species (ROS) accumulation than WT. Comprehensive RNA-seq analysis of rice roots revealed that a total of 1948 genes was differentially expressed in different conditions. These genes were involved in the response to salt stress, ROS, cell wall modification and auxin. Further ongoing analysis including cell wall rigidity and lignin staining microscopy analysis would reveal the genuine function of OsEXPA genes in salt-stress tolerance mechanism.

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Proteome analysis of sesame leaves in response to waterlogging stress at vegetative and flowering stages

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Waterlogging, major environmental stress, impairs the plant growth and development and induces the synthesis of anaerobic proteins. To understand the molecular mechanisms coupled with morphophysiological alterations underlying waterlogging tolerance, the LTQ-FTICR MS/MS technique was employed to map the proteomes of leaves of sesame under control and waterlogged conditions. The waterlogging treatment caused dramatic alterations in morphological and biochemical properties of the leaves of sesame. For proteome analysis, more than 75 reproducible protein spots were identified on 2-DE gels wherein 51 protein spots (≥ 1.5-fold) were used to analyze mass spectrometry. Among 51 differentially abundant proteins (DAPs), 20 spots were specific to the ten-leaf stage and 31 spots were specific to the flowering stage. Most of the differentially abundant proteins involved in metabolism, and energy and stress defense with oxygen-evolving enhancer protein 1, ATP synthase subunit and heat shock proteins, glutamine synthetase, glyceroldehyde-3-phosphate dehydrogenase, superoxide dismutase were upregulated under waterlogging stress. However, the photosynthesis- and protein biosynthesis-related proteins with ribulose bisphosphate carboxylase/oxygenase activase, Sadenosylmethionine synthase 1 were down-regulated under waterlogging stress. The protein interaction network indicated that energy metabolism- and stress and defense-related proteins were involved in the protein-protein interaction network that could form an indispensable network in sesame leaves. To this end, physiological results highlighted the deregulation of photosynthesis efficiency which was consistent with results obtained at the proteome level. The upregulation of metabolism- and energy, and stress defense-related proteins in response to waterlogging stress may provide new insights into the complex mechanisms underlying waterlogging tolerance in sesame.

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In Vitro screening of Soybean Mutant lines using PEG Under Drought Stress and Yield performance under dry Land

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The development of drought tolerant cultivar is an effective alternative to overcome this abiotic stress. Four soybean mutant lines were screened at 20 % polyethylene glycol (PEG) 20% under in vitro condition and under dry land during the dry season. The objectives of the study were 1) to evaluate soybean mutant lines to drought under vitro culture and 2), to evaluated yield soybean mutant lines under dry land. The first experiments were setting up in two factors with randomized complete block design Four soybean genotypes [A2, A3, A4, A5 and two variety namely Argomulyo (Parent) and Dering (control of drought)] were used in vitro study as first factor experiment. In vitro selection was in embryogenic callus and number of plantlet level using media containing PEG (0, and 20%) as second factor experiment was done to all genotypes. Then, the second experiment was to set up in one factors with randomized complete block design, four soybean mutant lines genotypes (A2, A3, A4, A5 and parent Argomulyo with variety control drought tolerant Dering). The results showed that after 3 months in the selection medium, Combination MS with Gamborg and Soybean Mutant A2 showed a higher on weight fresh embryonic callus and percentage number of embryonic callus, percentag of plantlet compared to Argomulyo and Dering. Meanwhile A5 (parent) had the lowest weight of fresh calls embryogenic and number of embryonic callus compared to other mutant control. PEG in high concentration decreased the percentage of fresh and number of embryogenic callus and percentage number of plantlet in all genotypes. A2 and A5 soybean mutant lines somatic embryos from PEG selection successfully regenerated into plantlet as drought-tolerant. The second experiment soybean mutant lines A3 and A4 (2.42 and 2.45 t/ha) had higher yield under dry land compare to two control variety (Argomulyo 1.97 and Dering2.17 t/ha).

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Leaf and root proteome analysis of Sorghum in response to lead stress

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Lead (Pb) is one of the most hazardous pollutants of the environment that is an ecological concern due to its impact on human health and the environment. The present study aimed to identify differentially accumulated proteins (DAPs) involved in Pb stress in Sorghum bicolor seedlings. After 15 days of Pb exposure, the total protein of the fresh leaves and roots was extracted and analyzed using label-free quantitative proteomics techniques. The growth characteristics of sorghum seedlings were elucidated by treated Pb. The morphological and physiological characteristics were reduced by Pb stress. The results revealed that the growth inhibition induced by Pb depended on the degree of heavy metal concentration. The quantitative proteome analysis led to the identification of 1392 proteins, of which 627 were differentially modulated in response to Pb stress. Of the identified 627 proteins, a total of 383 proteins were specific to leaf proteins, and 244 proteins were specific to root proteins. The DAVID Bioinformatics analysis showed that the proteins with increased abundance were mainly associated with energy metabolism, detoxification and stress defense and protein metabolism, whereas the proteins related to the cell growth/division, intracellular traffic and photosynthesis were downregulated. Protein-protein interaction analyses highlighted an energy metabolism centered sub-network that synergistically responded to Pb stress. Quantitative real-time polymerase chain reaction (qRT-PCR) analysis of 5 key DAP genes revealed that most genes showed consistency with proteins changes level. Taken together, our results provide essential reference protein and gene information for future molecular studies into the tolerance and accumulation of Pb in Sorghum.

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Phenotypic screening of North Korean rice varieties for phosphorus deficiency and drought stress tolerances

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Rice cultivation is affected by several abiotic stresses which significantly reduce yield. To select tolerant rice genotypes from 190 varieties of North Korean (NK) origin, rigorous screenings were conducted in hydroponic media. Experiments were conducted for drought and low phosphorus (P) stresses under greenhouse conditions with positive and negative control genotypes. Plants grown in normal nutrient solution for 4 and 5 weeks were subjected to 20 % polyethylene glycol (PEG) and 1 ppm phosphate solution to provoke drought and low-P stresses, respectively. Morphological traits such as seedling height, root length, shoot length, root fresh and dry weights, shoot fresh and dry weights, root/shoot weight ratios were recorded. Phenotypic scoring was performed based on a Standard Evaluation System developed by IRRI. In PEG-induced drought stress screening, 84 varieties were selected as tolerant genotypes with less leaf rolling and high recovery rate, and these are also being examined in water-deficient conditions in soil pot experiment. Meanwhile, in low-P stress screening, 74 varieties were selected as tolerant genotypes with higher root and shoot dry weight and many tillers. These selected varieties can be used as useful genetic materials to identify new alleles for drought and low-P stress tolerances through genome wide association study and further breeding.

Keywords: Rice, drought, low phosphorus, abiotic stress, phenotypic screening

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Characterization of Complete Chloroplast Genomes of Artemisia capillaris and Artemisia iwayomog

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Artemisia capillaris, commonly called “Sacheolsook” is used in folk medicine and has long been used for medicinal purposes in folk medicine. A. capillaris is now cultivated korea as the natural source of a 6,7-dimethoxycoumarin, scoparone. Similarly, Artemisia iwayomog called “Hanin-jin” has been used as a substitute for A. capillaris, despite the fact that its effect is different from that of A. capillaris. In the case of A. capillaris, it has been reported that it has the effect of removing inflammation from the liver and gallbladder to urine, and promoting hepatocyte regeneration in experimental hepatitis in dogs and rats. On the other hand, A. iwayomog is said that the heat buildup promotes the secretion of bile and it only plays a role of removing the waste of the body. To distinguish them, we analyzed the chloroplast genomes of A. capillaris and A. iwayomog to investigate phylogenetic relationships and discovered potential molecular markers. The chloroplast genomes of A. capillaris and A. iwayomog identified in this study will be useful tools for basic molecular understanding and future authentication between the two.

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Key words: Chloroplast genome, molecular marker, phylogenetic tree, authentication, Artemisia capillaris, Artemisia iwayomog.

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Development of InDel Markers Based on Transcriptome Sequences and Genetic Diversity Analysis of Mungbean Varieties from China

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Mungbean is an important legume in Asia as it is rich in proteins and vitamins. However, the insufficiency of molecular markers made it difficult to perform genetic analysis of Mungbean. In this research, transcriptome sequences of mungbean varieties Sulu-1 and cm (a mutant from V1197) were compared using BLAST. 140 transcript sequences carrying insertion/deletion (InDels) were randomly selected to develop InDel markers and determined that 84 of them (i.e., 57.1%) were polymorphic between the Sulu-1 and cm. Nineteen polymorphic InDel markers were selected to performed genetic diversity and fingerprint analysis of 42 mungbean varieties from China. The effective alleles of the InDel markers were between 1.0998 and 1.9955, with an average of 1.750. The expected heterozygosity(He) was between 0.0918 and 0.5049, with an average of 0.421. The variation of Nei’s gene diversity index was between 0.0907 and 0.4989, with an average of 0.416. The value of the polymorphic information content(PIC) was between 0.0866 and 0.3744, with a mean of 0.325. By utilizing UPGMA, 42 varieties were grouped into 2 classes when the genetic similarity coefficient is 0.522. Genetic analysis showed that the 42 mungbean varieties have been separated from the effect of regional isolation. The DNA fingerprints of 42 mungbean varieties were generated by these polymorphic informations and each variety could be accurately identified. Thus, taking advantage of user-friendly InDel markers, our results provided scientific basis or the fingerprint analysis that might be useful in clarification and protection of mungbean varieties.

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Draft genome of a cereal and medicinal crop, Coix lacryma-jobi, in the Poaceae family

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Coix lacryma-jobi, called adlay or Yulmu, is an annual herbal plant belonging to the Poaceae family and has been cultivated as cereal and medicinal crop in Asia. At present, its genomic resources were very limited for understanding and breeding of this plant species at molecular level. On this account, a draft genome of a Korean cultivar Johyun of C. lacryma-jobi variety ma-yuen was generated by de novo assembly of genome sequence data generated by PacBio and Illumina platforms, which consisted of 3,362 scaffold sequences with total length of 1.28 Gb, representing 90.8% of estimated genome size (1.41 Gb). About 77% of the draft genome were occupied by repeat sequences, most of which were LTR-type transposons such as Gypsy and Copia. Evidence-based gene prediction identified 47,263 protein-coding genes in the draft genome. The draft genome sequence and gene set for C. lacryma-jobi variety ma-yuen were firstly generated in this study and will be valuable for molecular breeding and pharmacological study of this plant species. Here, we will present the detailed results of the draft genome assembly.

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Nanopore sequencing and its application to genome assembly of various organisms

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Nanopore sequencing technology of Oxford Nanopore Technologies (ONT) is the latest 3rd generation sequencing technology released in 2014 and provides its own advantages beyond other sequencing technologies, such as cost-effective high-throughput sequencing of long DNA molecules in a short time. Therefore, this sequencing technology is now providing new opportunities for efficient and high-quality genome assembly. For example, so far more than 120 genomes of various organisms (viruses, bacteria, fungi, protozoa, animals and plants) have been successfully assembled using Nanopore sequencing technology. Phyzen (www.phyzen.com) has provided Nanopore sequencing service firstly in Korea since March 2018 and established an optimized experimental and bioinformatics pipelines for Nanopore sequencing in order to produce the best quality result for researchers in various fields of biology. We sequenced more than 140 samples and analysed total >750 Gb Nanopore sequencing data until now. Using the Nanopore sequencing data, we also performed de novo genome assemblies of bacteria, fungi, mushrooms, animals and plants and then generated assembled genome sequences with better quality than those of previously reported reference genome sequences. Here, we will present data obtained by our Nanopore sequencing service and some examples of genome assembly using Nanopore sequencing data.

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Identification of QTLs controlling seed weight and days to flowering in zombi pea (Vigna vexillata (L.) A. Rich), an underutilized legume crop

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Zombi pea (Vigna vexillata (L.) A. Rich) is a legume crop which is resistant to several biotic and abiotic stresses. Seed weight and flowering date are important agronomic traits contributing to seed yield. In this study, we identified quantitative trait loci (QTLs) for seed weight and flowering date in zombi pea. An F2 population of 198 individuals developed from a cross between “TVNu 240” (cultivated) and “TVNu 1623” (wild) were used to construct a linkage map of 11 linkage groups (LG) comprising 6,529 SNP markers. Comparative genome analysis revealed that high genome homology between zombi and cowpea (Vigna unguiculata (L.) Walp.). Inclusive composite interval mapping identified three major QTLs (PVE >10%) and one minor QTLs (PVE < 10%) for seed weight, one major QTL and two minor QTL for the flowering date. The major QTLs for seed weight were mapped to linkage groups 5 (qSdw5.1, qSdw5.2) and 8 (qSdw8.1). While the major QTLs for days to flowering date were mapped to linkage group 5 (qFld5.1). Our results will be useful for improvement of zombi pea and related legume species.

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Development of LOX-3 null near-isogenic *japonica* rice line and characterization of seed longevity and stale flavor

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Lipoxygenase-3 (LOX-3) is a key enzyme involved in the peroxidation of polyunsaturated fatty acid such as linoleic and linolenic acid in rice. The peroxidation causes the production of volatile constituents related to stale flavor of stored rice. This breeding program was conducted to develop the LOX-3 null near-isogenic *japonica* rice line in the genetic background of Saenuri, mega variety of Korea and elucidate the effect of introgression of the LOX-3 null allele. We developed the LOX-3 null near-isogenic *japonica* rice line, Jeonju624 by backcrosses to Saenuri, marker-assisted selection for LOX-3 allele, and phenotypic selection for similar agronomic characteristics of Saenuri. In the analysis using 406 KASP (Kompetitive Allele Specific PCR) markers, Jeonju624 was confirmed the near-isogenic line recovered the 95.8% genetic background of Saenuri. After storage in the high temperature condition (35°C), Jeonju624 showed higher germination rate, lower fat acidity and lipoxygenase activity than Saenuri. Hexanal, major component of stale flavor of stored rice, contents of Jeonju624 showed lower value and variation than that of Saenuri. Jeonju624 exhibited an enhanced seed longevity and an reduced stale flavor than Saenuri. Jeonju624 could be utilized in the breeding programs for enhancing the quality of stored rice.

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Sequencing of the tetraploid *Perilla (Perilla frutescens)* genome

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*Perilla* is an annual plant of the Lamiaceae family mainly cultivated in East Asia. Its seeds contain a high amount of unsaturated fatty acids (more than 60 % of total fatty acid), which is very beneficial to not only human health but a plant oil industry. Hence, interpreting the *Perilla* genome is essential to better understand this crop. Here, we report progress on the de novo genome assembly of *Perilla* variety ‘Deasildeulkkae’ (*P. frutescens*, 2n=4x=40). Fluorescence in situ hybridization (FISH) analysis was performed to draw chromosome specific genetic map and to identify molecular cytogenetic karyotypes. The assembly of a draft de novo genome by Illumina short read and PacBio sequencer platforms is on-going and we estimated the genome size of 1.379 Gb using Jellyfish program. Using a total of 130.2 Gb PacBio data merged with three assemblies (Falcon-Integrate, -Unzip and Arrow), the genome assembled into 3,470 contigs (N50, 528,499 bp) with a total length of 1.152 Gb. Though the process of Hi-C grouping, we analyzed contig clustering and ordering/orientation. Contigs genome was grouped to 20 superscaffolds total genome length of 953.4 Mb by Hi-C heatmap. We also identified chloroplast (cp) genome sequences of six cultivars and three wild *Perilla* species, and comparative sequence analysis of the complete cp genome sequences. Additionally we constructed recombinant inbred lines (RILs) between ‘Deasildeulkkae’ and ‘Ipdeulkkae-1ho’ cultivated *Perilla* for prepared high density genetic map. The results above will provide useful information of the genome structure to understand the functional genomics of *Perilla*.

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Analysis of the characteristics of transcriptomes in rice by submergence during the ripening stage

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Research on the submergence stress of rice has concentrated on the quiescence strategy to survive in long-term flooding conditions based on Submergence-1A (SLUBA). In the case of the ripening period, it is important that submergence stress can affect the quality as well as the survival of rice. Therefore, it is essential to understand the changes in the distribution of assimilation products in grain and ripening characteristics in submergence stress conditions. However, such studies have been insufficient at the physiological and molecular biological levels. We confirmed that the distribution rate of assimilation products in grain was decreased by submergence treatment. These results were caused by an increase in the distribution rate of assimilation products to the stem according to escape strategy. To understand this phenomenon at the molecular level, we analyzed the relative expression levels of genes related to sucrose metabolism, and found that the sucrose phosphate synthase gene (OsSPS), which induces the accumulation of sucrose in tissues, was decreased in the seeds and leaves, but not in the stems. Furthermore, the sucrose transporter gene (OsSUT) related to sucrose transport decreased in the seeds and leaves, but increased in stems. We also analyzed the biological metabolic processes related to starch and sucrose synthesis, carbon fixation, and glycolysis using the KEGG mapper with selected differentially expressed genes (DEGs) in seeds, stems, and leaves caused by submergence treatment. We found that the expression of genes for each step related to starch and D-glucose synthesis was down-regulated in the seeds and leaves but up-regulated in the stem. The results of this study provide basic data for the development of varieties and corresponding technologies adapted to submergence conditions, through understanding the action network of the elements that change in the submergence condition, as well as information regarding these DEGs.

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Fine mapping a major QTL associated with seed dormancy in mungbean (Vigna radiata (L.) Wilczek)

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Weather damage due to rains before and during harvesting of cereal and legume crops can impair seed yield and quality, thus reducing the value of the crops. Hardseededness (a type of seed dormancy) is considered a useful trait in mungbean (Vigna radiata (L.) Wilczek) breeding for weather-tolerant varieties. In this study, we fine-mapped a major quantitative trait locus (QTL) Sdp1.1 previously reported for seed dormancy in wild mungbean (Vigna radiata var. sublobata) using an F2 population derived from a cross between cultivated mungbean (Vigna radiata var. radiata) and wild mungbean. The results showed that the QTL Sdp1.1 is dissected into two QTLs, namely qSdp1.1a and qSdp1.2b. qSdp1.1a and qSdp1.2b accounted for 23% and 6% of the total variation in hardseededness. qSdp1.1a was mapped to a 1.1-Mb region, while qSdp1.2b was mapped to a 3-kb region of mungbean chromosome 7. Our findings are useful for further research to identify causal genes controlling seed dormancy and for genetic improvement of this trait in mungbean.

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Re-sequenced 235 wild and cultivated soybean accessions reveals genomic signatures for domestication and subsequent improvement

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Cultivated soybean experienced artificial and natural selection during domestication and improvement. These selections affected the cultivated soybean to increase their fitness for the environment and to improve human-favorable traits. A total of 235 soybean accessions consisting of 112 wild (Glycine soja), 79 landraces (Glycine max), and 54 improvements (Glycine max) were re-sequenced at an average of 11x depth that covered 98% of a reference genome, and approximately 19M of bi-allelic SNPs were finally obtained after genotype calling and strict filtering processes. The landraces and the improvements were divided into two groups each based on structure, phylogenetic tree, and principal component analyses (Landrace-1, n=22; Landrace-2, n=57; Improvement-1, n=35; Improvement-2, n=22). Through extensive studies to find signals of selection, we found the improvement-1 and the improvement-2 groups have selection signals for drought tolerance and disease resistance, respectively. In addition, the landrace-1 and the landrace-2 groups showed selection signals for cold acclimation and response to auxin stimulus, respectively. In the further study, we will focus on the genes identified in the selection signals of each group and present the missense SNPs fixed in the gene with haplotypes, linkage disequilibrium, and diversity patterns.  
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Transcriptome analysis for anthracnose resistance in watermelon reveals insights into the co-expression patterns of changeable expression

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Anthracnose is a representative disease in watermelon. Colletotrichum orbiculare can cause severe damages to the hypocotyl and the fruits of watermelon. Especially, when watermelon is infected in young plant stage, the pathogen causes water soaking lesions at the hypocotyl, resulting in death. Recently, single-nucleotide polymorphism markers related with Anthracnose resistance were identified through genetics approach, but the resistance mechanisms and pathogenesis based on the transcriptome are still poorly understood. We hypothesized that detailed mechanisms of the resistance can be understood by analyzing the expression pattern of the resistant and susceptible breeds. Herein we performed RNA-sequencing of 30 samples from two watermelon cultivars such as Dhls7250 and Ot09491. We considered three biological replicates at diverse time-points such as 0, 0.3, 24, 72, and 120 hours, after spray-inoculation with C. orbiculare race 1. We conducted a statistical analysis to identify differentially expressed genes (DEGs) between resistant and susceptible cultivars at each time-point, resulting in 473, 938, 592, 1026, and 5701 significant DEGs, respectively, at false discovery rate (FDR) adjusted P-value < 0.01. The 39 genes showed a certain trend between the two cultivars regardless of the elapsed time and these genes are significantly enriched in regulation of innate immune response (P=0.0038), response to virus (P=0.0019), and four circadian rhythm related pathways. We also performed co-expression network analysis to decipher complex expression patterns of the time-series data, finding in 30 co-expression modules through scale-free topology model at signed R2>0.9. The co-expressed genes of each module were enriched in the biologically relevant pathways. These results provide insight into gene-expression change by response to the watermelon’s Anthracnose race 1. We believe this study provides a step forward in deep understanding the mechanisms and pathogenesis of anthracnose resistance in watermelon.  
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Molecular mapping of the unstable Restorer-of-fertility (Rf) gene in sweet pepper (Capsicum annuum L.)

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Cytoplasmic-genic male sterility (CGMS) has been used for F1 hybrid seed production in several crop plants. The CGMS system is determined by interaction between cytoplasm male sterility (CMS) associated mitochondrial gene and the Restorer-of-fertility (Rf) gene in nucleus. In the previous studies, several Rf-linked markers and candidate genes were identified. However, the unstable Rf genes that are affected by environmental conditions have rarely been studied. In this study, we investigated the male fertility phenotype of the unstable Rf gene and developed markers linked to the unstable Rf gene. The male fertility phenotype was inherited as a 3:1 ratio in a population derived from a cross between MSGR-A with stable sterility (rf/rf) and SPR03 with unstable fertility (Rf/Rf) indicating that the unstable Rf gene is controlled by a single dominant gene in the permissive temperature. Genetic mapping revealed that 214.14MB-CAPS is co-segregated with the unstable Rf locus. Candidate genes were predicted using the sequences within the delimited region between 13T7-SCAR and G16-SCAR. Total 37 and 80 predicted genes were detected in the target region from Zunla-1 and CM334 (UCD 10X), respectively. Predicted genes related to unstable Rf couldn’t be found in Zunla-1. However, in CM334 (UCD 10X), pentatricopeptide (PPR) gene, protein gamete expressed 2 (GEX 2) and peroxidase were detected in the target region. When diverse breeding lines were tested, the genotype of 214.14MB-CAPS was correlated the phenotype of unstable fertile lines (91.6%). However, stable male sterile lines could not be clearly distinguished with this marker. Phylogenetic tree based on the genotype of several markers linked to the Rf locus showed that stable or unstable lines were coarsely clustered together.

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Draft genome assembly of the Korean sesame (Sesamum indicum) variety Goenbeak

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Sesame is known as one of the oldest oil crops in the world. Despite the fact that it is considered as an orphan crop, a significant effort for unravelling sesame genome structure has been done. During the last decade, next-generation sequencing technologies provided sesame assembly with 16 pseudomolecules. The recent improvement of the Chinese sesame "Zhongzhi 13" assembly through a high-density genetic map, suggested 13 genetic linkage groups. Here we report the first genome assembly construction of the Korean variety Goenbeak. The methodological approach involved a combination of short (Illumina), long (PacBio) reads sequencing technologies. The K-mer analysis showed that the estimated genome size was 322 Mbp and the heterozygosity ranged from 0.0485 to 0.0501%. Based on Falcon-Unzip assembler algorithm, we found that the total size of contigs was 281.7 Mbp resulting in 87.5% of the expected genome. The quality of our assembly was checked using several metrics. Illumina and PacBio datasets were mapped onto the reference genome using the new alignment algorithm BWA-MEM resulting up to 95.8% of mapping rate. Gene set orthologs quality control of our assembly performed by benchmarking our results to the BUSCO embryophyte lineage profiles showed 86.9% of complete and single-copy orthologs. To produce an accurate gene model of the Korean sesame, gene expression study was initiated. The high-quality chromosome scale of Goenbeak will be a highly valuable resource for sesame breeding and provide a blueprint for the genetic basis of biotic and biotic stress and functional genomics.

Keywords: sesame, Goenbeak, genome sequencing

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Barley RNA viromes in six different geographical regions in Korea

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Barley is a kind of cereal grass belonging to the family Poaceae. To examine viruses infecting winter barley in Korea, we carried out a comprehensive study of barley RNA viromes using next-generation sequencing (NGS). A total of 110 barley leaf samples from 17 geographical locations were collected. NGS followed by extensive bioinformatics analyses revealed six different barley viromes: Barley yellow mosaic virus (BaYMV), Barley mild mosaic virus (BaMMV), Barley yellow dwarf virus (BYDV), Hordeum vulgare endornavirus (HvEV), and Barley virus G (BGV). BaYMV and HvEV were identified in all libraries, while other viruses were identified in some specific library. Based on the number of virus-associated reads, BaYMV was a dominant virus infecting winter barley in Korea causing yellow disease symptoms. We obtained nearly complete genomes of six BaYMV isolates and two BaMMV isolates. Phylogenetic analyses indicate that BaYMV and BaMMV were largely grouped based on geographical regions such as Asia and Europe. This is the first study of barley RNA viromes in Korea.

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Molecular mechanisms of high-rutin content in tartary buckwheat revealed by whole genome sequencing

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Tartary buckwheat (Fagopyrum tataricum) is a valuable crop due to its characteristic functional component, rutin for medicine and health. We generated a high-quality draft genome of a high-rutin tartary buckwheat cultivar (F. tataricum cv. Daegwan). The genome of tartary buckwheat included higher copy numbers of genes encoding enzymes synthesizing precursors of rutin than those of common buckwheat and Amaranthaceae family crops. Notably, we identified an inverted tandem duplication of gene loci encoding paralogs of flavonol synthase 1 (FlLS1). The inverted tandem duplication was also present in the co-linear region in the genome of grape, another species known for high flavonol content, but absent in genomes of common buckwheat and Amaranthaceae crops. Comparative analysis of FlLS1 loci demonstrate that these genes of F. tataricum expanded through sequential tandem duplications different from common buckwheat (F. esculentum). The tandem duplicated FlLS1 showed flower-specific expression in F. tataricum. Correspondingly, rutin content increased in flowers of F. tataricum, compared to common buckwheat. In further work, by a dedicated qPCR array platform, the transcript levels of rutin biosynthetic genes, including paralogs, will be determined in flowers, leaves, stems and roots to elucidate the pathway regulatory mechanisms.

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Improvement of Button Mushroom (*Agaricus bisporus*) Genome Assembly via the Hybrid Assembly with Oxford Nanopore Technology and Illumina MiSeq

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The button mushroom (*Agaricus bisporus*) is a widely cultivated and consumed edible mushroom. In spite of economic significance, it is little known on the genomic study of *A. bisporus*. We performed a hybrid assembly using two types of platforms (Oxford Nanopore Technology MinION and Illumina MiSeq platforms) to obtain the complete *A. bisporus* ASI1011 genome. The completed new *Agaricus bisporus* ASI1011 genome was compared with two previously reported references (*A. bisporus* H9 and H97). As a result, It was possible to obtain 33 Mbp *A. bisporus* ASI1011 genome with more than 3 Mbp larger than the previously reported reference (30 Mbp) genomes. Gene prediction was performed on three genomes (*A. bisporus* H9, H97 and ASI1011), and the total number and gene density of *Agaricus bisporus* ASI1011 (present study) were 11,328 and 2,917, respectively, which were the highest among them. The gene distributions at the chromosome level of *A. bisporus* ASI1011 and *A. bisporus* H97 (Sanger sequencing) were very similar. *A. bisporus* ASI1011 and *A. bisporus* H9 (Pacbio sequencing) showed different genes on chromosome 6 and 11. As a result of comparison with two previously reported reference genomes (*A. bisporus* H9 and H97) to find additional 3 Mbp genome components (*A. bisporus* ASI1011), repeat masked (LINE, LTR, DNA), intron and exon regions were higher than the other two genomes. Consequently, the quality of *A. bisporus* genome could be improved by the hybrid assembly. Our results could provide useful information for establishing molecular genetic markers that could be used to improve the agricultural traits of *A. bisporus*.

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Investigation of single nucleotide polymorphism in glucosinolate biosynthesis related genes among subspecies of *brassica rapa*

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To better understand glucosinolate biosynthesis in *brassica rapa*, focusing on the glucosinolate biosynthesis related genes were needed. Thus, we have identified single nucleotide polymorphism (SNP) in the genes among subspecies of *brassica rapa*. For this, two types of sequencing platform, which contain Illumina HiSeq4000 for short-reads paired-end data and PacBio Sequel for long-reads Single Molecule Real Time (SMRT) data, were applied for 3 subspecies; chiifu, pakchoi, yellow sarson. And then, we performed assembly for the 3 subspecies genomes (chiifu 320Mbp, pakchoi 362Mbp, yellow sarson 307Mbp) using FALCON-Unzip and Plion for assembly and error correction, respectively. Furthermore, KEGG pathway database played critical roles in collecting 20 glucosinolate biosynthesis related genes (9 enzymes) in *Brassica rapa*. To compare similarity in the genes among the 3 species, the alignment was performed by GenomeThreader. From this, we could extract both nucleotide sequence in coding region and peptide sequence in translated region. Then, clustalw2 was used for multiple alignment with sequences of each gene. Finally, we have investigated single nucleotide polymorphism (SNP) in glucosinolate biosynthesis related genes by the alignment. Our approach is the first time for efficient discovery of glucosinolate biosynthesis related variation, and we hope that our result could be the potential sources for future development of genetic marker.

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Mutation of TF1 cause the Function Loss of regulating Anthocyanin Biosynthesis in Chrysanthemum

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Chrysanthemums, are known globally for the one of the most important plants in floriculture industry, have a variety of colors due to anthocyanins accumulation. Anthocyanin is the most well-studied secondary metabolite in plants. Anthocyanin biosynthesis is known to be regulated by several transcription factors (TFs). To investigate regulation of TFs in the anthocyanin biosynthetic mechanism, we analyzed three different Chrysanthemum cultivars OB, DP and RM, which showed white, pink and red ray floret colors, respectively. We identified that TF1 gene derived from OB was mutated in structure analysis whereas those derived from DP and RM was not. Through the subcellular localization, TF1 gene derived from OB was abnormally localized in Arabidopsis protoplasts. To validate the function of TF1 and TF2 in planta, we performed a transient assay with tobacco leaves. It revealed that simultaneous expression of TF1 and TF2 from RM accumulate anthocyanins, but that from OB did not show any pigment. Complementation of the Arabidopsis tt8-1 mutant, which lacks red pigmentation in leaves and seeds, with TF1 from RM restored red pigmentation, and resulted in high anthocyanin and proanthocyanidins contents in the leaves and seeds, respectively. On the other hand, TF1 gene derived from OB didn’t restored red pigmentation, indicating that the white colored OB was caused by TF1 mutation. Yeast one hybrid (Y1H) showed that TF2 from OB had the same function with that from RM, whereas the TF1 and TF2 from OB cannot interact with each other. Taken together these results suggested that interaction between TF1 and TF2 play an important role for anthocyanin biosynthesis in Chrysanthemum.

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**PCS02-19**

Integrative analysis of metabolome and transcriptome of large- and small- nut in Korean chestnut trees (*Castanea crenata*) during nut development

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Chestnut is extensively cultivated as a food crop in Asia and Europe for its highest commercial values. Chestnut contains high nutrient with low in fat which also act as alternative food source. Remarkably, the fruit quality is mainly determined by sugar contents and nut weight. To understand the correlated molecular mechanism between these determined factors, we compared metabolomics and transcriptomic profiling in two representative genotypes, Daehan (large nut bearing individual) and Jangwon (small nut bearing individual) during nut development. Metabolic analysis revealed that 17 metabolites were differentially accumulated between Daehan and Jangwon. Among these metabolomes, sugars and organic acids were identified during nut development. Furthermore, our metabolomics data showed the significant negative correlation between sugar contents and nut weight at stage III using test populations (n=30). We further performed Illumina platform transcriptome sequencing, and 141,895 unigenes including 705 up- and 416 down-regulation were differentially expressed more than 2-fold between Daehan and Jangwon. The expression level of granule-bound starch synthase (GBSSI and GBSS2) was higher in Daehan, while starch hydrolytic enzymes, B-amylase (BAMY1, BAMY2, and BAMY3) was lower in Daehan. Taken all together, these results indicate that both the sucrose contents and the expression levels of starch metabolic enzymes might be important factors involved in the determination of chestnut nut quality.

Keywords: *Castanea crenata*, nut development, sucrose, metabolic, transcriptome sequencing

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Whole genome wide sequence variation in dwarf derived from normal growth of F7 RILs of crossing between cultivar and wild type in soybean

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Plant height is an important component of plant architecture, and significantly affects crop breeding practices and yield. Here, we report the characterization of dwarf mutant (sample id 1282 and 1303) derived from crossing of G. max var. Peking and G. soja var. IT182936 in F5 RIL population. The dwarf mutant displayed reduced plant height and shortened internodes. With the help of Illumina high-throughput platform variant analysis was carried out and compared among normal and dwarf in triplicates in samples named 1282N, 1282D, 1303N and 1303D where “N” stands for normal and “D” stands for dwarf phenotype. We obtained 458,209 SNPs in 1282 of which 57,098 SNPs were of homozygous type. Likewise for 1303 sample 337,001 SNPs were obtained of which 253,032 SNPs were of homozygous type. A total of 51,622 INDELs were of homozygous types among 108,277 INDELs obtained in 1282 and 63,184 homozygous INDELs were found out of 100,267 INDELs in 1303 sample. We discovered a total of 33 homogenous non-synonymous SNPs that are happen at the same loci in each 2 sets of dwarf and normal soybean derived from normal growth soybean. Our results provide important information for improving our understanding of the genetics of soybean plant height and crop breeding. These could be useful genetic resource for plant breeders, geneticists and biologists.

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Genome-wide identification and characterization of bZIP transcription factor gene family in mungbean (Vigna radiata (L.) R. Wilczek)

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Basic region leucine zipper (bZIP) transcription factor family is one of the largest families in plant species, and is known to play crucial roles in plant development from various signaling responses to organogenesis. Because of its significance, genomic studies of bZIP transcription factor (TF) have been conducted in many important plant species, such as Arabidopsis, rice and maize. Mungbean (Vigna radiata (L.) R. Wilczek), although recognized as one of the major crops in Asia for its high level of protein and vital micronutrients, has not been studied for its identification and characterization of bZIP TF. Recently, reference genome sequence of mungbean has been published. In this study, based on the mungbean genome sequence and annotations, bZIP TF genes in mungbean were identified using sequence similarities of known Arabidopsis bZIP TFs, and further verified with domain search. Based on the maximum-likelihood tree constructed from bZIP TF sequences of Arabidopsis and mungbean, mungbean bZIP TF clades were classified and other conserved motifs were analyzed. Additionally, possible gene duplications and sequence variations within regions of bZIP TF sequences were found with synteny analysis of mungbean genome. To check expression level variations of bZIP TF genes among four tissues of mungbean, including leaf, flower, pod and root, expression heatmap was constructed using RNA-Seq data. Dimerization patterns of mungbean bZIP transcription factors were also analyzed and classified accordingly. With the genome-wide study of bZIP TF genes in mungbean, the data can further be utilized to elucidate the mechanisms behind various stress responses and development of mungbean.

Keywords: Vigna radiata, bZIP transcription factor

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Identification of microRNAs and their abiotic stress-related target genes in flood-treated soybean Cheongja-3

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MicroRNAs (miRNAs) are non-coding RNAs that regulate gene expression by cleaving mRNAs or disturbing translation process. They are known to act in plant development as well as in defense mechanisms against stress due to abiotic factors. Flooding is one of the critical abiotic stresses that influence crop growth and productivity. The flooding stress particularly causes negative effects on growth and productivity of soybean (Glycine max) that is relatively sensitive to wet soil environment, due to poor root respiration and nutrient uptake.

In this study, miRNAs' comparative study was conducted among flood-tolerant soybean Cheongja-3 (Glycine max), and soybean (Glycine max), rice (Oryza Sativa), Arabidopsis (Arabidopsis thaliana). In Cheongja-3, a total 247 conserved miRNAs are found and belong to 102 known miRNA families in miRBase. Of them, 21 common miRNA families were identified in the four crops and miR156, miR159, miR160 target Myb domain protein and auxin response factor which are stress-related genes. We showed that the target transcripts of miR156, miR159, miR160 between Cheongja-3 and WS82 (G.max) are in orthologous relationship. Especially, miR319 and miR390 are found in Cheongja-3, and they appear to be related to non-coding RNAs. Through this study, we will provide the epigenetic information on two components of abiotic stress regulation, miRNAs and their target genes in Cheongja-3.

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MutMap analysis reveals loci for growth traits in rice

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We analyzed three rice mutant lines which are Ds061942, Ds073406, and Ds074081 among the Ac/Ds insertion mutant population. These mutant lines showed phenotypes of reduced plant height and shortened culm length. The mutant lines were crossed with their wild type variety, Dongjin. All of F1 plants showed wild type phenotypes, and F2 segregation ratios were fit to 3:1 (wild type : mutant type), which indicated that single recessive gene controls mutant traits. Recession of the three mutant lines were performed using Illumina HiSeq 2000 platform. 13.9-15.2 Gbp sequence data were produced per mutant line. After quality trimming and read-mapping onto rice reference genome sequence (Nipponbare), 9.9-10.7 Gbp were mapped onto the reference sequence resulting in average mapping depth of 26.55-28.75x. By comparison with Dongjin resequencing data, 42,386-56,988 single nucleotide polymorphisms (SNPs) were found between each mutant line and Dongjin. MutMap analysis was performed by pooling mutant type F2 plants and resequencing the pooled DNA. It was found that the causative mutated genes were located on chromosome 3, 4, and 7. We developed cleaved amplified polymorphic sequence (CAPS), and derived CAPS (dCAPS) markers on these chromosomes based on the detected SNPs between mutant line and Dongjin, and did mapping by genotyping F2 plants derived from crosses between mutant line and Dongjin by these markers. Three loci for the mutant traits were successfully mapped on chromosome 3, 4, and 7. These results demonstrate that MutMap analysis are very helpful in mapping genes with mutant lines.

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Draft genomes of two medicinal plants, *Cynanchum wilfordii* and *Cynanchum auriculatum*

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The tuber extracts of *Cynanchum wilfordii* and *Cynanchum auriculatum* have been used as traditional medicine in Korea and China. In Korea, only *C. wilfordii* is listed as a lawful ingredient for food or herbal medicine, while *C. auriculatum* is not. Similar morphology of dried tubers from both *C. wilfordii* and *C. auriculatum* makes it difficult to discriminate them. Moreover, heterozygosity of *C. wilfordii* makes it difficult to identify particular variety of *C. wilfordii* in the market. Therefore, it is necessary to investigate the genomes of these two species to discover nuclear DNA markers that are able to authenticate *C. wilfordii*. The genomes of two *Cynanchum* species were sequenced using PacBio (Sequel) and Illumina HiSeq platforms. The expected genome size based on K-mer analysis of these two species were between 220 and 250 Mb. The contig numbers of 1,164 and 999, total lengths of 201.7 and 201.9 Mb, and N50s of 516 and 518 Kb were estimated in *C. wilfordii* and *C. auriculatum*, respectively. Predicted gene numbers were also very similar in these species; 28,178 and 28,770 in *C. wilfordii* and *C. auriculatum*, respectively. We identified genome-wide Simple Sequence Repeats (SSRs) in these two genomes, resulting in SSR number of 52,681 and 61,011 in *C. wilfordii* and *C. auriculatum*, respectively. Approximately 20% more SSR were found in *C. auriculatum*, which can serve as useful source of future DNA markers. This research was supported by a grant (17162MFDS005) from Ministry of Food and Drug Safety, Korea in 2019.

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Integrated genome structural and functional annotation pipeline for plants

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Next generation sequencing has triggered an explosion of available genomic and transcriptomic resources in the plant sciences. Although genome and transcriptome sequencing has become orders of magnitude cheaper and more efficient, often the annotation process is delayed. Here, we introduce a comprehensive plant genome annotation pipeline for plant species. The developed customized pipeline consists of three major parts which includes denovo assembly, structural annotation, and functional annotation. In detailed, NGS platforms are supported to conduct plant specific sequencing and denovo assembly was performed using Omicsbox to generate assembled fasta files. Structural annotation workflow was adapted from MAKER-P, collected supporting evidences for plant specific which includes RNAseq evidence, homology evidence, gene prediction methods (SNAP, Augustus, genemark) to generate consensus gene models. Further, post validation criteria and manual curation was followed for optimizing the final gene models. Then, functional annotation analysis was carried out to identify the functional descriptions by BLAST (Swissprot and NCBI nr), gene ontology (biological process, cellular component, and molecular functions), pathways (KEGG, Reactome), domains (interproscan), transmembrane prediction (TMHMM), and signal peptide prediction (SignalP). These customized plants specific gene annotation pipeline is will be help to plant researchers to conduct their genome annotation to functional annotation. Furthermore, we will incorporate additional bioinformatics tools, visualization tools for easier and data access.

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PCS02-26

Transcriptomic approach of FAD family proteins in *Perilla citriodora*

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Perilla is well known for its high α-linolenic acid (ALA) accumulation in seeds and as food source of edible vegetables and oils. Its ALA content is almost 60% of total fatty acid in seed compared to edible oils plants including hemp, peanut, sunflower, olive, grape and rapeseed which are generally less than 3%. ALA is not only considered as one of the most elemental nutrients for human health but also important for stress responses, pathogen defense-related signaling and cell maturation processes. Only a few genes encoding enzymes involved in fatty acid biosynthesis (such as fatty acid desaturases (FADs), sterol C4-methyl oxidase, 3-ketoacyl-ACP synthases, KAS I, II, and III) have been characterized in *Perilla*. In this study, we first focused on the FAD family proteins using transcriptomic analysis in diploid *Perilla citriodora*. By comparison with *Arabidopsis thaliana* FAD family protein genes in NCBI, 36 FAD related genes were selected in *P. citriodora* by BLAST program. Phylogenetic analysis of *A. thaliana* FAD family genes and *P. citriodora* genes was performed to confirm the similitude and the difference in production of ALA compared to the FADs genes in edible oil plants. To obtain time-series of variable FAD related genes expression during *Perilla* development, 12 development stages were analyzed for composition measurements. Significance in gene expression in the *Perilla* leaf, flower and seed development stages were analyzed for the variation of FAD related genes. These results can contribute to identify and control the genes related to unsaturated fatty acid biosynthesis in the sesame seeds.

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Genome-wide analysis of evolution of the TCP transcription factor family in soybean

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The TEOSINE BRANCHED/CYCLODEA/PROLIFERATING CELL FACTOR 1 and 2 (TCP) family is one of the plant-specific transcription factor family involved in development and growth. In recent studies, it has been revealed that one of the TCP transcription factors, named BRANCHED1, is tightly associated with branch development in soybean. Despite the importance of the TCP transcription factors on soybean development, comprehensive evolution and expansion of the TCP transcription factor family has not been investigated. The soybean has advantages in evolutionary study because paralogous genes have been retained after two rounds of whole genome duplication events (WGDS). In this study, we identified TCP transcription factors presented in soybean genome and analyzed its expansion and evolution. Bioinformatics analysis including phylogenetic relationships, motif conservation, gene structure, expression patterns, and duplication and divergence modes were conducted for 55 non-redundant soybean TCP genes. It was found that 54 TCP genes expanded by WGDS and tandem duplication events, and one gene, TCP11/21, was presented as single gene. Based on the synteny analysis, it was revealed that there was no significant difference in functional retention between old and young duplicates. Additionally, it appeared that 29 and 5 TCP gene pairs were transcriptionally and structurally diverged, irrespective of age. Interestingly, tandem duplicated segments containing TCP genes retained more partial long terminal retrotransposons compared to its syntenic counterpart. The findings of this study exemplify the fates of duplicated genes and provide profound understanding for the evolution and function of TCP gene family in soybean.

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142
Comparative genomic analysis of three isolates of *Phytophthora capsici*

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*Phytophthora capsici* is an oomycete pathogen responsible for damping off, root rot, fruit rot and foliar blight of popular vegetable and legume families, which cause yield and quality damage resulting in huge economical losses. The reference genome of the partially inbred isolate LT1534 was previously sequenced using 454 FLX and Titanium technology supplemented by Sanger reads (5X). In the present study, we report the *de novo* hybrid assemblies of three *P. capsici* isolates showing a striking variation in virulence. The sequences of three *P. capsici* genomes were obtained using Illumina HiSeq and single-molecule real-time (SMRT) sequencing technologies. Genome sequencing and characterization was performed of the three *P. capsici* isolates representing distinct virulence profiles. The *de novo* hybrid assemblies of three *P. capsici* isolates, using Illumina HiSeq and single-molecule real-time (SMRT) sequencing technologies were illustrated. In results, average number of 514 contigs with 50.96 % of GC contents, 698,937 bp of N50 and 16,398 predicted genes were obtained with assembly size of 76 Mb. Genomic analysis discovered the huge number of genes encoding potential secreted effectors in the genomes, including average 60 RxLR domain containing effectors, 42 Crinklers (CRN), 536 CAZymes grouped into 7 families, and several apoplastic effectors, such as cytochrome P450, phytoxins (PoF proteins), NPP1 families, LRR kinase as well as virulence and necrosis inducing proteins, in three *P. capsici* isolates. The comparative genomic analysis and GO term enrichment analysis for the polymorphism detection in various genes revealed, the numerous groups of genes which showed 10 polymorphisms on one CDS sequence. In addition, the characterization of the virulence profiles of the isolates in laboratory and field experiments were assessed which showed a striking variation in virulence of three isolates. This study provides a genomic landscape of three *P. capsici* isolates for the comparative genomic analysis, which may help to identify the genes under positive and negative selections, homology analysis with other *Phytophthora* spp. and effector assisted breeding.

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Identification of non-additively expressed genes at early developmental stages in an F₁ hybrid cultivar of Chinese cabbage

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The superiorit of the hybrid progeny compared to the parental lines is known as heterosis or hybrid vigor. It is one of the key criteria for selection of Chinese cabbage (*Brassica rapa* L. var. *pekinensis*) in the breeding program. In this study, we analyzed the phenotypic and cellular characters of a Chinese cabbage F₁ hybrid cultivar (W77) and its parental lines (S11-female, R09-male) from early to late developmental stages to assess hybrid vigor. The F₁ hybrid did not show significant increase of cotyledon area in mature seed or at 2 days after sowing (DAS) compared with its parental lines. Hybrid vigor was first observed at the 4 DAS cotyledon stage. Thereafter, hybrid vigor was observed in cotyledon size at 6 DAS, true leaves size at 14 DAS, and yield. Most of plant hormonal accumulation in F₁ hybrid showed mid-parent levels at 2 and 10 DAS. We identified non-additively expressed genes (differentially expressed genes compared with the mid-parent value) in F₁ hybrid at 2 and 14 DAS by RNA-sequencing. At 2 DAS, the expression of 107 genes were higher, and 69 genes were lower in the F₁ hybrid. At 14 DAS, the expression of 179 genes were higher and 606 genes were lower in the F₁ hybrid. Only 6 upregulated and 8 downregulated genes were common between 2 and 14 DAS. Our current results suggest that heterotic characters in F₁ hybrid started from the early developmental stages in Chinese cabbage, and the identified non-additively expressed genes might be involved in the molecular mechanism of hybrid vigor.

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Vernalization alters histone H3 lysine 27 trimethylation at FLC locus in *Brassica rapa*

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*Brassica rapa* L. is an important leafy vegetable such as Chinese cabbage and pak-choi. Prolonged cold exposure is required for flowering in *B. rapa* leafy vegetables, which is termed as vernalization. Before exposure to cold, expression of FLOWERING LOCUS C (FLC) represses flowering. Following prolonged cold exposure, FLC expression is repressed and allows plant flowering. Vernalization induces flowering (bolting) and restricts the head formation, which creates great losses to the economy of Chinese cabbage. Now-a-day’s producing high bolting resistant variety is a challenging issue to the breeders to overcome this problem in Chinese cabbage. We determined the histone H3 lysine 27 trimethylation (H3K27me3) distribution before and after vernalization by chromatin immunoprecipitation sequencing (ChIP-seq) in an inbred line of Chinese cabbage (RIKB- T24). At similar developmental stages, between non-vernalized and vernalized samples, H3K27me3 levels at the whole genome level had high correlation coefficients, suggesting that genome-wide H3K27me3 levels influencing vernalization is unlikely. Following four weeks of vernalization, H3K27me3 increased at the first exon and part of the first intron (nucleation site) in all four FLC paralogs. After vernalization following a return to 22 °C, an increase of H3K27me3 was observed in all four FLC paralogs, which started at the nucleation site and spread 5’ to 3’ along the genes. We also analyzed the expression levels of FLC, VIN3, and SOC1 by qPCR and found total amount of the four FLC paralogs were downregulated following vernalization. VIN3 and SOC1 were highly induced following vernalization.

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Genome-wide association study for trichome development in the *Brassica rapa* core collection

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Chinese cabbage (*Brassica rapa* spp. *pekinesis*, 2n=20) is one of the important vegetable crop in East Asian countries. Diverse breeding programs have been focused on improvement of yield and reduction of cost for cultivation. However, breeder’s interests are gradually moving to demand of consumers by considering taste, nutrition and other horticultural purposes for the breeding program. The trichome functions as a barrier in defense mechanism of plant against pathogen and herbivores to survive in the nature. However, high-density trichomes on the surface of edible leafy organ is unfavorable factor when one masticates it as salad or uncooked form. Thus, understanding genetic mechanism of trichome development is important to develop commercial cultivars with alleviated level of trichome in the *B. rapa* breeding. To research genetic regions involved in trichome development, we surveyed presence of trichome for 97 *B. rapa* accessions and generated 2,732.44 Gbp sequencing data by NGS (Next generation) sequencing. We identified 225.19 K SNPs from the *B. rapa* population using reference genome (ver 3.0). Subsequently, we performed genome wide association studies (GWAS) to investigate candidate genes involved in trichome development in the *B. rapa*. Several SNPs were detected in flanking region of known candidate genes, TBL 22 and QTL region on the chromosome 6 reported in previous study. Results from further studies will be presented.

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PCSO2-32

The characterization of the gene expression concern to plant growth in the dwarf mutants derived from F7 RILs crossed between cultivar and wild type soybean

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Soybean (Glycine max) is one of the most important economic crop for food and bioenergy resource in the world. Soybean growth is an element to increase high yield. There are key genes including homebox, gibberellin, and auxin that are concern to regulate plant growth. The gene expression is variable in the plant condition including plant root, stem, leaf and environment. To characterization of the gene expression in the specific plant growth tissue is important to understand the gene regulation to the plant growth. We found 6 soybean dwarf mutant derived from F7 RILs crossed between cultivar (G. max, Peking) and wild type (G. soja) soybean. We tested the genes expression between dwarf and normal growth soybeans by RT-PCR. The homeobox, gibberellin and auxin genes are differently expressed in the dwarf soybean against the normal growth plant. We guess the genes are keys to role soybean growth. Furthermore, we need to get the more information including transcription factors to understand the regulation why the genes are differently expression in dwarf soybean. This information provides to select target genes to engineering for plant growth.

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PCSO2-33

Transcriptome analysis and characterization of genes associated with leaf development and dimorphic chloroplast differentiation in Bienertia sinuspersici

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Bienertia sinuspersici belongs to the Chenopodiaceae family possess unique C₄ photosynthetic mechanism. B. sinuspersici performs C₄ carbon fixation through compartmentalization of central and peripheral chloroplast within in the single chlorenchyma cells. Spatial separation and formation of cytoplasmic domains are associated with the development of leaf. Therefore, this study was carried out to analyze the whole transcriptome using RNAseq in three development stages of leaf such as young (less than 0.3 cm), intermediate (between 0.3-0.6 cm), and mature (more than 2cm). Several numbers of genes were differentially expressed between the developmental stages. Interestingly, 199 genes were upregulated in the young stage in comparison with the mature leaves. Furthermore, young-specific differentially expressed genes (DEGs) were confirmed by qPCR analysis. In silico characterization showed that DEGs were involved in transferase activity (35%) followed by DNA binding (19%), ion binding (14%), oxidoreductase (12%), hydrolase activity (11%), and drug binding (10%). To noteworthy, 41% and 35% of DEGs were localized in integral component of membrane and nucleus, respectively. Genes responsible for the development of plant system, epidemic, post-embryonic development, cellular component organization, and cell differentiation were also identified. Result of this work will be helpful to elucidate genes actively involved in the younger stage of leaf development associated with unique peripheral and distal arrangement of a chloroplast, a vital factor for non-Kranz SCC₄ photosynthesis in B. sinuspersici.

Keywords: Compartmentalization, non-Kranz, C₄ metabolism, RNAseq, Gene ontology

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QTL Mapping with Stem Related Traits using Recombinant Inbred Lines based on High-Resolution Map in Rice (Oryza sativa L.)

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Rice (Oryza sativa L.) is one of the world’s important crops and major staple food for Asians. However, a major problem in rice breeding, lodging resistance, often cause decreases in yield and quality because of severe weather conditions such as heavy winds and rains. In this study, we cultivated ‘Milyang23’ and ‘Gihobyeo’ recombinant inbred lines (MGRILs) in both the field and greenhouse, and investigated the culm length (CL) and internode diameters. We discovered single nucleotide polymorphisms (SNPs) from 162 individuals through re-sequencing analysis by next generation sequencing (NGS). Additionally, recombination breakpoints were used for constructing the high-resolution genetic map. Quantitative trait loci (QTLs) with stem related phenotypes were analyzed using MGRIL population to identify highly effective QTLs. As a result, normal distributions in phenotype investigation were shown as the wide variations in all five traits; CL and each of four internode diameters (ID1, ID2, ID3 and ID4) from the field and greenhouse, respectively. Significant difference was also shown positively among internode diameters. 2,739 SNP-based markers were developed from re-sequencing, and then integrated with 463 PCR-based markers to perform QTL mapping. Finally, 22 QTLs were totally detected for five traits on both the field and greenhouse, and 10 of 22 QTL regions were overlapped with high accuracy. In the future, QTLs information in this study will be useful to identify genes related to lodging resistance traits.

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Analysis of glucosinolates content and related-genes expression in 88 Radish (Raphanus sativus L.)

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Glucosinolates (GLs) are secondary metabolites contained nitrogen and sulfur, mainly found in natural plants. Recently, GLs have been proven the effect of human health on inflammation, carcinogenesis and cardiovascular protection. Radish (Raphanus sativus L.) is an economically important crop belongs to the Brassicaceae family. Radish roots have been used for medicinal purposes because their phytochemical compounds. The radish roots contained a rich source of GLs and then they are degraded by the myrosinase, resulting in several derivatives, isothiocyanates, nitriles and thiocyanates, etc. In this study, we analyzed the GLs contents from total of 88 radish accessions. A glucoraphasatin (GRH), aliphatic glucosinolate, indicated high rate compared with other glucosinolates. Further transcriptome analysis showed several candidate genes related to GLs biosynthetic pathways. These results provide comprehensive information of GLs contents and related genes in radish. Also, this research may be useful for radish breeding of new valuable cultivars.

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Construction of A Linkage Map Using Axiom-driven SNPs for Genome Improvement and Molecular Breeding in Octoploid Strawberry

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The cultivated garden strawberry (Fragaria × ananassa) is an allooctoploid species (2n = 8x = 56) with an estimated genome size of 813.4 Mb. Despite of its commercial importance, the complex structure of genome prevented molecular breeding in strawberry. Here, we report construction of a linkage map of cultivated strawberry using strawberry Axiom array and an F2 mapping population (‘L80’) derived from inbred lines ‘Benihoppe 8-10’ and ‘Sachinoka 14-9’. A total of 138,099 markers were obtained for ‘L80’ populations with a standard threshold. Of selected SNPs, polymorphic markers were selected according to the Mendelian segregation ratio of 1:2:1. As a result, 5,370 SNP markers were used for construction of a linkage map. The linkage map of ‘L80’ population was consisted of 49 linkage groups containing 5,359 high-quality SNPs. This linkage map represents total of 28 chromosomes of the octoploid strawberry. This genetic map was used to validate of genome assembly of an inbred line. This Axiom-based linkage map will be a useful resource for molecular breeding of strawberry.

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 genome-wide identification and characterization of high affinity potassium transporter 1 (HKT1) and Na+/H+ antiporters (NHX) family in Bienertia sinuspersici

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Bienertia sinuspersici is a single cell C4 photosynthesis plant with non-krantz anatomy. It is usually grown in semi-arid regions of Central Asia and Persian Gulf. Though B. sinuspersici is classified as halophytes belonging to Chenopodiaceae, only limited studies were conducted on its salt tolerance mechanism(s). This study was carried out for genome-wide identification and characterization of high affinity potassium transporter1 (HKT1) and Na+/H+ antiporters (NHX) families in B. sinuspersici. Further, HKT1 and SOS1 genes expression level were examined under four different salt conditions (0, 100, 200 and 300 mM of NaCl) for two or three weeks in B. sinuspersici, respectively. Compared with A. thaliana (glycophyte), both HKT1 and NHX families were expanded in B. sinuspersici (halophyte). Distinguishable intron-exon arrangement was noticed from gene structural analysis between B. sinuspersici and A. thaliana. Converged and diverged motifs were observed in HKT1 family as well as among NHX subfamilies. Interestingly transmembrane topology analysis revealed BsSOS1 protein contains additional N-glyco motifs than AtSOS1. Both AtHKT1 and BsHKT1α were merely detected. Nevertheless, BsHKT1β was recognized as highly expressed, followed by BsHKT1c. Expression of BsHKT1β and BsHKT1c was higher in third week compared with second week. Similarly, significant difference was detected on BsSOS1 expression between two and three weeks treatment. In conclusion, results of this work provide deeper insight on evolutionary as well as functional differences exist between glycophyte and halophyte on HKT1 and NHX gene families.

Keywords: Glycophytes, Halophytes, Salinity, Exclusion, Tolerance.

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Identification, characterization, and comparative genomics study of YABBY gene family in *Brienertia sinuspersici*, a single cell C₄ plant

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Determinate dorso-ventral leaves evolved from the indeterminate radial branch system of plants. The emergence and expression of YABBY genes coincided with the evolution of leaves in seed plants were integral to early manifestations of laminar development. This study was conducted to identify and characterize YABBY genes in *Brienertia sinuspersici* (Bs), an important model plant for single cell C₄ (SCC₄) non-Kranz photosynthesis. In addition, a comparative genomic analysis were conducted on *Arabidopsis thaliana* (At), *Brassica rapa* (Br₄), and *Chenopodium quinoa* (Cq₄) to gain insight on evolutionary changes of YABBY gene family after whole genome duplication (WGD) events. With a lack of recent genome duplication, At and Br₄ had a single copy of each YABBY gene subgroup, while auto- and allo-tetraploidization led to the expansion of the YABBY gene family in Br₄ and Cq₄, respectively. The retention rates of duplicated or triplicated copies differed between species and subgroups. A distinct intron-exon arrangement was observed in orthologous copies of YABBY genes. Conserved, as well as lineage specific motifs, were identified in Brassicales (At and Br₄) and Caryophyllales (Bs and Cq₄). A deletion of amino acids in the functional YABBY domain region occurred in the CRC and YABB subgroups of B. sinuspersici. Consistently, CRC and INO were only detected in floral tissues of all the plant species studied. Nevertheless, both temporal and perpetual shifts in the differential expression of YABBY orthologs were observed in leaves and in different floral developmental stages. The results of this study provided an overview of the YABBY gene evolution and its retention rates subsequent to WGD in plant lineages along with understanding of structural and functional modifications between Brassicales and Caryophyllales.

**Keywords:** Angiosperm, Evolution, Development, Diversification, Leaf organogenesis, Floral morphogenesis

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The transcriptome identification for anthocyanin biosynthesis in black rice

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Anthocyanins are involved in many diverse functions in rice, but their benefits have yet to be clearly demonstrated. Our objective in this study was to identify anthocyanin-related genes in black rice plants. We identified anthocyanin-related genes in black rice plants using a combination of whole-genome resequencing, RNA-sequencing (RNA-seq), microarray experiments, and reverse-transcriptase polymerase chain reaction (RT-PCR). Using multi-layer screening from 30 rice accessions, we identified 172,922 single-nucleotide polymorphisms (SNPs) and 1,276 differentially expressed genes that appear to be related to anthocyanin biosynthesis. We identified 18 putative genes from 172,922 SNPs using intensive selective sweeps. The 18 candidate genes identified from SNPs were not significantly correlated with the RNA-seq expression pattern or other well-known anthocyanin biosynthesis/metabolism genes. We also identified nine putative genes from 1,276 differentially expressed genes using RNA-seq transcriptome analysis. In addition, we identified four phylogenetic groups from these nine candidate genes and 51 pathway-network genes. Finally, we verified nine anthocyanin-related genes using a newly designed microarray and semi-quantitative RT-PCR. We suggest that these nine identified genes appear to be related to the regulation of anthocyanin biosynthesis and/or metabolism.

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Development and application of KASP marker for high throughput authentication of 7 *Panax* species

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Ginseng is the collective name for a group of slow-growing fleshy-rooted deciduous perennial plants within *Panax* species belonging to the Araliaceae family. Fourteen ginseng species were identified throughout East Asia, Central Asia, and North America, including seven major species: *Panax ginseng*, *Panax quinquefolius*, *Panax notoginseng*, *Panax japonicus*, *Panax vietnamensis*, *Panax stipuleanus* and *Panax trifolius*. Ginseng roots are used as an important herbal medicine in health care and treatment of diseases for thousands of years in Asian countries, particularly in Korea, China, and Japan. Presently, ginseng is one of the best selling herbal supplements worldwide with many health benefits. Due to the continual increases in demand for ginseng health food and dietary supplements, economically motivated adulterations (EMAs) of ginseng products are growing, specifically, intentional substitution of the wrong species in commercial ginseng products is common issue and can cause adverse effects or even harm to the consumers. Therefore, establishment of analytical methods to authenticate and classify the various ginseng species is importance for efficacy and safety of ginseng materials and their products. Recently, LGC Genomics developed KASP the Kompetitive Allele Specific PCR (KASP) assay to genotype SNPs in several fields of study, including plant breeding, disease identification, and species identification. KASP assay is a uniplex SNP genotyping platform that are fixed for a more flexible markers, as useful SNPs are not limited to available restriction enzyme recognition sites. In the demand of a simple, high throughput and low cost assay with high resolution, in this work, we employed KASP technology to obtain 26 markers of Ginseng species-specific SNPs to authentication of 7 *Panax* species.

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Transcriptome analysis and identification of OsWRKY transcription factor associated with the leaf morphology in rice

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WRKY transcription factor was involved in plants. Diverse biological functions in plant disease resistance, abiotic stress responses, senescence, development, embryogenesis, and hormone-controlled processes. WRKYs contain the highly conserved amino acid sequence WRKYQK and the zinc-finger-like motifs Cys(2)-His(2) or Cys(2)-HisCys. Bind to the TTGAC(C/T) W-box cis-element in the promoter of their target genes. Therefore, it is important to identify the binding motifs of transcription factors to better understand the networks associated with development. Here, we used a rice promoter protein-binding microarray (RPBM) to identify the ATGGTG binding motifs of OsWRKY. Among these putative target genes, there were contained transporters, protein kinases within their 2-kb promoter regions. OsWRKY were transiently expressed as fusion proteins with green fluorescent fusion protein in *Nicotiana benthamiana*, where they were observed to accumulate in the nucleus. For the identification of putative targets of OsWRKY36, Transcriptome analysis of the overexpression OsWRKY36 plants, combined with the RPBM results. We considered exhibiting 1.5 up- and down- regulation under WT in leaves of 17days for microarray. This first selection resulted in 3,421 genes. In RNA-Seq data that analyzed 5 fold change regulation under WT in leaves of 50days, resulted in 2,758 genes. Also, We extracted 559 genes with ATGGTG binding motif in higher than cut-off intensity from RPBM. This analysis reduced the putative targets to 6 genes. These genes included: Serine/threonine protein kinase-related domain containing protein; Peroxidase P7 (TP7); spindle assembly Cytoskeleton, HALL complex; Telomere binding protein-1; Beta-amyrin synthase; Glycoseid hydrolase, family 17 protein. The transgenic plant showed a rolled leaf phenotype and reduction in grain yield. The shape of grass leaves possesses great value in both agronomy and developmental biology research. Leaf rolling is one of the import traits in rice breeding.

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Application of Korean japonica rice Kompetitive Allele-Specific PCR (KASP) markers in High-Throughput Genotyping system

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The next generation sequencing technology enabled massive discovery of single nucleotide polymorphisms (SNPs) in genomes. However, genotyping small number of SNPs in a large number of samples is still challenging task in plant breeding. For that end, several methods that are suitable for high-throughput SNP genotyping have been developed. Among them, Kompetitive Allele-Specific PCR (KASP) is becoming popular in plant breeding and research. Recently, genome-wide SNPs were discovered by resequencing 13 Korean japonica rice varieties. Among them, 1,010 SNPs were developed in KASP markers and are being tested in high-throughput genotyping system using Array Tape. Among tested 506 KASP markers, 79% was found to be polymorphic in tested rice varieties whereas 29% did not show polymorphisms or showed poor genotyping performance in Array Tape platform. The KASP markers for Korean japonica rice will be a valuable source for molecular breeding such as genetic map construction and variety identification.

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Functional Study of PAMP-responsive long noncoding RNAs in Arabidopsis

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Recently, long noncoding RNAs (lncRNAs) have emerged as important regulatory factors of diverse biological processes in both plants and animals. However, plant lncRNAs involved in innate immunity remain largely unknown. Plant innate immune responses are initiated upon the perception of PAMP (pathogen-associated molecular pattern) such as flagellin (flg22) and EF-Tu (elf18). In this study, we analyzed custom lncRNA array datasets generated from PAMP treatments. Overall, we identified 1,370 Arabidopsis lncRNAs induced or repressed by PAMP. Real-time RT-PCR validation confirmed the differential expression patterns of these lncRNAs in response to flg22 and elf18. Out of them, we chose 13 lncRNAs (ELENAs: elf18-induced long noncoding RNAs) that are induced by PAMP for further analysis. These lncRNAs include 10 lncRNAs (long intergenic noncoding RNAs) and 3 NATs (natural antisense transcripts). To determine whether these ELENAs regulate PTI (PAMP-triggered immunity) signaling, we examined the altered expression of innate immune response genes by overexpressing ELENAs using Arabidopsis mesophyll protoplasts. Further, we will genetically characterize the ELENA functions using gain- and loss-of-function mutants. Finally, we suggest that PAMP-responsive lncRNAs have great potential for breeding disease-resistant crops.

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Inter- and intra- chloroplast genome diversity and classification of germplasm in Cynanchum species

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Cynanchum wilfordii (Cw) and C. auriculatum (Ca) have long been used as traditional medicine source in Korea and China. Recently, the effect of reducing cholesterol levels and alleviating menopausal symptoms have been scientifically proven and the importance of Cw is increasing. Nevertheless, basic research including intra-species variation is lacking. In addition, recent economically motivated adulteration (EMA) problems have arisen, further emphasizing the need for genomic research. Cw and Ca are morphologically similar that makes them difficult to distinguish. Furthermore, various morphological diversities were found in the Cw germplasms collected from Korean farms. It is presumed that this may raise confusion between Cw and Ca. 45S rDNA and complete chloroplast genomes of four Cw collections were assembled for research of intra-species variation and development of more accurate species authentication markers considering the characteristics of Cw, which has many intra-species diversities. Genetic variations of chloroplast genome were identified with marker application on 27 Cw and 26 Ca germplasms collected in Korea. 250 InDels and 971 SNPs were identified between Cw and Ca, and five InDels and six SNPs were marked within chloroplast genome of Cw. Six species authentication markers successfully distinguished the two species without confusion derived from intra-species diversity. With five intra-species variation markers, 27 Cw and 26 Ca germplasms were classified into 14 and two subgroups. Inter- and intra- species variation specific markers developed in this research provide precise species distinguish system for Cw-based functional and medicinal products and basic information for breeding of two Cynanchum species.

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Whole Genome Scan Reveals the Positive Selection in Kohlrabi

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Brassica oleracea has been considered as an economically crucial food crop and has various morphology within species; cauliflower, broccoli, cabbage, kale, kai-lan, brussel sprouts, and kohlrabi. Especially, kohlrabi has a specific characteristic such as stem swelling whereas the others have not. Thus, we focused on exploring of the genetic signature related to stem swollen in kohlrabi. Several genomic analyses were conducted using 44 Brassica oleracea genome sequencing data in this study. Population structure and phylogenetic analysis based on whole genome data were constructed using 1,110,638 SNPs detected as high quality variants. Population stratification result revealed that three groups within species. To investigate the genomic regions under selection in kohlrabi, we performed several statistics such as XP-CLR, XP-EHH and Tajima D. We could discover several candidate loci that might be associated with tuberous stem in kohlrabi via this study. Among of these loci, 2 genes were observed as having SNPs undergone missense mutation, which indicated that might affect on function of protein. Consequently, the knowledge generated through this study will contribute to understanding the genetic signature related to stem swollen characteristics in kohlrabi.

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Unique features displayed in the chloroplast genomes of the *Selaginella* genus

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Selaginella is a sole genus of the Selaginellaceae family, belonging to early vascular plants. Around 800 species inhabit a diverse range of climates around the world and have various characteristics within the genus which make them good models for comparative analysis. They are used as medicinal and ornamental plants, as well as resources for bioenergy. The *Selaginella* genus also has a very special position in plant history which makes it a valuable resource when studying the evolution of vascular plants. In this research, complete chloroplast genome sequences of three Selaginella species (*Selaginella tamariscina*, *S. stauntoniana*, and *S. involvens*) were assembled using Illumina and Nanopore sequencing technologies. These three assembled sequences along with chloroplast genomes of seven other related species in the Lycopodiopsida class registered in NCBI were analyzed for unique features of *Selaginella* species as well as their phylogenetic relationships. As a result, very uncommon features of the chloroplast genome were observed within the *Selaginella* genus. *Selaginella* species had smaller chloroplast genome sizes, more than 30 gene losses as well as intron losses, high GC content of about 50%, and extensive RNA editing. Moreover, they displayed various structural rearrangement events throughout evolution that gave some species their unique direct repeat structure not found in typical higher plant species.

Haplotype analysis of the BADH1 gene and the association with salt tolerance in rice germination stage

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Domestication of the important genes is one of the most effective methods to enlighten the rice evolutionary history. The evolutionary path of BADH1 gene has not been fully explored. In this study, we scanned the BADH1 sequences of 421 cultivated rice, and 54 wild rice from worldwide to determine whether BADH1 could be used as a domesticated gene during investigating rice evolution. In our materials no BADH1 variations were detected from temperate and tropical japonica in exon region. This finding may suggest japonica indicated rare selection in BADH1 region. T/A SNP in exon 4 (badh1.3) and C/A SNP in exon 11 (badh1.5) were detected in both wild and cultivated rice, suggesting these two alleles were selected from wild rice during domestication. BADH1 gene was reported having a close correlation with salt tolerance in rice. Based on the data of six exonic SNPs of cultivated rice, 84 varieties could group into 9 different haplotypes (H1-H9). Two haplotypes (H1-H2) were common, representing 89.2% of the varieties which representing BADH1 variations. Salt tolerance levels at rice germination stage are well correlated with BADH1 haplotypes H1 and H2 in cultivated rice. BADH1 is a good candidate gene for salt tolerance in rice.
Signatures of differential selection in chloroplast genome between japonica and indica

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Cultivated rice is the world’s major crops, feeding nearly half of the world’s population. The process of domestication of rice is complicated. So far, extensive research has been conducted on the origin of rice, but it has not yet been uniformly conclusions. Recently, based on phylogenetic studies of the rice chloroplast genome, we have found interesting results supporting the independent origins of Oryza sativa. Here, a total of 475 rice samples were collected from 28 regions of the world’s rice-rich regions with high average sequencing coverage (~15.88X) and yields of ~3.42T raw data. We identified 1286 SNVs and 156 InDels in the chloroplast genome. To more fully understand cultivated and wild rice, we also classified these rice groups into subgroups for subsequent analysis. Phylogenetic studies have shown that the separation clusters of indica and japonica rice are obvious. We also identified specific selection markers in different regions of Asian rice. This indicates that different selection characteristics of indica and japonica may occur during the domestication.

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Genomic variations and evolutionary studies in diverse varieties of rice

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Asian rice is mainly divided into two major categories, namely japonica and indica. In general, indica type usually exhibits slender grain and is grown in tropical Asia; japonica rice usually presents short, sticky grains and is grown at high altitudes in South Asia. Indica and japonica are important food crops for nearly half of the world’s population. Therefore, exploring the genetic information of these varieties can provide insights for rice breeding. The domestication process of Oryza sativa L. is complex. It has been widely known that Oryza rufipogon is the ancestor of Asian rice, although the number of domestication scenarios still remains controversial. Recently, many nuclear genome studies have been conducted, but the results are quite different. Therefore, we conducted a genomic-based (nuclear genome, chloroplast genome and mitochondrial genome) study aiming to provide more evidence for the domestication of Asian rice.

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Evidence for selection events during domestication by extensive mitochondrial genome analysis between japonica and indica in cultivated rice

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Domestication of rice is the process of transforming the natural selection of wild characteristics into the stable desired traits from artificial selection. So far, the genetic architecture and evolutionary history of Asian rice based on nuclear genome has been extensively studied, but the results are quite different. Recently, we have found interesting results supporting the independent origins of Asian rice based on comprehensive studies of the rice mitochondrial genome. Here, a total of 412 germplasms were collected from the world sequencing with high average coverage (~15.88X) and product ~3.42T raw data. We identified 10632 variations from rice mt genome, including 7277 SNVs (68.4%) and 3355 InDels (31.6%). To explore the evolution and genetic of rice better, artificial selection (π w/ π c), FST, population structure, haplotype and phylogenetic analyses are combined to analyses. As describe above, our studies have shown the clearly separation of indica and japonica rice. We also exhibited japonica may experience a strong selection or bottleneck event during the domestication.

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Integration of Genome-Wide/Transcriptome-Wide Studies and eQTL Analysis on Preharvest Sprouting Trait from 378 Asian Cultivated Rice

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We performed genome wide association study (GWAS), transcriptome wide association study (TWAS) and Expression quantitative trait loci (eQTL) analysis on preharvest sprouting trait (PHS) using WGR (whole genome resequencing) and RNA-Seq data from 378 Asian cultivated rice varieties. These analyses were carried out to analyze various aspects of genetic factors affecting PHS. The result of GWAS response with the data tested in field for two years showed that a number of significantly associated SNPs with PHS. Some of the significantly associated SNPs with PHS which were identified by GWAS were also significantly associated with the results of eQTL and TWAS, indicating that certain genes were involved in PHS response as a way of influencing the expression of specific genes.

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Atlas of Omics Information on Badh2 in Rice

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Aromatic rice (Oryza sativa L.) is interesting to consumers. It holds huge economic importance and demands a premium price in the global trade. The fragrance in such rice results from the loss of function of the betaine aldehyde dehydrogenase (Badh2) gene on chromosome 8. In this study, a total of 3,475 rice accessions encompass the resequencing data of 421 accessions of Korean rice (KRICE), 54 wild rice accessions, and 3,000 accessions of Asian cultivated rice (by CAAS, BGI and IRRI). SNP and indel variant sites of 3,475 rice accessions were performed using the PowerCore software to search the functional, novel alleles in Badh2 compared with the Nipponbare genome. A total of 181 haplotypes based on nucleotide polymorphism were detected in the coding sequence of the Badh2 gene. The variations of SNPs and indels were classified into 87 haplotypes of fragrance alleles in the Badh2 gene, that were found in 644 rice accessions, including in 558 accessions from the 3,000 Rice Genome Project, 50 cultivated from KRICE, and 36 of wild rice. A total of 58 alleles in the coding region of Badh2 were detected in the sequence data. We found the 49 new fragrance alleles leading to synonymous and non-synonymous mutations in the coding region. Newly identified alleles, named badh2.24-badh2.37, contained 14 non-synonymous SNPs and deletion led to functional changes that appeared in 111 rice accessions. The evidence of 14 novel alleles was clearly distinguished SNP substitutions by DNA cloning and sequencing of 60 rice accessions. This discovery of the 14 novel functional Badh2 alleles and haplotypes will be used in a Badh2 diversity study to improve the breeding of new varieties of fragrant rice.

Keywords: Omics, fragrant rice, Badh2 gene, SNPs, indels

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Submergence 1 (\textit{SUB1}) Gene Diversity in 475 accessions of rice genetic resources

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Anaerobic germination (AG) is plays important role in submergence resistance which is an important trait for rice production in flood-prone lowland areas. Slow seed germination and delayed seedling establishment due to flooding become major problem for modern sowing methods such as direct seeding and environmental friendly good agricultural practices especially using young seedling age. In total, 475 diverse rice accessions were evaluated for anaerobic germination ability. Submergence 1 (\textit{SUB1}) which is induced ethylene response factors is suggestive because genes belonging to this gene family play a crucial role in rice tolerance to submergence. In this study, haplotype variations of three AG related genes, \textit{SUB1} (\textit{SUB1A}, \textit{SUB1B}, \textit{SUB1C}) were examined using whole-genome resequencing data of 475 accessions of rice core set. The new SNPs and InDels found in the exon of the subst1 loci would be useful in developing markers to screen the varieties with strong anaerobic germination ability in the future molecular breeding.

Keywords: Anaerobic germination, genetic diversity, \textit{SUB1}

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The genetic diversity related to vitamin E biosynthesis pathway using cultivated rice DNA chip data

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Vitamin E is necessary for humans and must be a component of a healthy diet. As rice is a major food source for half of the global population. Tocochromanols, also known as vitamin E are lipid-soluble molecules that belong to the group of vitamin E compounds. In this study, we quantified tocochromanols content in brown rice using GC instrument (GC 400 Varian) and performed re-sequencing data of 475 rice accessions including 54 wild rice and 421 cultivated rice from a diverse core collection for representing the genetic diversity of tocochromanols. The nucleotide polymorphisms of Oryza TMT gene (Os02g0710600) on chromosome 2 was found 52 SNPs and InDels nucleotide variation in coding region (CDS). Furthermore, we also implemented DNA chip analysis to measure the expression levels of large numbers of genes simultaneously or to genotype multiple regions of a genome. This analysis information will be used genetic diversity study of vitamin E for developing marker and breeding for improve the new varieties.

Keywords: genetic diversity, rice, tocochromanols, vitamin E

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Genetic Differentiation Analysis of Ecotype Interactions in Bacterial Leaf Blight Resistance Gene in rice

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Bacterial leaf blight (BLB) caused by Xanthomonas oryzae pv. Oryzae (Xox) is an important bacterial disease in rice. Breeding for disease resistant varieties remains very effective and economical in controlling the bacterial leaf blight (BLB) of rice. Breeders have played a major role in developing resistant rice varieties against the BLB infection which has been adjudged to be a major disease causing significant yield reduction in rice. The purpose of this study is to analyze the ecotype interaction in BLB gene in 475 accessions of Korean rice genetic resources including 54 accesses of wild rice. Ecotype interactions-Xa1, xa5, xa7, xa10, xa13, Xa21, Xa23, Xa25, Xa26, Xa39 and Xa41(i) were analyzed. By ecotype result, wild rice showed higher nucleotide diversity than the cultivated rice. The result using the analyses of Tajima’s D, Fu and Li’s D*, and F* predicted that the population size probably being increased sharply in the majority resistant genes, and that the wild and Aoe groups were close in genetically, but the Japonica and Aromatic groups were far.

Key words: Bacterial Leaf Blight (BLB), Xanthomonas oryzae pv.oryzae (Xox), Ecotype, eQTL

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Sequence and Haplotype Variations of Granule-Bound Starch Synthase I and II (GBSS-I, GBSS-II) Genes in Cultivated Rice and Wild Rice Based on Genome Information

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Granule-bound starch synthase (GBSS) is the enzymes involved in amylose synthesis during starch biosynthesis. This gene has two isoforms. GBSS-I is predominantly expressed in storage tissues such as endosperm and pollen. GBSS-II is expressed in non-storage tissues such as leaves and stems. We performed a bioinformatics analysis of GBSS-I and GBSS-II to find important sequence and haplotype variations for improving starch quality based on genome information in rice breeding. To investigate genetic variations of GBSS-I and GBSS-II, we implemented variant calling using a total of 475 resequencing genomic data including 54 wild rice accessions and 421 cultivated ones. As a result, we found a total of 14 non-synonymous SNPs from the 8 different exons of GBSS-I (Os06g0133000) on chromosome 6, and a total of 45 non-synonymous SNPs from the 11 different exons of GBSS-II (Os07g0412100) on chromosome 7. According to the Tajima’s D analysis, GBSS-I showed more selection signature than GBSS-II. These analysis results would be useful to provide important foundation for rice breeding.

Keywords: GBSS-I, GBSS-II, starch, diversity, cultivated rice

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Identification of eQTLs of a bacterial leaf blight resistance gene (Xa39) using RNA-Seq data of Korean rice coreset

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Bacterial leaf blight (BLB) caused by Xanthomonas oryzae pv. oryzae (Xoo), one of bacterial pathogens, is a vascular disease and it is one of the major diseases in rice. It attacks in most rice cultivating areas such as Africa and Asia. Depending on the growing season, it can cause 20-80% yield lost. In order to find out the regulatory factors affecting on the blight resistance gene, Xa39 which have been identified as the highest 95% heritability among the Xoo genes, we identified eQTLs using RNA-Seq data of 163 Korean rice coreset. According to the results, Os11g0588600 (Os11t0588600-01, Xa39) was presumed to be regulated by a SNP located 9Kbps in the same chromosome 11: 22,319,757 bp as cis-regulatory element. The expression level of Xa39 was high in the case of the thymine (T) at the SNP position, and the expression level was low in the case of the cytosine (C).

Keywords: Xanthomonas oryzae pv. oryzae (Xoo), bacterial leaf blight (BLB), diversity, haplotype

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Development of KNU Axiom Oryza 580K Genotyping Array

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As rice breeding methods become more sophisticated through the use of genomes, the utility of genomes is increasing. We have developed a multipurpose SNP/indel genotyping chip from the collection of genome information of 3,459 domestic and worldwide genetic resources, which can be used in various agricultural research fields. Due to the typical high-throughput methods, NGS requires high-performance computing resources when performing genome-wide SNP/indel genotyping from short-length nucleotide sequences of a sample output from a sequencing machine. However, the genotyping array will lower the barriers of research on the use of genomes in rice because the use of computing resources to call genotypes from the array is relatively low. We designed the chip in two groups in order to utilize the chip in a multipurpose way. The first group is the SNP/indel marker group that can be used for genomic selection, GWAS, and map-based mapping for breeding. The second group is a group of markers to be used in agricultural research, such as genotyping of agriculturally beneficial genes, subspecies specific gene analysis, plastid genome analysis, evolutionary studies. We obtained SNP/indel information from a total of 3,494 accessions including the Korean rice core set ver. 2 (KRICE_CORE v2) including wild rice and 3K IRRI world collections. A total of 558,281 SNP markers and 66,314 indel markers were selected through various stages of filtering. Among them, 528,758 SNP markers and 51,279 indel markers suitable for the genotyping chip probe were finally planted on the chip.

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Identification of Genetic Diversity in Korean Breeding Lines using Oryza 580K Genotyping Array

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Recently, as the high density genotyping chip (KNU Axiom Oryza 580K Genotyping Array) for rice has been developed, we analyzed the genetic diversity of 4,000 Korean breeding lines using the genotyping array. We performed genome-wide SNP/indel genotyping derived from 4,000 Korean breeding lines using the genotyping array. We selected only those genotypes found in the ‘PolyHighResolution’, which represents good cluster resolutions in terms of genotype signal strength and distinction. We traced marks of selective sweeps using indicators such as linkage distribution, genetic diversity, the normalized difference between observed genetic diversity and expected diversity, as well as haplotype lengths in 3,475 accessions. This was done through the use of variants, and the allelic and genic differentials between populations such as Indica/Japonica and wild/cultivated.

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Orthologs Phylogenetic Profile of 18 Plants

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The phylogenetic profile of a gene is a pattern of the absence/presence of orthologous genes under the phylogenetic relationship, which is presented as a vector with each component in the vector corresponding to either the absence or presence of orthologous genes represented by the digits 0 or 1, respectively. One of the important usages of the phylogenetic profile of orthologs was raised because phylogenetic profiles may be useful for recovering a given genes’ evolutionary history, as well as identifying its function. We selected a total 18 plants which have completed whole genome sequencing, 11 plants in the Oryza genus, including O. sativa subspecies such as Japonica and Indica, and 7 outgroup species including Arabidopsis thaliana. The results showed that a total of 13,215 profiles. Among them, the number of common genes to all the species was 2,341. The number of genes deleted from Indica only was 187. The number of genes deleted from Japonica only was 226. The number of genes existing in Japonica and O. rufipogon but not in Indica was 3,267, whereas the number of genes existing in Indica and O. rufipogon but not in Japonica was 6,451. The number of genes existing in Indica and Japonica but not in O. rufipogon was 2,693. The shared number of genes between Indica and O. rufipogon was more than that between Japonica and O. rufipogon, and more-so even than that between Japonica and Indica.

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A Strategy that Discovers Conserved Genes from Co-orthologs

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The use of orthology information is a fundamental and widely used strategy in functional analysis and comparative genomics even as demands increase for genome projects due to the rapid development of next generation sequencing. Thus, the identification methods for orthology have become sophisticated. However, orthology, especially co-orthology, does not guarantee their functional conservation essentially, and the current methods are focused on the discrimination of orthologs from out-paralogs. Hence, only one-to-one orthologs that do not cover total genes have been used for comparative genomics. We developed a strategy to extract the most likely conserved genes among co-orthologs. In comparison with the traditional method, the reciprocal best hit and a pilot analysis showed the ability to discover genes that could not be discovered by reciprocal best hits.

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Identification of Indels Causing Frameshift from 3,459 Asian Rice Collection using KNU Axiom Oryza 580K Genotyping Array

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For this analysis to be effectively used in gene function research, the Indel is an important variation that can cause frameshifts in a gene and change the gene function, depending on the location of occurrence. We performed the indel variant calling on 294 rice core accessions to identify indels which gave rise to frameshift indel before. Here, we identified the indel variants which gave rise to frameshift from the 3,459 Asian rice collection using KNU Axiom Oryza 580K Genotyping Array. The results will provide an infrastructure to identify the function of genes and breed new varieties which have agronomically beneficial genes.

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IT-PCR: a simple web-based integrated tool for picking CRISPR targets to facilitate functional genomics study in rice

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In the era of new breeding biotechnology, which is based on genome editing, it is important to choose an appropriate target gene and design specific guide RNA (gRNA). In particular, determination of an effective knockout strategy, such as a single or multiple knockouts, to deal with the functional redundancy of the target gene is essential when using a new breeding technology for rice, given that it has undergone substantial genome duplication. Although many computational tools are available to help researchers design precise gRNA, there is no software for the selection of target(s) for the new breeding technology. To address this bottleneck in functional genomics using genome editing technology, we developed a simple web-based software designated “integrating tool for picking clustered regularly interspaced short palindromic repeat targets to facilitate functional genomic study in rice” (IT-PCR). This is an integrated tool for calculating the similarity in both protein sequences and transcriptomes to predict the functional redundancy of a queried gene in rice, which is a model crop plant. Using IT-PCR, researchers can easily obtain information about functional redundancy or dominance of a queried gene using an informative graphical user interface, without computing power or substantial labor. IT-PCR is implemented in the Django web framework, Bootstrap, and Python. It is freely available at it-pcr.khu.ac.kr.

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Repeated Rank-based Marker Selection for Genomic Selection of Low Heritability

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Genomic prediction is the most popular part of genomic analysis in plants and is to predict a trait of interest from the pre-trained model which sets up using genomic datasets. Recently, sequencing technologies have evolved, whole genome scale data has been created and can be used for genomic prediction, but there are some problems in this case, such as high computational load and considering the correlations between SNPs, etc. RRMS is an R package designed to extract marker subset from repeated rank-based marker dataset induced by genome-wide association study or marker effects for genomic selection. (https://github.com/lovemun/RRMS) RRMS provides the optimized genome-wide biomarker set with the best predictability of phenotype by the implemented ridge regression using genetic information. Applying our method to human and plant dataset with various heritability, we selected hundreds to thousands of biomarkers for precise prediction.

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LegExpress: Construction of a translational bioinformatic platform for expression profiling in legume plants

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Genome-wide transcriptome analysis is one of the most powerful means to gain a broad and deep insight into the molecular mechanisms that underlie dynamic interactions among numerous genes in organisms. Although several bioinformatic platforms for gene expression profiling have been developed for individual species, platform for cross-species transcriptome analysis is not currently available. We employed the technical concept of translational genomics between different species and aimed to build the platform in user-friendly manner. This DB-linked platform, named LegExpress, harbors wide array of transcriptome data for three representative species with relatively the most comprehensive gene expression information, including Glycine max, Medicago truncatula and Arabidopsis thaliana. All these expression data were collected from publically available ArrayExpress(http://www.ebi.ac.uk/arrayexpress)DB and composed mainly of Affymetrix GenChip data. Raw data were processed to select high-quality transcriptome data and normalized by the RMA standardization method. We developed a program for visualization of the data and organized the user interface according to suitable criteria, such as organs, developmental stages, time courses and different stimuli (e.g., hormones, biotic/abiotic stresses). It is anticipated that LegExpress may play a useful role for breeder/researcher-friendly transcriptome analysis platform and can be applied to design breeding programs through helping breeders discover trait-associated genes.

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LegCompara: A real time-responsible DB-linked platform for the translational genome analysis in legumes

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Comparative genome analysis is a powerful approach to look into the genomic organizations among different, but evolutionary related, species, to predict function of certain genes of interest and to interpret evolutionary relationships between compared species. For such reasons, development of efficient and automated bioinformatic visualization tool is essential in this research field. To achieve this goal, we intended to construct an interactive and flexible bioinformatic interface for the comparative analysis focused on legume genomes, named ‘LegCompara’. This platform consists mainly of two parts: a web-based user interface and corresponding relational databases. The database harbors a diverse array of genomic information (e.g., functional annotation, ortholog groups) for seven legumes (M. truncatula, G. max, P. vulgaris, C. cajan, V. radiata, C. arietinum) and two model plants (A. thaliana, O. sativa). This genome browser, unlike other traditional genome browsers, was designed for researchers to dynamically interact with user interface, so it can navigate multiple chromosomes of different or same species simultaneously, resulting in genome-wide and/or regional comparisons by depicting corresponding syntenies with either blocks or lines between orthologous regions or genes. It is expected that LegCompara may provide researchers and breeders with useful resources for more efficient and user-friendly comparative genome analysis.

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GWAS-based dissection on genes and genomic loci involved in the pigmentation of soybean seeds

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Soybean (Glycine max [L.] Merr.) is the most important crop among all cultivated legume crops in the world. Seed coat has been significantly influenced during the period of domestication in that it is linked to seed dormancy, seed viability and cost factors in processing seeds for oil and soy foods. To identify loci linked with seed pigmentation, we collected the resequencing data of 438 accessions. A genome wide association study using all possible combinations of three traits revealed four loci (designated as SPI-SP4). More important, we identified a gain of function mutation affecting a CaaX-type endopeptidase gene (Glyma.01G198500), which was a chloroplast-targeted transmembrane protein, as a strong candidate for the green seed coat. Glyma.01G198500 gene was highly coexpressed with the genes associated with chloroplast development and shared CaaX protease self-immunity domain (PF02517) with SCO4 which is a chloroplast-targeted protein that plays important roles in development of chloroplast. Glyma.01G198500 protein of the green soybeans had all of the CaaX protease self-immunity domain and resembles alpha-helical bundle structure of major three transmembrane protein structures, whereas that of the yellow soybeans had a partial CaaX protease self-immunity domain and was far from the alpha-helical bundle structure. This study provides insights into how to effectively utilize the data accumulated in the public databases and the interaction of four loci controlling seed pigmentation.

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Dynamics of the gene regulatory networks of leaves in Brassica rapa

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Chinese cabbage (Brassica rapa ssp. Pekinensis) is one of the most important horticultural crops in Asian countries. Currently, domestic and overseas demand is steadily increasing. In the heading formation, differential regulation of production and growth between inner and outer leaves is the most important developmental process. In general, it is well known that the developmental process is determined by complex interactions among genes. Therefore, it is important to understand the developmental process of Chinese cabbage by studying the crucial genes involved in the cells constituting the inner and outer leaves, and to clarify their dynamical characteristics. A recent study showed that the gene expression patterns of inner and outer leaves are quite different but the tissue-specific gene regulatory networks of the two types of leaves are still largely unknown. Based on the RNA sequencing profiles of inner, outer and young leaves from Chinese cabbage and the gene regulatory network of A. thaliana, we reconstructed tissue-specific active subnetworks of inner and outer leaves of Chinese cabbage. Then, we analyzed the structural and functional characteristics of the two tissue specific active subnetworks. Interestingly, we found that coherent feedforward loops were prominent in the inner leaf whereas incoherent feedforward loops were abundant in the outer leaf. By exploring these results, we found that the coherent feedforward loops are necessary for maintaining the molecular states whereas the incoherent feedforward loops are crucial for adaptation.

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Transcriptome profiling reveals marker genes for seed dormancy and germination in *Arabidopsis thaliana*

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Plant seeds are an important genetic mediator for trait of progeny. Seed development and dormancy are affected and regulated by a large number of genes and environmental conditions. The antagonistic interaction between abscisic acid and gibberellin in plant hormones plays an important role in the regulation of seed dormancy and germination. Recently, studies of epigenetics have shown that seed dormancy and germination-related gene expression is regulated by DNA methylation and histone modification. However, the molecular mechanisms underlying seed dormancy and germination in seed development stage have not been clearly understood. In this study, we analyzed transcriptome of three different dormancy levels of seed development stage in *Arabidopsis* (*Arabidopsis thaliana*) ecotype Col-0 using mRNA library sequencing. The three different seed development stages are fresh harvest (FH), after-ripening (AR), and germination stimulated (GS). We investigated transcriptome-wide responses of long non-coding RNAs (lncRNA) and protein-coding genes during breaking seed dormancy. We found that differential expression of well-known marker genes associated with processes of dormancy and germination in Col-0 such as Dog1, ABI5, Ga3ox1 and Ga3ox2. To verified these data, we analyzed expression level of marker genes (Dog1, ABI5, Ga3ox1 and Ga3ox2) in each different dormancy stage by quantitative reverse transcription PCR (RT-qPCR). Also, we identified approximately 1,500 IncRNAs and some of them located near genes which are related to dormancy. This study provides a foundation for understanding dynamics of transcriptome during breaking seed dormancy in *Arabidopsis thaliana*.

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Transcriptome analysis in rice irradiated with different types of ionizing radiations

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Exposure to ionizing radiation (IR) has been regarded as a kind of abiotic stresses that can change the expression of genes in living organisms. This study aimed on investigating the variations in gene expressions induced by four different types of irradiations with different doses on rice. Rice seeds (cv. Ilpum) were irradiated with 100, 200, and 400 Gy gamma rays (GR), 20, 50, and 80 Gy ion beams (IB), 100, 200, and 400 Gy proton beams (PB), and cosmic rays (CR). Sequencing of RNA extracted from 3-week-old seedlings of the irradiated seeds yielded a total of 55.1 Gb reads with an average of 4.6 Gb per sample. Comparison of the gene expression levels between non-irradiated control and IR treated plants identified 1005 differentially expressed genes (DEGs). Among them, 50 and 44 DEGs were up- and down-regulated commonly by the four types of IR treatment. A total of 159 DEGs were mapped to 84 KEGG pathways, and “Metabolic pathways” (104 DEGs) and “Biosynthesis of secondary metabolites” (75 DEGs) were heavily represented. Gene ontology (GO) enrichment analysis of DEGs revealed that 134, 138, 111, and 45 GO terms were significantly enriched in GR, IB, PB, and CR treated groups, respectively. 11 GO terms, “catalytic activity” (GO:0003824), “defense response” (GO:0006952), “phenylpropanoid metabolic process” (GO:0009698), “phenylpropanoid biosynthetic process” (GO:0009699), “response to stimulus” (GO:0005690), “response to stress” (GO:0006950), “secondary metabolic process” (GO:00174748), “extracellular region” (GO:0005576), “cell wall” (GO:0005618), “external encapsulating structure” (GO:0043591), and “oxidoreductase activity” (GO:0016491) were found in the all IR treatment, indicating differential expression of functional genes in response to IR at the molecular level. This study will contribute to an understanding of the response mechanism to ionizing irradiation in plants.

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Web-application for finding the open reading frames (ORF) in diverse sugar cane genomes

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Sugarcane is one of most important multi-purpose crops that is native to the tropical regions. Because of the genome size of sugarcane (10 Gbase for the sugarcane cultivar that is polyploid interspecific hybrids), it has been hard to build the reference level assembly resulting in partial contigs or scaffolds. Moreover, the recently published assemblies with the name of “sugarcane” are highly heterogeneous as the template species are not the cultivar that actually being cultivated or other polyploidy form that may be representing donor species of sugarcane such as Saccharum officinarum and Saccharum spontaneum. As the genome-editing technology is advanced, the necessity of utilize genome sequence is also arising for sugarcane to find guide-RNA binding site by the pre-trained algorithms or human inspection. Here, we built web-application for the researchers to find the open reading frame (ORF) easily with a query sequence. This utilize various draft level contigs and scaffolds from NCBI database with RNAseq assemblies. Firstly, the query sequence will be matched with RNAsq assemblies and the matched transcript assembly would be spliced-aligned to set of sugarcane draft genomes. This enable the researchers to directly observe the ORF structure of the query gene and design precise guide RNA for genome editing.

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RTFDB: A web-based tool for the prediction of rice transcription factor function

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Transcription factors (TFs) are an important class of regulatory molecules. Despite their importance, only a small number of genes encoding TFs have been characterized in Oryza sativa (rice), often because gene duplication and functional redundancy complicate their analysis. To address this challenge, we developed a web-based tool called the Rice Transcription Factor Phylogenomics Database (RTFDB) and demonstrate its application for predicting TF function. The RTFDB hosts transcriptome and co-expression analyses. Sources include highthroughput data from oligonucleotide microarray (Affymetrix and Agilent) as well as RNA-Seq based expression profiles. We used the RTFDB to identify tissue specific and stress related gene expression. Subsequently, 273 genes preferentially expressed in specific tissues or organs, 455 genes showing a differential expression pattern in response to 4 abiotic stresses, 179 genes responsive to infection of various pathogens and 512 genes showing differential accumulation in response to various hormone treatments were identified through the meta-expression analysis. Pairwise Pearson correlation coefficient analysis between paralogous genes in a phylogenetic tree was used to assess their expression collinearity and thereby provides a hint on their genetic redundancy. Integrating transcriptome with the gene evolutionary information reveals the possible functional redundancy or dominance played by paralog genes in a highly duplicated genome such as rice. With this method, we estimated a predominant role for 83.3% (65/78) of the TF or transcriptional regulator genes that had been characterized via loss-of-function studies. In this regard, the proposed method is applicable for functional studies of other plant species with annotated genome.

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A comparison of two GBS pipelines to analyze a large onion genome

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Various genotyping methods based on sequencing have been developed with the fast development of NGS technology and the decline in prices. In particular, Genotyping-By-Sequencing (GBS) technology has become a useful technology in agricultural plant research with the announcement of the TASSEL-GBS pipeline in 2014. The genotyping pipelines used in GBS can be divided into two types the reference-based method and the de novo method determining genotype without a reference genome. Many agriculturally important crops had no reference genome so the de novo method pipelines have been used for the plants. However, there were reports even genotyping result by a reference-based method based on a poor quality draft genome is better than a de novo method. In order to check whether the reports are also correct for a huge genome, we tested two GBS pipelines, GBS-SNP-CROP and Stacks, which support both GBS methods with onion. As a result, genotyping result by the reference-based method shows better result even that we used a very first draft genome as the reference genome in both pipelines. The cost of genome sequencing is getting to decrease sharply. Thus, the reference-based GBS can be the better choice in a genotyping of a huge genome plant.

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Developing a model system to obtain genotype data of a mass of genetic resources

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Countries around the world are making various efforts to secure genetic resources, which are the necessary materials for agricultural research and development. NAC (National Agrobiodiversity Center) has secured more than 200,000 agricultural genetic resources in Korea. In the era of the genome, it is essential to obtain genotype information about genetic resources to utilize agricultural genetic resources efficiently. However, there is not yet a system for efficiently securing genotype data of the huge number of genetic resources. Therefore, we aim to construct a model system by using 3,300 sorghum genetic resources managed by NAC. As the first step, 12 seeds were sown in each sorghum resource after removing similar resources by the Powercore software based on the basic information of the resources. As a next step, we will determine the genotype data for all plants and carry out a comparative analysis in the genotype data to determine the degree of difference between seeds in a resource as well as between resources.

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RACSO: Toolkit for random seed orchard design and visualization

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Seed orchard is a stand planted with superior trees for mass-production of genetically improved seeds. In establishment of new orchard, clones should be arranged to minimize selfing and to facilitate cross-pollination for increase in genetic gain and variation. We present RACSO, an integrated collection of Perl scripts focused on building fast and flexible pipelines for random arrangement and visualization of clones in seed orchard. RACSO adopted stepwise arrangement method based on the iterative convergence that improved the performing speed of random arrangement. It consists of three parts: 1) random arrangement of the clones, 2) iterative revised search and repositioning of same clones that are placed in close proximity, 3) visualization of planting grid map. RACSO is available in designing the orchards with polygon shape and some vacant positions.

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Effect of Pinewood Nematode on the Water Content and Early Disease Development of Japanese Black Pine Seedlings

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Pine wilt disease caused by Bursaphelenchus xylophilus (steiner & Bührer) Nickle, the pinewood nematode (PWN), is a devastating disease and spreading in Korea since the first notice at Mt. Keumjeong in Pusan in 1988. In this study, the disease development such as resin drying, xylem drying, pith browning and needle yellowing in 4-year-old Pinus thunbergii seedlings, inoculated with pine wood nematode, and the change of water content, were investigated to find a reliable physiological index for early diagnosis. The results showed that internal and external symptoms appeared 20 days after inoculation, and there was drying of resin, drying of xylem and pith browning in stem xylem, then needle wilted occurred and pine seedlings died finally. Although population of pine wood nematode increased from 5 to 10 days after inoculation, it has increased dramatically from 10 to 20 days after inoculation when both internal and external symptoms appeared, but decreased 60 days after inoculation. As the number of nematodes increases, water content of stem and relative water content of current needles and branches decreased significantly. The stem water content decreased gradually, stem and leaf relative water content in a current branch began to decrease before symptoms appeared. It is suggested that stem water content could be used as a disease indicator for early diagnosis of the disease.

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Soybean endo-1,3-beta-glucanase interaction with Soybean mosaic virus -encoded P3 protein may contributes the intercellular movement

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Soybean mosaic virus (SMV), a member of the Potyvirus genus, is a prevalent and devastating viral pathogen in soybean-growing regions worldwide. Potyviral cell-to-cell movement was shown to target plasmodesmata (PD) by CI with the help of P3N-PIPO in a ratio-dependent manner. Potyvirus-encoded P3 is reported to participate in virus replication, movements, and pathogenesis. This study provides evidence that the soybean (Glycine max) endo-1,3-beta-glucanase protein (designated as GmGlu) interacts with SMV-P3 by using a two-hybrid yeast system to screen a soybean cDNA library. A bimolecular fluorescence complementation assay further confirmed the interaction, which occurred on the cytomembrane in Nicotiana benthamiana cells. Subcellular localization experiment indicated that GmGlu localized in the cytomembrane and GmGlu with PD (plasmodesmata) marker co-localization at plasmodesmata site. The transient expression of GmGlu can promote the coupling of Turnip mosaic virus replication and cell-to-cell movement in N. benthamiana. Under SMV infection, Callose deposition at PD was observed obviously by staining with aniline blue, which raise a physical barrier restricting cell-to-cell movement of SMV. Meanwhile, RT-PCR experiment demonstrated that the expression of GmGlu increased under SMV infection, which involved in regulation of callose. The interaction between the membrane protein SMV-P3 and GmGlu may contribute to the potyvirus intercellular movement, and GmGlu may be an essential host factor involvement in potyvirus infection.

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Fine Mapping of QTL Confering Cercospora Leaf Spot Resistance in Mungbean (Vigna radiata (L.) Wilczek)

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Cercospora leaf spot (CLS) disease, caused by the fungus Cercospora canescens Ellis & Martin is an important limiting factor in mungbean (Vigna radiata (L.) Wilczek) production. Yield loss due to this disease can be up to 50%. A previous study using mungbean F2 and BC1F1 populations developed from CLS-resistant mungbean ‘V4718’ and CLS-susceptible cultivar ‘Kamphaeng Saen 1’ (KPS1) has identified a major quantitative trait locus (QTL) controlling CLS resistance (qCLS). The objectives of this study were to finely map the qCLS and to identified candidate genes for the qCLS. An F2 and BC1F2 populations derived from crosses between KPS1 and V4718 were used for mapping population. The populations were genotyped with newly developed simple sequence repeat markers. QTL analysis the in F2 and BC1F2 populations located qCLS to a genome region between markers mCLS243 and mCLS203. The qCLS accounted for 66 and 57% of the disease score variation in the F2 and BC1F1 populations, respectively. Compared to the previous result, QTL region for qCLS was narrowed down from 29 Mb to 30 Kb. Annotated genes in the 30 Kb regions are considered as candidate genes for the CLS resistance. They will be sequenced and their expression will be determined.

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Novel Sources of Resistance to Pepper Yellow Leaf Curl Thailand Virus (*Begomovirus*)

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Likely, the most devastating pepper-infecting viruses, especially in tropical and subtropical regions, are members of the whitefly transmitted *Begomovirus*, including Pepper yellow leaf curl Thailand virus (PepYLCThV). Management of PepYLCThV has been based primarily on insecticides against the vector. However, the use of insecticides has been found to be only partially effective, costly for producers, and represents a hazard to farmers and the environment. An effective PepYLCThV management strategy is the development of resistant cultivars. For this project, 100 *Capsicum* entries comprising breeding lines, open pollinated varieties, genebank accessions and wild species were screened for resistance to PepYLCThV. The experimental design was a randomized complete block design with three replications and 10 plants in each replication and was conducted in field net-houses at two locations (Khon Kaen and Kamphaeng Saen, Thailand) using augmented inoculation by viruliferous whiteflies. Scoring was done at ~60, 90, 120, and 150 days after inoculation using a standardized 6-point scale (1 = no symptoms to 6 = very severe symptoms) and the average of the scores of 10 plants within each replication was used for analysis. While no accession was identified as being immune to the disease, several accessions (PP99, PBC 148, PBC 149, PBC 502, PBC 518, and PBC 601) were found to be highly resistant at both locations, with accession PP99 being the most resistant. The accessions PI 159236, VI012911, VI012528, and VI012642 were identified as being very susceptible, with high levels of symptoms occurring only 60 days after inoculation. Overall, the disease severity at the Khon Kaen location was greater compared to Kamphaeng Saen, highlighting the importance of multi-location testing for disease resistance. These resistant accessions can be used to study gene action and to move resistance genes into well adapted germplasm.

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Evaluation Phenotypic and Genotyping for Resistance Against Tomato Yellow Leaf Curl Thailand Virus (TYLCThV) Validated by Ty-2 Ty-3 and Ty-4 Genes in Tomato

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Tomato yellow leaf curl virus (TYLCV) caused by whitefly-transmitted begomovirus species one of the most destructive and causing heavy losses in tomato yields, especially in sub-tropic and tropic regions including Thailand. Therefore breeding tomato variety resistance to TYLCV is necessary. The purpose of this research was to evaluate Tomato variety which resistant to TYLCV for Thailand’s strain (TYLCThV) with agronomic traits. The 35 tomato accessions obtained from the World Vegetable Center (AVRDC) were compared with the susceptible variety (Seedatip: KKU-T12002). The results of field evaluation showed that the eleven tomato accessions performed moderately resistant to TYLCThV and their good agronomic traits. The results for resistance were classified into 3 groups based on their responses to TYLCThV. The first group, i.e. KKU-T24003 and KKU-T23160 were identified as highly resistant level. The second group, i.e. KKU-T23176 was identified as resistant level and the other seven tomato varieties were identified as moderately resistant level. In addition, Ty-2, Ty-3 and Ty-4 gene were validated by 2 SCAR markers and 1 SSR marker in the 12 tomato accessions.

Keywords: whitefly, SCAR markers and SSR marker

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**PCS04-06**

Inhibition of fusarium surface rot by sound wave treatment in *Arabidopsis thaliana*

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The effect of sound waves on growth of *Fusarium commune* was investigated to explore whether frequency specific sound could be used as a practical alternative to chemical fungicides to fusarium surface rot on sweet potato. Of the sound treatment tested, sound wave significantly inhibited spore germination and growth. Furthermore, the disease rate was also effective, when the specific sound wave frequencies are treated on detached arabidopsis leaves with inoculated fungus. We analyzed the gene expression of infected arabidopsis leaves and *F. commune* on the PDA media after sound wave treatment. The expression of ethylene (EIN2, etc.) and jasmonic acid (PDF1.2, etc.) responsive defense gene in *Arabidopsis thaliana* was increased in the sound wave treated leaves. While, the expression of germination and pathogenicity related genes in *F. commune* was decreased compared to the untreated group (SNF1, etc.). These results suggest that sound wave treatment could be used to reduce the occurrence of fusarium surface rot on sweet potato by regulation of plant defense and fungus pathogenicity related genes expression. It is possible that sound wave treatment could represent an environmentally-friendly alternative to chemical fungicides. These results broaden our knowledge regarding the effective management of noxious necrotrophic fungal pathogens by a nonchemical approach.

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**PCS04-07**

Sequential double screening method to identify accessions resistant to *Fusarium* wilt disease in the sesame world collection

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Sesame (*Sesamum indicum*) is cultivated for its high oil content and numerous health benefits, but the increase in its production area and productivity facing to a lot of factors. Among the major diseases affecting sesame, the wilt disease triggered by *Fusarium oxysporum* f. sp. *sesami* (Fos) can cause severe loss in seed yield. However, there is currently very little genetic material with high resistance to Fos among cultivated varieties. In this context, the identification of accessions with higher resistance to Fos would help to understand the occurrence of *Fusarium* wilt disease. During previous field assessments, five different strains of *Fos* were collected, identified and characterized for their pathogenicity. In this study, we selected one strain with high virulence to develop various screening methods to identify genotypes resistant to *Fos* among the different accessions in the Sesame World Collection stored at the National Agrobiodiversity Center. In order to establish a systematic screening method, an initial set including contrasting materials of the mini-core collection, wild and cultivated sesame were investigated for resistance to *Fos*. In three distinct screening platforms, the inoculation was performed at different development stage. In the first screening, the first *Fos* inoculation was conducted at germination and the second inoculation after 4 weeks. In the second method, the inoculation occurred 10 days after emergence by cutting roots of young seedling. In the third method, the inoculation was conducted 30 days after planting. The symptoms related to *Fusarium* wilt disease were accessed daily up to 4 weeks after inoculation. The screening methods were optimized to identify resistant(R) and susceptible(S) accessions among the Sesame World Collection. Ultimately, the results of this study will be used to develop recombinant inbred lines from the selected R and S genotypes and genetic markers associated with resistance to *Fusarium* wilt.

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Screening of Sclerotinia Rot Resistance in Korean Origin Perilla (*Perilla frutescens*) Germplasm Using a Detached Leaf Method

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Sclerotinia rot, caused by a fungus *Sclerotinia sclerotiorum*, is one of the most destructive and unpredictable yield losses in perilla (*Perilla frutescens*) leaf production in Korea. Screening disease resistant genetic resources is necessary to develop disease-resistant cultivars and conduct related research.

A total of 544 accessions of Korean origin, including 400 landraces, 29 cultivars, 24 breeding lines, and 1 relative wild type, and 90 unknown, were evaluated for resistance to Sclerotinia rot (*Sclerotinia sclerotiorum*) using detached leaf inoculation technique. *Sclerotinia sclerotiorum* isolate KACC40457 was inoculated at the seedling stage (five to six leaves). A mycelial plug was placed fungus-side down on the main leaf vein and incubated at 22 ± 1°C on moistened paper towel in a plastic box. 12 accessions including two landraces and 10 unknown accessions showed high level of resistance that is higher than 70% of resistance ratio (no. of plants showed below 1 cm of lesion size/total evaluated plants × 100). Two accessions, IT226504 and IT226533, showed 100% of resistance ratio.

12 accessions which showed strong and moderate level of resistance to Sclerotinia rot could be possibly used by breeders, farmers, and researchers to produce new disease resistant cultivars and use them commercially. However, research related to the exploration of appropriate materials (accessions) for breeding cultivars with good quality, high functional components, high consumer acceptability, etc. should be continued, considering pathogenicity test was conducted in young stage.

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The WY domain in the *Phytophthora* effector PSR1 is required for infection and RNA silencing suppression activity

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*Phytophthora* pathogens manipulate host innate immunity by secreting numerous RxLR effectors, thereby facilitating pathogen colonization. Predicted single and tandem repeats of WY domains are the most prominent C-terminal motifs conserved across the *Phytophthora* RxLR superfamily. However, the functions of individual WY domains in effectors remain poorly understood. • The *Phytophthora sojae* effector PSR1 promotes infection by suppressing small RNA biogenesis in plant hosts. We identified one single WY domain following the RxLR motif in PSR1. This domain was required for RNA silencing suppression activity and infection in *Nicotiana benthamiana, Arabidopsis*, and soybean. Mutations of the conserved residues in the WY domain did not affect the subcellular localization of PSR1 but abolished its effect on plant development and resistance to viral and *Phytophthora* pathogens. This is at least in part due to decreased protein stability of the PSR1 mutants in * planta*. • The identification of the WY domain in PSR1 allows the prediction of a family of PSR1-like effectors also possess RNA silencing suppression activity. Mutation of the conserved residues in two members of this family, PpPSR1L from *P. parasitica* and PcPSR1L from *P. capsici*, perturbed their biological functions, indicating that the WY domain is critical in *Phytophthora* PSR1 and PSR1-like effectors.

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**PCS04-10**

Gene effects of chili pepper with two different resistant sources to PepYLCV

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To improve chili variety for resistant to multiple strains of Pepper yellow leaf curl virus-Thailand (PepYLCV) with appropriate breeding methods, the gene effects of those different resistant sources are required. The objectives of this study was to investigate generation mean analysis of the two populations from different genetic reported-resistant sources; first resistant population was derived from Twari (code no. 101) and the other one from PSP-11 (code no. 103). Each of population consisted of six generations, i.e. two parents (P1, P2), F1, F2, back cross to female parent (BCP1) and male parent (BCP2). All plants of the two populations were infected by PepYLCV with whitefly transmission at 4 true leaves-stages. It was found that both populations with two resistant sources showed the main effects of additive by dominant epistasis gene for resistance to PepYLCV. However, the main effects for fruit yield were additive by additive epistasis gene. Therefore, backcross technique might be good for selection resistant chili variety to PepYLCV with good agronomic traits.

**Keywords:** Begomovirus, PepYLCV, chili resistance

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**PCS04-11**

Discover a new QTL for bakanae disease resistance in rice

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Bakanae disease is caused by several species of Fusarium and imposes serious limitations on rice production worldwide. The incidence of this disease is increasing in the top rice-growing countries. Thus, higher resistance to this disease may be a cost-saving solution preferable to the application of fungicides. In this research, we used tropical japonica rice variety, Zenith, was selected as resistant donor to bakanae disease. 180 RILs (F₃₋₅) were generated from a cross between Ilpum and Zenith. In primary mapping, a QTL was found on short arm chromosome 1 was 3.5 Mb region between RM1331 and RM3530 markers. The resistance QTL, qBK1², explained 30.93 % of the total phenotype variation with an LOD score of 13.43. Location of qBK1² was further narrow-downed to 730kb by finer mapping by using additional RM markers and those of previous study developed by lee et al.,(2017). Results of this study are expected to provide useful information toward developing resistant rice lines harboring single or multiple major QTLs by pyramiding genes and marker-assisted breeding against bakanae disease.

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**Genetic Mapping of *Chili veinal mottle virus* Resistant Gene 4 (cvr4) in Pepper**

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*Chili veinal mottle virus* (ChiVMV) is the notorious virus affecting the severe loss of pepper production in Asia and Africa. However, very limited resistant sources have been reported up to date. Through the evaluation of ChiVMV resistance, we identified four ChiVMV resistant accessions in this study. Among them, *Capsicum annuum* accession ‘CV9’ showed a broad spectrum of resistance against other potyviruses, Tobacco etch virus HAT (TEV-HAT) and *Pepper mottle virus* (PepMoV). Genetic analysis showed that the ChiVMV resistance in ‘CV9’ was conferred by single recessive gene, which was named to cvr4 in this study. pvr1 and pvr6, previously reported loci for ChiVMV resistance, were not co-segregated to CV9 × Jeju F2:3 segregating population. To map the new resistant locus, we performed bulked segregant analysis RNA sequencing (BSA RNA-Seq) in resistant and susceptible pools from F3 population. RNA-Seq pinpoints the telomeric region of chromosome 11 to the cvr4 locus. Previously developed genome-wide markers on pepper chromosome 11 could delimit the cvr4 locus to 33 Mb. To figure out the locus, we are saturating SNP markers in cvr4 target region using information from BSA RNA-Seq. This study will be helpful to make use of potyvirus resistant cultivar in pepper breeding program.

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**Change of yield by using rootstock in tomatoes**

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Bacterial wilt of tomatoes caused by *Ralstonia solanacearum* is one of the main reasons for reducing crop production. In high-temperature and humid conditions, *R. solanacearum* invades plant wounds and blocks the xylem. Damage to tomatoes by bacterial wilt is serious in Korea. *R. solanacearum* is soil born pathogen and its biological and chemical control is difficult. Currently, the best way to control the bacterial wilt is to use resistant rootstocks. This study was conducted to find the changes in yield between grafted tomatoes and non-grafted tomatoes. Tomatoes grafts were conducted 30 days sowing. The yield was investigated for 2 weeks from 100 days after planting. Non-grafted tomatoes and 4 kinds of grafted tomatoes with different rootstocks each other was used. As the result, 3 kinds of grafted tomatoes showed more yield than non-grafted tomatoes. In addition, there was no difference in the quality of fruit. Thus, the use of resistant rootstocks not only shows that resistant to disease but also increase the yield of fruit.

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**PCS04-14**

**Discovery of new haplotyped of a soybean cyst nematode resistant gene, GmSNAP18**

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Soybean Cyst Nematode (SCN) is a single most damaging pest, affecting soybean production all over the world. Therefore understanding the molecular nature for resistance to SCN, is important for good management. Soluble NSF attachment protein (SNAP) gene is related to resist SCN. SNAP gene is a family of constitute five members, among which SNAP18 is considered as resistant gene that confer to resist SCN. We studied the haplotypes of the GmSNAP18 with DNA sequencing and comparing of DNA variation in variable Korean cultivars, landraces, and wild type soybean with the different phenotypes. Objective of our research is to genotype 71 soybean lines based on SNPs found in target position along with SNP haplotypes for distinguishing resistant and susceptible cultivars. With the known phenotypes of the cultivars, i.e., Peking, PI88788, and Essex, we developed primers on exon 6 and 9 of GmSNAP18 followed by PCR and sequencing for the selection of resistant gene. 71 different Korean cultivars were targeted to the same region of GmSNAP18 and sequenced. With the multiple sequence alignments with known phenotype cultivar (published), genotyping was performed and SNP haplotypes were studied. The cultivars were differentiated as a resistant and susceptible as per the SNP haplotypes found. Additionally, new SNP haplotypes were found in three cultivars. Total 16 genotypes showed resistant haplotypes and forty-seven cultivars were found to be susceptible. Interestingly three cultivars showed a new SNP haplootype position in compare to known haplotypes and tagged as a new haplotypes. From these relevant research and reference we can further explore soybean breeding and develop resistant varieties through the manipulation of gene GmSNAP18.

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**PCS04-15**

**Microbial community analysis in cultivation soil with soft–rot disease of Gastrodia elata by metagenomics**

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*Gastrodia elata* (*G.elata*) belongs to the orchid family and has a myco-heterotrophic lifestyle that plant-fungi symbiosis depends on seed germination and vegetative growth rather than photosynthesis. *G.elata* is a traditional medicinal herb mainly used for convulsion ischemia, dementia, tremors, and vertigo. *G. elata* has been widely cultivated in the mountainous area of Korea, China, Japan, and India. However, the soft rot disease of *G. elata* has caused 60% of loss in the actual yield in South Korea in recent years. In this study, we aim to compare the fungal composition in cultivated soil to identify the fungi caused a soft rot of *G. elata*. For metagenome analysis, fungal genomic DNA (gDNA) was isolated from infected soil with soft rot disease. The isolated gDNA was identified by internal transcribed spacer (ITS)-barcoding amplicon sequencing approach. Initially, 5.24 Gb raw data was generated from Ion-S5 sequencing. After sequence quality control processing, the data was investigated further taxonomic classification. We compared the top 10 ranked fungal composition between normal and infected soil. *Guehomyces pulillare, Solicocozyma terricola, Cystofilobasidium infirmominutum, Coniochaeta mutabilis, Leucosporidium drummi*, and *Exophiala salmonis* are higher in infected soil than normal soil condition. Those fungal groups have well known in the dead plant biomass and postharvest disease. Thus, further study is needed to examine these fungal groups can act as a pathogen in *G.elata*.

Keywords: *Gastrodia elata* (*G.elata*), single internal transcribed spacer (ITS), metagenome, soft rot disease

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Multi-omics approaches reveals co-evolution of microRNAs and disease-resistant genes in pepper

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MicroRNAs play roles in various biological processes like defense in plants. Some plant microRNAs produce phased, secondary siRNAs (phasiRNAs), which regulate cascade of gene expression. We investigated the relationship of Solanaceae microRNAs and defense genes in evolutionary perspective by performing genome-wide comparative analysis of microRNAs and their targets in Solanum plants. Degradome analysis showed that many of genes related to defense response are regulated by microRNAs in Solanum plants. We found that novel pepper microRNAs targeted genes encoding nucleotide-binding leucine rich repeat or receptor-like protein, known as disease-resistant genes. In addition, these novel microRNAs triggered phasiRNA production indicating amplification of regulation of the disease-resistant gene families. Taken together, microRNAs might be generated and evolved to regulate diverse genes involved in plant immunity. This study provides an insight into the evolution of novel microRNAs targeting plant defense genes and possible co-evolution with their target genes. This work was supported by the Next-Generation BioGreen 21 Program (No. PJ0133001), Rural Development Administration, Republic of Korea

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Development of multi-resistant japonica rice with a constant extraction of panicle

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‘Jeonju596’, a multi-resistant japonica rice variety developed from a cross between ‘Boramchan’ having a high yield and ‘HR28354-AC3-4’ having brown planthopper (BPH) resistance, was developed by the rice breeding team of NICS, RDA. This variety has about 121 days growth duration from transplanting to harvesting in west-southern coast, Honam and Youngnam plain of Korea. It has 53 cm culm length and 20 cm panicle length. In reaction to biotic and abiotic stresses, it shows resistance to bacterial blast pathogen races from K1 to K3, stripe virus and brown planthopper. Also, we confirmed that it has a resistance gene by carrying out molecular marker test for blast leaf, bacterial blast, rice stripe virus, and brown planthopper. The milled rice of ‘Jeonju596’ exhibits translucent, relatively clear non-glutinous endosperm and medium short grain. The milled rice yield performance of this variety is about 5.05 MT/ha in local adaptability test for three years. ‘Jeonju596’ has a very good panicle shape with a constant extraction of panicle and can be used as a useful genetic resources for multi-resistance breeding program against disease and insect and eco-friendly cultivation.

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175
Title: Investigation of the virus infection ratio in different sweet potato (Ipomoea batatas) generations for mass and quality seed production

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Virus free seedlings production is the biggest challenge in sweet potato production system. We attempted to investigate the virus infection ratio in different sweet potato generations (virus free, 1\textsuperscript{st} to 3\textsuperscript{rd} generations and virus infected seed stalks) to define the renewal generations which could minimize the damage by virus infection. Virus infection were checked before transplants and after harvest on two varieties-Pungwonmi and Jinhongmi. The result showed that the virus free plants produced lowest viral disease incidence in each variety. In Pungwonmi, virus free did not show any disease, 1\textsuperscript{st} and 3\textsuperscript{rd} generation produce disease in low percentage (3\textsuperscript{rd} generation showed only single virus SPSMV 100%). After harvest, virus free showed less disease infection (SPSMV 100%, SPLCV 40% and SPFMV 20%), whereas virus infected showed higher virus infection. VI affected with 5 viruses: SPSMV 100%, SPLCV 95%, SPFMV 50%, SPLV 35% and SPGV 5%. On the other hand, virus infection ratio of 3\textsuperscript{rd} generation were SPLCV 95%, SPFMV 70%, SPLV 20% and SPSMV 100%. In case of Jinhongmi, virus infection rate was lower in virus free and 2\textsuperscript{nd} generation stalks and higher in other generations and virus infected stalks. Before transplanting 55% SPSMV were observed in VI of Jinhongmi and 2\textsuperscript{nd} generation showed 100% SPLCV, 55% SPFMV, 40% SPLV and 10% SPVC whereas the virus infection ratio of VI of SPLCV, SPFMV, SPLV, SPVC, SPV2 and SPSMV were 100%, 25%, 20%, 10%, 10% and 45%, respectively. Before transplanting and after harvest, a total of 6 viruses were infected to the virus infected stalks but different generations showed lower number of virus infection. For using virus free sweet potato stalk and effective production of sweet potato for minimizing the damage by virus infection, 2\textsuperscript{nd} generation of renewal virus free stalks in Jinhongmi and stalks of 3\textsuperscript{rd} Generation of Pungwonmi would be useful.

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Genome-wide SNP discovery and development of molecular markers for bacterial wilt resistance in tomato

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Bacterial wilt is among most important vascular diseases limiting tomato production in tropical and subtropical regions of the world. The disease is caused by soil-borne pathogen Ralstonia solanacearum species complex. Bacterial wilt resistance in tomato is known to be polygenic and two major QTLs on chromosome 6 (Bwr-6) and 12 (Bwr-12) have been reported in the well-known resistant line (Hawaii 7996). Genome-wide SNPs were discovered by whole genome resequencing of seven resistant and two susceptible tomato varieties. The highest number of non-synonyms SNPs were obtained in chromosome 12 (168) followed by chromosome 6 (53). Analysis of SNPs in chromosome 12 revealed molecular marker tightly linked to Bwr-12 QTL which was able to effectively discriminate resistant and susceptible tomatoes. The Bwr-6 is a broad spectrum QTL covering a large genomic region and there is no SNP based molecular marker to locate this important QTL. Hence, we used the newly discovered SNPs in order to develop closely linked marker to this QTL. Six CAPS/CAP5 markers were developed near Bwr-6 and were applied to resistant and susceptible tomato cultivars for genotyping. Our marker analysis shows that Ch6-4 and Ch6-5 are closely linked to the Bwr-6 QTL. Either of the two markers can be used to track Bwr-6 and using together with Ch12-1 will increase the efficiency of selection in marker assisted breeding of tomato.

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Investigation of the expression level change of phytohormones which induced SAR on sweetpotato by inoculation time of *Ceratocystis fimbriata*

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Black rot is a sweetpotato (*Ipomoea batatas* (L.) Lam.) disease caused by the fungus *Ceratocystis fimbriata*. Black rot can develop on any part of the plant below ground and at any stage of crop production, but it is observed mostly on roots. *C. fimbriata* damages a part of the plant, then the signal transmitted directly to the whole body of the plant, which leads to Systemic Acquired Resistance (SAR). To induce SAR, the signal like phytohormone transmitted infected-cout to the whole body of the plant. Salicylic acid (SA) and Azelaic acid (AZA) are the plant hormones that promote plant defense mechanisms such as SAR. Pipelicolic acid (PIP) also help to establish plant SAR. In this study, we observed changes in hormone content in the plant on the basis of time period (0, 24, 48, 72 h) after inoculation with *C. fimbriata*. We observed different resistance among the sweetpotato cultivars. KOTO-PUKI, 7IB8 and Darby classified as susceptible, moderate resistance and resistance respectively. In case of Darby, PA content increased about 3 fold at 24 h after inoculation, AZA content has been changed after 24 h, 48 h and 72 h of inoculation. Especially, the moderate resistance cultivars (TIB8) 200nmol/g FW (0 h) increased to 450 nmol/g FW (24 h) and also susceptible cultivars (KOTO-PUKI) 200 nmol/g FW (0 h) to 870 nmol/g FW (24 h).

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Phenotypic reactions of soybean differentials following inoculation of *Phytophthora sojae* isolates originated in South Korean

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*Phytophthora sojae*에 의한 콩 역병(*Phytophthora root and stem rot*)은 전 세계적으로 분포하여 생산량을 크게 감소시키는 빈인 중 하나이다. 콩 역병은 콩이 유일무이한 가주식물인 정도로 가주 범위가 매우 좁으며 토양 내에서 또는 식물체 파편 등에서 겨울 동안 생존이 가능하여 수년간 생존할 수 있어서 방제가 어렵기에 식물의 저항성을 이용하는 것이 지속 가능한 방제방법이다. 국내에서 콩의 논재배가 증가함에 따라 역병에 대한 피해가 증가하고 있지만 국내에서 콩 역병 저항성 및 역병균에 대해 알려진 것이 거의 없다.

본 연구의 목적은 저항성 유전자(*Rps gene*)을 가진 판별 품종을 이용하여 국내 콩 역병 균주의 병원체(*pathotype*)을 확인하는 것이다. 콩 역병 저항성 유전자를 가진 15개 판별제품중에 각각 3개 각각 판별하여 저항성 여부를 검정하였다. 판별 후 6일차 유출(=10개체/품종)에 하백출 증상 기술을 이용하여 각 균주를 판별하였고, 5-7일 후 콩균 수의 비율에 따라 저항성 여부를 판별하였다. 15개 판별 품종들의 저항성/감수성 반응은 균주에 따라 다르게 나타났다. 이 결과는 본 연구에서 사용된 콩 역병 균주 4개가 유전적으로 서로 다르고 서로 다른 병원체를 가지고 있다는 것을 뒷받침한다. 본 연구 결과는 국내에서 콩 역병에 대한 *Rps gene* 저항성 품종 육종을 위한 기초 정보를 제공한다.

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Evaluation of Resistance to Bacterial Stalk Rot Caused by *Dickeya zeae* in Maize

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Bacterial stalk rot (BSR) caused by *Dickeya zeae* is an important bacterial disease of maize. This disease has a great influence on the reduction of the yield of corn. The pathogen is soil borne and spreads from soil to plant or field through rainwater or irrigation such as sprinkler. When plant was infected with BSR, leaf sheath become a discoloration with brown. After then the lesion has a foul odor and the top of stalk can be easily removed from plant. The plant topples down to ground resulting in severe grain production loss. To date, however, there are no solution to manage against this disease. To solve this problem, resistance plant breeding is the most efficient method. However, there are limited available information to evaluation of BSR resistance screening in maize. Therefore, in this study, we evaluated the disease score 1-5 scale, which is based on symptomatology of inoculated seedlings using our own 17 inbred lines. Bacterial suspension was adjusted to 10^8 cfu/ml. Three-to-four leaf stage of corn seedlings were inoculated with *Dickeya zeae* using syringe in the second internode from base of maize stalk. Inoculated plants were incubated in a growth chamber at 28°C and 65% relative humidity. Disease score was recorded after 7 days post inoculation(dpi) for corn seedlings. Among 17 inbred lines, 4 lines were categorized as resistance, 1 as moderate resistance, and 12 as susceptible to BSR. Our results provide information on resistance lines screening of *Dickeya zeae* and expected to breed easily BSR resistance maize cultivars

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A novel resistance gene for bacterial blight in rice, *Xa43(t)* identified by GWAS, confirmed by QTL mapping using a bi-parental population

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Bacterial blight (BB) caused by the *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) pathogen is a significant disease in most rice cultivation areas. The disease is estimated to cause annual rice production losses of 20-30 percent throughout rice-growing countries in Asia. The discovery and deployment of durable resistance genes for BB is an effective and sustainable means of mitigating production losses. In this study QTL analysis and fine mapping were performed using an F2 and a BC1F2 population derived from a cross with a new R-donor having broad spectrum resistance to Korean BB races. The QTL *qBB11* was identified by composite interval mapping and explained 31.25% of the phenotypic variation (R²) with LOD values of 43.44 harboring two SNP markers. The single major R-gene was designated *Xa43* (*t*). Through dissection of the target region we were able to narrow the region to within 27.83-27.95 Mb, a physical interval of about 119-kb designated by the two flanking markers IBB27os11_14 and S_BB11.ssr_9. Of nine ORFs in the target region two ORFs revealed significantly different expression levels of the candidate genes. From these results we developed a marker specific to this *R*-gene, which will have utility for future BB resistance breeding and/or *R*-gene pyramiding using marker assisted selection. Further characterization of the *R*-gene would be helpful to understand variations of resistance mechanisms of BB resistance in rice

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Functional characterization of papain-like cysteine proteases genes in rice

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Papain-like cysteine proteases (PLCP) are key enzymes involved in cell death as response to biotic stress. Functional genetic investigation of cysteine protease family members has been performed in a fragmentary scale to understand its specific role in plants. Highlights of research milestone for these proteases provide strong evidence on their diverse and overlapping roles in basal immunity and effector-triggered immunity. The objective of this study was to provide useful insights into biological function of three cysteine protease genes, OsCP2, OsCP3, and OsCP5, in rice. Overexpression of rice cysteine protease attenuated the virulence of Xanthomonas oryzae pv. oryzae race K3a in all transgenic lines which displayed moderate resistance as indicated by shorter lesion lengths (OsCP2ox, 6.82 cm; OsCP3ox, 5.55 cm; and OsCP5ox, 5.40 cm) than wild type Dongjin (16.07 cm) whereas RNAi-mediated knockdown of OsCP3 resulted in severe bacterial leaf blight symptoms (17.1 cm). Abiotic screening revealed the biological significance of these three cysteine protease genes, especially of OsCP3, against salinity stress for which rice exhibited moderate tolerance (salinity score = 5.0 to 5.2). This study provides experimental evidence for roles of papain-like cysteine protease in improving resistance of rich against Xanthomonas oryzae pv. oryzae and tolerance against salinity stress, suggesting that these genes could be used as a valuable resource to be employed in rice breeding program to improve its ability to withstand biotic and abiotic stresses.

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Identification of soybean genotypes resistant to Phytophthora sojae from the Korean cultivated soybean core collection

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Phytophthora root and stem rot, caused by the soil-borne oomycete pathogen Phytophthora sojae, is one of the most destructive diseases of soybean. Although researches have been conducted to identify and characterize genetic resistance to P. sojae in soybean in many countries, little was reported in South Korea. This study was conducted to identify cultivated soybean germplasms that are resistant to P. sojae from the Korean cultivated soybean core collection. A total of 398 genotypes from the core collection were inoculated with isolate 2457 using hypocotyl inoculation technique. Briefly, 12 to 20 7-day-old seedlings per genotype were inoculated on their hypocotyl with mycelial slurry of isolate 2457 and kept in humid environment overnight following inoculation. Reaction of seedlings were evaluated 5–7 days after inoculation. Reaction was determined as resistance (survival of 80% or more), susceptibility (survival less than 20%) and intermediate (21–79%) depending on the phenotype ratio of seedlings. Of the 398, only 41 genotypes showed resistant reaction, and 335 and 4 genotypes did susceptible and intermediate reaction. This study will be a framework for selection of genetic resource with resistance to P. sojae and development of P. sojae-resistant soybean cultivars by introduction of resistance genes from the identified germplasms in the future.

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**PCS04-26**

**Functional analysis of NLR protein from pepper related to enhanced anthracnose resistance in tobacum**

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Anthracnose caused by *Colletotrichum acutatum* (*C. acutatum*) is one of the major diseases to pepper in worldwide, especially in tropical and subtropical regions. Little information is known concerning the interaction of the *Colletotrichum* species and anthracnose have been reported in pepper. Anthracnose resistant pepper has been bred by our country research team and the gene is known to be derived from *Capsicum baccatum* (*C. baccatum*). One or two major gene related resistance to anthracnose, in addition some minor gene assisted major gene. One of the things known to date, NB-leucine-rich repeat (NLR) protein interacts with defense response proteins to regulate plant immunity and cell death. To isolate NLR protein gene from *C. baccatum*, we researched after infection pathovar *C. acutatum* K1 in the susceptible An-S (*C. annuum*), the resistant PBC80 (*C. baccatum*), 3-type breeding pepper An-9R, An-12R and AR-Tanjeobaksa. We isolated two NLR protein (NLR0901 & NLR1202) genes in PBC80 and then constructed vector for overexpression in tobacum (*N. benthamiana*), and generated transgenic tobacum. Here, we analysed disease resistance to anthracnose and expression of tobacco PR genes in NLR protein overexpressing tobacum. These results may helpful to understand NLR protein- anthracnose interaction related to anthracnose resistance in tobacco and pepper.

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**PCS04-27**

**In vitro** elimination of Cnidium vein yellowing virus from infected *Cnidium officinale* through embryogenesis and shoot-tip culture

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Cnidium vein yellowing virus-1 (CnVV-1) and Cnidium vein yellowing virus-2 (CnVV-2) is known to infect *Cnidium officinale* in Korea. *Cnidium officinale* is importantly used as oriental medicine and health functional food ingredient. However it frequently occur viral disease including mosaic, vein yellowing, mild mottle and leaf roll. In this study was aimed to develop effective culture method of virus elimination on each stage. *In vitro* plants were derived from embryogenesis and shoot tip culture. For embryogenesis, callus were obtained from infected leaf explant on MS medium supplemented with 2 mg l⁻¹ 2,4-D and 0.2 mg l⁻¹ NAA. CnVV-1 and CnVV-2 were eliminated in somatic embryo-derived *in vitro* plants on 20 % even though only CnVV-2 was eliminated in callus stage. However, all *in vitro* and acclimated plants from shoot tip-derived were detected virus. We only focused on comparing culture type to eliminate virus, and it is need to combine optimum culture type with antiviral agent (ribavirin) for increasing virus elimination rate.

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Mining tomato leaf proteome in search of potential markers for tomato spotted wilt virus (TSWV) infection using a TMT-based quantitative proteomic approach

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Tomato (Lycopersicon esculentum), a member of Solanaceae family, is one of the most important vegetables worldwide with an annual production of 159 million tones. However, because of the rise in global mean temperatures, severity of diseases has been increased in the past decade, putting tomato productivity at a risk. In particular, tomato spotted wilt virus (TSWV), transmitted by small insects known as thrips, cause a serious economic loss and is one of the major threats to tomato productivity. Here, an attempt was made to generate of proteome profiles of tomato leaves of four cultivars (cv 2621/ 2622 and 2689/ 2707 -susceptible and resistant to TSWV infection) using shotgun proteomics approach coupled with Q-Exactive high resolution mass spectrometer. A TMT-based proteomics approach led to the identification of total of 5162 proteins of which 490 showed significant change in response to TSWV infection. Functional annotation of the identified proteins was carried out by DAVID functional annotation integrated with gene ontology and KEGG pathway, leading to the identification of potential biomarkers for TSWV infection. List of the potential biomarkers identified here could be utilized in future to develop TSWV tolerant tomato plants. Taken together, these results provide new insights into the changes in tomato leaf proteome upon interaction with TSWV.

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Developing Inbred Line of ‘Wonkyo20046ho’ Showing Resistance for the Clubroot Gangneung Inoculum and Deep Yellow Leaf Colour in Kimchi Cabbage (Brassica rapa L.)

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Kimchi cabbage (Chinese cabbage, Brassica rapa L.) is one of the top 10 vegetables in Korea. It is mainly used as the main ingredient of the Kimchi (fermented traditional dish of Korea) and its use is increasing for shabu-shabu, salad, and ssam. Due to the climate warming, the outbreak of clubroot disease is becoming serious in Gangwon province, which is the main place of summer production. These days, it is reported that the outbreaks are nationwide throughout 4 seasons. In the 21st century, varieties showing clubroot resistance have been developed, however they are being ignored by consumers because of their poor quality. Therefore, the National Institute of Horticultural and Herbal Science has collected and do the microspore cultivation to develop varieties showing clubroot resistance and high quality, together. In 2010, major domestic varieties were collected and cultivated in autumn to select yellow inner leaf colour. The seeds of five selected varieties were propagated through bud-pollination. In 2011, various doubled-haploid (DH) plants were obtained by microspore culture using the propagated F2 plant materials. In 2012, the DH plants were trans planted into soil and under gone cold treatment at 5°C for 3-4 months. In 2013, each plants were trans-planted into big pod to produce self-pollinated seed using bud pollination. In 2014, the developed inbred lines were selected for their horticultural trait through productivity test and purity test. In 2015, one inbred line derived from ‘Bulamplus’ were selected as showing clubroot ‘Gangneung’ inoculumm resistance and deep yellow inner leaf colour by commercial breeders and applied for variety protection(2018-670).

Keywords: Kimchi cabbage, inbred, microspore culture, Clubroot

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Genetic Parameters Analysis and Transgressive Segregants Detection on F2 Population of Peanut (Arachis hypogaea L.)

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Transgressive segregation selection gives an opportunity to get pure line faster than other selection conventional methods for selfing plants. This study aims to estimate the genetic parameters of two populations of peanut crosses, to estimate genetic control of characters studied, and to detect predicted transgressive segregant plants in F2 populations. This research was conducted at IPB Leuwikopo experimental station located in Darmaga, Bogor, West Java, from November 2014 to February 2015. The genetic material used was two groups of peanut crossing populations, i.e. GWS18A1 x Zebra and its reciprocal, consisting of P1, P2, and F2 generations. There were 44 plants for each P1 and P2, and 330 plants for each F2, and were planted in 40 cm x 40 cm spacing. All plants were observed for variables: plant height, fresh stover weight, number of primary branches, number of filled pods per plant, filled pods weight per plant, seed weight per plant, and seed-hull maturity index. The genetic parameters estimated were broad-sense heritability and genetic variability coefficient, while the gene action was predicted based on kurtosis and skewness of the F2 curves. The results showed that there were differences in the estimated values of the broad-sense heritability and genetic variability coefficient in the two populations, and the values were low based on almost all of the characters observed. The prediction of gene action in two populations of F2 peanut crosses showed different results between populations. There were characters which controlled by many or few additive genes with the effect of dominance or epistasis. There were 15 transgressive segregant individuals in the Zebra x GWS18A1 cross population and 3 individuals in the reciprocal based on the number of pods per plant which characterized by high fresh stover weight which reflects better resistance to leaf spot disease.

Keywords: heritability, genetic variability, gene action, kurtosis, skewness

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Evaluation of germplasm for development Fusarium resistant freesia cultivar

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Freesia bulb rot is caused by Fusarium oxysporum, which is one of the serious problem in domestic cultivation field. Bulbs infected with Fusarium oxysporum have blackish brown slightly concave irregular lesion spots on the bulbous surface, gradually growing and decaying, outer leaves growing on the ground gradually wilted and inner leaves also yellowed and wither. It occurs in bulbs that are preserved and growing time, do not germinate with infected bulbs, or germinate, but growth is bad and the leaves will not turn into brown before it develops 2 or 3 leaves. To screen the freesia cultivars resistant to bulb rot disease, F. oxysporum was isolated from Freesia bulbs and inoculated to the bulbs. The hynphae of F. oxysporum was effective to causing disease symptom. Totally 43 cultivars of freesia germplasm were estimated, at 26°C growth chamber for 96 hours after F. oxysporum inoculation. Freesia ‘Mauve Topaz’, ‘Pink Blossom’, and ‘Figaro’ were resistant which have less than 10% of the lesion size, and ‘Pure Angel’, ‘Gold Fantasy’, ‘Golden Frame’ were susceptible, and more than 50% after F. oxysporum inoculation, respectively.

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**PCS04-32**

**Germlasm Evaluation of *Aleurites moluccana* based on agro-morphological characteristics**

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*Aleurites moluccana* is an industrial commodity. Kernel of the seed have been utilized for many purposes, particularly as seasoning ingredient. In Indonesia there is only one variety which was re-released, the variety is “Alor”. In order to gain new variety, Indonesian Industrial and Beverage Crops Research Institute have been collected and evaluated *A. moluccana* accession. The aim of this study was to identify promising genotypes in Indonesian Industrial and Beverage Crops Research Institute for use in *A. moluccana* breeding program based on agro-morphological characteristics. The research was carried out at the Pakuwon Experimental Garden, at altitude of 450 m above sea level, Latosol soil type, and type B climate (Oldeman), from January to December 2018. Eighteen agro-morphological traits were studied in 55 accessions. Descriptive statistics-univariate analysis of variance (ANOVA) were used to determine variation among accessions. Cluster dendogram was generated based on between groups-linkage method. The result showed there are variation in leaf length, leaf width, leaf petiole length, fruit thick, seed thick, and seed weight. Cluster analysis showed relationships among all accessions divided in two distinct groups. There are eight candidate varieties with high productivity and oil content characteristics.

**Keywords:** *A. moluccana*, oil content, seed

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**PCS04-33**

**Evaluation of RICE Tungro Spherical Virus (Rtsv) Resistance from Tropically Adapted Japonica Lines (*Oryza sativa L.*) Expressing RTSV Resistance Gene elf4G**

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Previously developed BC4F2 lines of MS11 and JAP1 (recurrent) crossed with TW16 (donor of the RTSV resistance gene) were used to evaluate RTSV resistance along with six check varieties (MS11, Japonica 1, TW16, TN1, Dongjin, and IRRI 154). Lines were initially cultivated in the green house for RTSV inoculation via RTSV infected green leafhoppers (GLH). BC4F2 plants were subjected to marker assisted selection using two RTSV resistance-related markers, one InDel type and one SNP type. Lines were designated into three groups: homozygous to donor (RTSV), homozygous to recurrent (rtsv) and heterozygous. Check varieties were grouped as inoculated and non-inoculated. ELISA test was conducted to compare RTSV infection levels and to confirm the absence of RTBV (Rice Tungro Bacilliform Virus) infection. The homozygous donor plants exhibited infection levels which passes for RTSV resistance and the homozygous recurrent were found to be susceptible. Plants were transplanted into the field, where one row was allotted for one group. Significant stunted growth observed for all lines as compared to the non-inoculated controls was associated to GLH’s damage over RTSV infection. However, the RTSV lines outperformed rtsv lines. The respective field test will also monitor potential differences by comparing fundamental agronomic traits (heading date, yield-related parameters, and plant type) and visual symptoms associated to tungro infection.

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Characterization of a deficient mutant of alpha 1, 3-fucosyltransferase for N-glycan engineering in rice (*Oryza sativa*)

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N-glycosylation is a major modification of proteins in plant cells. The presence of N-glycans is necessary for efficient secretion of plant glycoproteins. α 1,3-Fucosyltransferase (OsFucT) serves to transfer α 1,3-linked fucose residues to N-glycans of rice glycoproteins. We characterized the mutant Osfuct with T-DNA inserted by knocking out the α 1,3-fucosyltransferase (OsFucT) gene in rice. Mutants showed defects in anther and pollen development. The mutant pollen grains are sharper and significantly smaller in size. In addition, the number and survival rate of pollen grains were significantly reduced in the mutants compared to the wild type. The mutants were shorter, less cultivated, and had shorter stems and branches under field conditions. In MALDI-TOF (matrix-assisted laser desorption/ionization time-of-flight) analysis, N-Glycans showed that mutants produce N-glycans lacking core α 1, 3-fucos residue. Therefore, Osfuct’s interacting partners can gain insight into the function of Osfuct’s growth, anchoring in anther and pollen growth by identifying and evaluating to dissect a complex regulatory gene network. Furthermore, we developed rice callus from rice seed for N-glycan engineering. For this purpose, rice seeds (Donjin and α 1,3-Fucosyltransferase mutant) were treated with N6 media containing 2,4-D and were incubated in dark at 28°C. We confirmed T-DNA inserts in homozygous (HM) rice callus by PCR method. In addition, we evaluated optimal concentration of phosphinothricin which inhibits the growth of non-transgenic cells. In this presentation, transgenic calli are useful for a potential system for the production of recombinant glycoproteins as therapeutic purposes.

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Characterization of *Oryza sativa* FLAVONOL SYNTHASE (OsFLS) exhibiting bifunctional catalytic activity

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Flavonol synthase (FLS) is a key enzyme of the flavonoid biosynthetic pathway, acting at the diverging point separating into the flavonol and anthocyanin subclass branch. FLS belongs to the 2-oxoglutarate iron-dependent oxygenase (2-ODD) family. We characterized OsFLS gene from “limi” rice (*Oryza sativa*) cultivar. OsFLS shared FLS-specific motifs, and the sequence was clustered with other FLSs in the phylogenetic analysis with various 2-ODDs. The in vivo substrate-feeding assay demonstrated that recombinant OsFLS exhibited FLS activity showing higher substrate preference for dihydrokaempferol (DHK) than dihydroquercetin (DHQ). Additionally, OsFLS also showed F3H activity that converts flavanones to dihydroflavanols, indicating that OsFLS has bifunctional properties. The expression of OsFLS was observed not only in pigmented rice seeds but also in non-pigmented rice seeds. However, the expression of most other flavonoid biosynthetic genes was hardly detected in the non-pigmented rice seeds. Transgenic tobaccos (*Nicotiana tabacum*) expressing OsFLS generated pale pink- or white-colored flowers, in which kaempferol significantly increased but anthocyanin dramatically decreased. Additionally, their pod size and weight were reduced compared to wild type. Several early and late flavonoid biosynthetic genes were downregulated in the transgenic flowers. These investigations demonstrated that OsFLS plays a functional role in the production of flavonol in planta.

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Transgenic expression of onion flavonol synthase in tobacco changes flower color

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The onion (Allium cepa L.) flavonol synthase (AcFLS-HRB) gene, responsible for flavonol biosynthesis in yellow onion, was recently identified and enzymatically characterized. Here, we generated transgenic tobacco (Nicotiana tabacum) expressing AcFLS-HRB. These plants displayed normal growth and development, but produced flowers that were lighter pink in color than those of the wild type. The transgenic petals displayed high levels of AcFLS-HRB mRNA and AcFLS-HRB protein and produced more flavonols but less dihydroflavonols and anthocyanin than the wild-type petals, indicating that AcFLS-HRB is an authentic FLS gene with functionality in plants. A gene expression analysis showed that the early and late biosynthetic genes in the flavonoid biosynthesis pathway were downregulated in the transgenic petals. To test whether this downregulation was due to the excess levels of flavonols generated by the expression of AcFLS-HRB, wild-type tobacco flowers were treated with exogenous flavonols. The flavonol-treated petals had decreased levels of anthocyanin and showed reduced levels of dihydroflavonol 4-reductase and anthocyanidin synthase expression, suggesting that the excess flavonols in the transgenic petals negatively regulated flavonoid biosynthesis. Our results demonstrate that AcFLS-HRB played a critical role in the regulation of flavonoid biosynthesis in tobacco flower.

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Overexpression of GmIFS1 gene leads to produce the genisteins in tobacco petals

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Flavonoids, phenylpropanoids derived secondary metabolites, are accumulated in a wide range of plants such as leaves, fruits, flowers and seeds. Also, several studies have revealed that flavonoids metabolites have pharmacological properties that may be beneficial for human health including cardioprotective, anti-inflammatory and anti-tumor activity. Among these flavonoids, isoflavones including genistein and daidzein produced predominantly in leguminous plants and have the abilities for enhancing the human health as dietary components as well as for providing the defense compounds against pathogens. For deciphering the mechanism of isoflavones biosynthesis in tobacco plants, we introduced the GmIFS1 gene derived from Glycine max cultivar Sojin, which showed the high level of isoflavones contents in seeds. Transgenic tobacco plants overexpressing with GmIFS1 gene showed the normal phenotypes compared to wild type plants. Through the HPLC analysis with tobacco flowers, it confirmed that transgenic GmIFS1 tobacco plants produced the high level of genistein compared to wild type. Gene expression analysis showed that genistein synthesis correlated with flavonoid biosynthetic pathway genes expression. Additionally, transgenic GmIFS1 tobacco plants showed the higher total flavonoid content compared to wild type. Taken together, these results indicate that the overexpression of GmIFS1 gene is very effective for the production of genisteins in tobacco plants.

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PCS05-05

Analysis of \textit{AMT1} (ammonium transporter 1)–Mediated Root Growth in Rice (\textit{Oryza Sativa})

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Rice is a paddy-soil grown crop plant using NH$_4^+$ as the major nitrogen source. NH$_4^+$ ions are taken up into the plant cell from the rhizosphere by plasma membrane localized ammonium transporters (AMTs). In this study, \textit{AMT1} RNAi mutant have been utilized to study \textit{AMT1}-specific root development. NH$_4^+$ suppressed lateral root development of the \textit{AMT1} mutants, which could not be rescued by NH$_4$NO$_3$. This suggests that the activity of \textit{AMT1} is essential for NH$_4^+$-mediated development of lateral roots in rice. NAA (1-Naphthalametic acid) rescues NH$_4^+$-induced growth defect of roots in the mutants. The action of NAA on lateral root development was strongly inhibited by NOA (NaphthOxyacetic Acid) an auxin influx inhibitor. Split-root assays show that NAA exerts systemic signaling to rescue NH$_4^+$-mediated growth defect of lateral roots in \textit{AMT1} mutants. However, the NAA systemic signaling was not detected when NAA and NH$_4^+$ are present in the same media. The metabolomic profiles revealed that \textit{AMT1} RNAi mutants are deficient in glutamine and asparagine amino acid synthesis after NH$_4^+$ induction. Furthermore, by comparative analysis of transcriptional profiles of \textit{AMT1} RNAi and wild type roots, differentially expressed genes (DEGs) were identified. Among NH$_4^+$-responsive genes, \textit{AMT1} and \textit{amtl} specific genes were able to be categorized. The \textit{amtl}-specific genes would be utilized to further analyze NH$_4^+$-mediated lateral root suppression in \textit{AMT1} mutants.

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PCS05-06

Identification and functional analysis of kelch-containing F-box proteins and their expression in wheat grain development

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The ubiquitin-proteasome system (UPS) is involved in protein turnover mechanism that plays important roles in the regulation of many cellular processes including cell cycle transition, signal transduction, metabolic control, and stress responses. SKP1-Cullin-F-box protein (SCF) complex is the largest class of ubiquitin ligases in plants. F-box proteins comprise the most important part of the SCF complex, through which in functions as substrate recognition and substrate recruitment for degradation by 26S proteasome. F-box proteins contain an F-box domain in the N-terminal region and a variable protein-protein interaction domain in the C-terminal region, such as leucine-rich repeats, kelch repeats, tetraicopeptide repeats, and WD40 repeats. F-box proteins can be categorized based on their C-terminal domain structures. The kelch repeats is one of the most common C-terminal domains of F-box protein in plants. However, little is known about functions of F-box proteins containing kelch repeats in the important crop, wheat. We obtained the full length sequences of five kelch repeat domain containing F-box genes (TaKFBs) at different stages of wheat grain development. The TaKFBs showed elevated expression levels at the pigmentation stage of grain development. Our data demonstrated that green fluorescent protein-tagged TaKFB proteins were targeted to the nucleus and cytoplasm. We confirmed that TaKFBs interacted with TaSKP proteins. Through yeast two-hybrid screening, we identified aquaporin1 (PIP1) as a TaKFB1-interacting protein. The biomolecular fluorescence complementation assay revealed the interaction of TaKFB1 with partner protein in the nucleus of tobacco cells. And also, TaKFB1 target substrate protein (aquaporin PIP1) is regulated by 26S proteasome-mediated proteolysis through MG132 treatment. Our study of TaKFB proteins will provide useful information of the functions of F-box proteins in wheat.

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Isolation of higher crossover rate mutants in Arabidopsis

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Meiotic recombination produces crossovers from SPO11-mediated DSBs by diverse interhomolog repair pathways. The crossovers affect genetic diversity in population and breeding. Crossover is limited to ~1-3 along chromosomes by three distinct anti-crossover pathways that include FANCM, RECQ4 and FIGLI factors in Arabidopsis. However, the mechanism underlying crossover suppression in which the DSBs (~40-50 per chromosome) are repaired to 1-3 crossovers remains explored clearly. We have performed high throughput genetic screenings of higher crossover rate (hcr) mutants by using fluorescent seed-based system, enabling the measurement of crossover frequency in individual plants of various mutant pools. Three hcr mutants (hcr1, hcr2, hcr3) were isolated and confirmed to be new anti-crossover mutants by genetic analyses and crossover measurements. The isolation and characterization of hcr mutants reveal new anti-crossover pathways, providing an insight into the crossover suppression mechanism in plants.

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PGR (plant growth regulator) substitution effect on the chrysanthemum transformants of SHI (Short Internodes) related genes

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Generally, growth retardation is an important breeding trait in horticultural plant production. Various chemical growth regulators are applied to horticultural plants but these compounds are hazardous to environment and human. From Brassica rapa L. ssp pekinensis, we isolated 2 genes (BrSRS, and BrSRS-gene) and introduced to pot type chrysanthemum (pot-mum) using four CmActin-BrSHI constructs (CmActin, Chrysanthemum morifolium Ramat actin promoter). The transgenic plants containing BrSRS 7 (short related genes 7) and SRS7-gene (same sequence of SRS7 including genomic region) were shown to have growth retardation up to 50.0% and 54.1% under the control of the CmActin promoter at first year. In the case of nutritionally propagated crops, it has been reported that the genes are silenced during the multiplication process. In addition, since the effect of in vitro proliferation also occurs, stable expression individuals were selected through cutting and wintering several times. After seven nutrient breeding cycles (about 3 years), several transgenic lines showed still dwarf phenotype and their stable RNA expression in real-time PCR. B9 and cut off sprout were performed once on stable transgenic lines to see the response to the actual growth regulator. Most of the plants responded to the treatment and the plant height was reduced as expected. Especially, P-33 (including BrSRS7 gene) was found to be about 20 cm in length. This is the optimum size of the commercialized pot-mum, and it is possible to secure a suitable plant length with 1/3 of the growth regulator generally used. In this experiment, it was confirmed that SHI(Short internodes) family gene is effective in decreasing the chrysanthemum plant length and can replace the growth regulator sufficiently.

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Trait and fertility analyses of F1 and F2 hybrids between genetically modified *Brassica napus* expressing *BrAGL20* and *B. rapa*

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A number of studies have been conducted on hybridization between transgenic *Brassica napus* and *B. rapa* or backcross of F1 hybrid to their parents. However, trait changes must be analyzed to evaluate hybrid sustainability in nature. In the present study, *B. rapa* and early flowering transgenic (*BrAGL20*) *B. napus* were hybridized to verify the early flowering phenomenon of F1 hybrids, and F1 hybrid traits were analyzed to predict their impact on sustainability. Early flowering transgenic *Brassica napus* L. ‘Youngsan’ (AAAC, 2n = 38) was transformed with CAMV 3SS-regulated bar and *BrAGL20*, and *B. napus* L. ‘Youngsan’ and *B. rapa* L. ssp. pekinensis ‘Jangkang’ (AA, 2n = 20) seeds were obtained from the National Agrobiodiversity Center (Jeonju, Republic of Korea). Interspecific crossability was determined using transgenic *B. napus* as the pollen donor and *B. rapa* as the seed parent, by means of artificial emasculation and crossing. F1 hybrids bloomed later than transgenic *B. napus*, but without vernalization, owing to the expression of the *BrAGL20* transgene. The size of F1 hybrid seeds was intermediate between those of *B. rapa* and transgenic *B. napus*, and ~40% of F1 pollen exhibited abnormal size and morphology. The form of the F1 stamens was also intermediate between that of *B. rapa* and transgenic *B. napus*, and the number of stamens was close to the parental mean. F1 hybrids could not be obtained, while BC1 progenies were obtained by hand pollination of *B. rapa* with F1 hybrid pollen, with an outcrossing rate of 50%. Our results suggest that introgression of transgenes from transgenic *B. napus* to *B. rapa* will be slowed down in nature.

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Optimization of protocol for particle bombardment system in *Alstroemeria* to produce multiple tolerance against abiotic stresses

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Alstroemeria is a monocotyledonous plants and is renowned for beauty flowers with a variety of colors. Over the decades, alstroemeria breeding was carried out by cross-hybridization and selection between several varieties and wild species. These conventional techniques had some limiting factors for developing horticulturally useful traits. To solve this, transformation systems including particle bombardment and *Agrobacterium*-mediated transformation should be introduced in *Alstroemeria* breeding program. In this study, rhizome tissues were transformed to produce transgenic alstroemeria plants containing *bar* gene for herbicide-resistance and *AtSIZ* gene for multiple abiotic stresses such as salt tolerance and drought tolerance. Using experimental factors optimized from the previous study, effect of number of shooting on transformation efficiency was tested. Also, to reduce damage of cells and tissues from particle bombardment process, osmoticum treatments were employed with mannitol and sorbitol. As results, transgenic alstroemeria plants were produced with an optimized factors such as 6 cm of target distance and 1,100 psi as well as size of 1.0 μm of gold particle with double shooting and showed herbicide resistance through basta treatments. Moreover, 0.5 M of mannitol treatment showed 30% better than that of control in transformation efficiency. Although this protocol developed here should be improved for further progress, particle bombardment system used in this study can be applied for the production of herbicide and multiple tolerance against abiotic stresses in *Alstroemeria* plants in the near future.

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PCS05-11

Overexpression of the alfalfa DNAJ-protein enhances drought tolerance in transgenic plants

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Heat shock proteins (HSPs) are generally considered as important molecular chaperones; they are known to perform critical functions in plant development and abiotic stress response processes. In this study, we examined the role of a HSP, the alfalfa DnaJ-like protein, in alfalfa. As a co-chaperone DNAJ proteins play pivotal role in abiotic stress responses in plants, but the biological functions of DNAJ are poorly documented. In order to reveal the function of MsDNAJ proteins, physiological and molecular responses were investigated using transgenic tobacco plants. In this study, drought bioassay showed that the transcript level of transgene MsDNAJ was elevated under drought treatment. The ectopic expression of MsDNAJ in transgenic tobacco reduced malondialdehyde (MDA) and hydrogen peroxide (H2O2) under drought condition. The transgenic lines showed better growth with high chlorophyll fluorescence (Fv/Fm) and proline content than wild type (WT) lines. In addition, overexpression of MsDNAJ improved drought stress tolerance in transgenic plants. These results suggest that overexpression of tobacco MsDNAJ protein enhances drought tolerance in transgenic tobacco plants.

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PCS05-12

Ginseng-derived PgpPLAIIIβ reduces plant longitudinal growth and lignin content in Arabidopsis and hybrid poplars when overexpressed

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Patatin-related phospholipase A (pPLAs) are major lipid acyl hydrolases that participate in signal transduction, membrane remodeling, and lipid metabolism. pPLAIII group members, which lack a canonical catalytic serine motif, have been less studied than other PLAs. Based on Arabidopsis pPLAIII genes sequences, 11 members of pPLAIII genes in ginseng and 6 putative pPLAIII genes in poplar were identified using each genome database. The PgpPLAIIIβ transcripts were expressed in all organs of 2-year-old ginseng and the highest in leaves. The transcripts of endogenous pPLAIIIβ in poplar showed the highest expression in vascular tissues such as phloem and xylem, which supports that the major role of pPLAIIIβ is in the development of vascular tissues and cell wall. Overexpression of PgpPLAIIIβ caused shortened primary root and reduced plant height with transversely hypertrophied cell growth. The secondary cell wall structure was altered as well, showing a reduced lignification of xylem. Concomitantly therewith, the expression of lignin biosynthesis related genes was decreased significantly. Altogether, cytohistological and its relevant biochemical analysis as well as transcripts changes suggest that ginseng derived PgpPLAIIIβ plays a role in plant growth with secondary cell wall development.

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Corresponding solutions that overexpressed enzymes diversity Cytochrome Department of in the process and generations, T-DNA genome. The T-DNA copy number, absence of transformation plasmid backbone and generational stability of the event. Once characterized, single events are often combined into a stacked trait product through conventional breeding. This conventional breeding process does not affect the stability of the TDNA, preventing the need for a repeated characterization of the events. Instead, the presence and intactness of the stacked events can be confirmed by comparing the sequence of the characterized single event and the sequence of the event in the stacked product. NGS, specifically NGS of event specific amplicons, is well suited for this purpose.

NGS is an efficient and accurate way of characterizing genetically modified products and determining the presence and intactness of T-DNA in stacked event products. The conclusions drawn from NGS are similar to those historically provided by Southern blotting with the addition of a nucleotide by nucleotide overview of the DNA sequence being investigated.

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Ginseng-derived two CYP genes functions on plant growth and phenylurea herbicide tolerance

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Cytochrome P450 enzymes (CYPs) are a superfamily of monoxygenases that are found in all living organisms. They represent extraordinary diversity in their reaction chemistry. Beside their physiological functions in hormone biosynthesis, lipid, and secondary metabolites, P450 enzymes function to tolerate harmful exogenous chemicals such as herbicides. Two CYP genes from ginseng, PgCYP736412 and PgCYP76893 were highly expressed in the root, rhizome, and leaves of ginseng. The expression level of the two CYP genes was regulated against a variety of abiotic stresses such as abscisic acid, chilling, chlorotoluron, hydrogen peroxide, jasmonic acid, NaCl and salicylic acid. Heterologous overexpressed two CYP genes in Arabidopsis shows reduced plant height and resistance to phenylurea herbicide, chlorotoluron. It indicates that the functional roles of two ginseng CYP genes in plant growth and herbicide tolerance. Ginseng as a perennial plant offers more sustainable solutions to herbicide resistance. Therefore, this function can be used as an important agricultural trait in the breeding of crops.

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Identification of ‘Haryejosaeng’ mandarin using multiplex SNP markers

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Most satsuma mandarin (Citrus unshiu Marc.) cultivars are difficult to distinguish from the cultivars supplied to farmhouses based on morphological traits only because the these are seedlings obtained from the nucellar embryos and bud mutations, and are genetically very similar between to each other cultivars. Accordingly, this study was carried out to develop markers that could specifically quickly distinguish ‘Haryejosaeng’ from other satsuma mandarin cultivars used on farms. Polymerase chain reaction (PCR) was performed to distinguish ‘Haryejosaeng’ from other eight satsuma mandarin cultivars using six single nucleotide polymorphism (SNP) markers specific for ‘Haryejosaeng’ and one SNP primer pair, which was used as negative control. The SNP markers P1 (HL-SNP-SCAF_2-23997586-F and HL-SNP-SCAF_2-23997586-R) and P5 (HL-SNP-SCAF_9-30793978-F and HL-SNP-SCAF_9-30793978-R) simultaneously yielded 165- and 526-bp amplicons, respectively, in ‘Haryejosaeng’ only in a multiplex PCR, and the detected SNP markers were quickly revalidated by high resolution melting analysis. The multiplex PCR was also used to identify ‘Haryejosaeng’ on a farm growing 17 different cultivars of satsuma mandarin. Thus, we developed specific molecular markers for accurate identification of ‘Haryejosaeng,’ which can be performed by multiplex PCR to save the time and cost associated with the supply of ‘Haryejosaeng’ to farmhouses.

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Doubled haploid production using two-step regeneration method for shed–microspore culture in pepper (Capsicum spp)

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It is very important to have genetic resources with excellent traits for each target market in order to expand seed export market and volume. Genetic resources utilized in pepper breeding program in Korea have a limited range of variation and, therefore, a variety of useful traits must be incorporated in breeding program for the diversification of export markets. Haploid/double haploid production techniques are useful tools to produce superior homozygous lines in a short period of time, which greatly reduce the time for developing new cultivars. This study was carried out to increase regeneration rate by preventing microspore-derived embryos from enlarging and aging without shoot production in shed microspore culture. Regeneration rates were investigated in both one-step regeneration method that subculture induced embryos in the conventional regeneration vessel (100×40 mm) only once and two-step regeneration method that subculture embryos in 100×20 mm vessel for 2-4 weeks followed by subculturing in 100×40 mm vessel. The regeneration rate increased significantly from 3.3 - 9.8% (one-step method) to 59.1 - 77.4% when two-step methods was applied. The two-step method that simply include one more subculture with smaller regeneration vessel (100×20 mm) can be very useful method to increase the number of doubled haploid plants in pepper shed-microspore culture.

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Development of the analysis and content evaluation technology for allergens in Rice

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Allergic reaction means when organism comes into contact with an exotic substance that result in damage to cell in the body due to hypersensitive antigen-antibody reaction. Allergic diseases are classified as skin diseases and respiratory diseases depending on the target organ with symptoms. Especially when antigens are food, they are called food allergies. Currently, the food safety assessment of GM crops specifies the results of the substantial equivalence evaluation through the comparative analysis of nutrients and anti-nutrient components with existing crops, and research is being carried out to establish natural variations on the composition of domestic crop varieties, but the information on allergy substances contained in domestic crops is insufficient. So, this study was carried out based on information on the previously reported sequence of rice allergen to develop antibody-based allergen detection methods for quantitative analysis of them. It is expected that through this process, it will be possible to establish a database for natural variation and allowable range of allergy protein content for domestic rice varieties and to provide data on the safety assessment of GM crops.

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Characterization of biomass improved gibberellin biosynthesis related gene in rice

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Dwarfing is one of the most important traits in rice, because regulatory mechanisms for plant growth and development. In rice, more than 60 dwarf mutants are well known and its present different phenotype, such as small grain, more tiller and leaf shapes or plant height. In last decade, manifold GA biosynthesis and signaling genes have been characterized in rice that are regulated cell division, development, hormones and various stress. In this study, a novel gene OsGASD (Oryza sativa Gibberellin Acid Sensitive Dwarf) was identified that an efficient system to create rice mutant by Ac/Ds transposon insertion mutagenesis, such as selected homozygous mutant in dwarf phenotypes. To research the function of dwarf OsGASD gene in GA biosynthesis pathway, we generated transgenic rice plants overexpressing OsGASD plants for analysis of GA signaling and uptake. Overexpressing OsGASD plants shown that internodes length, height, number of tillers and biomass were increased compared with wild-type plant, whereas osgasd mutant through Ac/Ds decreased. osgasd mutant includes smaller amount of active GAs than wild-type. osgasd mutant plant of GA biosynthesis pathway causes GA deficiency and dwarf plants, and endogenous GA supplementation can restore the wild type phenotype in this mutant. The result indicated that OsGASD gene regulated the elongation of shoot, stem, plant height and biomass. The increased expression of OsGASD gene dramatically induces expression of the factors associated with GA biosynthesis such as CPS, KO, KAO, GA20ox and GA2ox, whereas osgasd mutant suppression of the factors associated with GA biosynthesis, leading to dwarf phenotypes. That applied GA3 at the plant development stage to survey the response of OsGASD gene to GA3. We suggest that OsGASD gene is related to factors of GA biosynthesis pathway regulating rice biomass improvement.

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Nutritional comparison of genetically modified tomato

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Tomatoes are one of the largest in the market and are widely cultivated around the world. Therefore, studies have been conducted to improve genetic traits to facilitate cultivation, harvest and distribution from the earliest days of GM studies. Unfortunately, since the first commercial GM crop, FlavrSavr™, has been turned away from consumers, there are no commercial transgenic tomatoes, but since then research and development have been steady, with eleven current events registered for commercial use. There has been no request for approval for transgenic tomatoes in Korea until now, but it is necessary to establish criteria for the safety assessment of tomatoes preemptively. In this study, we tried to perform safety assessment through analysis of nutrients of tomato. Here, the tomato with two genes, the pepper-derived MADS-box transcription factor(CaTF5) to increase the yield and herbicide(phosphinothricin) resistance gene as an agronomic trait, were used for the study. Nutritional components such as dietary fiber, fat, protein, carbohydrate, vitamins, minerals, amino acids and sugars were compared between CaTF5 introduced tomatoes and its non GM comparators.

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Phenotypic characteristics of citrus allotetraploids

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The production of somatic hybrids through protoplast fusion has become an important tool for developing interspecific or intergeneric genotypes and tetraploids, which are difficult achieve via conventional breeding. Consequently, In the this study, two citrus species (navel orange and kumquat) that are difficult to produce sexual hybrids because of polyembryony and different flowering times, were selected and protoplast-fused to develop intergeneric citrus that have the edible peel trait of kumquat and the high soluble solid content of navel orange. Phenotypic characterizations of allotetraploids were performed. Four allotetraploids among the 16 plants produced by protoplast fusion produced fruits in 2017, and fruit size, weight, presence of seeds, soluble solids content, and acidity, were determined. Leaf length of allotetraploids was shorter than that of navel orange, but longer than that of kumquat. The leaf width of allotetraploids was wider than that of both diploids. The fruit of allotetraploids showed intermediate size and weight between those of navel orange and kumquat. Thus, we could see difference in phenotype between allotetraploids and diploids. And the allotetraploid plants generated in this study might be useful breeding materials for developing a new variety of interspecific or intergeneric hybrids.

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Breeding and utilization of hybrid rice and male sterility rice line 134BtA expressing transgene *Bacillus thuringiensis*

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Stern borers and leaffolders are the main pests that cause severe damage in rice (*Oryza sativa* L.) production worldwide. In recent years, lots of studies have been performed to create insect-resistant rice using *Bt* gene. We recently have successfully bred new transgenic rice “Xiushui134Bt” with *cry1Ac1* Bacillus thuringiensis (*Bt*) gene which is high and stable resistance to stem borers and leaffolders. Hybrid rice has a 25.6-45.6% yield advantage over inbred varieties. In our study, in order to improve the yield of *Bt* rice Xiushui134Bt, used Xiushui134Bt line as maintainer line and male sterile line Xiushui123A as receptor parent, we developed a male sterility rice line 134BtA in the field by backcross method, which was crossed with different predominant restorer lines to identify the excellent cross combinations. The result showed that the 134BtA presents excellent agronomic characters, such as completed male sterility, resistant to leaffolder and high combination ability. Using 134BtA, three combinations BT134A/17R47, BT134A/17R50 and BT134A/17R104 were bred, and they presented outstanding features: all of the plants were highly resistant to leaffolder, whereas all of the control plants were susceptible. The yields of the above combinations were all about 20% more than that of the control Xiushui134Bt. Our result indicates a broad potential application prospect of hybrid rice and the 134BtA with insect resistance in the future.

Keywords: Transgenic rice; Insect resistance; *Bacillus thuringiensis*; male sterile line

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Production of transgenic overexpression population to discover genes related grain size in rice

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The growing population has put more pressure on maintaining food security worldwide. As rice is a staple crop, the increase of rice yield by genetic improvement is indispensable. There are various agronomical traits affecting rice productivity, which include morphological and yield phenotypes of seed and plant. Here, we focus on seed size - a primary trait of the important determinants in crop yield. To discover novel genes regulating seed size, the gene-overexpression pool has been utilized for the screening.

To elucidate novel functions of crop genes, there have been numerous efforts to generate a lot of loss-of-function resources by mutagenesis with chemicals, insertions of transposable elements or T-DNA. Also, activation-tagging lines have been developed using random insertion of enhancers. Recent progress in DNA sequencing technology has enabled the collection of full-length cDNAs with ease and at a cheap price. We have generated genome-wide transgenic pool overexpressing endogenous genes in rice. Unlike loss-of-function resources or activation tagging lines, it is more likely that a mutant phenotype could be conferred on the overexpressed full-length cDNA. Full-length insertions fragments of the constructed cDNA library were selected and the clones were transformed into rice (*Oryza sativa* cv. Dongjin). After the mass transformation into rice through *Agrobacterium* mediated co-cultivation, we obtained T0 transgenic seedlings and also harvested their seeds. To check the difference of seed size, the seeds of T2 generation were utilized. The selection strategy based on the transgenic overexpression pool has been demonstrated as a useful tool in identifying genes and phenotypes for application in crop breeding.

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Analysis of soybean seed traits using image technology

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Soybean [Glycine max (L.) Merr.] is a major source of vegetable protein and fat in the world. Among the 843 accessions in the soybean core germplasm population developed by the National Institute of Crop Science, 400 cultivars were used for the analysis of seed phenotype while 100 kernels were measured per each cultivar. RGB images were acquired using an in-house developed imaging device, and analyzed using an image analysis program (ImageJ) for seed size and shape related traits. The moisture content of the analyzed seeds was 8% on average. With regard to the reliability of the image analysis, the R² value was higher than 0.9 in the correlation analysis between the image analysis data and the actual measurement data. Eight traits including area, girth, width, etc. were measured by image analysis. Based on these seed phenotype data and soybean genome-wide SNP genotype data, GWAS was conducted. As a result, three significant loci were detected in soybean chromosome 6, 14, and 15 for seed weight, and the candidate genes were identified. Further gene function analysis will be carried out with the candidate genes.

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Measurement of plant growth rate using high throughput phenotyping with soybean core collections

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Soybean is one of the most important food crops in the world. Soybeans show different growth rates at each stage during growth. It also grows at a very fast rate, especially in certain stages. The overall growth process through photosynthesis and absorption of water and nutrients can be figured out by analyzing time-scale growth-related traits data. The differences in growth rates might be related with various important traits such as productivity, stress tolerance and healthful nutrient content. We have obtained images of 400 varieties of soybean core collection grown in the environment-controlled phytotron. For four weeks after seeding, images were taken five times every day at 3 hour interval from 9 to 21. A total of 56,640 images were acquired in a uniform environment using a high throughput device. The growth rate of each variety was analyzed from seed germination to the V3 stage of the vegetative growth. Through image processing, nine index data were extracted including area, perimeter, roundness, compactness, etc. of the plant, and were analyzed for each stage of vegetative growth. As a result, it was possible to check information on the growth rate of each variety from germination to V3 stage. In the future, we will take images of vegetative growth and reproductive growth stages and use them for breeding soybean suitable for harsh environment, such as high temperature and drought, by comparing the growth rates of the varieties in each stage.

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A trial of image based analysis for determination overgrowth of micro-tome

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Overgrowth of plant represents a stress situation which causes late harvest and decreased fruit quality. The major factor of overgrowth is low light quantity, low daylight integral, high temperature, too much watering, etc. In this study, we challenged to determine the method for classification of overgrowth using image based analysis. We used image of micro-tome after 4 weeks from germination. we separate 2 kinds of light quantity environment using different distance from the light source to plant get overgrowth condition. The light condition is 10k lux, B was 5k lux. we used SM-G955N camera for measuring image. ImageJ for analyzing plant image. For prepressing, we cropped and removed background then we used Trainable weka plugin(open source) to segmentation. To determine overgrowth of micro-tome, we separated 4 quarter of the image follows the height. Then, the density of each quarter was calculated for determination overgrowth. The Result shows accuracy was 76.8%, FDR was 0.30. In this study we try to determination overgrowth of micro-tome using image based analysis.

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Evaluation of Red Pepper Growth and Mineral Nutrient of Farm-made Liquid Fertilizers for Sustainable Agriculture

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This study was carried out to evaluate the growth promotion effects on red pepper crops and assess the mineral nutrients of farm-made liquid fertilizers used in organic cultivation in South Korea. We hope that this study will help in the development of a standardized manufacturing technique for these organic liquid fertilizers. We collected 62 farm-made liquid fertilizers made from various raw materials including 14 from fish, 8 from seaweed, 5 from food scraps, 23 from plant and crop by-products, and 12 from other materials. Two groups of red pepper seedlings were treated at different times, one at 20 days after sowing and the other at 40 days after sowing. We used both foliar and soil applications. These seedlings were treated using liquid fertilizers at various dilution rates (1000, 500 and 100 x original material). When foliar application was used, seedlings 20 days after sowing had over 31% increases in shoot fresh weight with 12-15 fertilizers and seedlings 40 days after sowing had over 31% increases in shoot fresh weight with 8-16 fertilizers. When soil application was used, seedlings 20 days after sowing had the same increases in shoot fresh weight with 4-6 fertilizers and seedlings 40 days after sowing also saw the same increase with 5 fertilizers. Therefore, our studies showed that foliar treatments were more effective than soil treatments regardless of application times. We also observed that higher concentrations of fertilizer, particularly when applied twice rather than just once, produced higher rates of growth which impacted shoot fresh weight more than plant height. Our results implied that mineral nutrients are the probable cause for the red pepper growth promotion that we observed, however more study is required to determined exactly which mineral nutrients are most effective.

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QTL mapping for anthocyanin content in bulb onion (*Allium cepa* L.)

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Bulb onion (*Allium cepa* L.) is one of the most economically important vegetable crops in Korea. Anthocyanins, the pigmented flavonoids, in red onion are considered as important phytochemicals due to their strong antioxidant activity and other health-beneficial properties. In this study, we constructed a genetic linkage map of onion in an F₂ population derived from a cross between ‘SP3B’ (yellow) and ‘H6’ (red) using genotyping-by-sequencing (GBS) based on reference transcriptome data, as well as identified three QTLs, *qAS7.1*, *qAC4.1*, and *qAC4.2*, for anthocyanin content in bulbs using a composite interval mapping (CIM) method. The map, consisting of 319 GBS-derived SNPs and 34 HRM markers, contained eight linkage groups with a total linkage distance of 881.4 cM. The linkage groups were assigned to the onion chromosomes by comparing with the previous high-density linkage map using the HRM markers developed from common transcripts. The major QTL, *qAS7.1*, responsible for anthocyanin synthesis, was located on chromosome 7 with a phenotypic variation of 37.74%. This result implied the QTL is associated with a dihydroflavonol 4-reductase (DFR) gene, which is also located on chromosome 7. Other two QTLs, *qAC4.1* and *qAC4.2*, for anthocyanin content, were separately positioned on chromosome 4, which showed $R^2$ values of 19.99 and 26.28%, respectively. This QTL information will be useful for marker development and onion breeding with a high content of anthocyanin.

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Sound waves affect the total flavonoid and the ascorbic acid contents in sprout vegetables

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Sound waves alter the physiology of seedlings and mature plants, but their effects on sprout vegetables are unknown. Compared with mature plants, many sprouts have higher levels of health-promoting antioxidants such as flavonoids and ascorbic acid. Here, to test whether sound waves could be used to enhance the levels of these nutritional compounds, we examined the effects of sound treatments on flavonoid and ascorbic acid production in alfalfa (*Medicago sativa*), broccoli (*Brassica oleracea*), and red young radish (*Raphanus sativus*) sprouts. We used short- and long-term treatments with 250, 500, 800, 1k, and 1.5k Hz sound waves to identify the optimal treatment conditions, growth stage, and treatment time needed to increase the total flavonoid contents of each sprout vegetable and ascorbic acid contents of alfalfa sprout vegetable. The expression levels of flavonoid and ascorbic acid biosynthesis-related genes and antioxidant activity were altered in sprouts in response to sound wave treatment. Therefore, treatment with sound waves could be used to increase the levels of beneficial compounds in sprout vegetables.

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Construction of a linkage map flanking the / locus controlling the dominant white bulb color in onions (Allium cepa L.)

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An F2 population originating from the cross between white and yellow breeding lines was produced. Red, reddish white, yellow, and white bulb colors segregated following the expected ratio. F2,3 populations were produced by self-pollination of reddish white F2 plants whose genotype of the / locus was assumed to be heterozygous. Ten bulbs of each red and white F2,3 plants were selected to perform combined analysis of bulked segregant analysis (BSA) and RNA-seq. A total of 5.1 Gb and 7.2 Gb raw reads were obtained from red and white bulked RNAs, respectively. Trimmed reads were separately mapped to both reference onion transcriptome and de novo assembled contigs. Contigs containing homozygous single nucleotide polymorphisms (SNPs) between red and white bulbs were screened by a stepwise process and resulted in 70 contigs. Among them, one contig showed 100% nucleotide sequence identity with a locus positioned at chromosome 3 of an onion linkage map constructed by a previous study. After verification of SNPs in this contig, a HRM marker was developed. Tight linkage of this marker to the / locus was confirmed by analysis of 190 F2,4 individuals. To further confirm position of the / locus, two contigs showing high homology with other loci in chromosome 3 were identified. Two HRM markers based on these contigs showed linkage to the / locus, indicating that the / locus was positioned at chromosome 3. Annotation of screened 70 contigs showed that no contig was related to flavonoid biosynthesis. Contigs containing more than two SNPs were selected, and their SNPs were verified by PCR amplification and subsequent sequencing of PCR products. Eight additional HRM markers were developed based on SNPs, and all of them showed linkage to the / locus. Among them, three markers showed perfect linkage to the / locus when 190 F2,4 individuals were analyzed.

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Selection of Suitable Triploid Cultivars for Production of Small-Sized Watermelon using Vertical Cultivation

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Watermelon consumption patterns are gradually changing to smaller ones due to the decline of family members and the spread of value-consuming trends. However, in the case of small-sized watermelon cultivation, the productivity per unit area is lower than that of the large-sized ones, and the economical efficiency in terms of price is disadvantageous. In order to overcome these drawbacks, it is possible to increase the yield per unit area by high density cultivation 3 to 4 times by using vertical cultivation which can utilize the cultivation space efficiently. Therefore, this study aims to select triploid cultivars suitable for vertical cultivation for standardized production of small-sized watermelon.

Four varieties were used in this study: 'Uniquesgum', 'Ajouen', 'Blackboy' and 'Seedlessplus'. Vertical cultivation type was I - shaped, planting distance was 20cm, and 2 stalks were attracted. The planting was carried out on April 5th and the harvest was carried out on June 26th. The growth conditions, fruit characteristics, and yield were investigated. As a result, there were no significant differences between the initial and later growth characteristics according to cultivars, and all four cultivars showed excellent tendency. The weight of all four varieties was 3.1-3.4kg, and small-sized watermelons production was possible. The sugar content was in the range of 11.0-11.9°Brix, and 'Blackboy' was the highest. According to the varieties, the percentage of watermelon was 1.5-4kg, which was the highest at 76.0-88.8%. The fruit quality of 'Blackboy' was 83.3%, the commercial yield was 7,747kg/10a, and the yield index was 111, which is considered to be the most suitable variety for vertical cultivation.

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Effect of Cultivar and Location on Oil, Fatty Acid, Protein and Tocopherol Content of Peanut (*Arachis hypogaea* L.)

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Peanut (*Arachis hypogaea* L.) is grown worldwide in the tropics and temperate zones primarily as an oilseed crop (38-54%). It is also important as nutritional source with 25-30% protein. The aim of this research was to study and compare the oil, protein, tocopherol content and fatty acid composition of five peanut cultivars from two different planting locations. For all measured parameters (oil, fatty acid, protein, tocopherol) significant impact of cultivar and location has been determined. Linoleic and oleic acid were the predominant fatty acids in all cultivars. ‘K-ol’ has the highest percentage of oleic acid (82.5%) whilst ‘Sinpalkwang’ has the lowest (43.5%). Oleic acid and linoleic acid were negatively correlated ($r = -0.998$, $p = 0.001$), as well as protein and oil.Linoleic acid ($r = -0.750$, $p = 0.001$). The highest total tocopherol (210.8 ± 19.4 mg/g) and a-tocopherol (112.5 ± 12.1 mg/g) content were found in ‘Sinpalkwang’. Especially, the relatively high oil content and the high oleic acid composition, suggested that ‘K-ol’ seed could be used as a source of edible oil. ‘K-ol’ oil can be considered nutritionally healthy because of the relatively high amount of monounsaturated fatty acids.

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High Yielding and High Oleate Peanut Cultivar ‘Hae-Ol’

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Peanut is grown worldwide in the tropics and temperate zones primarily as an oilseed crop (38-54%). It is also important as nutritional source with 25-30% of protein. The fatty acid composition of the endogenous fats plays an important role in determining shelf life, nutrition, and flavor of food products. Among them, especially, oleic acid has a healthful function of reducing coronary heart disease mortality. We have conducted peanut breeding program to develop high oleate and high yielding peanut cultivar. A new cultivar ‘Hae-Ol’ (*Arachis hypogaea* ssp. *hypogaea*) was developed with high yield and better agronomic characteristics such as lodging and disease resistances. ‘Hae-Ol’ has short stem and Virginia plant type. It has 22 branches per plant and its length of main stem was 39 cm. Each pod has two grains with brown testa and long ellipse-shaped kernel. Its yield components showed 45 pods per plant, 96g of 100-seed-weight and 78% of pod shelling ratio in the regional yield trials (RYT). Seed contains 32.3% of protein, 50.8% of crude oil, and 83.0% oleate and 3.0% linoleate (O/L ratio : 27.7) in fatty acid composition. The changes of acid value and peroxide value of its oil by 20 liter aeration per hour at 120°C also showed high stability with low value. Abiotic and biotic tolerances against lodging, early and late leaf spots, web blotch and stem rot were good in field. In the RYT’s for 3 years ‘Hae-Ol’ was more productive than a reference cultivar ‘Daekwang’ by 16% with 4.88 M/T/ha for grain production. Thus ‘Hae-Ol’ would be a suitable cultivar for peanut consumer and farmer and competitive in the markets with the function of improving human health and shelf life owing to high oleate property.

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Evaluation of Natto Processing Qualities and Sensory Properties of Soybean Varieties

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In Korea, soybeans have been mainly consumed as traditional food materials such as soy sauce, soybean paste, and tofu. Currently, however, the consumption pattern of these bean products has shifted the preference to new fermented soybean product called natto. With the increasing demand and the absence of soybean variety developed specifically for natto, this study was conducted to screen existing varieties of soybean with suitable characteristics for natto processing. In 2018, twenty-eight small-seeded soybean varieties were screened for their growth characteristics and performance in the field. Based on the evaluation of the growth characteristics, twenty cultivars were selected for natto processing. The processing qualities of natto were studied after fermentation using commercial Bacillus. The crude protein and crude oil content showed significant differences among 28 varieties, showing that the plant materials have a wide range of genotype. The crude protein content ranges from 35.5 to 44.0 percent with an average yield of 38.8 percent. The crude fat ranges from 6.0 to 20.4 percent with an average yield of 18.7 percent. The Dachae variety produces the highest natto yield of 253 percent while the Sowonkong variety has the lowest natto yield of 226 percent. Slime content including g-PGA was the highest in the Sowonkong and Hoseo varieties, while Pungsannamulkong and Dachae varieties produced the lowest slime content. In amino nitrate content, Seonam variety has the highest while Pungsannamulkong variety has the lowest yield. After evaluating the results, Hoseo and Haepum showed the greatest attributes for natto processing. Sensory evaluation showed that the overall acceptability and the amino nitrate content were negatively correlated.

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Genetic Mapping of a Novel Locus Controlling Pungency in Capsicum annuum

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Capsicum is an early domesticated genus synthesizing unique pungent substances including capsaicin and dihydrocapsaicin. Despite of its commercial importance, only three genes (acyltransferase (Pun1), putative aminotransferase (pAMT), ketoacyl-ACP reductase (KR)) have been identified as genes controlling biosynthesis of capsaicinoid in pepper. To better understand capsaicinoid biosynthesis, a total of 89 F₂ plants obtained from a cross between a non-pungent mutant line C. annuum ‘221-2-1a’ and the pungent accession C. annuum ‘Lan32’ were used in this study. In the F₂ population, the segregation of pungency and non-pungency was fit to a 3:1 ratio, which supports that non-pungency in ‘221-2-1a’ is controlled by a single recessive gene. To map the target locus, a total of 153 SNP markers were genotyped and 22 markers were linked to pungency trait on pepper chromosome 6. Furthermore, we used MutMap analysis to identify candidate genes. Then, we annotated pepper peptide sequences using protein database. A total of 21 annotated proteins were detected as capsaicin biosynthetic gene homologs, and 10 genes can be candidate genes in the target region.

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Perilla cultivar ‘Deulchan’ with high oil content and favorable oil quality

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Perilla (Perilla frutescens (L.) Britton) is an annual short-day plant and is widely cultivated in Korea not only as an oil seed crop but also as a vegetable leaf. The range of oil content is about 25-50%. Perilla oil contains a unique fatty acid, omega-3 polyunsaturated fatty acid (PUFA), α-linolenic acid (C18:3) composition as high 50-60% in vegetable oil. Perilla oil has the ability to inhibit colon cancer development in rats and prevent atherosclerosis and chemically induced cancer. In view of high demand of value added products in market, it need to development of perilla variety with added functional traits from various germplasms. To cope with this need we developed a new perilla cultivar for edible oil at the Department of Southern Area Crop Science, NICS, Miryang in 2018. The ‘Deulchan’ was developed from a cross between ‘IT240105’, white seed with few-branches, and ‘Milyang15’, high oil content and early maturity traits, in 2005. ‘Deulchan’ has dense flower and stem with few-branches and the kernel has white color. The flowering date of ‘Deulchan’ is at the beginning of September (5-6th) and the maturing date is at the beginning of October (5-6th). The thousand grain weight of ‘Deulchan’ is 4.1g, although seed hardness is softer than that of the check cultivar ‘Dayu’. The yield of ‘Deulchan’ was recorded up to 1.25 ton/ha in the regional yield trial. It contains approximately 44% of ω-3 fatty acid and 66.8% of α-linolenic acid. Nevertheless, ‘Deulchan’ was conducted as for seed, yet yield of this cultivar may decrease when used as leaves.

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Evaluation of Lutein and Rosmarinic acid Contents in Perilla Leaves

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Perilla (Perilla frutescens (L.) Britton), which belonging to the Labiatae family, is widely cultivated oil crop and used vegetable leaves in Korea. The perilla oil has unique fatty acid compositions; ω-3 polyunsaturated (PUFA) and α-linolenic (C18:3) acids those are high proportions (50-60%) in vegetable oil. Perilla leaves are frequently served with meat and seafood, because the leaves are thought to eliminate a fishy smell and to protect from inflammatory disease. A number of studies have revealed that the beneficial health effects of perilla (seed and leaf) are caused by its several phytochemicals contents, such as rosmarinic acid, luteolin, and lutein. Consequently, increasing the content of functional components in perilla has become a major breeding objective. Lutein, one of carotenoids, decreases the risk for eye diseases such as macular degeneration. Rosmarinic acid, a polyphenolic phytochemical, is one of the most important constituents of extracts and inhibits allergic reactions. In this study, a total of sixteen perilla cultivars and lines for leaves were evaluated for lutein and rosmarinic acid contents by HPLC (high performance liquid chromatography). Total lutein contents of perilla leaves were ranged from 0.86 mg/g to 1.17 mg/g with the average of 1.06 mg/g, which were higher than that of kale(0.87 mg/g) and broccoli(0.48 mg/g). Rosmarinic acid contents were ranged from 11.58 mg/g to 25.89 mg/g with the average of 17.41 mg/g.

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A modified colorimetric method for the determination of sucrose content in soybean seeds

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The soluble sugar content of soybean seeds affects the final flavor of soybean and soybean products. The purpose of this study is to develop a rapid, simple and low-cost colorimetric method for the determination of sucrose content in soybean seeds. The colorimetric method is based on the enzymatic reactions of invertase and glucose oxidase (GOD). 30 different soybean varieties were used to quantify sucrose content. To extract carbohydrates, 150mg of grounded seeds were added to 1.5ml water and the mixture was incubated at 50°C for 15 min and 30 min, respectively. The extracted sucrose was hydrolyzed to glucose and fructose by β-fructosidase (invertase). Hydrolyzed glucose was reacted with glucose oxidase (GOD) reagent and absorbance was measured at 490nm wavelength using a spectrophotometer to estimate sucrose content. In order to verify the colorimetric method, sucrose content was measured with high performance liquid chromatography-PAD (HPLC-PAD). The HPLC method and the GOD/invertase method at 15 min incubation showed a high level of correlation (r = 0.97 **). This colorimetric method is a simple and in-expensive tool for quantitative determination of sucrose in soybean.

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Phytoene synthase-2 Controls Yellow Fruit Color in Capsicum annuum 'MicroPep Yellow'

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Peppers (Capsicum spp.) show diverse mature fruit colors depending on the carotenoid composition and content. Phytoene synthase (PSY1) and capsanthin-capsorubin synthase (CCS) are two major genes responsible for fruit color variation in pepper. Nonetheless, numerous non-red fruit colors cannot be explained by variations of these two genes. To discover the genetic factor controlling yellow fruit color of a dwarf cultivar C. annuum 'MicroPep Yellow' (MY), candidate genes were analyzed. Among seven carotenoid biosynthetic genes including PSY1, PSY2, PST3, Lyb, CriZ-2, ZEP, and CCS, PSY1 and CCS had structural variations in MY: complete deletion of PSY1 and 7 kb LTR retrotransposon insertion in CCS. SCAR markers based on these structural variations showed perfect co-segregation of phenotypes and genotypes in an F₂ population. Despite complete deletion of PSY1 catalyzing the first step of carotenoid biosynthesis, MY and F₂ plants with the mutation displayed distinct yellow color and accumulated basal levels of carotenoid, which indicates that PSY1 homologs may complement PSY1 in these plants. qRT-PCR analysis demonstrated that PSY2 is constitutively expressed in fruits. Color complementation assay using E. coli with carotenoid biosynthetic genes revealed that PSY2 has catalytic activity to synthesize carotenoid backbone. Virus-induced gene silencing (VIGS) of PSY2 in MY showed white fruit color. These findings suggest that yellow color of MY is due to the functional complementation of PSY1 with PSY2. In conclusion, this study demonstrated that the PSY2 activity contributes yellow color in MY.

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Fibrillin2 is involved in high-light dependent photoprotection and jasmonate dependent senescence inhibition

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Fibrillins (FBNs) are major structural proteins of plastoglobule (PG) in chloroplast. PG is associated with defense against abiotic or biotic stress as well as lipid storage. Even though FBN2 is abundant component in PG, the independent function of FBN2 have not been identified under the abiotic stress. In this study, the targeting of FBN2 in PG was clearly demonstrated by FBN2-YFP fusion protein. FBN2 gene showed higher expression in green photosynthetic tissues than other non-green tissues and upregulated transcription level under high-light stress. The fbm2 knockout mutants were generated by CRISPR/Cas9 gene editing. The photosynthesis capacity in fbm2 knockout mutants decreased rapidly than wild-type plants under the high-light stress. In addition, the fbm2 mutant was highly sensitive to methyl jasmonate (MeJA), which exhibited root growth inhibition and pale green phenotype due to reduced chlorophyll content. Consistently, the fbm2 mutation showed faster senescence and rapid chlorophyll degradation with decrease of photosynthetic ability than wild-type plants by treatment of MeJA combined with dark. These results suggest that FBN2 is involved in light protection under high-light stress and acts as an inhibitor of JA-induced senescence in Arabidopsis.

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Development of the nutritional composition database for GM crop risk assessment

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Hectares of genetically modified (GM) crops have increased greatly world-wide since 1996. Together with conventional breeding, GM technology has become the main approach to improve agronomic traits of crops. Comprehensive safety assessment of the GM crops is required to evaluate the unintended alteration by the introduction of exogenous genes. It requires comparative assessment of nutritional compositions in GM crops, its non-GM counterpart, and commercially available crops, based on the concept of “substantial equivalence”. The Biosafety Division, National Institute of Agricultural Science (NIAS), has developed a ‘Crop Composition DB (CCDB)’ that provides data on the natural variability in the nutritional composition of key crop species. NIAS-CCDB is a compilation of data on the nutrient, antioxidant, and secondary metabolite compositions of rice and red-pepper grown in two or more growing regions for more than two years in Korea. Compositional analysis was conducted under the guidelines of the Association of Official Analytical Chemists or methods previously reported on the papers. The data is provided as average, minimum, and maximum values to assess whether the statistical differences between the GM crops and the comparative non-GM crops fall within the biological differences or tolerances of existing commercial crops. NIAS-CCDB is an open-access source and easy to access based on the user selected query. This study introduced the feature and usage of NIAS-CCDB which is a valuable tool for characterizing the composition of conventional crops.

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A comparative study on genetic and environmental influence on phenolic acid profiles in Korean red pepper varieties

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Phenolic acids play significant role in plants and human health as antioxidants. Therefore, it is important to assess the phenolic acid contents of the edible plants including fruits, vegetables, and grains. This study was conducted to determine the content of phenolic acids in various red pepper cultivars and to evaluate the impact of genotype versus environmental influence on the phenolic acid profiles of red pepper fruits. Two forms of phenolic acids (methanol-solubles and -insoluble) were identified using tert-butyldimethylsilyl (TBDMS) derivatization and gas chromatography-time-of-flight-mass spectrometry (GC-TOFMS) in samples of twelve Korean red pepper (Capsicum annuum L.) grown together at two different locations during two years. For a comparative investigation on the impact of genotypes versus environmental influence on phenolic acid profiles, twelve Korean red pepper cultivars were grown together under two different environmental conditions for two years. The phenolic acid profiles were subjected to data mining processes, including principal component analysis for identifying the specific chemical composition of red pepper samples depending on geographic origin, planting year, or genotypes. This study illustrates the utility of metabolite profiling combined with chemo-metrics, as a tool for identifying metabolic differences between crop samples from different regions of cultivation.

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Enhancing forage yield and nutritive value through maize × legume intercropping systems on paddy fields during the summer season

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The aim of this study was to evaluate the impact of maize and legume intercropping systems on crop growth, yield, and nutritive value. A total of eight cropping systems, three sole cropping systems (Zm-32P75, Gm-Chookdu1, and Gm-Chookdu2) and five intercropping systems (Zm-32P75 × Gm-Chookdu1, Gm-Chookdu2, Ps-SA, Lp-Longai, and Pv-burgundy), were planted using a randomized complete block design. The soil pH level and organic matter (OM) content were relatively higher after cultivation of maize and legumes, whereas the legumes in the intercropping system enhanced OM content. Legume growth was significantly increased by intercropping, but the total dry matter yield was not significantly increased. Interestingly, intercropping with Gm-Chookdu1 resulted in better neutral detergent fiber (NDF), acid detergent fiber (ADF), crude protein (CP), and total digestible nutrients (TDN) profiles compared with other intercropped legumes. The highest digestible dry matter (DDM), dry matter intake (DMI), and relative feed value (RFV) were found in Gm-Chookdu1, while Lp-Longai showed the highest digestibility value. These results suggest that the intercropping system has greatly enhanced the nutritive value of forage legumes. The above results concerning the impact of intercropping system on dry matter yield and nutritive value provide a new insight into the role of alternative cropping in forage improvement in paddy fields.

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Effect of sound waves treatment on agronomic traits of crops

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Plants have complex sensory networks that help them monitor their surroundings and modify their growth and development. Intracellular signalling pathways for the appropriate responses are activated in plants upon the reception of stimuli from external factors such as water, light, temperature, wind, microbes and insects. The molecular mechanisms that modulate physiological and metabolic processes for the correct response to occur at the right time after the recognition of an exogenous signal are highly complex. These physiological and developmental changes result from rapid and dramatic fluctuations in gene expression; studies have revealed increases in stress resistance in plants via the regulation of stress-related genes, which also influence plant growth and metabolism. We observed that treatment with 1-kHz sound waves delayed ripening in tomato (Solanum lycopersicum) fruit by regulating the expression of genes encoding transcription factors involved in ethylene biosynthesis. In addition to antioxidant contents altered by controlling the expression of flavonoid biosynthesis-related genes in three sprout vegetables in response to specific sound wave treatments. We also showed that spore germination and mycelia growth of plant pathogenic fungi can be inhibited by frequency-specific sound. Recently, we are exploring for the sound waves effect on the plant growth promotion.

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The effect of roasting temperature and time on the rate of oil extraction and functional components in Perilla oil

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Perilla (Perilla frutescens (L.) Britton) is a staple crop grown in Korea, with 45 percent of the seeds made up of fat. Its oil contains more than 60 percent of alpha-linolenic acid which is highest among plant species. Currently, perilla oil-producing industry includes either fresh oil which forgoes the roasting process or those that undergo roasting at various temperatures before pressing. The purpose of this study is to analyze the changes in the extraction rate and functional components depending on various roasting temperatures. The yield of oil extracted from the 650g of perilla seeds pressed without roasting was compared with those processed at 160, 180, 200, 220, and 250 °C for 10 and 20 minutes respectively. The levels of alpha-linolenic acid and policosanol from each sample were measured. Perilla oils had different colors depending on extraction conditions. The yield rate of oil was 38.9% when pressed without roasting, and 41.7% with extraction condition of roasting at 250°C for 20 minutes, indicating that oil yield was influenced by roasting time and temperature. However, the alpha-linolenic acid content of oil samples were about 63.4 % and stable without any significant difference for roasting temperatures. Perilla oil also had policosanol consisting of hexacosanol (81.38 μg/g) and octacosanol (85.69 μg/g). No significant change of polycosanol content was observed with different roasting temperatures. As the roasting temperature was higher than optimum range, the color of perilla oil became darker, resulting in poor quality of oil and a potential rise in benzopyrene, a carcinogen.

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Expression of Ripening–Related Genes by Calcium Compounds and Chitosan in Trees Extends Shelf–Life in Peach Fruits

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Peaches have soft tissues compared to other fruits, and are vulnerable to softness, wounds, and loss of marketability due to the weak fruit hardness after harvest. It is required to develop a technology to improve the shelf-life of the fruit to expand distribution of peaches. Calcium compounds and chitosan play an important role in improving the shelf-life of fruit by maintaining the hardness, reduction of decaying occurrence, activating cell wall related substances, and reducing the respiration rate in peach fruits. In this study, to select useful compounds in improving shelf-life of peaches, calcium chloride (calcium citrate 275 mg · L⁻¹, calcium chloride 4000 mg · L⁻¹, calcium nitrate 200 mg · L⁻¹, GH-Ca 340 mg · L⁻¹, OS-Ca 340 mg · L⁻¹, chitosan (200 mg · L⁻¹)), and chitosan (200 mg · L⁻¹) dissolved in calcium chloride 4000 mg · L⁻¹ were sprayed to trees. The fruit characteristics of the harvesting period were investigated after the treatments in ‘Kumhong’ and ‘Madoka’ peach trees. The hardness of fruit was kept highest in combined treatment and remained highly in treatments of calcium citrate, chitosan and calcium nitrate. Ethylene production and respiration were effectively inhibited by GH-Ca and chitosan treatment. There was no significant difference in soluble solids content, acidity, and skin coloration in fruits treated with each chemical. Real-time PCR showed that the expression of pectin lyase and polygalacturonase gene was lower in chemical-treated fruits than in the untreated control in ‘Kumhong’ cultivar. Pectin methyl esterase gene expression was lower in all treatments than in untreated treatments in two peach cultivars. Ca compounds were found to be delivered into tested fruits and trees in chemical analysis. These results suggest that Ca treatment increased shelf-life by increase of the Ca content and ripening related gene expression in peaches.

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Changes in rutin and quercetin properties of common and tartary buckwheat seeds and groats induced by roasting

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Common buckwheat (Fagopyrum esculentum Moench) and tartary buckwheat (Fagopyrum tataricum Gaertn.) are well known for their nutritional values and medicinal properties. A buckwheat seed contains high levels of rutin (quercetin 3-rutinoside) which has antioxidant and anti-inflammatory properties. The buckwheat tea quality is dependent on the raw materials and applied processing methods. This study is focused on the evaluation of changes in rutin and quercetin contents during the processing of common and tartary buckwheat for tea production. Raw common buckwheat seed has rutin content of 21.6 mg/100 g D.W. Dehulled groats and steamed seed are slightly lower in rutin content having 17.8 and 9.8 mg/100 g D.W, respectively. Raw tartary buckwheat seeds contain the highest quantities of rutin (1,679.9 mg/100 g D.W.). Soaking in water and steaming the whole seeds of tartary buckwheat significantly decreased its rutin contents. The rutin content of dehulled groats is lower than the whole seeds. Roasting process at 70-80°C for 2-3 min decreased the rutin (1010.5 mg/100 g D.W.) and quercetin contents (27.7 mg/100 g D.W.), respectively. The rutin content in the processing of tartary buckwheat tea was reduced by more than 40% while the roasted buckwheat contains more than 1% (1,000 mg/100 g D.W.) compared with using raw whole seeds. Steam and heat treatment of raw and roasted tartary buckwheat groats affected their flavonoid content (rutin and quercetin). In comparison with untreated common buckwheat seed, the rutin content in the processing of common buckwheat using roasted groats was almost similar. In view of the findings, further studies in buckwheat tea procedures are required to determine the quality and amount of flavonoid in the final product.

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Multiple Functional Rice “Milyang320” for Complex of Various Protein Property

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In order to overcome the problem of excess rice supply and stock increase, strengthening research on functional rice cultivation has been focused. However, antioxidant black rice, the key subject in functional fields, failed to overpass the limitation of rice consumptions and still under the stamping stage. Therefore, in order to enhance the functionality of functional rice, it is necessary to cultivate diversity of varieties according to consumption type such as consumer age for children (high nutrient) and old (easy to digest), obesity (high fiber), anemia (high iron), dementia (high GABA), allergies (low globulin) along with complexity of traits and enhancement of planting stability. Thus, to meet the demand of the consumers, we developed the ‘Milyang 320’, a high-lysine line.

‘Milyang 320’ showed a multiple functional trait as a combination of LGC, LA, and low amylose contents. Furthermore, ‘Milyang 320’ has a lysine content of 3.4 mg/g, which is 10% higher than that of Nampyeong. Especially, the lysine content of ‘Milyang 320’ cultivated at five regional test sites was confirmed that ‘Milyang 320’ had a stable lysine content as about 111% higher than that of regional test varieties meaning lysine contents is genetically controlled rather than environmental circumstance. The ‘Milyang 320’ is a low amylose content (10.0%) rice with a heading date of August 1, resistance to rice stripe virus, but susceptible to other pests and insects. The yield capacity was about 4.5MT/ha in milled rice, somewhat lower to high quality rice.

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Effect of physicochemical characteristics of Korean wheat flour on different types of steamed bread, Korean and Chinese styles

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The objective of this study is to identify the effect of physicochemical characteristics of 11 Korean wheat cultivars flour on different types of steamed bread, Korean and Chinese styles. The quality attributes of two different styles of steamed bread, Korean style steamed bread (KSSB) and Northern style Chinese steamed bread (NSCSB) were evaluated. Korean consumers prefer white and glossy surface and soft crumb. For the reason, KSSB prepared more ingredients and higher optimum water absorption of dough than NSCSB. For surface and crumb structure of steamed bread, KSSB showed lower height, larger diameter and volume of steamed bread, higher stress relaxation, and softer texture of crumb than NSCSB. The correlation between flour characteristics and quality of steamed bread was different in KSSB and NSCSB. About 90% of variability in the height and volume of KSSB could be predicted from protein content, mixing tolerance of Mixograph, average particle size of flour, final viscosity and solvent retention capacity. Protein content and quality parameters also could explain the variation of steamed bread height in NSCSB. For only KSSB, the effect of Glu-A3c allele was higher than Glu-A3d allele for volume of steamed bread (704.7 cc vs 645.8 cc, respectively). Also, Glu-D1d and Glu-A3c alleles had softer texture of crumb than Glu-D1f and Glu-A3d alleles in KSSB. Glu-B3i allele also showed lower hardness of crumb than their counterpart allele in NSCSB. KSSB showed that hard wheat showed higher height and volume of steamed bread, and lower stress relaxation and hardness of crumb than soft wheat.

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Correlation of eating quality traits in a RILs population derived from a cross between Hwayeong and Wandoaengmi6

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Eating and cooking quality is very important to breeding system and economic value in rice. A total of 174 recombinant inbred lines (RILs) population derived from the cross between Hwayeong (japonica type of high grain quality in Korea) and Wandoaengmi6 (weedy rice with high eating quality from Korea) was sowing on May 2 for each year during the period 2017 to 2018. We evaluated 13 physicochemical properties such as amylose contents, protein contents, glossiness of cooked rice by Toyo-taste meter (GCR) and rapid visco analyzer traits (RVA) of peak viscosity, trough viscosity, final viscosity, breakdown and setback, which affected the eating quality. The sensory test of cooked rice including glossiness, stickiness, hardness, taste and overall evaluation by panels. A positive correlation showed amylose contents (0.34**), GCR (0.44**), breakdown (0.15) and texture (0.91**). A negative correlation showed protein contents (-0.36**) and setback (-0.11**). The high GCR and overall sensory test average was observed in Wandoaengmi6(88.9, 0.42) while Hwayeong (71.72, -0.05) showed the low value. Principal component analysis (PCA) was explained 77.6% eating quality that PC1 was amylose contents, setback and GCR, PC2 was breakdown and overall. Thus, we have selected 7 RILs that high eating quality in traits. These results suggested that main factors to improve the taste of cooked rice could be utilized breeding program to selected elite lines with high eating and cooking quality.

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Identification and characterization of MYB-bHLH-WD40 regulatory complexes controlling purple pigmentation biosynthesis in wheat (Triticum aestivum L.)

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Wheat contains high levels of important antioxidants, like proanthocyanidins and anthocyanins, related to their seed coat color, which have been recognized as health-promoting nutrients. Transcription factors (TFs) naturally act as master regulators of cellular processes and the transcription complex composed of a WD40, a bHLH and a MYB protein regulates the expression of multiple distinct target genes in a range of plant species. It has been reported in rice, A. thaliana, petunia hybridra and Zea mays, that the bHLH interact with several MYB proteins, furthermore, it has been reported the requirement for a WD40-bHLH-MYB transcription complex for the control of anthocyanin biosynthesis. This research is focus in the discovery of the TFs related to the seed coat color in wheat. We had performed transcriptome analysis of two samples of wheat seeds, Deep Purple and Yellow during three developmental stages (early, middle, and late stage); moreover, we performed a Differential Expression Analysis to investigate which TFs (MYB, bHLH or WD40) are up or down-regulated and in which stage, and to analyze if there was difference between Yellow and Deep Purple samples. Additionally, we performed Y2H (Yeast 2-Hybrid) and GFP assays for confirmation of these putative genes that interact for the generation of the seed coat color in wheat. Wheat is one of the most consumed crops around the world, that's why our study will help elucidate the genes related to seed coat color generation, helping breeders and biotechnologists to use this information for the creation of new highly-nutrient wheat crops.

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Comparison of productivity and functional components for selection of vegetable sweetpotato variety

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Sweetpotato (Ipomoea batatas L.) is one of the most important food crops and have been recognized as the healthy food. Sweetpotato leaves and stalks are used as vegetables in small quantities in Africa and East Asia including Korea. But they contain a variety of functional components with antioxidant activity such as carotenoids and flavonoids. Report suggested that the functional components and antioxidative activity of young leaves and shoot tip is very high. So the present study was conducted to select suitable varieties for vegetable cultivation through analysis the productivity information, usefulness of ingredient content and antioxidant activity in young leaves of sweetpotato. The used materials were shoot tip (20 cm) including stems, petioles and tender leaves cultivated in greenhouse. The yield and amount of harvest were very different in each variety. The total productions during the cultivation period was over 6 kg/m² in 9 different varieties. Among them, ‘Gogeonmi’ was the highest production yield with over 9 kg/m². Lutein content ranged from 21.7 ~ 47.0 mg/100g in varieties and was the highest value in ‘Juhwangmi’ (47.0 mg/100g). Whereas the lutein content of ‘Hayann’, ‘Yeseum’, ‘Matnami’ and ‘Danjum’ was 42.8, 41.3, 40.6, 40.5 mg/100g, respectively. β-carotene content was in the range of 25.5 ~ 183.4 mg/g and the highest value was 183.4 mg/g of ‘Hayann’. DPPH radical scavenging activity was high level in ‘Hayann’ and ‘Gogeonmi’ which were 91.4 and 91.0 %, respectively. The DPPH activity on other varieties were over 80%. The leaves of ‘Hayann’ contained the high level of lutein & β-carotene and showed high DPPH radical scavenging activity as well as productivity. ‘Gogeonmi’ was the highest in the yield of production and contained high levels of DPPH radical scavenging activity. In conclusion, sweetpotato variety with high yield and abundant functional components are recommended as fresh vegetables.

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Validation of candidate gene associated with biosynthesis in pericarp using bi-parental population in Capsicum

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Chili peppers, characterized by pungency are important vegetable crops with a wide variety of uses, such as food additives and pharmaceuticals. Generally, pungency is dependent on genetic constitution, developmental stage of the fruit and environment. In the perspective of biology, the pungency comes from the presence of compounds known as capsaicinoids. Capsaicinoids are synthesized by the condensation of vanillylamin with a branched-chain fatty acid in the placental tissue. Recently, the biosynthesis in the pericarp was discovered, but the exact capsaicinoid biosynthesis in the pericarp has been unknown. A previous study revealed the candidate genes controlling capsaicinoid biosynthesis in the pericarp by using QTL mapping and RNA sequencing. Capsaicinoid biosynthesis in pungent pepper pericarps was associated with one major QTL on chromosome 6. Therefore, the objective of this study is to validate whether one of the candidates affects pungency in pericarp. In this study, extremely pungent pepper C. chileense ‘Trinidad Moruga Scorpion’ and nonpungent pepper ‘SNU11-001’ were used as plant material. ‘Scorpion’ shows the accumulation of capsaicinoids in the pericarp tissue as well as the placenta, leading to the elevation of capsaicinoid content in the whole fruit. ‘SNU11-001’ x ‘Scorpion’ F₁ population was genotyped, and phenotype was investigated by the measurement of capsaicinoid contents. Verification of gene expression was conducted between ‘SNU11-001’ and ‘Scorpion’. By comparing genotype and phenotype data it explains that candidate gene is associated with the phenotype.

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High-Throughput Identification of HMW-GS in Common Wheat Varieties by MALDI-TOF-MS

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High-molecular weight glutenin subunits (HMW-GSs) play an important role in bread making quality. In this study, matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF-MS) was established to identify HMW-GSs. Four major factors influencing mass spectra including solvent components, resolving volume, matrix II components and treatment with alkylation reagent in glutenin extraction were optimized using HMW-GS of Chinese Spring. To obtain accurate molecular weights for individual HMW-GSs, 24 standard wheat cultivars covering all HMW-GSs in hexaploid wheat were analyzed 3 times using this optimized MALDI-TOF-MS method. 38 Korean wheat cultivars previously determined using RP-HPLC and SDS-PAGE were used to verify the allelic compositions. 675 wheat crossing blocks that were harvested by RDA National Institute of Crop Sciences were also used to analyze the composition of HMW-GSs. Results showed that some varieties have 1Ax2*, 1Bx7*, 1Bx17 + 1By18, 1Dx5 + 1Dy10 which are specifically associated with good breed making quality. Although 3-5 subunits are usually expressed in common bread wheat cultivars, but two lines have only two subunits. HMW-GSs of a wheat cultivar are analyzed within one minute by MALDI-TOF-MS, so it is expected to be suitable for the high-throughput analysis of HMW-GSs. MALDI-TOF-MS will be useful to improve end-use quality in wheat breeding programs.

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Accurate identification of alleles for Wheat Low-Molecular-Weight Glutenin Subunits using Aroona Near-Isogenic Lines and a Set of Standard Cultivars by 2-DGE, MS/MS and RP-HPLC

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It is well known that the composition of low-molecular weight glutenin subunits (LMW-GS) in wheat flour is important for end-use quality. However, the contributions of specific LMW-GS to quality have been difficult to assess because of the complexity of LMW-GS within a cultivar as well as the allelic variation between cultivars. Thus, the accurate and reliable determination of LMW-GS alleles in wheat germplasm is very important for breeding efforts. To locate individual LMW-GS corresponding to different alleles encoded by the Glu-A3, Glu-B3 and Glu-D3 loci, we analyzed a set of 15 near isogenic lines (NILs) from Aroona containing unique LMW-GS alleles in the same genetic background. Proteins in glutenin fractions were separated by two-dimensional gel electrophoresis (2-DGE) and the resulting protein patterns were compared to the pattern from Aroona. For most lines, the identifications of protein spots corresponding to LMW-GS alleles were consistent with results using a set of standard wheat cultivars for Glu-3. However, some spots in lines containing the Glu-B3h, Glu-B3g and Glu-D3c alleles differed from the previous study. To confirm their identities, these spots were excised from 2-D gels, digested with chymotrypsin and subjected to tandem mass spectrometry (MS/MS). We also developed a practical and optimized method for RP-HPLC analysis of LMW-GS using a Waters Xbridge BEH, C4 peptide column that results in better resolution than previous studies. The results will be used to identify LMW-GS alleles in germplasm prior to breeding and to screen for desirable LMW-GS alleles in wheat quality improvement.

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A MYB Transcription Factor is a Candidate to Control Pungency in *Capsicum annuum*

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Capsaicinoid is a unique compound that gives hot peppers (*Capsicum* spp.) their spicy taste. The *Pun1* and *Pun2* loci are known to control pungency in Capsicum species. Whereas *Pun1* encodes an acyltransferase, the identity of *Pun2* is currently unknown. Here, we used recombinant inbred lines and F2 plants derived from a cross between the non-pungent *C. annuum* accession ‘YCM34’ and the pungent *C. annuum* cultivar ‘Tean’ to identify a novel non-pungency locus. Inheritance studies showed that non-pungency in *C. annuum* ‘YCM34’ is controlled by a single recessive gene, which we named *Pun3*. Using a high-density SNP map derived from genotyping-by-sequencing, *Pun3* was mapped to chromosome 7. By comparing physical information about the *Pun3* region in the *C. annuum* ‘Zunla-1’ and *C. chinense* ‘P1159236’ reference genomes, we identified candidate genes in this target region. One cDNA sequence from ‘P1159236’ was homologous to an unannotated gene in ‘Zunla-1’. This sequence was also homologous to *CaMYB31*, which is expressed only in ‘Tean’ and harbors one stop codon in the non-pungent accession ‘YCM34’. RNA-Seq analysis showed that major structural genes in the capsaicinoid biosynthetic pathway were significantly downregulated in ‘YCM34’ compared to pungent pepper. Therefore, *CaMYB31* is a candidate gene for *Pun3*, which may act as a master regulator of capsaicinoid biosynthetic genes in pepper. We analyzed capsaicinoid contents and, *Pun1* and *CaMYB31* genotype of 215 germplasms. 29 non-pungent accessions showed *Pun1* and *CaMYB31* homozygous genotypes, which didn’t have deletion mutation in *Pun1* allele and no stop codon in *CaMYB31* allele. Novel allele of *CaMYB31* was investigated to confirm relationship between allelic variation and capsaicinoid biosynthesis.

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Effect of Kernel Properties and Storage Temperature Condition on Popping Qualities of Popcorn

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Popcorn is one of the popular snacks and the amount of consumption is reasonably high in South Korea, but the majority of popcorn is imported from outside. We have developed two commercial popcorn hybrids in South Korea, Oryun-popcorn and G-popcorn. The purpose of this study is to evaluate the popping properties and to figure out the optimum popping condition of the Korean popcorn hybrids. Expansion volume, kernel size, moisture content and storage temperature were determined for two popcorn cultivars in this study. We investigated expansion volume under various conditions using the two cultivars. When the kernel diameter is increased, the expansion volume is also increased. The expansion volume at the diameter 5.6 and 4.8mm were 31.1㎝³/g and 30.2㎝³/g, respectively. Moisture content is also one of the important factors for popping. We tested expansion volume of the two cultivars at the moisture range from 10 to 13 %. The highest expansion volume, 29.3㎝³/g and 30.7㎝³/g for the two hybrids, were detected at the moisture range from 12 to 13%. In order to see the popping properties by the storage condition, the popcorn kernel was stored for seven months at room temperature, 15℃, 5℃ and -16℃. Expansion volume was decreased from 32.3㎝³/g to 27.7㎝³/g at the room temperature only, and there was no significant variation at other temperatures. This kernel properties and storage condition will be useful for farmers to use the Korean popcorn cultivars.

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QTL mapping for AGI (α-glucosidase inhibitor) activity of pepper leaf extract using genotyping-by-sequencing

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Diabetes mellitus, a metabolic disorder characterized by high blood sugar levels over a prolonged period, is one of the most important diseases in the world because the number of cases is increasing rapidly every year. It is caused by inherited and/or acquired deficiency in production of insulin from pancreas (Type I), or by the ineffectiveness of insulin produced (Type II). Alpha-glucosidase inhibitor (AGI) suppresses the activity of α-glucosidase, so it can prevent the absorption of carbohydrates. Although microbial agents for control blood sugar are used as a treatment, their long-term taking is accompanied by side effects such as digestive disorders. Therefore, it is required to develop AGI materials originated from natural products. There have been reports that pepper leaves show higher AGI activity than fruits. Therefore, the aim of this study was to identify QTLs controlling AGI activity of pepper leaves using an F2 population derived from the F1 plant (114-1) with high AGI activity (34.2% α-glucosidase inhibition rate). AGI activity of 96 F2 individuals was analyzed by using dried pepper leaf extracts with three repeats, and DNA from the F2 plants was subjected to genotyping-by-sequencing (GBS) analysis. In result, the AGI activities ranged from 25.07% to 65.57% and a total of 17,427 SNPs were genotyped. Linkage analysis of the SNPs revealed a pepper genetic linkage map with a total linkage distance of 2,514.8 cM, consisting of 12 linkage groups. In addition, QTL analysis for the AGI activity detected four QTLs, qAGI1.1, qAGI4.1, qAGI4.2, and qAGI11.1, with LOD scores of 3 or higher. In genotype analysis, two QTLs, qAGI4.1 and qAGI4.2, were thought to be false positive, whereas other two QTLs, qAGI1.1 and qAGI11.1, were valid. While a QTL qAGI1.1 was located on chromosome 1 with a phenotypic variation of 14.53%, a QTL qAGI11.1 was positioned on chromosome 11 with a $R^2$ value of 16.38%. These QTLs will be useful for pepper breeding programs with high AGI activity.

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The Effects of Root Pruning on the Growth Characteristics in Quercus acutissima and Q. variabilis

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Quercus spp. is characterized by weak development of lateral roots and rootlets compared to those of tap roots resulting low rooting and growth rates. Root pruning is one of the ways of improving the rates by promoting root differentiation, lateral roots development and increasing surface area of roots to take nutrition and water. This study was conducted to examine the effects of root pruning on the above-ground growth and development of roots of 1-0 seedlings of Quercus acutissima (sawtooth oak) and Q. variabilis (oriental oak). The treatment was applied with 1/3 and 1/2 intensity to the seedlings produced from seed orchard. Height (H), diameter at root collar (DRC), the number (NL) and length (LLA) of lateral roots were assessed for root pruning treatment group and control group. In Q. acutissima, the significant differences in treatment and control group were observed in the growth traits observed. H, DRC, NL and LLA were increased in the root pruned seedlings than those of the control group. In Q. variabilis, the same tendency was revealed in the all the traits except in DRC.

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Characterization of ‘GolSam’ lines developed from the cross between Samgwang and 5MT resistant lines in rice

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Rice grain quality is usually observed by its chalkiness and is affected by genetic effects of endosperm, cytoplasm and maternal plant. Controlling the chalkiness in rice can be a very challenging task because it is affected by genotype and environmental factors. The present study aimed to introduce 5-methyl tryptophan (5MT) resistance from the 5MT resistant mutants into Samgwang, a high grain and eating quality Korean variety by introgression of, resulting to elevated tryptophan content in grains. The progenies generated from single crosses of two different crossing combinations were phenotyped based on agronomic traits and by 5MT growth inhibition test. Through direct PCR sequencing, the inheritance of single base mutation (F124V) in OsASA1 was selected among the progenies. The latter generations were used to analyze the grain and eating quality of the selected lines. Inbred lines (S4-10, S4-28, S5-11) carrying the point mutation in OsASA1 and with reduced chalkiness plus good eating qualities were successfully generated. Tryptophan content in the milled grains of the selected lines showed 2-4 times higher (mg/100 mg) than the maternal parent. The three selected lines, S4-10, S4-28, S5-11 were later renamed as GolSam-1, GolSam-2, and GolSam-3 respectively.

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Identification of SNP marker related to high eating quality using GWAS analysis in rice (Oryza sativa L.)

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Next-generation sequencing (NGS) provides opportunity for developing DNA-based molecular markers. Various molecular markers have been developed for analysis of genetic diversity. Moreover, single nucleotide polymorphisms (SNP) have been identified as powerful selection markers for association with agronomic traits.

In this study, we identified genes related to high eating quality using 243 rice core collections by genome-wide association study (GWAS) analysis for their physico-chemical characteristics (peak viscosity, breakdown viscosity, final viscosity, setback viscosity, gelatinization temperature, peak time) and cooking quality (hardness, springiness, adhesiveness, stickiness, thickness) using standard methods and investigated correlation between genes related to physicochemical properties and starch synthesis. As a result of analysis for cooking and eating quality traits including amylose content and protein content, each trait showed a different distribution and basic statistics based on normal distribution curve. Total 1,842,517 SNPs (29.5% of total SNPs) were finally confirmed through SNP quality control. Manhattan plot analysis of GWAS using 14 physico-chemical and cooking quality data showed that statistical significance was associated with chromosome in each group. In the vicinity for significant SNPs, candidate genes were observed through NCBI database and selected candidate genes with a high significance. Among them, candidate genes related to seed storage protein and lipid metabolism, grain yield and starch content are detected. We selected the foreground selection (FS) markers by searching SNPs between ‘Samgwang’, ‘Goshihikari’, ‘Gopum’. The candidate gene detected through GWAS would be useful in developing new rice varieties with improved yield potential through future molecular breeding.

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Genetic and functional analysis of genes related to eating & processing quality of brown rice through GWAS analysis

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Brown rice (Oryza sativa) is rich in nutrients such as protein, fat, dietary fiber and vitamins and the consumption of brown rice is increasing annually in Korea. The objective of this study is to investigate physico-chemical, textural properties related to eating quality of brown rice including ‘Seolgaeng’ and ‘Keunmun’. To identify candidate genes related to synthesis of aleurone layer and starch in rice grain. As a result of X-ray diffraction analysis for brown rice, it showed strong X-ray peaks in ‘Keunmun’, ‘Seolgaeng’, ‘Samgwang’, ‘Hong Jinju’, and ‘Yonghojinni’ and was found to have a uniform starch granule. High quality brown rice varieties including ‘Seolgaeng’ and ‘Keunmun’ had a generally thin aleurone layer structure, but pigmented rice such as red rice and black rice showed thick aleurone layer structure in investigation of seed cross section and aleurone layer analysis. We also carried out a genome-wide association study (GWAS) to detect significant single nucleotide polymorphism markers and candidate genes affecting major eating and processing quality of brown rice. As a result, Os11g016800, which is significant in regard to amylose content, was correlated with quantitative yield component and Os04g0420300 and Os04g0420600 related to cooking properties had correlation with shape and quantity of panicle. Starch synthesis genes in endosperm were selected and sgRNA was designed. Plant transformation vector was constructed and transgenic rices edited with CRISPR/Cas9 were developed. Further analyses will be carried out to identify SNP markers related to eating and processing quality of brown rice.

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Determinations of α-glucosidase inhibitory (AGI) activity and flavonoid content from pepper leaves (Capsicum sp.)

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Type 2 diabetes mellitus is one of the most important metabolic diseases that are characterized by hyperglycaemia, high blood glucose levels. α-glucosidases are enzymes of digestive tracts that hydrolyze carbohydrates into glucose. Hence, inhibition of their activity using synthetic drugs is one of the strategies developed to treat type-2 diabetes. However, these inhibitors are usually associated with gastrointestinal side-effects and the development of inhibitors from natural products presents an alternative option for the control of hyperglycaemia. This study has investigated AGI activity of pepper leave’s extracts from 89 pepper lines. In the preliminary AGI analysis, the enzyme assay was done as follow, 50µl of extract and 200 µl yeast α-glucosidase enzyme (1U/mL) were incubated at 37°C for ten minutes. Then 400 µl of PNPG (3mM) were added to the mix and incubated for another 20 minutes at 37°C. The reaction was stopped in 4.35mL Na2CO3 (20mM) and absorbance of the solution was taken at 405nm. Inhibitory activity of the extracts ranged from 2% to 36% while the positive control acarbose (25mM) showed 30% AGI activity. Also five pepper lines with high and three lines with low activity were selected. Methanol extract of leaves collected from shoot tips, middle and lower part of these plants will be investigated for their flavonoid contents and AGI activity. PNPG, maltose and sucrose will be used as substrates for yeast and rat intestinal α-glucosidase enzymes. Inhibitory activity will be measured based on the amount of glucose produced in the presence or absence of leave’s extracts. Glucose oxidase kit will be used to measure glucose in the assay. Correlation analysis will be done between flavonoid content and inhibitory activities. Plant parts with high AGI activity and flavonoid content may be identified. The result may lead to instigate the identification of flavonoid compounds that could be potential inhibitors.

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Selection of β-Carotene High Content Corn Using Molecular Markers

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β-carotene is a main component of carotenoids that can be converted into vitamin A through animal’s metabolism, and plays a very important role in the prevention of vision-related retinal diseases and cataracts. Carotenoids are mainly contained in red, yellow and orange fruits or vegetables, and are said to have medical effects on heart disease and cancer. Recently, studies have been conducted to utilize natural pigments, dietary fibers, and protein raw materials of these plants, and cultivation of varieties with high pigment content has become a major goal of breeding price. In this study, we selected F1 segregating generation(18Cr112) corn using two molecular markers(5'TE, 3'TE) to select the hydroxylase 1(crtRB1) gene related to β-Carotene production developed by CIMMYT(International Maize and Wheat Improvement Center). In addition, high performance liquid chromatography(HPLC) analysis was performed to evaluate the β-Carotene content of the selected lines. In this study, 885 separate lines were evaluated, and each DNA was extracted from leaves and analyzed by two primers, crtRB1-3'TE, 5'TE. The β-Carotene content analysis of the selected lines showed 34.8㎍/g in 18Cr112. The result of this study suggests that selection of high-β-Carotene-containing corn line using crtRB1 molecular marker is expected that time and effort will be reduced and accurate selection compared with naked eye selection by color.

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TMT labeling based proteomics and metabolomics analysis to deciphering the effect of warm water imbibition in soybean seeds

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For production of soy-foods or supplements, imbibition of soybean seeds in the water is required step for generation of tofuf, soy-milk, and other soy-products. With an aim to get new insight into effects of different imbibition temperature (4, 25, and 55℃), this study conducted integrated proteomics and metabolomics analysis of soybean seeds. For total proteome analysis, we applied TMT labeling based quantitative proteomics combined to FASP (Filter-Aided Sample Preparation) with high-throughput LC-MS/MS. A total of 2,616 proteins were identified out of which 801 proteins showed significantly difference of protein abundance (≥1.5 fold change, Benjamini-Hochberg FDR <0.05) among 4, 25, and 55℃ imbibition seeds. Functional analysis of identified proteins showed an increased abundance of proteins functioning as glycosyl hydrolase enzymes such as beta-glucosidase, alpha and beta-galactosidase, and alpha-mannosidase, or protease, and PTMs related enzymes as well. UPLC TOF-MS analysis showed increase in isoflavone aglycones (daidzin and genistin) while isoflavone glycosides (daidzin and genistin) were decreased in 55℃ imbibition seed, in agreement with proteomics results which we assume positively related to increase abundance of glycosyl hydrolase. A metabolomics analysis revealed 64 metabolites were significantly altered, for example, various free amino acids showed accumulation patterns by increased abundance of various protease enzymes and further confirmed the accumulation of isoflavone aglycones and degradation of raffinose and stachyose in 55℃ imbibition seeds. Based on these results, we recommend the use of 55℃ for soybean seed imbibition to increase the quality of soy-food products.

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Crucial Role of Sucrose and Sucrose Transporter Genes in Regulating Flowering Time in the Triticeae Tribe

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Wheat, Barley and Rye are three very important cereal crops with distinct properties and high economic value hence a lot of research and efforts are put into these three cereal grains to produce a much viable, sustainable and nutritious cultivar. Flowering is a very crucial stage in plant growth and development. Early flowering in plants indicates faster fruit development which in turn promotes faster production and distribution. Wheat, barley and rye grains belong to the Triticeae tribe however, their flowering times are quite different from each other. This research focuses on the transport of sucrose and the critical role of sucrose transport genes (SUT) in the peduncle of the three grains in order to promote early flowering. In order to study this phenomenon peduncle from four different Waddington Stages had been sampled from three different cultivars of wheat (Keumgangag, Yeongkwang, Chinese Spring), two cultivars of barley (Bunong, Oweol), and two cultivars of rye (Uri, Kokwoo). Along with the peduncle, flag leaf and spike were also sampled for comparison purposes. Maturity time graphing has been done to determine the maturity time gap between cultivars along with sucrose extraction and quantification. Moreover, gene expression studies have been done by qRT-PCR in all three sample tissues. Discovering the proper flowering mechanism causing flowering time differences in wheat, barley and rye cultivars would be a big breakthrough in cereal crop research as with this very vital knowledge, researchers would be able to make tremendous advances in creating a much-improved quality of the current cultivars.

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RFS acts as a flowering inducer independent of photoperiod in rice

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Chromatin remodeling plays crucial roles in regulation of proper gene transcription for various developmental process in eukaryotes. Recent studies reported that transition from vegetative stage to reproductive stage is controlled by epigenetic factors in plants. RFS encodes a CHD3/Mi-2 chromatin remodeling factor which consists of two chromodomains, a plant homeodomain (PHD) and a SNF2 (Sucrose Non-Fermenting)-related helicase/ATPase domain. In two mutant lines of RFS, late flowering phenotypes were observed under both SD and LD conditions. On the other hand, vegetative growth was almost simultaneously occurred as wild-type plants before flowering, indicating floral transition was delayed in rfs mutants. To identify genes affected by rfs, we investigated diurnal expression of flowering regulatory genes when flowering signal begins to induce. Transcription of two rice florigen genes, Hd3a and RFT1, were significantly decreased under both SD and LD in rfs. In addition, Ehd1, which is an activator of florigen genes, was down-regulated in rfs mutant. However, several upstream regulators of Ehd1 did not displayed significant changes in the rfs mutant. These results suggest that RFS promotes flowering by activating transcription of Ehd1 independent of photoperiod in rice.

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Growth and Profile of fatty acids from *Nigella sativa* L and *Nigella Damascena* Planted in Indonesia

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Black cumin seeds are plant products of *Nigella* ssp. that have economic value in Indonesia, which are widely used as raw material for herbal medicines and have been made with various formulations. The benefits of the seeds for treatment are also related to the beliefs of Indonesian Muslims. The effort to plant in Indonesia is a strategic step in order to meet these needs. Differences in climate and soil conditions between regions of production center and Indonesia are likely to cause differences in growth and fatty acid profile. This study aims to study the characters of growth and fatty acid profile of *Nigella sativa* and *N. damascena* which is grown in Indonesia. The research was conducted at the Sirungge research station and at the Food Science and Technology Laboratory, IPB University. Planting black cumin is done in polybags and harvested when the capsules have dried color. Harvested seeds were extracted and injected in GC-MS to determine the fatty acid profile. The results showed that the two *Nigella* ssp. could grow and complete their life cycle completely, with a shorter life cycle than in some production centers. Both species of *Nigella* have several types of fatty acids, namely capric acid (C10: 0), lauric acid (C12: 0), tridecaryl acid (C13: 0), myristic acid (C14: 0),pentadecylic acid (C15: 0), palmitic acid (C16: 0), palmitoleic acid (C16: 1), margaric acid (C17: 0), stearic acid (C18: 0), oleic acid (C18: 0 cis), linoleic acid (C18: 2), Δ9 linolenic acid (C18: 3), arachidic acid (C20: 0), gadoelic acid (C20: 1) behenic acid (C22: 0). The most abundant types of fatty acids are *Nigella sativa* and *N. Damascena* are linoleic acid (C18: 2), which is 54.55% and 64.51% of the amount of fatty acids detected.

Keywords: Black cumin, habbatussaudah, GC-MS, production

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QTL mapping and validation of whitefly (*Bemisia tabaci*) resistance derived from *Solanum galapagense* in tomato

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Whitefly is one of the major constraints in tomato production by directly feeding as well as indirectly virus transmitting worldwide. In several wild relatives reported as resistance against whitefly, *Solanum galapagense* is closely akin to the cultivated tomato and promising breeding material for insect resistance including *Trialeurodes vaporariorum, Bemisia tabaci, Myzus persicae, Frankliniella occidentalis* and *Spodoptera exigua*, also aphids and thrips as well. The objective of the present study was to identify whitefly resistance QTLs and construct a high density genetic map using SNP markers derived from genotyping-by-sequencing (GBS) using a set of 167 F2 population produced from the cross between CLN9682C (susceptible, *Solanum lycopersicum*) and VF07099 (resistant, *S. galapagense*), in addition, validate CAPS markers converted from SNP markers associated with whitefly resistance QTL using an 112 BC1F2 population. A total of ~218 million SE reads comprising 22.1 Gbp sequence information were generated for 167 F2 population and the parents using the Illumina sequencing platform. All genotyped markers were attributed to 12 LGs representing the 12 chromosomes of tomato, spanning ~793 Mb with an average distance of 0.49 Mb between neighboring markers. Among morphological and phytochemical traits of tomato, high density of type IV trichome (V), low density of type V trichome (V), and high acyl sugars content (AS) were closely related to high adult whitefly mortality (AWM) in the no-choice bioassay and reduced numbers of eggs (NE) in the choice assay. Quantitative trait loci (QTL) was found on Chromosome 2 for IV, AS and NE, Chromosome 3 for V, and Chromosome 2, 3 and 9 for AWM. Through validating effective effects of three QTL regions using BC1F2 population, it was confirmed that genes associated with IV, V, AS, AWM and NE were significantly located on Chromosome 2.

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Construction of single nucleotide polymorphism markers based QTL map and validation of resistance loci to bacterial wilt (Ralstonia solanacearum) in tomato

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Bacterial wilt (BW), caused by Ralstonia solanacearum is one of the major biotic factors limiting tomato production in the humid tropics. Pyramiding of resistance genes through marker-assisted selection is an efficient way to develop durable BW resistant cultivars. Tomato line ‘Hawaii 7996’ (H7996) is a stable and robust resistance source against various R. solanacearum strains. Major BW resistance QTLs Bwr-12 and Bwr-6, and several minor or strain specific QTLs have been coarse-mapped in this line, but none has been fine-mapped and validated. The objective of the current study was to construct a high density genetic map using SNP markers derived from genotyping-by-sequencing (GBS), fine-map Bwr-12 and Bwr-6 and determine the effects of these QTLs using a near isogenic line (NIL) population. A high density genetic map using 1,604 SNP markers with an average distance of 0.82 cM was developed for 188 F2 recombinant inbred lines (RILs) derived from the cross H7996 × WV1700. A total of seven QTLs associated with BW resistance to race 1-phytophthora 1 or 1/ and race 3-phytophthora II strains were located on chromosomes 6 (Bwr-6.1, 6.2, 6.3 and 6.4) and 12 (Bwr-12.1, Bwr-12.2 and Bwr-12.3) with LOD scores of 6.2-15.6 and 6.2-31.1, explaining 14.2-33.4% and 15.9-53.9% of the total phenotypic variation contributed from H7996, respectively. To validate the genetic effects of the two QTL regions, a set of 80 BC3F1 NILs containing different sections of Bwr-6 with or without Bwr-12 was phenotyped for disease severity after challenge with either race 1-phytophthora 1 Pss4 or race 3-phytophthora Pss1632 BW strains over two seasons. Bwr-6.1 specific to Pss4 and Bwr-6.3 specific to Pss1632 were mapped to an interval of 50 cM (P < 0.05) between 6.33,444,000 SLM-61 and 6.33,868,000 SLM-6-124 SNP marker, and to 2.7 cM (P < 0.01) between positions 6.35,949,000 _SLM-6-107 to 6.36,750,000 _SLM-6-82 marker, respectively. In addition, the specific effect of Bwr-12 for resistance to Pss 4 (LOD score of 5.8-16.1, P < 0.01) was confirmed and markers for this QTL have already been made available previously.

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The promise of genomic selection in breaking yield ceiling in rice

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Conventional rice breeding reached at an exhaustive state leading lower genetic gain in most rice breeding program globally. Modern rice breeding approaches made a profound impact on rice yield breaking the potential yield ceiling and the bottleneck of the yield barriers. However, the major paradigm shift in breeding got the momentum over the last two decades since the availability of molecular marker technology along with genomic selection (GS) would lead and reshape crops breeding programs and facilitate rapid genetic gain. The advent of molecular marker technology enables reducing the genotyping cost immensely. Such low cost genotyping and ability to select individuals at earlier generation through rapid generation advance (RGA) would substantially cut the plant breeding cycle, enhancing gains per unit time. IRRI is focusing its breeding program on GS method with modern operations and data driven breeding decision support tools to accelerate genetic gain in rice. In Bangladesh, total 769 advance breeding lines were evaluated at four agro-environments e.g. Satkhira, Rangpur, Mymensingh and Cumilla in 2018 season wet (T. Annan season) to identify superior progenies (having higher breeding values, BVs) with superior agronomic performance. The trials were established with partially replicated (P-rep) design and the plot size (for each entry) was 5.4 sqm meter with 20 x 20 cm plant to plant transplanting spacing. Results revealed that few entries shown high yield potentials (3.5 to 7.9 t/ha) with 110 - 130 days growth duration. Pedigree-BLUP model was used to estimate BVs where a bunch of breeding lines were identified with higher BVs. Ranking and selection of superior lines with higher BVs and recycle them in the following crossing program would lead to a substantial increase of genetic gain in grain yield in the subsequent progenies sustainably.

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QTL mapping of powdery mildew resistance in cucumber

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Powdery mildew (PM) is a very important disease of cucumber (Cucumis sativus L.). Resistant cultivars have been deployed in production for a long time, but the genetic mechanisms of PM resistance in cucumber are very complex and depended on the resistance germplasms. For QTL mapping study of PM resistance, we made 132 F2:3 families derived from two cucumber inbred lines DB1278 (resistant) and DB2652 (susceptible). A genetic map covering seven linkage groups was developed with BSA sequencing approach. Multiple QTL mapping analysis of molecular marker data and disease index of the true leaf for responses to PM inoculation identified three genomic regions in two chromosomes harboring QTL for PM resistance in DB1278. Results of this study provided new insights into phenotypic and genetic mechanisms of powdery mildew resistance in Korea style cucumber inbreeding line.

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Genome-wide association study for seed weight in soybean (Glycine max)

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One of a yield component, Seed weight (SW) is a complex and agriculturally important trait in soybean (Glycine max (L.) Merr.). In this study, we performed to identify major and minor candidate QTLs through GWAS on seed weight in 430 accessions with genetic diversity. A total of 430 soybean accessions, including landraces and improved lines, were applied to evaluate the variation of 100-seeds weight. All accessions were bulk-harvested individually after full maturity in field of the National Institute of Crop Science, Rural Development Administration (Jeonju, Korea) in 2016, 2017 and 2018. A sample of 100 cleaned seeds from each accession was randomly taken and weighed. We measured 100-seed weight in 430 accessions in 2016, 2017 and 2018. 100-seed weight of 430 accessions was distributed 7.3 ~ 59.4 g in 2016, 9.1 ~ 48 g in 2017, and 8.7 ~ 45.6 g in 2018. We identified SNPs with a significance (-log(p) ≥ 3.0, p ≤ 0.001) related to 100-seed weight in whole soybean chromosome through GWAS. In results of GWAS, the number of significant SNPs identified 171 in 2016, 137 in 2017, and 122 in 2018. Of these, 29 SNPs showed commonly significance in both years. As a results, we found a number of candidate genes in 17 loci of 12 chromosomes. In addition, we will explore and validate candidate genes that are closely related to 100-seed weight. Consequently, the results of the present study could provide fundamental and practical materials and information for both genetic research and breeding programs in soybean.

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QTL analysis regulating seed α-tocopherol ratio in wild soybean

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Soybean (Glycine max) is one of the most important agriculture crop that major source of tocopherols (Tox). Tocopherol exists in 4 forms in nature α, β, γ, and δ. Among them, α-toc has the highest vitamin E activity in humans. As a antioxidants that have a positive impact on humans health, the most predominant form in soybean seeds is γ-Toc and the ratio of α-Toc is only lower than 10%. Therefore, low content of α-toc was regarded limit the soybean uses in the food and medical industries. So improving the content of α-Toc in soybean seeds expands the use of soybean in food and medical industries.

Here, we report the results obtained from the quantitative trait loci (QTL) analysis for a high seed α-Toc ratio detected in a wild soybean accession (B04009). Using recombinant inbred lines (RIL) population derived from a cross between B04009 and a soybean cultivar TK780, three QTLs associated with the high α-Toc ratio were detected in chromosomes 9, 11, and 12. In QTLs at chromosome 9 and 12, B04009 alleles gave positive effects for the high α-Toc ratio, whereas in chromosome 11 QTL, TK780 allele increased the α-Toc ratio.

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QTL analysis for pod shattering tolerance in soybean [Glycine max Merr (L.)] with RIL populations derived from ‘Daewonkong’

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Pod shattering at maturing stage causes a yield loss and is a main limiting factor for mechanization in soybean cultivation. ‘Daewonkong’ is an elite cultivar which occupies more than 80% of soybean cultivation area in Korea because of its strong tolerance to pod shattering. The objective of this study was to find QTL associated with pod shattering tolerance in the RIL population derived from ‘Daewonkong’. Two RIL populations using ‘Daewonkong’ as a female parent were used in this study; ‘Daewonkong’ x ‘Taewonkong’, ‘Daewonkong’ x ‘Sacollkong’. SNPs were used to construct genetic map using a 180K SoyaSNP array. Linkage map construction and QTL mapping were conducted using Icemapping ver. 4.1. The linkage map was constructed with approximately 116 markers per chromosome and 1.2 cM average distance between each SNP. A major QTL was found on chromosome 16. This region was located at 45~64cM on the genetic map, and its physical position was 29.5~30.1 Mbps, which includes the previously reported gene pdh1 related to pod shattering tolerance. This result indicates that pod shattering tolerance of ‘Daewonkong’ is derived from the pdh1 gene. QTL from ‘Daewonkong’ has the relatively high PVE (82.8%) and LOD (67.1) values than the QTL previously reported. Therefore, QTL information found in this study will be useful for developing varieties with pod shattering tolerance comparable to ‘Daewonkong’.

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220
Genome-wide Association, Breeding Signatures and Epistatic interactions among Flowering Time in Korea Soybean

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Genome-wide association studies (GWAS) have enabled a deeper understanding of the genetic factors of many complex traits in plant genomics. A GWAS of a population of 3,632 germplasm accessions from the Affymetrix Axiom 180k SoyaSNP array has been conducted to evaluate the representative nature of the Korean cultivated soybean. As more GWAS have been performed focusing on single-nucleotide polymorphisms (SNPs), many researchers have started exploring breeding signatures along with epistatic interactions. Also, genomic prediction enables markers on breeding programs to focus on insightful markers. Especially, epistasis, the genetic interactions among genomic loci, has started receiving interest as a potential source of missing heritability in single-locus analyses of GWAS. Complex traits such as flowering time are important components in Korean soybean and known to be controlled by many genomic regions modulated by many factors. Limitations in the knowledge of these effects resulting from genotype can be one of the main achievement in improving selection process in soybean breeding. In this study, we identified the markers estimated by GWAS, breeding signatures and genetic interactions on the complex traits of flowering time in the Korean soybean population.

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Functional Analysis of *Ruby* Alleles Controlling Anthocyanin Pigmentation in *Citrus*

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Blood oranges (*Citrus sinensis*) are believed to have significant health-promoting properties, combining the high content of vitamin C, carotenoids, citrus-specific flavonoids, and dietary fiber with health benefits of anthocyanin pigments. The high anthocyanin content in blood oranges has been generally known to reduce cardiovascular risk factors due to their high antioxidant activity. In a mouse model, blood orange juice consumption has been shown to prevent obesity caused by a high-fat diet. Up to now, six different alleles on *Ruby* locus encoding a MYB transcriptional activator of anthocyanin production were identified. For the marker-assisted selection of citrus cultivars with red flesh trait, we developed PCR-based DNA markers for the genotyping of each *Ruby* allele. During the marker development, we identified the 7th *Ruby* allele from a citrus hybrid, ‘Shiranuki’, and traced its origin from the genotyping on parents and grandparents of ‘Shiranuki’. We finally concluded that the 7th *Ruby* allele was originated from *C. unshiu* ‘Miyagawa Wase’, a grandparent of ‘Shiranuki’. Several Ruby alleles such as R, r-1, R5-2 were introduced into *Arabidopsis thaliana* to study their functional analysis. Accumulation of anthocyanin pigments was observed in cotyledon and hypocotyl of the transgenic lines expressing R5-2 dominant allele under cold growth condition, but not in the transgenic lines expressing R and r-1 alleles.

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221
Study of Quantitative Trait Loci (QTLs) Associated with Allelopathic trait in Rice (Oryza sativa L.)

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QTL analysis for Allelopathic trait were conducted with 167 F8 RILs developed from the cross between the high allelopathic parents of ‘Nong-an’ and non-allelopathic parents of ‘Sath’. The performance of allelopathic traits were evaluated with inhibition rate on root length, shoot length, total length, root weight, shoot weight, and total weight of lettuce as a receiver plant. With 106 polymorphic DNA markers, linkage map was constructed showing total 1,042 cM genetic length and 11.2 cM of average genetic distance between each adjacent markers. QTL analysis detected two additive QTLs regions where three QTLs were on the chromosome 3 and three QTLs were on the chromosome 6. The qTL-3 explained 6.8% of the phenotypic variation for the inhibition on the total length and The qRL-6 explained 9.7% of the phenotypic variation for the inhibition on the root length. Five digenic epistatic QTLs were detected for root length trait. The interval between marker id3009433 and id3015453 on chromosome 3 showed interaction with other three genomic regions on chromosome 5, 7 and 9. And the interval between marker chr7_2014342 and SLG7-GC on chromosome 7 showed interaction with other two genomic regions on chromosome 1 and 3.

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Assessment of the molecular markers selected for genotyping of soybeans by agricultural traits

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The present investigation was conducted to assess the selected molecular markers for genotyping of soybeans. We selected 50 SSR markers which were reported by several studies for QTL mapping of soybean agricultural traits and investigated the agricultural performances of 11 soybean varieties from China (Harbin, Yanji, Dalian, and Qingdao) and Republic of Korea (Suwon and Jeonju) to assess performance of the selected markers. We constructed an UPGMA dendrogram separately by traits using the SSR markers significantly associated with each trait. The dendrogram for days to flowering (DTF) showed five subclades at a genetic distance of 0.5. Soybean varieties in subclades III and IV showed the shortest DTF. The soybean varieties classified into subclade II showed longer DTF than other soybeans. Members of subclade VI in the dendrogram for stem length (STL) had the longest STL on average, while members of subclade V showed the shortest STL. Hannamkong, which had the longest DTF and the shortest days to maturity (DTM), was categorized in subclade III and average DTM of the varieties in this subclade was the shortest. The dendrogram for 100-seed weight (HSW) displayed three subclades; subclade I, including Hannamkong, Tawonkong, and Doyoukong, was the most distant genetically and the HSW of these soybean varieties was the lowest on average. The dendrogram for yield (YLD) also showed three subclades. Subclade I, including Hannamkong and Kaumgangkong, differed genetically from the other subclades and the YLDs of the four soybean varieties within subclades I and II were higher than that of soybean varieties within subclade III. These results suggest that genetic characteristics contribute to the DTF, DTM, STL, HSW, and YLD of soybean varieties and the selected markers are able to use for genotyping of soybeans. This work was supported by the National Institute of Crop Science Research Program (Project No. PJ012548032019).

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Assessment and selection of molecular markers for analyzing cross of F1 soybean plants

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This study was conducted to assess and select molecular markers for analyzing cross of F1 soybean plants. We prepared genomic DNA samples from 20 soybean parent varieties and 325 F1 lines (24 combinations) and selected 8 SSR and 7 InDel markers for preliminary tests. Predicted product sizes of PCR by the SSR and InDel markers were 219 bp and 104 bp on average, respectively. We confirmed that the products by markers were formed in ranges of predicted sizes. On average, number of allele by SSR and InDel markers was 4.6 and 2.0, respectively. Products sizes of PCR by Satt009 were very diverse but all InDel markers showed only 2 bands each other. We calculated polymorphic information content (PIC) of marker to assess usefulness of the markers. PIC of all SSR markers were over 50 but under 50 by the InDel markers. Satt009 showed the highest PIC (0.83) while Sindel_06_05 had the lowest (0.10). Among the 325 F1 soybean plants, we confirmed that 36 lines (11.1%) were self-fertilized: all lines of Milyang 315/Fukuibuki and Hannamkong/Suwon 273 combinations were self-fertilized but all lines of 10 combinations including Daewonkong/Cheonga were completely crossed. We investigated analytical degree of the markers to assess the markers. SSR and InDel markers were averagely able to analyze 16.6 and 7.7 combinations, respectively: Sat_197 analyzed 22 combinations but 5 combinations by Sindel_06_05. For this study, we concluded that SSR markers formed more diverse allele and were more suitable marker for analyzing cross of the F1 soybean plants than InDel markers. Taken together, we selected 5 SSR markers, Satt009, Satt184, Satt216, Satt424 and, Sat_197 which showed PICs of over 0.70, as suitable markers for analyzing cross of F1 soybean plants with similar combination. This work was supported by the National Institute of Crop Science Research Program (Project No. P9012548012019).

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Migration heading date of descendants by selection early maturity lines in oats

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The use of oat races in artificial crossing with cultivated oat (Avena sativa L.) has been used as a way of increasing the variability. This work aimed to identify the variability for heading date of descendant groups of crossed oat genotypes, and segregating the populations of crosses between early heading cultivar and late heading cultivar. Wide genetic variability was observed for heading date trait in the descendant groups. The descendant group of crossed early maturated parents showed narrow range early maturity, but in the descendant group of crossed early heading parent and late heading parent, there was wide rage maturity. This studied in this work can be used in oat breeding programs to increase early maturity characters into the cultivar.

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Genotyping 1,969 wheat accessions using SSRs to build a core collection

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Wheat (*Triticum aestivum* L.), one of the major crops in domestic, currently has a low self-sufficiency rate of 1.1%. For this reason, most wheat consumed in Korea depends on imports. Therefore, it is necessary to collect the genetic resources of domestic and overseas wheat, to accumulate breeding sources. By evaluating the characteristics of these genetic resources in Korea and abroad, it is possible to find useful genetic materials for agriculture and the efficiency of breeding will also increase. These useful germplasms are expected to be used for resource-specific evaluation and molecular genetic studies of genetic resources. In recent years, molecular markers for basic and applied studies have been used in plant systems. These molecular markers are not affected by the environment and are used for genetic diagnosis, characterization of transformatants, genome organization studies, and phylogenetic analysis. In bread wheat, the restriction fragment length polymorphism (RFLP), amplified fragment length polymorphism (AFLP), and random amplified polymorphic DNA (RAPD) marker systems have detected only low levels of intraspecific polymorphism. In contrast, microsatellite markers are consistently found to be highly polymorphic, easily visualized, stable, and co-dominant. The minimum length of SSRs was defined as 14-21 bp. The maximum length ranged from 24 to 87 bp, depending on the length of the repeat unit itself (1-7 bp). DNA polymorphism was analyzed using genomic DNA extracted from leaves of 1,969 wheat accessions collected from domestic and foreign genetic resources using genomic simple sequence repeat (SSR) markers. The SSR markers used in the research consisted of 18 primer sets and about 35,500 PCR reactions were performed. All these microsatellite markers come from IPK-Gatersleben (WMS SSRs from Röder et al.1998), except CFD71, which was developed by INRA Clermont-Ferrand (Guyomarc'h et al. 2002). The genotype data for those accessions will be used to build a core collection for a Korea wheat breeding program.

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Assessment of Molecular Markers Related to Spike Properties and Tiller Number of Long Spike Korean Wheat Populations

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This study was conducted to identify molecular markers of long spike Korean wheat populations which were evaluated to improve the yield potential of Korean wheat breeding programs. The recombinant inbred lines derived from a cross between Korean wheat cultivar and Ilsean 370, which large kernel number line carried with the longer spike length and higher kernel number/spike than Korean wheat cultivars. Spike length, kernel number/spike and spike density were investigated from replicated field trials in Korea. A genetic map was constructed with 92 microsatellite marker loci and a total of nine QTL were identified on six chromosomes for spike length and kernel number. The six QTL, *Xwmc 44*, *Xbarc 205*, *Xgwm 292*, *Xgwm 135*, *Xgwm 495* and *Xiwg 285* were explained phenotypic variation for spike length, spike density and kernel number/spike in F₃ populations. The tiller number of long spike Korean wheat cultivar populations differed according to the *Ppd-D1* allele, affecting the yield. These molecular markers could be used in marker assisted selection wheat lines with higher kernel numbers and improving tiller number in Korean wheat breeding programs.

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**Genome-wide SNP selection associated with protein and oil contents in wild soybean using multi-locus genetic models**

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Soybeans are one of the most important crops as a source of protein and oil, not only for humans but also for livestock feed. Therefore, many studies are being conducted on the search for genes that can change the content of protein and oil. However, genetic diversity has decreased due to the genetic bottleneck caused by the development of cultivated soybeans. Therefore, we searched for SNPs related to protein and oil content using wild soybeans, which were originated from cultivated soybeans and large in genetic diversity. Protein and oil contents of 311 wild soybean accessions were analyzed from harvested seeds in 2016 and 2017. Genome-wide association studies were performed using multi-locus genetic models (LASSO and ELASTIC-NET) as well as single-locus genetic model in GAPIT. The average contents of protein and oil were 48.14 ~ 49.79 and 7.26 ~ 7.48, respectively. Also, protein and oil contents showed negative correlation (\(r = -0.558**\)). The LD estimate for the whole genome was 18.7 kb. Twenty SNPs were detected simultaneously in at least two models, and they were located around previously reported QTLs associated with protein and oil content in the Wm82 Genome Browser at https://www.soybase.org/. Based on these SNPs, we identified 13 candidate genes for protein and oil at https://phytozome.jgi.doe.gov/. These SNP markers will be useful for breeding materials in soybean.

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**Genome-wide association studies for flowering time variation in cowpea (Vigna unguiculata L. Walp)**

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Cowpea (Vigna unguiculata L. Walp., 2n=2x=22) is one of the most important legume crops which has dietary protein and essential nutrients for the people in sub-Saharan Africa, East-Asia, and other developing countries. Generally, the flowering time is controlled by various environmental factors as well as developmental growth. Furthermore, flowering time is an important effect of maturity and adaptation in different geographical regions. In this study, we identified SNPs associated with flowering time by using GWAS analysis. A total of 384 cowpea germplasm were genotyped with 51K Cowpea iselect consortium array. Genome-wide association analysis was conducted with Compressed Mixed Linear Model (CMLM) using GAPIT (Genomic Association and Prediction Integrated Tool). We discovered 21 SNPs located on three different chromosomes (chr. 2, chr. 3, and chr. 9) that might be significantly associated with flowering time. Previously, the position of chr. 2 and chr. 9 were discovered through GWAS and QTL analysis with another cowpea germplasm. However, the remaining SNPs on chr. 3 appeared to be in novel location. We identified candidate genes including AP2 (chr. 2, and chr. 9), NAC domain-containing (chr. 2), and Jmjc&Histone H3MK9 demethylase that (chr. 3) are involved in flowering time and plant development. As a result, this study provides the sources that could be helpful to research genetic and breeding program of cowpea.

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Application of a novel, targeted sequencing-based genotyping approach for cost effective marker assessment in *O. Sativa*

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Decreases in sequencing costs have increased the availability of public SNP databases while necessitating development of targeted genotyping assays for use in marker assisted genomic selection for a variety of crop species. NEBNext Direct is a novel, hybridization-based target enrichment approach that has been optimized for use in genotyping applications to increase the number of assays that can be performed in a single reaction, while providing sequencing coverage depth suitable for SNP identification. The approach enables high-levels of multiplexing of both isolates and markers, allowing enrichment of hundreds of thousands of SNP targets in a single hybridization reaction, and the protocol is easily completed in a single day. We developed a panel covering 1989 single nucleotide polymorphisms previously identified as markers for polymorphism detection in *O. Sativa*. We applied this panel to detect polymorphisms in 24 diverse lowland and upland accessions of *O. Sativa*. Each sample was sequenced to >150X unique coverage to enable robust genotyping calls of the targeted SNPs. Using this genotyping data, the diverse rice DNA samples could be correctly categorized into unique cultivars, demonstrating that this genotyping approach enables a robust and cost-effective method to distinguish cultivars of *O. Sativa*.

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Genetic architecture of soybean flowering-time using a variation block analysis

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Flowering time is strongly influenced by climate and day-length adaptation in soybean (*Glycine max* L.), yet they remain untapped due to the genetic linkage between the few useful alleles and hundreds of undesirable alleles. In this study, a variation block analysis of flowering time was conducted with a diversity panel comprising 96 soybean cultivars and inbred lines grown in three agro-ecological conditions. In total, 7,087 variation blocks (VB) were mined by analyzing whole genome sequencing data of 96 soybean genotypes. Phenotypic associations with flowering time and seed yield were calculated in the panel over the year 2016-2017. We identified 290 VBs associated with the onset of flowering among all soybean cultivars. Three clusters were inferred by STRUCTURE analysis, which is in good agreement with a neighbor-joining tree. In addition, soybean orthologs for a number of candidate genes for adaptation were detected, including soybean maturity locus *E1*. Further, backcross recombinant inbred lines (BC:F1, ‘Hwangkeum’ X ‘Daepoong’) exhibited significant variations in their onset of flowering, with a range of 18-20 days due to obvious difference in *E1* locus. Hence, VB analysis of candidate regions suggested that, selection of genes involved not only in flowering time but also in other trait may have high impact on diverse soybean cultivars. Furthermore, our study provides a valuable framework to improve the genetic resources of crop plants under changing environments.

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Genome-wide association study for seed sucrose content of soybean (*Glycine max* [L.] Merr.)

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Sucrose is one of major factor determining sweetness of soybean, however, genetic factors regulating seed sucrose of soybean have been barely studied. In this study, we assessed seed sucrose of Korean soybean collection consisting of 201 landraces and 99 elite variety bred by Korean breeders. Phenotype assessment showed that seed sucrose content had not been targeted during soybean breeding. We identified 25,984 SNP loci using genotyping-by-sequencing (GBS) for conducting genome-wide association study (GWAS) and fixation indices analysis to identify genetic factors regulating seed sucrose content of soybean. GWAS showed three SNPs were associated with seed sucrose content and seed sucrose content was significantly affected by alleles of the SNPs. Two candidate genes, sucrose phosphate synthase 3F and 3-ketoacyl-acyl carrier protein synthase were identified. By the fixation indices, a sucrose synthase 4 and two seed sucrose QTLs were located on the blocks with high FST. One of three SNPs identified in Korean soybean collection by GWAS showed consistent association in the germplasms consisting of 59 high and 59 low sucrose contents obtained from USDA by single marker association analysis. From blocks with high FST in the USDA germplasms, one QTL for sucrose content and four sucrose regulating genes, sucrose transporter 4, sucrose synthase 4, sucrose phosphate synthase 1F and sucrose synthase 3 were identified and all of them was different with the genetic factors detected from Korean soybean collections. The sucrose content may be controlled by different genetic factors because of different genetic structures between the Korean soybean collection and USDA germplasms. This study provides genetic factors regulating seed sucrose content of soybean and contributed to breed soybeans with diverse sucrose contents suitable for specific table use.

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Genome-wide association study of fruit traits and testing genomic selection models in pepper

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In Korea, pepper (*Capsicum.spp*) is an important crop for spices as well as fresh fruit. Among the various traits, fruit related traits are critical determinants of marketable quality in pepper. Fruit traits are controlled by a number of genes. To develop an effective breeding method on these traits, we examined the potential of genomic selection in pepper. We used the two populations, pepper core collection and PD RILs, and generated SNPs by genotyping by sequencing (GBS) and whole genome re-sequencing. After filtering and imputation, a total of 18,663 SNP markers common in both populations were selected. As target traits, fruit length and fruit weight data of 2018 were used. To select the most effective genomic selection model, we conducted 10 fold cross-validation using our core collection data for training. Based on the training results, we selected three models, ‘gblupRR’, ‘RKHS’, ‘Random Forest’ and tested prediction models. Using the selected models, SNP markers were subjected to estimation of breeding values in the testing population (PD RILs). Then, model performances were evaluated by comparing correlations between predicted values and observed phenotype values of PD RILs. For fruit weight, ‘RKHS’ showed the highest accuracy with an average value of 0.558. For fruit length, ‘RKHS’ and ‘gblupRR’ showed the same accuracy with an average value of 0.290. In general, differences of linkage disequilibrium pattern and genetic diversity between training and test population could lead the lower prediction accuracy in testing populations. In our case, even though parental lines were included in the training population, the prediction accuracy was lower than expected in the testing population.

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A Maiden Attempt of Genomic Selection in Korean Red Pine (Pinus densiflora) Trees

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Genomic Selection (GS) is one of the accelerating breeding methods. With the advent of high throughput molecular technology, numerous molecular markers distributed throughout the whole genome can be developed to characterize many genetic entries involving new perspectives in methodology of selection. In tree breeding the GS could significantly reduce the cost of genetic improvement schemes by limiting the size and number of field experiments. In this study, we used 5,228 trees of 46 half-sib F1 families from 6 environments in Korea and we got 97,647 SNPs via GBS (Genotyping by Sequencing). And then, we designed the high-resolution DNA chip (200K chip) to validate whole SNPs. Finally, we selected and produced the 50K SNPs chip for genotyping of Korean red pine trees. Now, we are preparing to analyze 4,412 trees which are confirmed the pedigree. In order to successfully performed GS, not only the genetic analysis of trees but also accurate phenotypic analysis is very important. Here, we present a novel approach to automatically measurement of tree phenotypes using drone and ground-based scanner. The actual utility of this scanner depends largely on the efficacy of point cloud data (PCD) analysis. The quantified data of each tree was validated using laborious measurements. The results showed that the individual tree growth was accurately reproduced using our method from three dimension registered scans, with a relative deviation of less than 5%. Therefore, we want to apply this method of phenotype analysis for accelerating breeding and management of large-scale progeny test site.

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Tiny Inflorescence controls internode length of inflorescence and shoot in tomato

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In crops, internode growth of stem is a major determinant of plant organ size including inflorescence size, and the length fitness of inflorescence has been selected to take benefits for farming such as high yield in the field or in the building. Here, we report tomato ERECTA (ER), a LRR (leucine-rich repeat) receptor-like serine/threonine-protein kinase known as regulator of cell division in stem cell, controls plant organ size including inflorescence and stem size. tiny inflorescence (tinyin), a mutant line induced by EMS (Ethyl Methane Sulfonate), produces extremely short internodes in inflorescences and other stems, but normal sized leaves and flowers relatively. Map-based cloning revealed tinyin was resulted from single nucleotide change creating a premature stop codon in the middle of leucine-rich repeat domain of TINYIN. Multiple Sequence Alignment (MSA) indicated TINYIN is the orthologue of ERECTA of other plant species. In addition, we created tinyin s double mutant producing multiple branches with very short internode length in all internodes of inflorescence like the one of grape. Moreover, we could engineer the internode length of inflorescences in double determinate cherry tomato (cv. Sweet 100) by TINYIN promoter bashing with multiple target genome edition. Therefore, we suggest that the elaborate manipulation of TINYIN function could offer a new window to improve crop productivity with controlling size of plant organs in the building, greenhouse and field.

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Functional haplotype and eQTL analyses of genes affecting cadmium content in cultivated rice

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This experiment was conducted to investigate genetic factors affecting Cd uptake because the current molecular understanding of Cadmium (Cd) uptake-transport mechanisms remains insufficient. Associations between genotypes and gene expression levels of Cd-related genes (e.g., the Nramp, MTP, and HMA gene families) in the rice core set were analyzed at the genomic level. Os01g0595700, Os05g0128400 and Os11g0485200 showed strong associations between expression level and genotype in the rice core population, and the regulatory candidate genes that affect these genes in cis and trans were examined. The association between the expression level and genotype of a candidate gene (Os01g0611300: metal tolerance protein) predicted to affect Cd content in rice by a previous genome-wide association study (GWAS) was also analyzed. Furthermore, the correlations between Cd and other inorganic components (Mg, Mn, Fe, Cu and Zn) in the roots, stems, leaves and unpolished grain of selected rice cultivars were analyzed. As a result of the phylogeny and haplotype analyses of the candidate gene, high-Cd tolerance cultivars were selected. Therefore, these results may be useful for understanding the uptake-transport mechanisms of Cd and other inorganic components via molecular genetics and may help rice breeders develop new low-Cd varieties in the near future.

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Deciphering the genome of octoploid strawberry (Fragaria × ananassa)

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Advancements in the next generation sequencing (NGS) approaches have revolutionized the whole genome de novo sequencing in several plants. In addition, the reconstruction of chromosome level whole genome sequences of even non-model organisms has become affordable with long read sequencing technologies such as Single molecule real-time sequencing (SMRT) and nanopore sequencing methods. The present endeavor deals with sequencing, de novo assembly, and annotation of the high-quality reference genome of Fragaria × ananassa ‘Benihoppe’. The whole genome has been sequenced using PacBio RSh in combination with IlluminaNovaseq. A total genome size of 804 Mb has been generated for Fragaria × ananassa ‘Benihoppe’, with an estimated depth of coverage of 80×. This allowed us to assemble each genome with contig size of 805,664,111 bp and scaffolded the genome to chromosome scale by using Hi-C in combination with the HiRise pipeline (Dovetail). Further, the gap-filling and error-correction have been performed for PacBio reads with PBJelly. A genetic map for Fragaria × ananassa was used to correct any misassemblies, and comparisons to Fragaria vesca were used to identify homeologous chromosomes. Further, the whole genome annotation has resulted in the identification of higher number of genes on comparison with the existing reference genome of Fragaria × ananassa ‘Camarosa’. Taken together, the draft genome sequenced for cultivated strawberry using cutting-edge genome sequencing approaches will facilitate the strawberry genomics research and enhance the strawberry breeding.

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Integrated bi-parental quantitative trait loci mapping and genome-wide association provides novel candidate genes for plant height and habits in pepper (Capsicum annuum) using a superior Dempsey reference genome

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Plant height (PH) and habit (PHa) are important plant architectural traits that can influence photosynthetic efficiency, early maturity, lodging resistance and yield performance of pepper (Capsicum spp.) plants. Here, we constructed a genetic map based on 116 F2 plants from a cross between Ca. annuum ‘Jeju’ and ‘Micropep Red’ to identify the PH and PHa quantitative trait loci (QTL). Subsequently, a panel of 350 core collection accessions was used for genome-wide association studies (GWAS) to discover significant signals of marker-trait association and co-localized regions. A genotyping-by-sequencing approach was used for genotyping and 897 and 97,531 single nucleotide polymorphisms (SNPs) were detected in F2 plants and core collection accessions, respectively. Composite interval mapping identified a total of two PH QTLs on chromosomes 4 and 7 and eleven PHa QTLs on chromosomes 1, 2, 3, 6, 7 and 9. In GWAS, we identified 70 significant SNPs for PH and PHa. The significant QTLs and GWAS-SNPs commonly found on chromosomes 4 and 7 for PH without co-localized regions, however, two GWAS-SNPs co-localized to earlier reported PH QTLs. Four PHa GWAS-SNPs from chromosomes 1 and 3 were co-localized with two PHa QTLs. A cluster of three GWAS-SNPs on chromosome 6 was co-located to the fasciculate gene a homolog of the self-pruning (SP) gene in tomato. We identified multiple candidate genes with low effects in response to plant hormonal biosynthesis mostly gibberellins for PH which alters the numbers and length of internode cells and strigolactone hormones for PHa. The knowledge of the genetic basis of such complex quantitative traits, together with relevant novel alleles from QTL and GWAS can contribute effectively for the improvement of plant architectural and yield-related traits in pepper.

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Development of SNP marker set related to Crown gall disease in Grapevine by GWAS

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The grape is one of the most popular fruit trees produced in the world, yield 74 million tons within 6.9 million hectares per year. The crown gall disease caused by Agrobacterium vitis has occurred in worldwide vineyards and induce serious economic losses. These pathogens form galls in the stem of the grapevines and reduce the vitality of fruit trees, resulting in reduced yields. Because the Agrobacterium vitis is soil-borne disease, they can survive in soil for several years in the vineyards and are which difficult to control. The most effective control method is breeding of resistant varieties. To make the resistant variety, using Marker-Assisted Selection (MAS) enables fast breeding with low cost. In this study, we applied Genome-Wide Association Study (GWAS), by combination of Genotyping-By-Sequencing (GBS) and phenotyping, for development SNP marker set related to crown gall disease using the grapevine core collections. First, phenotyping analysis results of 350 varieties showed 10.6% resistance, 73% moderate susceptibility and 16.4% highly susceptibility. Second, about 70,000 SNP data were obtained by carrying out GBS analysis using 350 varieties of grapevines. Finally, GWAS results data revealed that the two candidate genes which were related to the crown gall disease. To confirm these two candidate genes, High-Resolution Melting Analysis (HRMA) was performed using Luna probe to distinguish the heterozygote and homozygote. Our data provide that these SNP markers are expected to be helpful for evaluation of resistance against grapevine crown gall disease and breeding.

Key Words: Genotyping-By-Sequencing, Genome-Wide Association Study, Crown gall, Agrobacterium vitis, Grapevine, Marker, Marker-Assisted Selection

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Construction of High Density Linkage Map and QTL Analysis of Plant Height and Height of First Capsule in Sesame

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Sesame (Sesamum indicum L.) has long been cultivated and used as one of the most important vegetable oil sources. It has been known that some of the agronomic components such as plant height (PH) and height of first capsule from the soil surface (HFC) were positively related with seed yield in sesame. In this study, a total of 90 F₃₅ recombinant inbred lines (RIL) derived from a cross of Goenbaek × Osan were genotyped by using genotyping-by-sequencing (GBS) technology. A high-density genetic map was constructed with 1761 SNPs, covering 2205.9 cM of the whole sesame genome. The parental cultivars and RILs were grown and measured for PH and HFC in two different locations, Miryang and Andong in 2018. In total, eight QTL for PH on chromosomes 11 and 12 and ten QTL for HFC on chromosomes 1 and 11 were detected. The identified QTL explained phenotypic variation in the range of 10-23% for both PH and HFC. The QTL were detected in one or two locations, indicating genotype and environmental interactions for phenotypic variation for PH and HFC. In combined data of two locations for HFC and PH, two QTL with two different regions were overlapped on chromosome 11. These overlapped QTL may suggest that there could be putative genomic regions for further genetic manipulation of yield-related traits such PH and HFC.

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QTL Analysis of Phytophthora blight Disease Resistance in Sesame by Linkage and Association Mapping

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Phytophthora blight disease (Phytophthora nicotianae) is the most serious threat to sesame. The objective of this study was to identify QTL and markers for resistance to phytophthora blight. The strain ‘KACC.40121’ provided by the NICS, was used for inoculation. The sesame accessions and lines with five replications were inoculated when the unifoliolate leaves began to unfold stage in a shade house. Disease resistance was scored as binary trait: seedlings with either resistant or susceptible. In the case of genome-wide association (GWA) analysis of accessions, plants were rated for disease resistance on a 1-9 scale basis after inoculation. We found that 37 loci significantly associated with phytophthora disease resistance on chromosome 10 in the GWA analysis. A few number of the SNPs associated with resistance in GWA analysis might be closely linked to or are in high LD with the resistance QTL. Genetic mapping of phytophthora disease resistance was performed using 90 F₃₅ recombinant inbred lines (RIL) from a cross between a resistant cultivar ‘Goenbaek’ and a susceptible cultivar ‘Osan’ with a genetic map consisting of 1762 SNP markers. QTL analysis employed composite interval mapping (CIM) in WinQTL Cartographer identified seven QTL (LOD >2.0) on chromosomes 7, 9, 10, and 11. The phenotypic variance (PVE) of QTL was in the range 8.2-17.5%. On the other hand, the analysis of GWA allowed us to genotype additional five simple sequence repeat (SSR) markers which were associated with disease resistance in the common region on chromosome 10. Based on SSR markers, three major QTLs (qPh-10_1, qPh-10_2, qPh-10_3) were detected with high LOD score (LOD >10.0) and PVE range of 33, 41, and 79%, respectively.

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A promising multifunctional crop *Miscanthus* and its breeding strategies

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*Miscanthus* is a perennial grass which inhabits in a wide range of climates around the world. It has been considered as an invasive weed which cannot be easily managed due to its rhizomatous trait and strong adaptability to various climates. Nowadays, it is also being considered as a new biomass and horticultural crop due to its high biomass production potential with low resource consumption and its unique appearance in gardening. However, breeding new *Miscanthus* cultivar is regarded as a challenging project due to its heterozygosity, self- incompatibility and long period of time for full development. Such traits led to only few cultivars of *Miscanthus* being commercially utilized. Thus, we adopted new breeding strategies for *Miscanthus* including genome-wide association studies, polyploidy breeding, and mutation breeding to overcome obstacles and make new commercial cultivars. GWAS was adopted to search for genetic markers related to favorable traits, which is an effective tool to find new markers for *Miscanthus* which lacks already-known trait markers. Polyploidy breeding will enable crossbreeding between *Miscanthus* species with different ploidy levels, leading to a totally new cultivar which is naturally unable to appear. Mutation breeding will lead to generation of cultivars with new traits which may be useful in breeding commercial cultivars or finding new markers. By conducting multiple breeding approaches, we hope to overcome obstacles, establish a whole new breeding strategy, and generate various cultivars with multifunctional traits. This work has been carried out with the support of "Next-Generation BioGreen21 Program for Agriculture & Technology Development (Project No. PJ01324501)", Rural Development Administration, Republic of Korea.

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QTL mapping for grain size with Korean *japonica* rice varieties


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Grain size is one of important agronomical traits closely related to yield in cultivated rice (*Oryza sativa* L.). In order to obtain genetic information governing grain size for rice breeding of Korean *japonica* varieties, grain traits (length, width, area, and weight) of 160 recombinant inbred lines (RILs) derived from cross between two *japonica* rice varieties, Odae and Unbong40, were investigated for correlation and quantitative trait loci (QTL) analyses. Also, to construct a genetic map, 160 RIL plants were genotyped by kompetitive allele-specific PCR (KASP) markers which have major advantage of improved cost-effectiveness. In results, positive correlations were shown between all grain traits. Correlation coefficient between grain length and weight was higher than that between grain width and weight, and correlation between grain length and area was higher than that between grain width and area. Furthermore, a genetic map was successfully constructed using more than 150 KASP markers which showing polymorphisms between parental varieties. Subsequently, when QTL mapping was performed with phenotypic data and genetic map, a major QTL of almost same region on chromosome 3 was detected from grain length, area, and weight but was not detected from grain width. Thus, our results suggesting that grain size and weight would be determined by grain length than grain width and would be controlled by a major QTL on chromosome 3. Our knowledge on grain size will be helpful for studying molecular mechanisms of grain size regulators and breeding program for yield improvement in Korean *japonica* rice varieties.

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Genetic analysis of morphological and agronomic traits using progeny between *japonica* rice

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Plant height and grain shape are important for high-yield rice. Josaengiado has small and round grains with short plant height. Daeribbyeo 1 has large grains and is widely used as a genetic material for grain size. To identify the QTL associated with grain size and plant height, 120 F$_2$ plants derived from a cross between two *japonica* cultivars “Josaengiado” and “Daeribbyeo 1”, were measured for 11 traits including plant height. A genetic map was generated using 89 KASP (Kompetitive Allele Specific PCR) markers for the selected 120 F2 plants. One major QTL was detected in a region between KASP markers KJ05009 and KJ05041 on chromosome 5 and this QTL appears to be allelic to *D1*, a gene controlling plant height and grain size. Another QTL was detected in a region between KASP markers KJ02005 and KJ02029 on chromosome 2. Genetic analysis of apiculus and sterile lemma colors is underway. Gene sequencing will be conducted to clarify the allelism of the *D1* and the QTL plant height on chromosome 5.

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Identification of Quantitative Trait Locus (QTL) for spikelets per panicle using near isogenic lines derived from an interspecific cross between *Oryza sativa* and *O. minuta*

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In rice (*Oryza sativa* L.), grain yield is determined by three yield components: panicles per plant, spikelets per panicle and grain weight. Among them spikelets per panicle (SPP) shows the wide variation and makes the large contribution to yield output. Therefore, the identification of the SPP-related genes will play a vital role in high-yield rice breeding. In our previous study, one putative QTL affecting the number of spikelets per panicle (*qSPP7*) was identified on the long arm of rice chromosome 7 using near-isogenic lines (NIL-SPP7) derived from an interspecific cross between the *Korean japonica* ‘Hwaseongbyeo’ (HS) and *O. minuta*. In the current study, we confirmed this QTL using 540 BC$_1$F$_2$ plants for genotyping and 13 recombinant BC$_1$F$_2$ lines for traits evaluation. The *qSPP7* was mapped between two simple sequence repeat (SSR) markers RM4952 and RM21605. The *O. minuta* segment on chromosome 7 introgressed into the HS background was associated with an increase in the number of spikelets per panicle. The panicle structure of NIL-SPP7 further revealed that, not only the number of spikelets per panicle increased significantly, but also the primary branches per panicle and the secondary branches per panicle increased significantly as compared to HS. Although NIL-SPP7 has reduction in 1000-grain weight and number of panicles per plant, but grain yield per plant was significantly higher than that of HS. Additional experiment under short-day length condition indicated that NIL-SPP7 was photoperiod-sensitive and *qSPP7* was not associated with the heading date. To find out candidate genes associated with the difference in heading date between NIL-SPP7 and HS, KASP (Kompetitive allele specific PCR) assays were carried out. As the result, *qEhd1* on chromosome 10 appears to be involved in the difference in heading date of NIL-SPP7 or HS and this was confirmed using 62 BC$_1$F$_2$ plants.

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Genome-wide association study of drought tolerance in maize

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Globally rainfed agriculture is practiced in 80% of agricultural area and generates 62% of the world’s staple food. However, the impact of climate change is affecting the magnitude of rainfall and its distribution which in turn has adverse effects on crop production. In present situation agricultural scientist face dual challenge of breeding adoptable and climate resilient varieties at a fast pace. Thus it is imperative that the scientific community use all the avenues available to improve the drought tolerance in crops. In the present study we intend to dissect genetic factors contributing to drought tolerance in maize (Zea mays spp. mays) based on Genome wide association studies (GWAS). Maize is among the most predominant food sources and prone to drought stress affecting the overall productivity. Our objective is to 1) Identify maize genotype tolerant to drought stress 2) To identify genetic regions contributing drought tolerance based on 55K SNP chip. We evaluated 150 maize inbred lines in a randomized complete block design with five replication each and drought stress was imposed in a green house. The germinate, survival and recovery rate were measured and we observed a significant difference between genotypes under stress environment. We shortlisted 15 maize inbred accessions categorized based on a) drought tolerant b) moderatley tolerant c) Drought susceptible. Our further step is to perform a GWAS scan on the shortlisted inbred lines. This will enable us to identify marker trait association with candidate genes related to traits under drought conditions. Functional annotations of these putative candidate genes will give a valuable insights for maize breeding under drought conditions.

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Mapping Quantitative Trait Loci related to salinity tolerance at the seedling stage in rice

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Vietnam is one of the most vulnerable countries to climate change in Asia. Rice is a principle food in Vietnam and plays an important role in the economic activity of this country. However, rice yield and its cultivating areas are adversely affected by the threats of devastation of a rise in sea level. Molecular marker provides powerful tools for the development of stress-tolerant varieties that can cope with these devastating changes. Eighty-six F₂ plants and 86 F₂:F₃ families derived from a cross between salt tolerance “VN193” and salt sensitive “Huong Viet” were used in this study. Salt tolerance was evaluated at the seedling stage at concentrations of 0.7% and 0.9% NaCl. A total of 423 SSR markers were screened for polymorphism between VN193 and Huong Viet. Among them, 147 markers produced polymorphic bands between two parents and were used to mapping the F₂ population. Analysis of quantitative trait loci (QTLs) related to seedling stage salinity tolerance was conducted and three QTLs, qST1, qST6, and qST11 conferring salt tolerance at the seedling stage were mapped on chromosomes 1, 6, and 11, respectively. They explained 10.5%, 11.2%, and 11.7% of the total phenotypic variation, respectively. The favorable alleles of qST1, qST6, and qST11 were contributed by the salt tolerant “VN193”. The results obtained in 0.7% and 0.9% NaCl were similar for 2 years indicating that the QTLs would be useful in selecting salt tolerance in the breeding program.

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QTL mapping for rice grain quality-related traits, nutritional value traits, and heading date using recombinant inbred lines derived from a cross between japonica cultivars

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Research on grain quality and nutritional value has enormously one of the targets in rice breeding programs. By strategically exploiting the different molecular approaches and advanced genomic technologies such as Kompetitive Allele-Specific PCR (KASP) approach and Genotyping-By-Sequencing (GBS) technology, the identification of useful or novel genes present in a specific rice cultivar is becoming more straightforward. However, application of genomic technologies like GBS on closely-related rice species like japonica/japonica population background is poorly reported. In this study, 92 F6 recombinant inbred lines (RILs) derived from a cross between two japonica cultivars, Dodam (high in resistant starch (RS)) and Hwayeong (a non-waxy cultivar), were generated and evaluated to construct QTL map for some agronomic traits. A total of 1,848 single-nucleotide polymorphisms (SNPs) were identified using GBS technology and only 215 of these SNPs were used to construct a physical map. However, big gaps were observed in genomic regions of the F6 RILs resulting to non-detection of SNPs in some specific regions. Thus, a total of 41 KASP markers were used to analyze the gaps. Thereafter, single marker analysis identified seven, five, ten, three, five, five, and seven QTLs for RS content, amylose content (AC), iron (Fe) content, zinc (Zn) content, manganese (Mn) content, calcium (Ca) content, and heading date, respectively from the combined GBS and KASP results.

Keywords: Genotyping-By-Sequencing, Kompetitive Allele-Specific PCR, Single-Nucleotide Polymorphism

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Development of successful technology transfer system based on the systematic assessment of large R&D outcomes of PMBC

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As R&D results of PMBC (Plant Molecular Breeding Center), 830 SCI / non-SCI papers, 432 patents, 91 new plant varieties were generated for last 8 years. In this study, we carried out comprehensive analysis of large PMBC R&D outcomes, and sorted out the excellent patents with IP rights, as well as new plant varieties with improved agronomic traits. Total of 202 patents registered at KIPO (Korean Intellectual Property Office) were first evaluated using the SMART3 (System to measure, analyze and rate patent technology) patent rating algorithm, and sixty registered patents rated above BBB levels were selected. Selected patents were later classified into 6 groups according to the tech tree and market needs. Market needs and competitors were investigated by surveying on the worldwide technology development and patent trends in plant molecular breeding field in respond to climate changes. The results were published as a report and provided as an article in PMBC newsletter. In 2018, the patents for molecular markers to enhance breeding efficiency for citrus, radish and pepper, as well as new rice and chili varieties with high crop yields or disease resistance were then repackage to strengthen the IP portfolio. For technology marketing, we designed 8 sales and marketing kits (SMKs), composed of 7 patents, 2 know-how technologies, a new rice variety. These SMKs were distributed to the seed companies by e-mails as well as on site during technical briefings for marketing purposes. In addition, strategic IP management and future R&D directions for each researcher have been suggested individually during official IP R&D sessions. The synergistic networks between the researchers of PMBC and technology demand institutes/companies were established, as well. As a result, two cases of successful technology transfers were followed in 2019, and more are expected in future.

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A study to develop a systematic IP R&D support system to promote technology transfers of SSAC R&D outcomes

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Since 2011, SSAC (Systems & Synthetic Agrobiotech Center) have funded the research projects on developing applied technology and system biology based on agricultural organisms. Advanced synthetic biology as well as metabolism engineering approaches resulted in large scale R&D outcomes (1360 SCI / non-SCI papers and 712 patents) and showed several cases of successful technology transfers. In order to increase the cases of technology transfer, in this study, we developed a systematic IP R&D support system, and have provided assistance for the SSAC researchers who are in need of in-depth consults for IP management and technical transfer process. Comprehensive analysis of the R&D outcomes of SSAC revealed that 453 patents were registered at KIPO (Korean Intellectual Property Office), and 26 patents were registered internationally. However, only 277 patents (38.9% of ATIS uploaded patents) remained live at KIPO, due to changes in legal status. We employed an online patent evaluation system called SMART3 (System to measure, analyze and rate patent technology) to sort out the patents with excellent intellectual rights. As a result, 110 patents rated above BBB levels were first selected, and classified according to technology trees based on their technology. Thirty four patents (31%) out of 110 were identified as the technology of mass production of functional substances for cosmetics, food, medicines. We packaged the related patents to build up strong IP portfolios, and 6 Sales Material Kits (SMKs) were created to introduce technologies to various green-, red-, white-bioscience companies. In addition, surveys on patents in mass production technology of highly profitable functional substances using agricultural systems were performed, and the survey results were published as a report. Patent managements and future R&D directions for individual researcher were also provided during IP-R&D consulting sessions.

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'AR Tanjeobaksa', commercial F1 variety resistant to anthracnose in chili pepper

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Pepper anthracnose caused by Colletotrichum spp. is one of the most destructive diseases in many Asian countries. In order to reduce the damage of the disease, we have developed and released the commercial F1 variety, 'AR Tanjeobaksa', resistant to anthracnose in Korea. From the genetic resource to commercial variety, we carried out 4 related research steps as follows; 1) searching for genetic resources, 2) interspecific hybridization between Capsicum annuum and C. baccatum, 3) developing molecular markers and 4) using male sterility system for F1 seed production. As the genetic resources resistant to anthracnose, PBC80 and PBC81 belonging to C. baccatum were selected. There was double genetic barriers such as embry abortion and hybrid sterility in interspecific cross between C. annuum and C. baccatum. To overcome the genetic barriers, partial compatible C. annuum line and embryo rescue techniques were used. The hybrid sterility was overcome through intensive backcrosses with their maternal line used as pollen parent. From the segregating populations including BC1F1 and BC1F2 generations, molecular markers associated with anthracnose resistance were successfully developed by using QTL mapping and reference genomic information of C. annuum. The maternal line, '8047', resistant to CMV and having good traits was bred from Korean commercial variety. The paternal line, '92-13-3', resistant to anthracnose and Phytophthora root rot was developed by using consecutive backcrosses between resistant plants selected from the interspecific BC1F2 progenies. The 'AR Tanjeobaksa', having excellent horticultural traits and strong resistance to several serious diseases in Korea was finally developed and commercially released to famer's field in 2017. Now a days, the varietal performance of 'AR Tanjeobaksa' and their relative varieties are satisfied to be one of the great F1 varieties and their seed market share will be getting increase every year.

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Effect of soybean moisture contents according to the artificial drying

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Soybean is majorly used as the raw material of tofu, soy sauce, soymilk, and moeju (fermented soybean lump), and sprout soybean after harvest in South Korea. Due to the recent climate change such as rain during the harvest period and the large amount of cultivation using the combine in the paddy field, the importance of artificial drying in soybean is more increasing than the past. However, the matter in application of artificial drying to soybean high temperature is change in the surface quality because surface quality affects quality of the processed goods.

Experiment material is two cultivars such as Daewonkong which is used for tofu and fermented products and has large seed size, 25.0 grams per 100 seed and Haepum which is used for sprout soybean and has large seed size, 11.0 grams per 100 seed. The tested moisture contents of soybean seeds are from 19.0 percentage to 14.0. The tested drying temperatures of soybean seeds are from 45.0 degree celsius to 30.0 with circulating soybean during the drying plus hot air. The surface quality experimented surveyed the ratio of crack and rupture in soybean seed coat.

During the drying process, soybean damage is occurred crack in drying (A), mechanical damage by rotary during the circulating (B), A plus B. The higher moisture contents and the higher drying temperature are the higher crack in soybean. There are different drying patterns between Daewonkong and Haepum. Haepum had the rapid drying speed and smaller ratio of crack compared with Daewonkong.

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조, 기장 기계정식을 위한 모판흙 산발 및 육묘 영향 분석

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경남 밀양시 경밀대로 20, 50424, 국립식량과학원 남부작물부 생산기술개발과

본 연구는 잡곡 조(Foxtail millet, Setaria italica)와 기장(Panicum miliaceum L.) 작물개체에서 조, 기장과 같은 소립 잡곡 콩종은 쌓이 매우 작아 정밀파종이 어렵고 발아율이 낮을 뿐만 아니라 접착성으로 생육이 부진하여 재파종하는 일이 자주 발생하는 것을 개선하기 위해 기계정식에 적합한 접착⋅산파의 모판흙을 선발하고 육묘의 생육특성을 조사하였다.

시험재료는 조 '삼당قتل', 기장 '이백قتل' 품종으로 트레이 접착은 120℃, 200℃을 사용하였고, 산파는 비 육묘상자를 이용하였다. 모판흙은 모판흙협회에 가시된 16개가 170℃에 대해 용도별, 종류별로 생육특성을 검토하고, 수도율 및 육묘율로 구분하여 평균 생육율에 해당하는 11곳을 선발하여 사용하였다. 모판흙 선발을 보면 수도율은 황도 15-44%, 질식 25-41%로 큰 비중을 차지하였고, 원육율은 코코포트 63-72%, 팔라이트 6-12%로 특이하게 포함되어 있다. 2017년부터 4월 하순에서 6월 하순까지 6차례 트레이에 접착한 후 생육특성이 우수한 육묘별 4개 모판흙을 선발하였고, 2018년 5월 상순에서 8월 하순까지 선발된 수도율(S1, S2), 원육율(W1, W2) 4개품 모판흙은 대형적으로 트레이 접착과 육묘상자 산파에 대한 생육특성을 분석하였다. 조 또는 기장 잡곡은 조가 15cm 이상 생육이 되어야 기계정식에 적합하기 때문에 트레이접착, 모판흙접착, 산파육묘의 생육특성을 분석하였다. 2017-2018년 시험에서 모판흙 11개품에 대한 접착 육묘의 생육은 트레이접착 > 접착곡 > 모판흙 순서였다. 결론적으로 조와 기장 접착⋅산파육묘에서 조가 산파육묘에 적합한 접착(40%~41%), 코코포트(12%~31%), 황도(15%~20%), 피트모스(6%~8%)으로 구성된 수도율제어가 적절하였다. 적절 육묘율선발은 산파 120℃공 트레이에서는 15일, 220℃공 20일 정도의 육묘가 적합하였고, 산파육묘에서는 15일 정도가 적합하였다. 앞으로 산파육묘의 기계정식 적합성을 평가하기 위한 적절 접착량, 접착접착, 접착법등 연구를 계속 추진하고자 한다.

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Comparative phenotypic and metabolic analysis of *Carthamus* species

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Safflower belongs to the family of *Asteraceae* and it is known as Oriental traditional medicine. It holds abundant crucial active compounds hence it is the lucrative subject to the researchers. Until now, the single compounds and its application have been isolated and studied from *Carthamus lanatus* (*C. lanatus*) species. In addition, a numerous *Carthamus* species have been commercialized to get oil extraction for commercial market in all over the world. In this study we dealt with comparative analysis of plant phenotypic characteristics and important metabolites identification among five different species of *Carthamus* spp (*C. tinctiorius, C. lanatus, C. palaestinus, C. tenus, C. turkestanicus*). We conducted phenotypic analysis based on several analytical criteria like seed germination, leaf shape, plant height, color of flower and seed weight. Most of safflower seeds showed conical or oval shape. All species except *C. tinctiorius* have rosette formation. Considering the phenotypic analysis criteria, the results showed that *C. palaestinus* is suitable for cultivation among relatives. Each flower sample was analyzed using ultra performance liquid chromatography mass spectrophotometry. We detected 29 metabolites with negative mode, and 22 metabolites with positive mode from flower extract using LC-MS. Metabolomic data are related in KEGG pathways like flavonoid synthesis (Luteolin 7-O-β-D-glucoside, Safflomin A, saflor yellow A, Anhydrorflor yellow B, Apigenin, Chrysins, Epigallocatechin, Fisetin), phenylpropanoid synthesis (Caffeic acid, Esculetin, Ferulic acid), flavone and flavonol synthesis (Astragalin, Kaempferol, Quinic acid) and nicotirine and nicotineamide metabolism (Trigonelline). Furthermore, the identified flower metabolites were subjected to principal component analysis (PCA) and it existed three combination groups, within the species. This study ascribes to identify the potential and valuable biomarkers among the *Carthamus* spp. Also, this result might be helpful for future studies to breeding safflower resources containing more useful metabolom.

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Diversity of flower characters of Jerusalem artichoke germplasm in Thailand

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Flowers of Jerusalem artichoke (*Helianthus tuberosus* L.) are beautiful, bright and yellow, have various forms of morphologies and bloom continuously for 1-2 months. The crop is used mainly as a functional food crop because of its high inulin containing tubers and it also has aesthetic value for use as a pot plant or an ornamental plant. The objective of the present study was to evaluate the variations in floral traits among Jerusalem artichoke accessions. Seventy-three accessions were evaluated in a randomized complete block design with two replications for three seasons in the late rainy season 2008, the early rainy season 2009 and the late rainy season 2009 at Khon Kaen University agronomy farm, Thailand. The data were recorded for days to flowering, number of flowers per plant, flower size (diameter), number of petals per flower, flower color and petal character. Differences in the seasons were significant for days to flowering, number of flowers per plant and flower size (P≤0.01). High variations were found among Jerusalem artichoke accessions for days to flowering, number of flowers per plant, flower size and number of petals per flower (P≤0.01). Days to flowering varied from 47 to 71 days after planting. Number of flowers per plant ranged from 5 to 30 flowers. Flower diameters varied from 6.4 to 8.9 centimeters. Number of petals per flower varied from 7 to 12 petals. Jerusalem artichoke accessions were classified by the color of petal (yellow to yellow-orange) and petal character (elongated, ovoid-elongated and ovoid). The correlation coefficient between days to flowering and the number of flowers was negative and significant (r=0.43, P≤0.01). The information is useful for horticulturists to select the best genotypes for use as an ornamental plant and plant breeders to select suitable parents in breeding programs.

Keywords: aesthetic value, morphology, ornamental plant, variation

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Amaranthus cruentus with a low-amylose synthesis phenotype lacks amylose in starch granules in the perisperm

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This study aimed to understanding the genetic mechanism underlying low-amylose synthesis in the amaranth perisperm. Chain-length distribution profiles measured by high-performance size-exclusion chromatography showed that the amylepectin structures of waxy, low-amylose, and non-waxy phenotypes differed significantly from each other. Only the non-waxy phenotype had detectable amylose levels. In contrast, the content of high molecular weight amylepectin was higher in the low-amylose phenotype than other phenotypes. Thus, the low-amylose phenotypes (including the waxy phenotype) contained no amylose. This could be attributed to changes in starch phenotypes caused by variations in chain-length distribution in amylepectin. This hypothesis is supported by data from sodium dodecyl sulfate-polyacrylamide gel electrophoresis and DNA sequencing. Electrophoresis revealed that non-waxy phenotypes had approximately 67 kDa of protein, while no protein band was visible for waxy and low-amylose phenotypes. Moreover, the coding sequences of low-amylose and waxy phenotypes were identical, and contained a nonsense mutation. The absolute low-amylose content is considered to reflect a decrease in the amount of granule-bound starch synthase I (GBSSI) protein. These results suggest that an unknown genetic modification has altered the starch (amylepectin) structure of the low-amylose phenotype of amaranth. We conclude that GBSSI mRNA is not synthesized in the amaranth perisperm of the low-amylose phenotype. Additionally, the low-amylose content of A. cruentus is probably not absolute amylose but apparent amylose.

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Waxy strains of three amaranth grains raised by different mutations in the coding region

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The waxy strains raised from waxy mutation have been found in three amaranth grains. Three genes encoding waxy protein isolated from Amaranthus caudatus (Wx-ca), A. cruentus (Wx-cr), and A. hypochondriacus (Wx-hy). Sequence analysis indicated that the Wx-ca, Wx-cr, and Wx-hy genes contained the same exon (13 exons) and intron (12 introns) structure. The lengths of the Wx-ca, Wx-cr, and Wx-hy genes were 3236 bp, 3237 bp and 3225 bp, respectively. The alignment of the coding sequence of the three Waxy genes showed 12 polymorphic sites including 11 SNPs (in exons 10 and 12, in introns 1, 3, 4, 9, and 11) and 5 indels (in introns 4, 9 and 11). In particular, major polymorphism was detected in 8 bp and 3 bp indels in intron 4. Moreover, the mutation in the waxy alleles (wax-ca, wax-cr, and wax-hy) of all three species was also isolated and characterized. Comparison of coding sequences of the three Waxy genes and their waxy alleles indicated one base insertion (wax-ca: insert of T base in exon 8) and a base substitution (wax-cr: a G to T base substitution in exon 10, wax-hy: a G to A base substitution in exon 6), which occurred as internal termination codon in three Waxy genes, suggesting the involvement of a nonsense or frame shift mutation. Therefore, these different mutations in coding regions were considered to be the cause of the waxy (amylose-free) phenotype.

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Cryopreservation of vegetatively propagated crop germplasm: achievements and challenges

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Though recent advances in developing cryopreservation techniques open the routine application of cryobanking for important agricultural crops, the selection and development of plant cryopreservation have been based upon the application of the technique available and screening of the conditions and thus the process often relies on trial and error. Among the vitrification-based cryopreservation techniques, droplet-vitrification, a combination of droplet-freezing and vitrification, produces high post-cryopreservation recovery. However, the protocol cannot universally solve all challenges in plant cryopreservation. Specifically, not all materials have the same tolerance to desiccation and cytotoxicity to the most widely used cryoprotectant solutions. This presentation briefly introduces diverse options of cryopreservation procedures and current status of cryobanking worldwide. It also suggests alternative approaches to the development of cryopreservation protocols based on the initial characteristics of plant materials, by introducing specific steps in a vitrification-based method. The osmotic tolerance of samples can be classified based on their response to overnight preculture at sucrose concentration of 10%, 17.5% or 25%. Based upon the cytotoxicity and size of the samples, some alternative vitrification solutions to the popular plant vitrification solutions 2 and 3 can be considered. Using this systematic approach we can identify whether the material is tolerant or sensitive to the osmotic stress and chemical toxicity of cryoprotection with vitrification solutions. And we can design a droplet-vitrification procedure, i.e. preculture, osmoprotection, cryoprotection, cooling and rewarming, and regrowth. This approach will facilitate the development of cryopreservation protocols and large-scale implementation of clonal germplasm.

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Cryopreservation of Dysophylla yatabeana Makino, an endangered wild species, using a droplet-vitrification procedure

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Dysophylla yatabeana Makino is an endangered species of ornamental value in urgent need of a comprehensive conservation strategy. Thus this study aims to develop droplet-vitrification protocol using in vitro shoot tips to complement traditional conservation approaches in case when seeds are not available or their amount is not sufficient for conservation programs. The standard procedure includes preculture with 10% sucrose for 31, followed by osmoprotection with C4-35% (17.5% glycerol + 17.5% sucrose) for 40 min, and cryoprotection with A3-80% (30% glycerol + 15% ethylene glycol + 15% dimethyl sulfoxide + 0.4M sucrose) on ice for 60 min, cooling in liquid nitrogen using aluminum foil strips, with a survival rate of 81.9% after cryopreservation. But for the regeneration, cryopreserved shoots need to be sequentially recultured with ammonium free medium, normal MS medium (GA3 0.5 + BA 0.2 mg/l), and MS free medium. Using a droplet-vitrification method we optimize the preculture, osmoprotection, vitrification solution (VS) and duration, cooling, and regrowth media and conditions as a model species of endangered wild species in Korea.

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Genetic Diversity of Pisifera Elite Parent Using SSR Markers in DXP Sriwijaya Population

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Molecular markers can be used as specific tags of certain genes and even as markers of some individuals. The individual specific markers or variations can be SNPs or microsatellites such as SSRs. A number of molecular tools are now widely used to form diversity profiles can be used for plant genetic identification. The function is to identify genetic diversity within the population, distinguish between accession, cultivar and also species that may be difficult to characterize due to similar morphology. The purpose of this research is a preliminary stage of DNA fingerprinting to analyze genetic variation and identify specific Sriwijaya DXP varieties which later, can be used to prevent counterfeiting of Sriwijaya DXP seeds in the field. A total of 16 progenies from 6 origins of Pisifera elite parent were analyzed using 19 molecular markers (SSR). Overall, 108 alleles were detected by markers analysis varying from three to eight alleles. There are 34 unique alleles identified in the parents as a diagnostic tool. From varieties SJ1 to SJ6, the % P value obtained only on the SJ6 Pisifera elders shows 100% while the others ranged between 63-95%. The polymorphism information content (PIC) ranged between 0.389-0.844. This shows a high level of diversity. The pairwise FST analysis indicated significant differentiation (0.372). This result also corresponds with principal coordinate analysis (PCo) that the SSR markers used in this analysis can group Sriwijaya Pisifera parents separately. Finding from this study suggest that the fingerprint can be developed using SSR marker to identify specific varieties of DXP Sriwijaya.

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Molecular Characterization of 170 New gDNA–SSR Markers for Genetic Diversity in Button Mushroom (Agaricus bisporus)

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We designed 170 new simple sequence repeat (SSR) markers based on the whole-genome sequence data of button mushroom (Agaricus bisporus), and selected 121 polymorphic markers. A total of 121 polymorphic markers, the average major allele frequency (MAF) and the average number of alleles (Na) were 0.483 and 5.7, respectively. The average number of genotypes (Nc), observed heterozygosity (Ho), expected heterozygosity (He), and polymorphic information content (PIC) were 6.6, 0.267, 0.638, and 0.589, respectively. Pearson’s correlation coefficient showed that MAF was negatively correlated with Nc (-0.683), Na (-0.600), Ho (-0.584), and PIC (-0.941). Nc, Na, He, and PIC were positively correlated with other polymorphic parameters except for MAF. UPGMA clustering showed that 26 A. bisporus accessions were classified into 3 groups, and each accession was differentiated. The 121 SSR markers should facilitate the use of molecular markers in button mushroom breeding and genetic studies.

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Molecular Chracterization of New gDNA SSR Markers for Glycyrrhiza lepidota and Cross–Amplification of other Glycyrrhiza Species

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LICORICE (Glycyrrhiza L.) is used as a natural sweetener and medicinal herb. Molecular studies have been conducted to find differences between wild species and cultivars, as most wild species are highly resistant to abiotic and biotic factors compared with their cultivated counterparts. However, for licorice, only a limited number of molecular markers has been developed for studying the genetic diversity and population structure to find differences between cultivars. In this study, we aimed to develop genomic simple sequence repeat (SSR) markers in licorice for molecular genetic studies. We designed 100 SSR markers based on the whole-genome sequence data of wild G. lepidota and selected 62 SSR markers. The genetic diversity analysis using the markers helped identify 2-23 alleles, and the major allele frequency, observed heterozygosity, genetic diversity, and polymorphism information content were 0.11-0.91, 0.090, 0.17-0.94, and 0.15-0.93, respectively. Interspecies transferability was 93.5%, 91.6%, and 91.1% for G. echinata, G. glabra, and G. uralensis, respectively. Cluster analysis resolved the cultivated (Group 1) and wild species (Group 2) into three and two subgroups, respectively. The SSR markers developed can be applied in studies on genetic diversity of licorice species, population structure analysis, cultivar differentiation, and breeding.

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Genetic Advance and Evaluation Transgressive Segregant on Two Population Bird Pepper (Capsicum frutescens L)

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Genetic advance showed how much increase value is obtained from the selected characters. Genetic advance is influenced by intensity of selection, characters variance and heritability. The research was conducted from September 2016 to April 2017 at Alam Sinarsari Research Station, Dramaga, Bogor at 202 m above sea level. The aim of the study was to obtain candidates for transgressive segregant genotypes in two selected populations of bird pepper. The results showed on the population F3-285290 and F3-321290, the genetic advance value were positive for all characters. Broad sense heritability of F3-285290 population were moderate for weight per fruit and number of fruit per plant. Heritability in F3-321290 population was high for weight per fruit, fruit length and fruit diameter. Transgressive segregant genotypes in the F3-285290 population was found in fruit length. Transgressive segregant verified genotypes for fruit length were F3-285290-205, F3-285290-248 and F3-285290-257. Transgressive segregant genotypes in F3-321290 population was found in weight fruits per plant. Transgressive segregant on weight fruits per plant were verified in F3-321290-33 and F3-321290-293 genotypes.

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Recent Progress on the Ornamental Pepper Breeding in Indonesia

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Pepper or chili (Capsicum annuum L.) is mainly consumed for its fruit. Besides that, many varieties of pepper have been used as ornamental plants such as pot, bedding, and garden plants. However, availability of commercial pepper varieties that are actually declared as ornamental plant is still very limited in Indonesia. The general aim of this program was to develop new varieties of the ornamental pepper. The program was initially started in 2013. Crossings between selected genotypes/collection from IPB University (Bogor Agricultural University) have been made. The pedigree method was used to obtain good candidates based on the uniqueness of fruits and leaf color, shape and size, as well as the whole plant shape, compactness and size. In addition, consumer preference tests have also been performed. Eleven new varieties have been produced from this program, namely Ayesha IPB, Lembayung IPB, Syukin IPB, Namira IPB, Jelita IPB, Triwarsana IPB, Nazla IPB, Viola IPB, Violetp IPB, Adelina IPB dan Batrisiya IPB.

Keywords: chili, new varieties, ornamental plant, pedigree method, selection

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Analysis of Glucoraphanin and Sulforaphane Contents in Germinating Broccoli Sprouts

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The aim of this study is to investigate the amount of glucosinolates (GSLs) in broccoli sprouts (Brassica oleracea L. var. italica) (‘kingdom’) according to different development stages, different plant hormones application and MgSO4.7H2O supplementation. Broccoli sprouts were cultivated in a growth chamber for 15 days. Broccoli sprouts were treated with ABA (Absic acid), MJ (Methyl jasmonate) and SA (Salysalate). In addition, the effects of MgSO4.7H2O supplementation also measured. Amount of two types of GSLs (glucoraphanin and sulforaphane) were measured in broccoli sprouts after harvest. In this conference, the accumulation of glucoraphanin and sulforaphane in broccoli sprouts following developmental stages, hormone application and MgSO4.7H2O supplementation in the growth media. This study will give clues for higher accumulation of glucoraphanin and sulforaphane in broccoli sprouts cultivation.

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Different Types of Mutation in Pepper Inbreeding Lines Result in a Loss of Pungency

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The pungency of pepper (Capsicum annuum L.) is due to the presence of capsaicinoids, which are synthesized through the convergence of the phenylpropanoid and branched-chain fatty acid pathways. The first study of non-pungent trait of pepper fruit reported genetic causes of its loss of pungency are mutations in acyltransferase (Pan1). To date, several different types of mutations in the genes encoding capsaicinoids biosynthesis involved enzymes, such as putative aminotransferase (pAMT), ketocycl-ACP reductase (CaKR1) and etc. Furthermore, several reports present that these genes involved in capsaicinoids biosynthetic pathway could be regulated signaling cascade of WRKY and MYB transcription factors. In this study, several different types of mutation in pepper inbreeding lines result in a loss of pungency would be presented.

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Phytochemical and Yield–Related Traits of Winged Bean and Another Substitutive Crops

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Winged beans (Psophocarpus tetragonolobus L.) are vegetable plants that can substitute most local food in Indonesia, because it has very high protein content, low-fat and also become an alternative source of vitamin C and calcium. Supporting technologies to improve vegetable production and quality need to be developed through integrated and sustainable research. One of the supporting technologies is superior varieties. The general objective of this study is to produce high-productivity winged beans varieties with high protein content by utilizing local genetic resources. Furthermore, germ plasm is characterized by important characters. From the information of traits obtained, crossbreeding is made between germplasm in order to obtain new lines that have a relatively complete superior character. Selection was begun from the second generation to the sixth generation. The results showed that the protein content of some lines in the sixth generation similar to soybean (p <0.01), higher than cowpea and snap bean. The highest fat content belongs to soybean, cowpea and snap bean. In general, the results reported explaining the phytochemical and yield-related traits determine potential targets for developing plant ideotypes to direct this breeding program.

Keywords: fat content, ideotypes, protein content, selection, winged bean

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Overexpression of a novel RING-type E3 ubiquitin ligase gene induces formation of coiled branches in Arabidopsis

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To investigate the molecular mechanism of stem coiling, a screening was carried out from Arabidopsis activation tagging lines obtained by activation T-DNA treatment. A mutant with a wavy and curly morphology, and coiling branches, named cbr, was identified. Plasmid rescue and genomic southern blot analysis revealed the site of T-DNA insertion in the genome. RT-PCR was performed to monitor expression levels of the genes adjacent to the T-DNA integration site and showed the activation of an E3 ubiquitin ligase gene. Database search revealed that the protein with the C3HC4 type RING domain belongs to a family of E3 ubiquitin ligases. Complementation test by overexpression and RNA interference of the gene showed that activation of the novel gene caused the cbr mutant phenotypes. Ubiquitination affects every cellular process including plant development. E3 ubiquitin ligase has been reported to recognize target proteins that are needing to be ubiquitinated for further degradation by the proteasome complex. We have obtained eight candidate substrates for E3 ubiquitin ligase by performing a yeast two-hybrid screening. Currently we are performing correlation analysis between the selected substrates and CBR protein.

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Profiling of agronomic characteristics and phytochemical compounds in sweet sorghum (Sorghum bicolor L. Moench) germplasms

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Sweet sorghum (Sorghum bicolor L. Moench) is one of the most multifunctional crop, which is utilized as source of biofuel, functional foods, and forage. In this study, we assessed 153 sweet sorghum based on 8 agronomic characters and phytochemicals to selected elite lines. Seven of eight agronomic characters displayed a normal distribution except for the number of tiller. Plant heights and panicle length ranged from 70 (SS.2) to 430 (SS.99) cm and 7 (SS.181) to 55.8 (SS.16) cm, with an average of 262.48 and 26.66 cm, respectively. Stalks diameter and leaf number ranged from 11.6 (SS.180) to 38.4 (SS.174) mm and 5 (SS.22) to 25 (SS.21) ea, with an average of 24.26 mm and 11.76 ea. Leaf width and length ranged from 4(SS.10) to 14 (SS.68) cm and 38 (SS.224) to 121 (SS.134) cm, with an average of 8.45 cm and 71.53 cm, respectively. Sugar content and Tiller number ranged from 4.5 (SS.97) to 21.6 (SS.226) brix and 1 (SS.2) to 10 (SS.124) ea, with an average of 15.29 brix and 2.48 ea. In addition, we analyzed phytochemicals, including 3-deoxyanthocyanins, flavonoids, and tannins from eight selected sweet sorghums. Among these plants, SS.74 contained the highest luteolinidin content 2-25 fold higher than that of other accessions, SS.113 contained the highest apigeninidin and glycosides of apigeninidin content 5-22 and 7-27 folds higher than that of other accessions, respectively. As a result, SS.113 had 3-9 folds higher total 3-deoxyanthocyanins, while SS.129 does not contain 3-deoxyanthocyanins. Total tannin content ranged from 2.4 (SS.7) to 5.0 mg/g (SS.174) and the total flavonoid content ranged from 1.84 mg/g (Danssus 4ho) to 7.52 mg/g (SS.129), with an average of 4.9 mg/g. This study will be helpful for desirable selection of agronomic traits and phytochemicals for breeding source of sweet sorghum in a temperate climate.

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Genetic variation of Chinese maize inbred lines using morphological character and SSR marker

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We selected 68 Chinese maize inbred lines to understand the genetic diversity, population structure, and marker-trait associations for eight agronomic traits and 50 simple sequence repeats (SSRs) markers. In this study, effective traits, such as days of anthesis (DA), days of silking (DS), ear height (EH), ear height ratio (ER), plant height (PH), and leaf width (LW) were divided into PC1 and PC2 by PCA analysis for maize inbred lines. Genetic diversity analysis revealed a total of 506 alleles at 50 SSR loci. The mean number of alleles per locus was 10.12. The averages of genetic diversity (GD) and polymorphic information content (PIC) values were 0.771 and 0.743, respectively. Based on a membership probability threshold of 0.80, the population structure revealed that the total inbred lines were divided into three major groups with one admixed group. A marker-trait association using Q+K MLM showed that nine SSR markers (bnlg1017, umc2041, umc2400, bnlg105, umc1229, umc1250, umc1066, umc2092, and umc1426) were related with seven agronomic traits. Among these SSR markers, eight SSR markers were associated with only one agronomic trait (DA, DS, ER, LL, LW, PH, and ST), whereas one SSR marker (umc1229) was associated with two agronomic traits (DA and ST). These results will help in optimizing the choice of inbred lines for cross combinations, as well as in selecting markers for further maize breeding programs.

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Genetic diversity analysis based on SSR Markers in Perilla Crop between Korea and China

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In this study, 25 simple sequence repeat (SSR) markers were used to evaluate the genetic diversity and population structure among 90 Perilla accessions from Korea and China. 153 alleles were identified with an average of 6.12 alleles per locus. The average polymorphic information content (PIC) and genetic diversity (GD) values were 0.582 and 0.625, respectively. The level of genetic diversity index for weedy var. frutescens had highest value among different types of Perilla, weedy var. crispa, cultivated var. frutescens and cultivated var. crispa. This study was also compare genetic diversity between Korean and Chinese accessions. As a result, Chinese accessions had higher diversity than Korean accessions. Based on the UPGMA dendrogram, all accessions were classified into four major groups with a genetic similarity of 34.0%. Moreover, on the population structure analysis, 90 Perilla accessions were divided into two main groups and admixed group based on a membership probability threshold of 0.8. However, both of methods were not clearly discriminated in all Perilla accession for different types or their geographical location. Finally, the findings in this study will provide useful theoretical knowledge for further study on the population structure and genetic diversity of Perilla and benefit for Perilla crop breeding and germplasm conservation.

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Morphological variation among accessions of cultivated types of Perilla crop and their weedy types in Korea and China

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In this study, we detected the morphological variation of 83 Perilla accessions from Korea and China by the measurement of 7 quantitative and 8 qualitative characters. Statistical comparisons of means (P<0.05) revealed that between accessions of cultivated var. frutescens and cultivated var. crispa showed significantly different for effective number of branches, number of branches and number of internodes. Most accessions of cultivated var. frutescens from Southern China showed higher plant height than those accessions from Korea and Northern China. And also, these accessions of cultivated var. frutescens from Southern China have almost lately flowering time, while the accessions of cultivated var. frutescens from Korea and Northern China have three types: early-maturity, middle-maturity, and late-maturity. These results indicate that latitude with geographical distribution may be an important factor affecting the flowering time in Perilla species in East Asia. In principal components analysis (PCAs), 4 quantitative traits and 5 qualitative characters contributed in the positive direction on the first axis. The accessions of cultivated var. frutescens were clearly separated from accessions of cultivated and weedy types of var. crispa in the PCAs. While the accessions of cultivated and weedy types of var. crispa were not clearly separated in the PCAs. In addition, most accessions of weedy type of var. frutescens were not clearly separated with the accessions of cultivated and weedy types of var. crispa. In this study, we have provided the information regarding the morphological variation of accessions of two cultivated types of Perilla crop and their weedy types from Korea and China. These findings demonstrated in this study could assist us to further understand the morphological variations and differentiation of Perilla accessions with different geographical distributions in Korea and China.

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Genetic Analysis of Ratooning Ability in Sorghum for Perennial Grain Crop

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Perennial grain crop can reduce soil damage and water usage. Sorghum is a good candidate for perennial grain due to its ability to develop ratoon as a second crop. This study aims to obtain information about the genetic control of sorghum ability to form ratoon. This study evaluate 103 F_{2:3} generation from the cross of var. B69 x var. Numbu. The study was conducted at the experiment field of the Bogor Agricultural University from June 2014 to October 2014 for the main crops and from October 2014-January 2015 for the ratoon plants. The results showed that there was a difference in the ability to develop ratoon between the parental lines, where Numbu had a higher ability to develop ratoon than B69. Of the 103 F_{2:3} genotypes, only 72 genotypes were able to form ratoon, while the rest were unable to form ratoon. There were 14 genotypes with the ability to form ratoon that were higher than var. Numbu with average productivity higher than 50% of the main crop. Segregation analysis showed that the ability to develop ratoon in Indonesian sorghum is controlled by additive genes. Selection for ratooning ability in the segregating population will result in high genetic gain.

Keywords: additive gene action, ratoon, ratoon productivity, segregating population

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Heterosis and Combining Ability of F₁ Hybrid Grain Sorghum in Korea (*Sorghum bicolor* L.)

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A few inbred grain-sorghum varieties were developed and grown in Korea and they all have low productivity. Hybrid cultivars have been demonstrated to be more productive and resistive to unfavorable environmental conditions than pure line varieties. However, no hybrid cultivars are available or never have been planted before in Korea; therefore, information on combining ability of landrace based parental materials is needed for breeding program to increase production. This study was, conducted to determine the combining ability of Korean landrace varieties and cultivars. Two cytoplasmic male-sterile lines (Arg-1, A03017) were crossed with 13 male-fertile lines to generate 26 experimental hybrids. The hybrids were evaluated at two sites in Daegu and Miryang in Korea in 2018. Grain sorghum hybrids were planted with three replicate and standard agronomic practices were followed at both sites. There were significant (P=0.001) variation among genotypes for yield and secondary traits. For each trait, general combining ability (GCA) and specific combining ability (SCA) effects were estimated using the line-tester method. The positive heterosis for grain yield and plant height was observed in hybrid. The A03017 × ‘Sodumchal’ hybrids exhibiting heterosis of up to 154%. The lines 18AYT-S04 and Sodumchal displayed significant and positive GCA effects for grain yield, while Arg-1 × 18OTY-S01 crosses showed positive and greatest SCA effects. These lines were the crosses Arg-1×18OTY-S04, A03017 ×18OTY-S02 and Arg-1 × Miryang14, which combined high mean performance with positive SCA effects, would be recommended for produced and used in grain sorghum breeding program in Korea.

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Profiling of transcriptome from immature seed after flowering in 50 accessions by RNA-seq in soybean (*Glycine max*)

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The purpose of this study is (1) to provide transcriptome information with genome and metabolite information of Korean soybean [*Glycine max* (L.) Merr.] core collection obtained from previous research through transcript analysis in 50 accessions, and (2) to analyze patterns of expression genes through transcript analysis at immature seed of 10 and 30 days after flowering, which is the seed development stage in soybean growth. A total of 50 accessions with genetic diversity were selected based on genome and metabolite analysis results from 430 Korean soybean core collection. Each RNA samples obtained from immature seed of 10 and 30 days after flowering, consisting of three independent biological replicates in 50 accessions. We confirmed 27,576 significant genes with satisfies \( \text{fc} \geq 2 \) and raw. \( p < 0.05 \) conditions in at least one of total comparison pairs. Of the 50 accessions, CRS39 showed the highest 10,413 genes, whereas CRS6 showed the least 18 genes. In gene ontology enrichment analysis, the biological processes associated with the DEGs mainly focused on translation and carbohydrate metabolic process. The molecular function of the DEGs were structural constituent of ribosome and oxidoreductase activity. The cellular components mainly included chloroplast and ribosome. In differentially expressed genes (DEGs) analysis, there were no genes that commonly increased expression more than 2-fold (up-regulated) between 10 and 30 days after flowering in 50 accessions. However, 44 genes showed commonly increased expression more than 2-fold in 49 accessions except CRS6. In addition, only one gene showed commonly decreased expression more than 2-fold (down-regulated) in 50 accessions, whereas 89 genes showed commonly decreased expression more than 2-fold in 49 accession except CRS6. This work could provide important insights into the molecular networks underlying soybean seed development as well as transcript information to be linked to genome and metabolite information in Korean soybean core collection.

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**Analysis of Antioxidant Activity in Safflower (Carthamus tinctorius L.) Germplasm Collected from Middle Eastern Region**

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Safflower (Carthamus tinctorius L.) seed is an important source of bioactive substances with potential pharmacological properties. The aim of this study was to evaluate and analyze antioxidative capacity of 43 safflower accessions collected from five countries. Total polyphenol content (TPC) was determined by Folin-Ciocalteu method and antioxidant activities were estimated by 2,2-diphenyl-1-picryl-hydrazil (DPPH), 2,2'-azino-bis(3-ethylbenzothiazoline-6-sulphonic acid) di-ammonium salt (ABTS), ferric reducing antioxidant power (FRAP) and reducing power (RP) assays. TPC was ranged from 28.25 to 90.53 μg gallic acid equivalent (GAE)/mg dried extract (DE). ABTS, DPPH, FRAP, and RP were ranged from 48.91 to 163.73, 18.76 to 93.98, 3.80 to 132.29 and 26.32 to 80.08 μg ascorbic acid equivalent (ASC)/mg DE, respectively. TPC values showed a significant correlation with ABTS and DPPH (r= 0.821, 0.903, respectively), and FRAP and RP were not significantly correlated with TPC, ABTS, and DPPH. Based on the antioxidative capacity data of the safflower seed, samples were divided into two groups (I and II) in cluster analysis. Group I showed higher values of TPC, ABTS, DPPH and FRAP than group II (p<0.05). Principal component analysis (PCA) based on the data revealed that the first two principal components (PC1 and PC2) together explained 78 % total variation. Accessions IT321214 and IT321215 which had high antioxidant capacity could be utilized in research and food processing industries for developing new functional materials.

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**Genetic diversity in Napier grass (Cenchrus purpureus) collections as revealed by genotyping by sequencing method of the DArsseq platform**

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Napier grass, also called elephant grass, is an important tropical forage grass primarily used as cut-and-carry feed and of growing potential as an energy crop. The ILRI genebank holds a diverse set of Napier grass accessions and a collection from the Brazilian Agricultural Research Corporation (EMBRAPA). One-hundred-five accessions were subjected to genotyping by sequencing using DArsseq, which generated high-density genome-wide SilicoDaRT (116,190) and SNP (85,452) markers together with short sequence reads. The reads, averaged 54 nucleotides (nt), were mapped to the pearl rattle genome. Approximately 17% SNPs and 33% SilicoDaRTs were mapped, and the closest genes and annotation information identified and used to select candidate genes for important forage traits. A total of 980 highly polymorphic SNPs distributed across the genome were used to assess population structure and diversity. Seven-subgroups were identified using phylogenetic analysis and the major subgroups were supported by the admixture model in STRUCTURE and by principal component analysis (PCA). A few representative accessions were identified with the objective to distribute subsets of a manageable size for further evaluation. Genome-wide linkage disequilibrium (LD) analyses revealed a fast LD-decay, on average 2.54 kbp, in the combined population with a slower LD-decay in the ILRI compared to the EMBRAPA collection. This genotyping initiative generated high-density markers with a good distribution across the genome. The diversity analysis revealed the existence of a substantial amount of variation in the ILRI collection and identified some unique materials from the EMBRAPA collection, demonstrating the potential of the overall population for further genetic and marker-trait association studies.

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Early Matured, Pod Shattering Tolerant and Large Seed Soybean cultivar, ‘Nuriol’ for Double Cropping

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Early matured soybean cultivars can be double-cropped with various summer or winter crops such as potato, maize, garlic, onion and wheat in Korea. When soybean cultivars are double cropped with other winter crops, cropping period of soybean from planting to harvest shouldn’t be overlapped with those of others. With regard to this, soybean cultivars need to be early-matured with short growth periods of about 100 days. Most of the soybean cultivars with early maturity developed in Korea are commonly susceptible to pod shattering. On the other hand, a new soybean cultivar, ‘Nuriol’ is not only tolerant to pod shattering but also early matured with about 106 days from sowing to maturity. ‘Nuriol’ was developed by crossing ‘Chamol’ with ‘Jangol’ in 2010. An elite line (YS2312-B-2G-150-2-2-1) was selected by pedigree method and evaluated for early maturity and pod shattering tolerance in its preliminary and advanced yield trials. The selected line of Milyang316 was evaluated in the regional yield trials in four locations (Suwon, Ilsan, Dalseong and Jinju) for three years, 2016-2018. Milyang316 was chosen as a new variety and named as ‘Nuriol’ in 2018. ‘Nuriol’ is a semi-indeterminate in growth habit and 67cm long in plant height. It has on average 15 nods, 3 primary branches and 48 pods per plant. Its number of seeds per pod is 2.2 and its 100-seed weight is 25.0g. ‘Nuriol’ is resistant to Bacterial pustule (Psuedomonas glycina Xanthomonas axonopodis pv. glycines) and Soybean mosaic virus, but is relatively susceptible to purple seed stain disease. The rate of pod shattering of ‘Nuriol’ is 0 without any pods shattered in a dry-oven test. Yield of ‘Nuriol’ is 2.85 ton ha⁻¹ which is 25% higher than that of ‘Saolikong’, a standard cultivar in Korea.

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20-seed Evaluation Method for Sprout Using Perforated Conical tube for Soybeans

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Sprouts characteristics for breeding purpose are generally evaluated with bulk-seed, but it is not adequate to select plant in lower generation due to small seed quantity. To develop evaluation method for sprouts with few soybean seeds, small number of seeds were grown for sprouts and compared with bulk-seed method for whole length(WL), hypocotyl length(HL), root length(RL), hypocotyl thickness(HT), decayed seeds(DS), hard seeds(HS), un-germinated seeds(US) and yield(SV) of sprouts. To cultivate sprouts, soybean seeds were irrigated 3 times every 4 hours and cultivated for 5 days at 20°C. 22 soybean cultivars developed for sprouts were used for this study. First, 10 seeds, 20 seeds or 30 seeds of ‘Pungsannamulkong’ and ‘Wonheug’ which have definitely different sprout characters were cultivated for sprouts in 50ml perforated conical tube and bulk seeds in plastic basket. Difference in sprout characteristics between each seed quantity (10, 20 and 30 seeds) and bulk seeds was evaluated. Sum of difference of 10 seeds, 20 seeds and 30 seeds were -34.3, 24.5 and -33.6 in ‘Pungsannamulkong’ and 124.6, 70.3 and 147.2 in ‘Wonheug’, respectively. Sprouts grown with 20 seeds indicated most small difference. Second, 20 seeds and bulk seeds of 22 cultivars were cultivated for sprouts. The WL, HL, RL, HT, US and SY were significantly different by genotypes and methods. Although rankings among 22 genotypes for the eight sprout characteristics were not exactly the same in both tests, rankings for the top and bottom genotypes were similar for both tests. WL, HL, RL, DS and SY were exactly same in the best cultivar ‘Wonheug’. Correlation coefficient of WL, HL, RL, HT, DS, HS, US and SY were 0.94, 0.94, 0.91, 0.73, 0.72, 0.00, 0.28, 0.96, respectively. Especially, correlation coefficient of WL, HL, RL and SY were over 0.9 and it is quite desirable result for sprouts test with a minimum seeds quantity.

Result of this study showed that the 20-seed evaluation method in 50ml conical tube could be used to test the sprout traits for breeding purpose as well as for other experiments.

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Selection of triticale genetic resources with early maturity and good adaptation in the middle-northern area of South Korea

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Triticale (Triticosecale Wittmack) is a man-made intergeneric hybrid of wheat (Triticum sp.) x rye (Secale cereale L.). It incorporates favorable alleles from both progenitors (wheat and rye), enabling adaptation to environments that less favorable for wheat yet providing better biomass yield and forage quality. In South Korea, triticale is well adapted nationwide as forage crops but has late maturity leading to unstable seed self-supply system. So, it is necessary to develop cultivars with early maturity. For ninety seven triticale accessions provided by GRIN, USDA-ARS, USA, we evaluated agronomic traits such as lodging tolerance, cold tolerance, and disease occurrence as well as heading date (HD). We used cv. Shinyoungryemil and cv. Joseong, the most popular one with early HD among Korean elite cultivars as a plant control. The accessions were evaluated at the experimental station of NICS (Suwon, South Korea) in 2018. Heading date ranged from May 1 through May 13. Joseong and Shinyoungryemil headed on April 26 and May 3, respectively. It is found that five accessions had earlier HD than cv. Shinyoungryemil but no accessions earlier than cv. Joseong. Among them, two accessions were finally selected considering lodging tolerance, cold tolerance, and disease occurrence. Particularly these two accessions had stronger lodging tolerance and less disease occurrence than cv Shinyoungryemil, suggesting that these may be used as breeding materials.

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Comparison of FT–IR Spectra for Identifying Functional Extract Differences in Core Segregant Population of Tea Plant

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High-function tea breeding is needed because tea is one of the most popular beverages. However, it takes a long time to breed new cultivars due to the physiological characteristics (woody plant, self-incompatibility, etc.) of the tea plant. Recently, new techniques such as molecular marker development and metabolite analysis for major components have been applied to shorten breeding time. In particular, the data comparison analysis using FT-IR equipment is a relatively simple test method, and a large amount of analysis samples can be simultaneously compared and analyzed. That’s why it is possible to perform rapid screening using functional extracts of samples, and various quantitative statistical analysis techniques can be used for accurate quantitative analysis and correlation analysis. In this study, multivariate statistical analyzes were performed using FT-IR spectra using some of the hybrid seeding to build a system that can quickly select high-function tea plants. The differences and interrelationship among the hybrid seeding were confirmed by functional extract. Further analysis such as quantitative analysis of major functional materials and regression analysis is needed to establish a more reliable selection system.

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Origin diversity of Cereals in the Genebank of Republic of Korea

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Organisms including plants have phenotype variations according to their environment even though belong to same species. With increasing demands on cereals, RDA is trying to breed new varieties which can adapt Republic of Korea well. It is important to conserve genetic resources with various origins of origin as having genetic resources with various phenotypes is essential for breeding. In this study, we investigated the origin of three representative cereals-f/oxtail millet (Setaria italica), sorghum (Sorghum bicolor) and prose millet (Panicum miliaceum) which have been conserved in the Genebank of National Agrobiodiversity Center. We compared the information with the origin data available in the International Crop Research Institute of Semi-Arid Tropics (ICRISAT), which plays a pivotal role in conservation and utilization of cereals and pulses as a main research organization under UN/FAO/CGIAR. There were 2,438 foxtail millets, 9,307 sorghums and 1,550 prose millets accessions in Korean Genebank, which are classified according to their countries of origin. The study revealed that the origins of cereals in Korea were more focused on specific countries than those in ICRISAT. It also shows that origin duplicate ratio between Korea agencies and ICRISA is only about 50%. Thus, we suggested enlarging origin diversity is important to breeding new varieties and meeting the needs of various users.

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Evaluation of Fagopyrum esculentum and Fagopyrum tataricum germplasm for sprout growth and rutin and quercetin contents under spring cultivation

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Buckwheat seeds contain many proteins, vitamins, minerals and polyphenols such as rutin and quercetin. These Buckwheat seeds ingredients make seeds effective for vascular disease. Buckwheat sprouts also provide similar components contained in seeds. In several countries, buckwheat sprouts are used as functional vegetable because of its healthy ingredients. Especially in Korea, people reap raw buckwheat sprouts to consume sprouts with juice and salad. The present study was conducted with the objective of evaluating sprouts of 87 Fagopyrum esculentum and 13 Fagopyrum tataricum buckwheat germplasm for growth characteristics and rutin and quercetin contents under spring cultivation. The germplasm of esculentum type buckwheat showed significantly higher leaf length, leaf width, fresh shoot weight and extract weight than the tataricum type buckwheat showed. However, the rutin and quercetin contents were significantly higher in the tataricum type germplasm. In esculentum sprouts, the contents of rutin ranged from 323.7 mg/100 g dry weight (DW) to 750.6 mg/100 g DW with an average of 553.3 mg/100 g DW. However, in tataricum sprouts, the contents of rutin ranged from 2220.0 mg/100 g DW to 3185 mg/100 g DW with an average of 2729.9mg/100g DW. Similarly, in esculentum, the contents of quercetin ranged from 0.27 to 1.82 mg/100 g DW. In tataricum, the contents of quercetin ranged from 5.51 to 30.41 mg/100 g DW. In the case of esculentum sprouts, growth traits didn't show significant correlation with the rutin contents whereas in the case of tataricum sprouts, only the leaf length showed positive and significant correlation with the rutin contents. The sprouting of the identified esculentum and tataricum germplasm, with higher contents of rutin and quercetin, could be used as a dietary source of phenolic components to lower down the risk of various chronic diseases.

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Which Species They Are? - Genetic Resources and Molecular Phylogeny of Ornamental Freshwater Plant Bucephalandra sp, in Trade Market Based on cp DNA Marker

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Bucephalandra sp. is one of the most exotics and endemic aquatic plants on the Borneo island and hunted by aquarium plant hobbyists which has become popular in recent years. In taxonomy, Bucephalandra sp are divided into three scientific names including B. gigantea, B. motleyana, and B. catherinea. These species have a special attraction for naturalists and aquatic flora enthusiasts. They have distinctive growth and are always present anywhere in moist and runny areas. Variation in their morphological character is one of the most attractiveness ones in the aquatic flora market. At present study, a total of 194 Bucephalandra sp. genotypes were collected from the market with different commercial names. Many commercial names of certain species given by sellers is kind of sales strategy for the increase of its economic value. However, it provides confusion in botanical systematics and plant taxonomy. The objective of this study was to identify the real species of Bucephalandra genotypes collected from fresh water plant market based on chloroplast DNA barcode. Chloroplast DNA region, ribulose-bisphosphate carboxylase gene (rbcL) was chosen as DNA barcode marker in present study. Phylogenetics analysis were constructed using Mega7 software based on UPGMA analysis, the evolutionary distances were computed using the Maximum Composite Likelihood (MCL) and maximum parsimony (MP) methods. Three topologies reconstructed by UPGMA and MP from specimens used in this study were congruent in which trees major clades. A total 120 genotypes in clade I was positively correlated with B. gigantea, with 0 % of genetics distance. Clade II consisted of 62 genotypes which correlated to B. motleyana and clade III was out of the group with 12 genotypes.

Key Words: Aquatic plants, Bucephalandra, Commercial names, RbcL marker, phylogenetics

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Male Parents Assignment in F1 Populations of Cacao using SSR Markers

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Cacao (Theobroma cacao L.) is a tropical plant that is widely cultivated in Indonesia because of its benefits. All parts of cacao pod can be used for industrial purposes, such as chocolate, beverages, jams, cosmetics and bio-fertilizers. To meet industrial demand, a higher yield of cacao by developing high-yielding variety is needed. High level of genetic diversity which can be investigated through exploration or crossing between selected cacao clones provides opportunity to plant breeders to develop new cacao varieties with desirable traits. At present study, the 204 F1 cacao progenies derived from several cross combinations were successfully developed. However, the genetic purity of each clone by tracking the true identity of male parents remained undetermined. The study was aimed to identify the male parents of F1 cacao populations derived from crosses between ten parental combinations using SSR markers. A total of 38 SSR markers were applied to screen polymorphism among five parental clones. Of these, 11 markers showed polymorphism and were used to amplify 204 cacao F1 hybrids. The genotype data were then analyzed using the Cervus program in order to identify the true genotype of male parents. The result showed that 87 out of 204 F1 progenies were identified as the true genotype of male parents at a 95% confidence level, whereas the true male parents of 51 other F1 progenies was identified at a confidence level of <95%. Overall, we found 138 selected F1 progenies that generated from crosses between ten parental combinations. This study demonstrated the utility of SSR markers to detect the true identity of male parents, which helps breeders to select F1 progenies known to their parents’ identities. These selected F1 progenies would be potential to use as genetic material for assembling new cacao varieties.

Keywords: Cacao, F1 population, male parents, SSR markers, true identity

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253
Development of bacterial blight and rice strip virus resistant, early maturing japonica rice cultivar ‘Jodam’

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In Korea about 85% of rice cultivar is mid-late maturing variety and every year repeat inefficiency of machine use, loss from falling price because of concentrate shipment. Development of early maturing cultivar with high yield, multi-resistance, machine high yield can resolve the problem of price, machine efficiency.

‘Jodam’ is a new japonica rice variety developed and registered by the rice breeding team of Sangju substation NICS, RDA in 2018. It was derived from a cross between Ungwang with good grain quality, resistant to bacterial blight and HR25425 crossed Sambaek and Hwayneong with high quality rice. From F2 plants were selected pedigree method and tested main disease, cold tolerance and rice quality. It has multiple resistant to leaf blast(BL), bacterial blight (BB) and rice strip virus (RSV). But viviparous germination ratio is 29.8% some higher than Odabyeong. The agricultural traits of ‘Jodam’ are heading in 24 July, 69cm in height, short culm and lodging resistance, and 13 in panicle number per hill, 109 in number of grains per panicle, 84.8% in percentage ripened grain and 25.5g in 1,000 grain weight of brown rice. The milled rice exhibits translucent, relatively clear non-glutinous endosperm and head rice milling recovery ratio is 61.9%.

During 3 years of local adaptability trials (9kg/10a for N), the yield potential of ‘Jodam’ was estimated as 559kg/10a in milled rice, which was 5% higher than that of ‘Odabyeong’ ‘Jodam’ is expected to be utilized as early harvest cultivation in northern plain, mid-mountainous and southern mountainous area in Korea. ‘Jodam’ is early maturing cultivar adapting to northern plain, mid-mountainous and southern mountainous area in Korea.

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A New Small Redbean Cultivar ‘Honggyeong’ with Lodging Resistance and Large Bright Red Seed

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For small redbean(Vigna angularis var. Nipponensis) productivity improvement, One of big problem at small redbean cultivation is a lodging and it open makes hard to mechanical cultivation. So, we developed small red bean ‘Honggyeong’ that strong lodging tolerance enough to compete with imported small redbean cultivars.

‘Honggyeong’ was artificially crossed between IT236172 and SA0001 in 2008, fixed excellent agronomic characters by pedigree breeding method, and selected for the further trials with the name of ‘Miryang 36’. It was prominent and showed good result, such as high grain quality, lodging resistance and high yield in the regional adaptation yield trials (RYT) for three years from 2016 to 2018.

Lodging tolerant variety ‘Honggyeong’ is a medium-late having a bright red seed coat. The plant height of ‘Honggyeong’ was 56 cm and its yield components showed 7.5 pods per plant, 18.4g of 100-seed-weight in the regional yield trials (RYT). The L-values, a-values and b-values of ‘Honggyeong’ seed coat were higher than that of ‘Chungju’. In the regional yield trial for three years, the average yield potential of ‘Honggyeong’ was 2.06MT/ha, which was 9% higher than that of ‘Chungju’. Mechanical cultivation variety ‘Honggyeong’ could be help saving labor and cost of farmer.

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Changes of growth period and cumulative temperature according to seeding times of soybean varieties in the central plain region

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The purpose of this research was to analyze the effect of different sowing times on the flowering and maturing of major domestic soybean cultivars by varying day length and temperature in the central plain region. The average of growth period and cumulative temperature in five test cultivars by sowing times were 128 days and 3,022°C on June 1, respectively and gradually decreased to 87 days, 2,050°C, respectively on July 20. Analysis of the flowering response according to the sowing times showed that flowering was greatly influenced by the decrease of photoperiod until the sowing on July 10, and the minimum number of days and cumulative temperature for flowering were 30 days, 800°C, respectively in the central plains, irrespective of sowing time and ecotype. Daepung 2 is so excellent in the characteristic of resistant to environmental stress and high yielding, and the mid-late maturing cultivar in ecotype. Compared with Daewonkong which is classified to the same ecotype of Daepung 2, the total number of growing days was not different, but ripening period (R2-R6) was longer by 5 days and yield was higher by 11%. The maturity rate was also high and safe enough to maintain more than 90% through the entire sowing times. Analysis of these results suggest that as the ripening period of soybean is extended, the amount of absorption of solar radiation increase and thereby affecting the number of nodes and the amount of assimilation products translocation, finally the yield and maturity rate are improved. The cumulative solar radiation increase by the extension of reproductive growth period, is quantitative or indirect effect among the photoperiodic effects involved in increasing the yield. It is finally concluded that the resistant to environmental stress and high yielding of Daepung 2 is attributed to quantitative effects.

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Genotypic variability of major carotenoids and fruit characteristics of 107 tomato wild germplasm

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Tomato has been a great food because of its high content of health-related compound, especially like carotenoids. Lycopene is a major carotenoid that is responsible for the characteristic red color of tomatoes. Wild germplasm has been utilized for tomato improvement, disease resistance and superior fruit quality characters. For that, the screening of large numbers of genotypes is important for crop improvement programs with respect to nutritional quality. This study evaluated the content variation of major carotenoids in 108 tomato wild relatives germplasm also with agricultural fruit characteristics to search for good quality breeding resources. One hundred and eight accessions were composed of 65 accessions of S. pimpinellifolium, 35 accessions of S. peruviamum, 4 accessions of S. habrochaites, and 3 accessions of S. conelionmullerii. Three individual carotenoids, lutein, lycopene, and β-carotene were quantified using fully matured tomato fruits at harvest using HPLC. The lutein content of 107 tomato wild relatives showed a variation ranging from 1.2 to 11.6 mg/100g, DW. The lycopene contents were varied from 17.3 to 802.0 mg/100g, DW. The content of β-carotene was evaluated from 8.8 to 71.7 mg/100g, DW. The eighteen accessions including IT173710 could be selected as potential high-lycopene resources over 500 mg/100g, DW. IT173887 showed the highest lycopene and soluble solid content with 802.0±31.2 mg/100g, DW and 10.1±0.2 °Brix, respectively. These accessions could be used as potential breeding resources with respect to contents in sugar or functional chemicals, and further research is needed for the antioxidative and anticancer activities.

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Selection of soybean varieties highly adapted to high altitudes

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Cultivating soybean crops has the effect of reducing the use of pesticides and chemical fertilizers and preventing the loss of soil in highland areas. It is important to confirm the adaptability of soybean varieties because the highland area is short of frost-free days and frequent weather disasters compared with the plains. As a result of examining the yield characteristics of 147 Korean soybean varieties in lowland (Gangneung) and highland (Daegwanryeong), 90 varieties with excellent adaptability to highland areas were selected. Among them, there are 37 cultivars including ‘Taekwang’ and ‘Daepung’ for soy sauce and tofu, 10 including ‘Hupungjeonjo’ for cooking with rice, 25 including ‘Pungsanamni’ for bean sprouts and 18 including ‘Danmi 2’ for vegetable and early maturity. The soybean varieties cultivated in high altitude area above 800m above sea level showed high isoflavone content compared to those cultivated in low altitude area. Especially, ‘Daepung’ increased the isoflavone content up to 1.2 times in the highland area (4,246μg/g) compared to the lowland area (3,654μg/g). This is about 1.7 times higher than that of ‘Daewon’ (2,423 μg/g), which is cultivated mostly in Korea. In addition, in highlands, yield was increased by 15% when sowing is increased to three seeds from two per hole, which is generally a cultivation method. Sowing 3 seeds a hole can prevent the diameter of the main stem from becoming thick, which is especially beneficial for harvesting. The use of soybean crops in highland areas could improve the agricultural environment in highland areas. In the future, it will be possible to raise the income of farmers in highland areas and protect the environment through studying cultivars and cultivation techniques suitable for highland cultivation in the future.

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Evaluation of Crop Characteristics of Sweetpotato (*Ipomoea batatas* L.) Germplasms

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This study was conducted to investigate the crop characteristics of 506 sweet potato genetic resources collected from Korea and abroad. The longest vine length was observed in *DJ-6-31* cultivar with 315cm in length and shortest was 27cm in *Mokpo 45*. Maximum number of branch and nodes produced by *PA* (20.8) and *Sanvon 123* (76.0), respectively. In Rapid Visco Analyser profiles, differences were observed in pasting parameters such as pasting temperature, peak, trough, final, breakdown, and setback viscosity. The peak and breakdown viscosity was the highest in *Happyuni* starch at 457.9 and 299.8 Rapid Visco Unit (RVU), respectively. The trough viscosity was the lowest was in *kogane sengan* starch at 84 RVU. *CIP440116* showed the highest final and setback viscosity value of 274.24RVU and 82.3RVU, and the pasting temperature of *chilbock* starch was the highest at 83.7 °C and *Happyuni* starch was the lowest at 61.9 °C. Among 354 germplasm, the starch contents showed that the highest frequency proportion was 52% of the group of 10 - 15% starch, and the next was 30.8% of the group of 5 - 10% starch. Sugar contents ranged from 2.4 to 6.7 % with 4.8% in average and the highest frequency distribution of it was the group of 4 - 5% with the proportion of 46.3% and next was the group of 5 - 6% with the proportion 35.6%. Water contents showed that the highest frequency proportion was 49.2% of the group of 60 - 70%, and next was 44.6% of the group of 70 - 80%. These results can be used as basic data of selection of useful resources, and development of new variety.

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Evaluation on agricultural traits and valuable composition of pigeonpea (*Cajanus cajan* (L.) Millsp.) genetic resources in Korea

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Recently, interest of diverse legume crops has increased, and pigeonpea seems to be one of the useful crops in the future. Therefore, this study was conducted to examine domestic adaptation through agricultural traits, to increase utilization to evaluate useful components of pigeonpea germplasm. A total of 112 pigeonpea genetic resources were used as material, and seeds were sown on April 4, 2018 and planted on April 27. We investigate days to flowering, growth habit, flower color, days to maturity, seed color etc. as agricultural traits and the content of crude fiber and dietary fiber for useful components. Of the 112 accessions used as materials, eighteen were not harvested due to unflowering and immaturity, and 94 accessions were carried out the composition analysis. The flowering period of pigeonpea germplasm distributed from 8th June to 31th October, 93% of 102 flowered accessions bloomed before the early of July, those after middle of July were not fruitless or low in yield. The crude fiber content of pigeonpea was ranged from 4.7% to 8.6% with an average 6.9%, dietary fiber was ranged from 15.8% to 36.0% with an average 24.4%. The content of crude fiber and dietary fiber in pigeonpea was higher than that of lentil, chickpea and hyacinth bean and lower than that of guar. We selected two accessions, IT170312, IT170450, with early maturity, high yield per plant, erect type of growth habit, higher than average content of crude fiber and dietary fiber. We are going to evaluate the content of crude protein and polyphenol and antibiotic activity to utilize new crop to provide useful information of pigeonpea.

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A Study on the Effects of Early Shipment of Cymbidium through Cooling in Plain Land in the High-Temperature Season

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The breeding of Cymbidium has mainly focused on medium and large species for exporting to China. The general cropping type is to cultivate tissue-cultured seedling in a house for about three years and ship out flowering stocks. For Cymbidium that has large shipments in winter, slightly early maturity of existing early-cultivated species can earn higher prices, and shortening the three-year cultivation period to two years can directly improve the farm household income due to the reduced operating cost. The distribution and consumption can be expected to increase for Cymbidium that has decreased in size. For earlier shipments, most farmhouses move Cymbidiums to a high altitude cool region in summer in the early floral differentiation stage to prevent the withering of flower stalks and increase the occurrence of peduncles. However, this requires much time and labor. Therefore, this study examined the possibility of replacing movement to a high altitude cool region with cooling in a plain land to save production cost. For experimental materials, two early maturing species including “Gold Sun” developed by the Rural Development Administration and “PN416,” which is a Japanese early maturing species, were used. One group of Cymbidiums were moved to and cultivated in a high altitude cool region (average temperature 21°C) for two months in summer in 2017 and 2018 and another group of Cymbidiums were cultivated in a plain land (Gongju, Chungnam) by cooling (average temperature 24°C) at low temperatures during the night. The growth patterns were compared between the two groups by investigating the bulb number, bulb diameter, plant length, and leaf number every one to two months. The results showed that the bulb diameter was smaller in the cooling section in general than in the plain land section and the plant length was longer in the plain land. In the cooling section, the foreign species showed a larger bulb number by 1 or 2, but the difference between treatment sections was not significant. “Gold Sun” showed a longer leaf length than other species and the leaf length was longer in the plain land high temperature section. In the future, we plan to establish the two-year cultivation technique for Cymbidium through combined technologies including supplemental lighting and nutriculture.

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Discovery and Evaluation of SNP Markers for Downy Mildew Resistance in Maize Population

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Maize (Zea mays) is C4 plant and 3 major crops for mankind in the world. However, several diseases infection of maize are considered as one of huge problems for maize production. Downy mildew (DM) caused by Peronosclerospora and Sclerospora species is the most destructive diseases for maize crops in the lowland tropics, especially in tropical Asian countries. In Asia, DM is the most important biotic stress in maize. Despite efforts toward the development of DM resistant cultivars or seed treatment with metalaxyl fungicide, DM still emerges in localized areas as a severe pathogen. DM infected plants at early stage is likely to die approximately 4 weeks after DM occurrence. In late-infected plants, disease progress usually starts with the characteristic pale green halfleaf shape. Previous study, we expect that the DM resistance is related to the Bk1. Full length, 2212 bp, Bk1 gene was isolated using GRMZM2G121565 sequence information. A total of 26 SNP and 116 bp of InDel fragment were identified. Eventually, 3 SNP markers (150 bp, 92 bp, 93 bp) were determined as a DM resistance molecular marker. B73 X Ki11 population was analyzed using 3 SNP marker. A total of 67 genotyping data out of 117 RIL from population was identical to DM resistance phenotype. Further analysis will be discussed.

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Change of Agricultural Characteristics of Core collections of Proso millet of International Crops Research Institute for the semi-Arid Tropics (ICRISAT) in South Korea

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Plant genetic resources are fundamental materials for crop improvement to enhance productivity. Using passport data, characterization and evaluation data, core collections have been developed in proso millet (Panicum miliaceum L.) at ICRISAT, Patancheru, India. Core collections (~10% of the entire collection) have been suggested as a gateway to enhance utilization of germplasm. Evaluation of these subsets has resulted in identification of new sources of genotypic variation. National breeding program in RDA (Rural Development Administration) Korea have shown immense interest in evaluating core collections for identification of new sources of variation for use in proso millet breeding program. Those core collections cultivated in Korea shown various heading days after seeding date, from 25-30 days to 46-50 days comparing to 53 days of ‘Ibaekchal’. In the case of lodging tolerance, which is one of important trait in proso millet cultivation, most of (77%) the core collections shown high risk of lodging, and only 4% were tolerant. In 1,000 grain weight, those collections shown various distribution from 4.0 g to 5.5g. Discovery of new sources from genetic variation could be favored by accurate identification of sources with favorable traits and their efficient use.

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Genetic diversity of fatty acid compositions in brown rice of mini-core collection of Korean rice core set (KRICE-CORE)

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The genetic diversity in grain fatty acid among mini core collection consisting of 137 rice accessions which represent 25,604 germplasm were investigated. In order to neutralize environmental impacts, selected accessions were cultivated in 3 different locations and fatty acid compositions of harvested brown rice were analyzed by using a gas chromatography. Total 9 fatty acids were quantified, among which linoleic, oleic, and palmitic acids were the 3 major ones which showed average composition of 36.8%, 34.1 %, and 24.1%, respectively. Additional minor fatty acids were stearic (1.9%), linolenic (1.1%), myristic (0.9%), arachidic (0.5%), behenic (0.3%) and eicosanoic acid (0.3%). Among 137 accessions minor fatty acids such as myristic and arachidic acids exhibited higher genetic variations by showing high relative standard deviation (RSD) values of 28.4% and 23.1%, respectively, while major fatty acids such as linoleic (RSD=6.2%) and oleic (RSD=8.8%) acids showed lower variations. Accessions IT005878, IT211283, and IT001908 showed highest compositions in linoleic (43.2%), oleic (41.9%), and palmitic (30.6%) acid, respectively. Ecotypes of accessions also affected fatty acid composition in that Aus-, tropical japonica-, and temperate japonica-type rice exhibited relatively high compositions of saturated, monounsaturated, and poly-unsaturated fatty acids, respectively. Palmitic acid composition showed negative correlations with oleic (r=-0.66**) and eicosanoic (r=-0.62**) acids, while positive correlation (r=0.58**) could be observed between oleic and eicosanoic acids. All these results suggested diverse fatty acid composition in 137 rice accessions of mini-core collection of Korean rice core set, which can be further utilized for breeding a superior rice variety of higher nutritional value.

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Breeding of High Productivity Italian Ryegrass Plant in Southern Part of Korea, Breeding Line ‘ARX 2’

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Italian ryegrass (*Lolium multiflorum* Lam.) has been cultivated mainly in southern part of Korea due to the cold weather. However, during the last 20 years, the NIAS (National Institute of Animal Science) has developed and supplied more than ten varieties including 'Korwinearly' of Italian ryegrass resistant to cold, which greatly increased the area of Italian ryegrass cultivation throughout the country. According to the statistics in 2018, among the cultivated area of winter forage crops, Italian ryegrass cultivation area occupies 97%. Nevertheless, it still grows imported Italian ryegrass varieties in the southern part of Korea. This is because the productivity of imported varieties is higher in southern regions than in domestic varieties. The ‘ARX 2’ line developed in this study was strong against cold and 33% higher than that of ‘Korwinearly’ in Haenam-gun, Jeollanam-do (southern part of Korea). In the three-year study from 2015 to 2017, the average dry matter yield per cohort was 10.6 tones of ‘Korwinearly’ and 14.2 tones of ‘ARX 2’. The heading date of ‘ARX 2’ is May 15, a late variety than that of ‘Korwinearly’, and chromosomal drainage is diploid. The plant length of the ‘ARX 2’ in the heading time is 5 cm longer than that of the ‘Korwinearly’, and the stem thickness is medium. The feed value of ‘AEX 2’ analyzed in heading time was 58.5% of TDN and 67.2% of dry matter digestibility, which was similar to that of ‘Korwinearly’. We are going to apply ‘ARX 2’ as a new variety next year. If this new varieties are introduced in the future, it is expected that it will become a popular variety in southern part of Korea.

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Selection of Breeding Lines for Improving traits in Forage Crop ‘Teosinte’

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Teosinte (*Zea mays* L. subsp. *Mexicana*) as a forage crop has advantages about strong in wet injury and good palatability for livestock in Korea but has weakness about low germination rate by hard seed coat and lodging damage by a weak and soft stem. Therefore, it is very important to develop a new teosinte variety with good germination rate and lodging protecting plant. This experiment was carried out to develop a breeding line of teosinte with a good germination and low lodging at Cheonan of Korea on 2016 to 2018. Breeding lines of teosinte for new variety were made by selecting of good germination plant from existing varieties for three years consistently. Among different breeding lines, total 15 breeding lines of early maturing(heading of 12 Sep.), middle maturing(heading of 18 Sep.) and late maturing(heading of 25 Sep.) were selected, respectively. Seeds of these breeding lines were got by self-crossing, and germination rate of breeding line seeds was tested by petri dish test and nursery box soil test, respectively. Germination rates of breeding lines were different between petri dish and nursery box soil test. In petri dish test, germination rate of breeding lines was 16 to 98% between breeding lines but in nursery box soil test, germination rate of breeding lines was 93 to 100%. Among breeding lines of these teosinte, 2016KDS-11-17, 2017USA-6 and 2017KDS-15-6 were more 80% of very high germination rate. These results suggested that three of these breeding lines are very important for breeding a teosinte variety with characteristic of good germination.

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Characteristics of inbred lines from octoploid strawberry varieties

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Strawberries are an allo-octoploid crop. A new variety has been developed by selecting a single progeny with good traits from the F1 hybrid groups. However, the traditional breeding program is not efficient to find the one that has the target traits. In order to select octoploid strawberries efficiently and to perform systematic breeding, a molecular genetic tool is required. To do that sufficient genomic research is necessary. Strawberries are one of the famous allopolyploid plant which makes it difficult to analyze the genome. To lower down the complexity of the genome, the inbred lines of 8 to 10 selfing generations was developed through repeated self-pollination in National Institute of Horticultural & Herbal Science. Their horticultural characteristics were also investigated. The population of octoploid strawberry inbred lines was derived from 8 cultivars. Details about the field cultivation and phenotypic evaluation of the inbred lines were performed according to the RDA standard method. These genetic resources and phenotypic traits are expected to be used for the future strawberry breeding materials.

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Current Status and Prospects of Rice Breeding in Central Region of Korea for 40 Years after the Development of ‘Tongil’ rice varieties

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Korea achieved self-sufficiency in rice, the staple food, in 1970 with the development of the ‘Tongil’ rice varieties. After that, in the 1980s, the development of high-quality cultivar was carried out on a continuous basis. Since then, in central region of Korea, 92 species of Japonica and 20 species of Tongil type have been developed over 40 years from 1980 to 2017. It is composed of 40 cultivars of early maturing type (such as Jingwang, Haedaul, Aseni, Aseni1. etc.), 32 varieties of medium maturing type (such as Hwaseong, Sanggwang1., Cheongpum etc.), 20 cultivars of late maturing type (such as Ilpum, Sanggwang, Kopum, etc.) and 20 species of ‘Tongil’ type rice including 8 varieties of whole crop rice. In order to overcome climate change and to expand genetic diversity in rice breeding system, it was used as a genetic source to introduce new traits through characterization tests of domestic and foreign genetic sources. To develop varieties that have high quality rice taste and resistance to disease/pest, and abiotic stress tolerance, characteristics tests were carried out for each relevant trait and quality related tests. These high quality rice varieties of early/medium maturing types developed in central region of Korea are produced in farming households, contributing to the overall improvement of the rice taste in Korea. Also, cultivars with disease-resistance and abiotic stress tolerance will be used to develop new varieties that can preemptively respond to climate change and contribute greatly to enhancing the competitiveness of Korean rice.

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Analysis the genetic diversity of watermelon (*Citrullus lanatus L.*) germplasm using genotyping by sequencing

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Watermelon (*Citrullus lanatus L.*) is an economically important vegetable fruit crop worldwide. The objective of this study was to find the single nucleotide polymorphisms (SNPs) and analysis the genetic diversity of 68 watermelon accessions. Genotyping by sequencing (GBS) was used to discover SNPs and assess genetic diversity using discriminant analysis of principal components (DAPC) analysis in watermelon accessions. Two different watermelons resources were used: 1) 41 highly utilized watermelon accessions from the National Agrobiodiversity Center (NAC) at the Rural Development Administration in South Korea; and 2) 27 Korean commercial watermelons. The results of GBS showed that 80.3% of raw reads (approximately 2.1 billion) were mapped on reference watermelon genome with an average mapping region of about 2,024 Kb. In the SNPs filtering process, a total of 1,770 SNPs were obtained. To understand the genetic relationship of 68 watermelon accessions, DAPC was carried out with 1,770 SNPs. Results revealed that the presence of four clusters within the populations, which are differentiated principally by seed companies. In addition, there were higher genetic differentiation among commercial watermelons of each company. The genetic distance revealed in this present study shows the importance of watermelon accessions for conservation and use in breeding programs.

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한국 재배중 검정콩의 \( \gamma \)-tocopherol methyltransferase-3 유전자 염기서열에 따른 알파토코페롤 함량

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Molecular Diversity and population structure of Korean ginseng (Panax ginseng) germplasm as revealed by microsatellite markers

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Korean ginseng (Panax ginseng C.A. Meyer) is one of the most favored herbal medicinal plants valued by local Korean consumers as well as those based overseas. In this study, 899 Korean ginseng accessions conserved at National Agrobiodiversity Center, RDA were genotyped using 20 SSR markers to reveal the genetic diversity and population structure in the ginseng germplasms. The study revealed that the number of observed alleles were ranged from 2 to 9 (an average of 4.4), Simpson index from 0.375 to 0.675 (with an average of 0.510), Nei’s genetic diversity from 0.376 to 0.676 (with an average of 0.510), and allelic evenness from 0.716 to 1.000 (with an average of 0.935). Using the discriminant analysis of principal components, a total of 10 sub-populations have been identified within 899 ginseng accessions, which contains from two to 140 accessions. Variance analysis showed that there was a significant difference among populations in genetic diversity. The genetic differentiation coefficient indicated that 5% of the variation occurred within populations, which indicates that substantial genetic differentiation occurred within populations. The quantitative analysis of the genetic diversity and population structure in this study could be useful for genetic and genomic analysis and utilization of the genetic variation in ginseng breeding.

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The Complete Chloroplast Genome Sequence of Japanese Millet Echinochloa esculenta (A. Braun) H. Scholz (Poaceae)

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Japanese Millet, Echinochloa esculenta is a weed-suppressing cover crop that was grown once as a staple food crop in Japanese regions when rice cultivation failed. Here, we report the complete chloroplast (cp) genome sequence of E. esculenta for the first time to understand the diversification of this species in the family Poaceae. The size of the circular chloroplast genome is 139,851 bp in length with 38.6% overall GC content which exhibits a typical quadripartite structure, containing pair of inverted repeats of 22,748 bp, flanked by large single copy and small single copy regions of 81,837 bp, 12,518 bp, respectively. The cp genome encodes 111 unique genes, 76 of which are protein-coding genes, 4 rRNA genes, 30 tRNA genes and 18 duplicated genes in the inverted repeat region. The phylogenetic analysis indicated that the E. esculenta is closely related with the wild relative barnyard grass (E. crus-galli).

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263
Interspecific hybridization between *Capsicum* spp. for introgression of alien genome

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The interspecific crosses were made between *Capsicum annuum* 'CM334' and *Capsicum baccatum* 'PBC81'. The F1 hybrid plants were obtained using embryo rescue to overcome embryo abortion. To advance generation, the F1 hybrids as a maternal parent and ‘CM334’ as a paternal parent were backcrossed for BC1F1 population and each BC1F1 lines were reciprocally backcrossed for BC2F1 lines. The BC1F1 population was genotyped using genotyping-by-sequencing (GBS) and Fluidigm EP1 system. To develop selection tools for next backcrossed line, Genotyping-in-Thousands by sequencing (GT-seq) which is multiplexed targeted SNP sequencing to generate genotypes were used. A total of 288 pairs of specific target amplification (STA) primers and locus-specific primers (LSP) derived from Fluidigm EP1 system and 110 SNPs derived from GBS analysis were converted to GT-seq targeted sequencing primers for foreground and background selections of the BC2F1 lines. Among the converted 288 sets of GT-seq primers, 67 sets of primers showed polymorphism in the BC2F1 lines. These marker sets were used to select the next introgression lines. The final set of interspecific introgression lines will be very useful for future pre-breeding program and interspecific incompatibility study.

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Genetic Diversity and Population Structure of Worldwide Cucumber Germplasm

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Conservation of genetic diversity is an essential prerequisite for developing new cultivars with desirable agronomic traits. Although a large number of germplasm collections have been established worldwide, many of them face major difficulties due to large size and a lack of adequate information about population structure and genetic diversity. Cucumber is the fourth most important vegetable crop worldwide and is a model system for other Cucurbitaceae, a family that also includes melon, watermelon, pumpkin and squash. To explore genetic diversity and population structure, a genotyping-by-sequencing (GBS) approach was used to provide dense genome-wide marker coverage (>12,082 SNPs) for a 264 cucumber accessions collected from 37 various countries. Using GBS platform, high density haplotype map was constructed and various stratification methods, including distance based phylogenetic methods, principal component analysis (PCA), and Bayesian phylogenetic methods (STRUCTURE) were performed to show the genetic diversity and population stratification. As a result, three sub-clusters were divided based on population structure analysis and it reflected their geographic regions. These results will not only find genetic variants among cucumber accessions but also provide powerful evidence for reducing first positive error to perform Genome-wide association study (GWAS) in large scale studies.

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Genetic parameters estimation of growth trait of *Pinus koraiensis* in 35-year-old half-sib progeny trial

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Genetic parameters of growth traits of *Pinus koraiensis* were estimated from 35-year-old half-sib progenies of 21 plus trees. *P. koraiensis*, Korean white pine, is one of the major conifer species in northeastern Asia. Tree improvement program of the species has been performed since 1959 in Korea followed by plus trees selection based on their superior phenotypes. Genetic effects on growth trait were estimated by restricted maximum likelihood (REML) analysis from the open-pollinated progeny trial in three sites. Family and site effects were significant for the traits observed. Mean heights by site were ranged from 10.88m to 12.58m showing the lowest growth in GP site. DBH average was high in the order of CC, GP and CJ sites ranging from 19.27cm to 26.02cm. Volume index was highest in CC site compared to the other two sites. Individual narrow-sense heritability (h²) estimates of height, DBH and volume index were 0.02, 0.23 and 0.19 respectively in the site combined analysis. Among the plus trees, gg61 and kw21 showed high breeding values (BV) for volume growth. Each of them had high BVs for height and DBH growth across the sites. gg51 showed high BV for volume growth though the predicted values were relatively decreased in CJ and GP sites. BVs for volume growth of gg62, gg63 were consistently low in the sites as the estimates for DBH growth.

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Characterization of twelve Korean waxy maize (*Zea mays* L.) landraces by RNA sequencing

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In the Korean peninsula, maize (*Zea mays* L.) is the second-most produced crop after rice and has been continuously cultivated since the 16th century. Even with such long cultivation history, the diversities and characteristics of Korean landraces have not been intensively studied especially at the genome sequence level. Twelve landraces with various flowering times were collected and used for RNA-seq in the early vegetative stage. The transcriptomes of 12 Korean landraces have been analyzed for their genetic variations in coding sequence and genetic relationships to HapMap2 maize population which include wide diversities of maize germplasm. The Korean landraces showed specific genetic characteristics and were closely related to a Chinese inbred line showing its origin. Flowering-time related gene profiles pointed to multiple causes for the variation of flowering time within Korean landraces; the profiles revealed significant positive and negative correlations among genes, allowing us to infer possible multiple mechanisms for flowering time variation in maize. These results showed the transcriptome-based genetic and gene expression profiles is efficient for collecting information on possible breeding resources, which is particularly needed in Korean maize germplasm.

Key words: landrace, corn, flowering time, SNP, genetic diversity

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265
Physicochemical Properties of dry-milling flour endosperm elite line

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‘Suweon542’, an elite rice line with floury endosperm suitable for dry-milling, was developed to revitalize rice flour industry. However, it is susceptible to viviparous germination and other diseases. New rice lines with floury endosperm, ‘Jeonju614’ and ‘Jeonju615’, were developed to strengthen multiple disease resistance by crossing ‘Suweon542’ with ‘Jopyeong’, an early-maturing cultivar with multiple disease resistance. The physicochemical properties of ‘Jeonju614’ and ‘Jeonju615’ were evaluated in comparison with soft endosperm rice cultivars (Seolgang, Hangaru) and normal nonglutinous rice cultivars (Jopyeong, Sindongjinn). The average grain sizes of ‘Jeonju614’ and ‘Jeonju615’ were 84.52 μm and 81.83 μm, respectively, which were lower than those of soft endosperm and normal nonglutinous rice cultivars. The average damaged starch contents of ‘Jeonju614’ and ‘Jeonju615’ were 6.08% and 5.64%, respectively, which were lower than those of soft endosperm and nonglutinous rice cultivars. Other physicochemical properties of ‘Jeonju614’ and ‘Jeonju615’ such as protein content, amylose content, color, and ash did not differ significantly from those of the other cultivars.

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Development of InDel Markers Based on Chloroplast DNA from Korean wild Codonopsis lanceolata for Genetic Diversity Analysis

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Codonopsis lanceolata is a perennial vine plant belonging to the Campanulaceae, and in Korea, it has been used for traditional medicine since ancient times due to its therapeutic characteristics. However, C. lanceolata has begun to be imported from foreign countries and distributed to the Korean herb market and it raised a concern about the mixing of Korean C. lanceolata and foreign C. lanceolata. In this study, we collected wild C. lanceolata in Korea, developed chloroplast-based molecular markers, and analyzed the genetic diversity of Korean C. lanceolata and imported C. lanceolata. For this study, 26 wild C. lanceolata were sequenced using NGS (Next Generation Sequencing), and for the analysis of C. lanceolata genetic diversity, we collected 20 foreign C. lanceolata which were originated from China in the Korean herb markets. As a result, 31 insertion-deletion (InDel) loci were found between chloroplast sequences of Korean C. lanceolata and we developed 29 InDel markers. In addition, we constructed phylogenetic tree of C. lanceolata collections based on genetic differentiation using the developed markers. The chloroplast-based molecular markers developed in this study could be used in the study of inference of genetic origins based on the maternal inheritance and study for variety development of Korean C. lanceolata.

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Screening of *FT* (*FLOWERING LOCUS T*) homologs in pepper (*Capsicum annuum* L.) based on genome database

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Members in PEBP (phosphatidylethanolamine-binding protein) family that include *FT* (*FLOWERING LOCUS T*) gene, which is well-known as florigen, conduct important roles in regulating flowering. In determinate tomato, it has been reported that the yield of the plant is greatly increased when the *FT* ortholog gene SFT (*SINGLE FLOWER TRUSS*) is heterozygous. Although the determinate inflorescence phenotype in pepper has been reported to be due to the frameshift mutation of the CaSP gene belonging to the PEBP family, there has been no research on *FT* orthologs. We are trying to characterize *FT* homolog after screening of candidate genes PEBP family based on pepper genome information. The pepper ortholog of tomato SFT showed frameshift mutation, thus it was estimated to be non-functional. Therefore, we selected other ten candidate genes that are homologous to *SFT* using pepper genome information, and analyzed the gene expression profiles of PEBP family genes using pepper transcriptome database reported previously. In addition, we performed phylogenetic analysis for these genes and other PEBP family genes reported in other solanaceae crops. As a result, five candidate genes showing similar expression patterns were grouped with genes known to be flowering inducer and repressor in other plants. Expression patterns of five candidate genes were confirmed by RT-PCR. The functions of candidate genes will be clarified by transformation to Arabidopsis thaliana. We will also screen pepper lines having mutation on the final *FT* candidate gene by TILLING (Targeting induced local lesion in genomes) use them as the breeding resources for higher heterosis.

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The circadian rhythm differences among four Korean soybean cultivars [*Glycine max* (L.) Merr.] with different flowering time [*Glycine max* (L.) Merr.]

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It has been reported that plants recognize seasonal change through daylength change through the circadian clock to allow them to synchronize multiple physiological and developmental responses. There are a number of genes, which are involved in circadian clock events in plants, to regulate of flowering time through the photoperiodic signaling pathway. Soybean (*Glycine max* (L.) Merr.) is a facultative short day plant, which is widely cultivated all over the world as important source of protein and oil. It is flowered only when daylength decreased below a certain threshold. To enhance crop yield and agronomic interest traits, manipulating the central oscillator, circadian clock, has been suggested, and it is assumed that various soybean cultivars, that showed wide-range of flowering time, maintained the different diurnal internal circadian rhythm. In this research, diurnal expression of circadian clock genes of four soybean cultivars with different flowering time under short day condition (16 hours of dark) was investigated to identify the circadian rhythm differences among these soybean cultivars. Plants were grown in green house for 10 days, and transferred to growth chamber under day condition for 5 days. mRNA was extracted in every 4 hours and quantitative reverse transcription-PCR analysis for important clock genes were conducted. This research could contribute to improve the understanding of flowering-time-regulated genes between soybean cultivars as well as soybean breeding program

Keyword: Glycine max, Soybean, Circadian clock, Flowering time

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Intensive selection of wheat world collections for introduction breeding

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Wheat is the second most important food crop in Korea after rice (annual consumption per capita: 32.4kg for wheat and 61.8kg for rice in 2017) and consumption rate of wheat in food crop is increasing. Although, the demand of hard wheat is increasing, it’s self-sufficiency is negligible in Korea. Most of Korean wheat cultivar is not suitable for bread making owing to poor gluten quality as well as quality. National Agrobiodiversity Center selected 200 wheat lines/cultivars/landraces obtained from the world based on the based on the field test and HMW-GS compositions. Numerous agronomic and quality parameters is now on evaluation for the 200 selected wheat lines. The filed test sites are allocated based on the climate difference (Mid-North: Korea University, Middle: National Institute of Crop Science, South: Gyeongsangnam-do Agricultural Research and Extension Services)

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Genetic Diversity Analysis of Angelica Species Using Chloroplast DNA Markers of Angelica gigas Nakai

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Angelica species are representative medicinal plants and it has been used in traditional medicinal methods, especially, in the traditional Asian medicine. The Angelica species used in conventional medicine varies by country according to specific regulations, i.e. A. gigas Nakai in Korea, A. sinesis Diels in China, and A. acutiloba Kitagawa in Japan. Because of the similarity between the names among Angelica, they can be confused in the market. In this study, twenty-four chloroplast insertion or deletion (cplnDel) markers were developed from chloroplast DNA of A. gigas Nakai and tested for the classification of Angelica species. Primer sets were designed from flanking sequences of the discovered InDel loci from chloroplast DNA of A. gigas Nakai using CLC Main Workbench with the following parameters: primer length = 18 ~ 26 bp (Opt. 23 bp); GC% = 50 ~ 70% (Opt. 60%); Ta = 55 ~ 62°C (Opt. 58°C); product size range = 120 ~ 300 bp. Polymorphism and genotype analysis of 13 Angelica species (A. gigas, A. acutiloba, A. archangelica, A. taiwaniana, A. hendersoni, A. atropurpurea, A. keiskei koidzumi, A. dahurica, A. hispanica, A. pachycarpa, A. temuissima, A. arguta, A. sinesis) were performed using the developed cplnDel markers. The 24 cplnDel markers developed in this study could be used for genetic diversity analysis and classification of Angelica species.

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Active Compounds Content of Flower-color Mutants in Angelica gigas Nakai

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Angelica gigas Nakai has two main cultivars such as ‘Manchu’ and ‘Yeongheung’ and native variety by home seed production. We have collected genetic resources at habitat and plantation for breeding of A. gigas. Since, it was very difficult to select of phenotypic variation, we were selected flower-color variation in the chief producing district of Bonghwa, Jecheon and Pyeongchang. In order to investigate the active compounds, such as nodakenin, decursin and decursinol angelate, we analyzed color phenotype and active compounds content. As a results of this study, decursin content of A. gigas was 0.250% in purple flower(purple), 0.260% in pink flower(pink) and 0.285% in white flower(white). Decursinol angelate content of A. gigas was 0.595% in white and was the higher than purple and pink. In addition, the total content of active ingredients was high in the order of 0.905% of white, 0.880% of pink and 0.875% of purple.

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Genotyping of selected wheat germplasms for grain quality tagging

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Introduction of new genetic source into current genomic background is important and its requirement is increasing in Korean wheat breeding program especially in hard wheat breeding strategies. Total 200 wheat lines were selected for their adaption in Korean environment. Heading date and plant height as well as high-molecular weight gluten scores were considered for selection and selection criteria were set high. Grain quality related genotyping is prerequisite before large scale filed observation. Genotyping of major genes tagging grain and quality parameter were conducted and the genotypic distribution of selected world germplasms were analyzed.

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Development of InDel Markers Based on Chloroplast DNA for Classification of Zizyphus jujuba Mill

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Jujube (Zizyphus jujuba Mill.) is broad-leaved arbor belonging to the family Rhamnaceae. Origin of the species is Southern Europe or Western Asia. The size of jujube is usually 2-3 cm and the weight is 10-13 g. Flowers bloom in yellowish colors from May to June, and fruit is ripe from September to October. Jujube is an economically important crop, and fruit is used for raw fruits, snacks, cooking as well as for medicine. We need methods to distinguish the varieties of jujube because it is very important in the protection of genetic sources, the cultivation of jujube, and the distribution of jujube in the markets. In this study, we tried to distinguish the major varieties of jujube using the InDel markers developed from chloroplast DNA of jujube. We collected 24 jujube varieties include Boljo and extracted DNA using CTAB method. We designed the primer sets using CLC Main Workbench based on chloroplast DNA InDel regions identified from the comparison of the chloroplast sequences of the varieties. PCR and electrophoresis were performed to confirm the polymorphism. As a result, several polymorphic loci were found. The InDel markers developed in this study could be good tools to differentiate the jujube varieties cultivated in Korea.

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Development of SSR Markers for the Genetic Diversity Analysis of Schisandra chinensis

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Schisandra chinensis is a deciduous vine plant belonging to Schisandraceae and is a medicinal plant. The red fruit of the plant is used as herbal medicine and food raw material. One domestic S. chinensis variety is registered and there are few studies on the development of molecular markers. In this study, S. chinensis was collected nationwide and genomic DNA was analyzed in 13 regions using next generation sequencing (NGS). As a result, 2,392 tri-motifs, 1,247 tetra-motifs, and 512 penta- or hexa-motifs were found. Among them, primers were designed by selecting 48 loci with a large number of genotypes between S. chinensis and motif repeats. The extracted candidate microsatellite markers were applied to 12 collections of S. chinensis and verified that they actually showed polymorphism among the genetic resources. PCR amplification products were tested by fragment analyzer. In addition, genetic relationships of the 12 accessions were analyzed using phylogenetic analysis. The molecular markers developed in this study could be used for the genetic diversity analysis of S. chinensis species.

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Identification of standard type chrysanthemum cultivars using SSR markers

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Chrysanthemum is one of the well-known ornamental plants and is a popular cut flower across the global flower market with higher economic value. Chrysanthemum is commercially important for the floral industry in Korea. Propagation of chrysanthemum cultivars by vegetative cuttings and having substantial genetic variations that can be manipulated under cultivations leading to a wide range of phenotypic variations, enabled to commercialize several hundreds of cultivars. Morphological characteristics alone are not sufficient to identify the cultivars as they are not stable and are influenced by the environment. However, cultivar identification is highly essential to ensure the right labelling in the floral market and to protect the intellectual property of the breeder. Hence, an effective and reliable method to identify and discriminate the cultivars is required. Present study was focused to identify the suitable molecular markers that can discriminate the standard type chrysanthemum cultivars. SSR markers were used to identify a collection of 11 standard type inbred and commercial cultivars. Among the total 23 markers screened, we identified one SSR marker which could detect polymorphism and could discriminate all the tested standard type cultivars. The PIC values ranged from the low of 0.25 to the high of 0.60 with an average PIC value of 0.41. Two markers are considered as informative markers for the identification of standard type chrysanthemum cultivars. Hence, these SSR markers can be effectively applicable to provide the data for genetic similarity among the chrysanthemum cultivars and for cultivar discrimination.

Key words: Chrysanthemum, cultivar discrimination, polymorphism, SSRs, variety protection.

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Selection Efficiency of Chrysanthemum Segregation populations Using White Color Related molecular Markers

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Chrysanthemum (Dendranthema grandiflorum Kitamura) is one of the leading cut flowers in the international market and is grown worldwide in glasshouses and in the field. In respect of cultivated area and total production value it is the most important floricultural crop in Korea. Fast altering trends drive chrysanthemum breeders to create a large number of new and attractive varieties each year. In turn, wholesalers and retailers expect a good shelf-life, resulting in a satisfactory vase life of both leaves and flowers for the consumer. Moreover, it is of increasing importance that these varieties should be compatible with environmentally favorable and sustainable production systems. This study was carried out to develop for breeding selection system a stable color cultivars without regard to temperature. The white associative markers developed in the white OhBlang were distributed by the Academy of Sciences and applied to the selection of white flowers. The selection efficiency in the three posterior separation groups crossed with OhBlang varied from one combination to another. In Segregation populations of the green and white mating combination, the selection efficiency was 70% and 100% in Segregation populations of the white and white mating combination. In Segregation populations of the yellow and white matings, the phenotype and marker selection results were inconsistent. The development of more color-related markers and the addition of fewer selection efficiency tests will be necessary.

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Breeding of a new cultivar ‘Charmgreen’ of Hardy Kiwi (Actinidia arguta)

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Hardy Kiwi (Actinidia arguta (Siebold&Zucc.) Planch. ex Miq.) is a native fruit tree in Korea. Compared to other kiwifruits, Hardy kiwifruit is sweet and used as medicinal purposes, however, less productive because of its small size. During almost twenty years, Hardy kiwi varieties that has superior traits, desirable size and high-yield were bred. Among them, a new cultivar ‘Charmgreen’ is a hybrid of ‘Saehan’ which had already selected as an excellent cultivar and ‘Machua’ introduced from New Zealand as a pollinator. Fruit of Charmgreen had circular shape. Its average longitudinal and transverse diameter was 30.6 and 33.4 mm, respectively. Average fruit weight was 18.9 g and was regarded as a big-sized kiwifruit. As well, yield per tree was 15.3 kg. Charmgreen was registered as a new cultivar in National Forest Seed and Variety Center on 2017 (No. 2017-48).

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Proteomic analysis of the life cycle of marine red alga, Pyropia tenera

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The understanding life cycle of valuable marine crop, Pyropia sp, is associated with productivity, control of seedling, cultivation of Pyropia sp. Their life stage is determined by environmental factors such as temperature, light intensity and light periods. A few studies for genetic and proteomic approaches have been available until now. In order to understand proteomic differences between sporophyte and gametophyte, comprehensive analysis of proteome was performed using 2-dimensional gel electrophoresis (2-DE) combined with mass spectrometry for protein identification. Totally, 400 proteins were displayed on the 2-DE gel. Among them, about 100 proteins which were differentially expressed in each stage were selected to identify the proteins. The expression pattern was showed quite different between sporophyte and gametophyte. A lot of high molecular weight proteins (over 40 kDa) were disappeared in a sporophyte sample otherwise expressed in a gametophyte sample. Interestingly, most of identified proteins were related to photosynthesis. Proteins produced in sporophytes were involved in light capture in photosynthetic machinery otherwise gametophytes specific proteins were related to Calvin-Benson cycle which involved in energy metabolism. Allophycocyanin(AP), Phycocyanin(PC) and Phycoerythrin(PE) proteins were showed maximum 4.68 log2 fold changes which more than 25 times higher expressed in sporophyte. The expression level of Calvin Cycle related proteins were more than 2-fold higher in gametophytes. The transcription level of photosynthesis involved genes was confirmed by using RT-qPCR. These results support the theory that the life stage was controlled by photosynthetic efficiency via retrograde signaling pathway.

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Genetic Diversity and Population Structure to Construct Core Collection from a Large Pumpkin Germplasms

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Conservation of genetic diversity is an essential prerequisite for developing new cultivars with desirable agronomic traits. Although a large number of germplasm collections have been established worldwide, many of them face major difficulties due to large size and a lack of adequate information about population structure and genetic diversity. Pumpkin is one of squash plant originated from Mexico and became important nutritious vegetable containing β-carotene and vitamin A, etc. The objective of this study is to clarify genetic diversity of 618 germplasms from 83 various countries. A total of 37 sets of phenotypic data including morphological traits and, resistance to abiotic and biotic stress were recorded. 2,019 single nucleotide polymorphisms (SNPs) were selected among 1,200,400 SNPs derived from genotyping-by-sequencing (GBS) approach by multi-criteria (Minor allele frequency<0.05, SNP coverage>0.6, Inbreeding coefficient>0.8). 60 accessions were selected using heuristic search with genotypic data. Using GBS platform, we constructed high density haplotype map and analyzed genetic diversity by various stratification methods. By combining 2,019 SNPs and 37 phenotypic/morphological traits, we can construct core collection and perform Genome-wide association study (GWAS) for breeding useful new pumpkin cultivar.

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Evaluation of mutation frequencies induced by gamma-ray irradiation of faba bean seeds using TRAP markers and their application

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Faba bean (Vicia faba L.) is an agriculturally important crop which is grown for food, feed, and vegetable in many countries. The aims of this study were to determine the optimal gamma ray dose for faba bean mutation breeding and to identify genetic variations and mutation frequencies among mutant individuals using target region amplification polymorphism (TRAP) markers. The seeds of 10 elite faba bean lines were irradiated with gamma rays (50-700 Gray), and germination, survival rate, and representative morphological traits were measured. Germination percentages significantly decreased at doses >100 Gray. Survival percentages and morphological traits decreased with elevation in dose. The optimal gamma dose showed in 100-150 Gray on the basis of survival percentage and morphological response analysis. The extent of DNA damage was investigated using comet assays which were revealed that high irradiation doses decreased head DNA levels. For evaluation of genetic variation, genetic diversity, and mutation frequencies, eight primer combinations (PC) of TRAP system were applied with 555 individual faba bean plants. The highest polymorphism level (80.8%) was obtained using the MIR159A + Sa4 pc, whereas the lowest polymorphism level (48.0%) was obtained using the B14G15B + Sa12 pc. Phylogenetic, population structure, and principal component analysis of 555 individuals resolved eight major groups. Genetic variation between controls and mutants was limited to within groups. Mutation frequencies were associated with gamma dose in each mutant line. Ultimately, The TRAP markers distinguished mutant lines and showed association between mutation frequency and gamma doses. This study will be useful for faba bean mutation breeding and may be applicable to other crops.

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Evaluation of phenolic content and antioxidant activity in two different color chrysanthemum tea cultivars

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Chrysanthemum morifolium Ramat is a perennial flowering plant widely cultivated to use in a tea infusion and as a popular beverage. To identify and evaluate the tea infusion made with a γ-irradiated mutant chrysanthemum cultivar with dark purple petals (cv. ARTI-Dark Chocolate), its phytochemical composition and antioxidant activity were tested and compared with those of the commercially available chrysanthemum cultivar with yellow petals (cv. Ganugale) by HPLC-DAD-ESIMS, as well as DPPH and ABTS radical scavenging assays. The purple chrysanthemum tea contained anthocyanins and linarin, which were not detected in the yellow chrysanthemum tea and the content of chlorogenic acid, acacetin-7-O-β-glucoside, and luteolin was higher compared with the yellow chrysanthemum tea. In contrast, the yellow chrysanthemum tea had higher luteolin-7-O-β-glucoside, 3,5-dicaffeoylquinic acid, apigenin-7-O-β-glucoside, and apigenin contents in comparison with the purple chrysanthemum tea. In addition, the content and antioxidant activity of the two chrysanthemum teas were investigated according to different water temperatures and infusing time. The yellow chrysanthemum tea did not show any significant differences according to infusing time and temperature, while the purple chrysanthemum tea was more influenced by the infusing time than water temperature, showing the highest total compound content in the infusing condition of 100 °C and 4 min. In the DPPH radical scavenging assay, the purple chrysanthemum tea broadly showed greater antioxidant activity than did the yellow chrysanthemum tea, corresponding to the high content of anthocyanins known as the powerful antioxidant. Further, both chrysanthemum flower teas exhibited strong ABTS radical scavenging effects ranging from 76% to 61% under all infusing conditions. Therefore, the purple chrysanthemum cultivar, ARTI-Dark Chocolate, is worthy of breeding as a new tea cultivar.

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Characterization of a novel Sg-10 gene responsible for the soyasaponin biosynthesis in soybean

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Soybean [Glycine max (L.) Merr.] seeds are abundant in high-quality proteins and fats. In addition, soybean seeds are also rich in secondary metabolites, such as isoflavones, lecithin, and saponins. Saponins are one of major components among the physiologically active metabolites in soybean seeds and mainly classified into two groups such as group A and DDMP saponins. Soybean saponins and their derivatives are beneficial to human health when consumed as a regular diet. Therefore, a need exists for a full understanding of the saponin biosynthesis pathway to engineer the saponin metabolism in soybean through genetic approaches. In this study, we have isolated an EMS-induced mutant line (PE1653) with reduced total saponin accumulation to identify and characterize the gene involved in the early stage of saponin biosynthesis. LC-PDA/MS/MS analysis showed that this mutant has low saponin concentration compared with the wild-type soybean. A breeding cross has been made with the mutant PE1653 along with a soybean cultivar Jinpung to study the segregation and physical mapping analyses. The segregation analysis showed that the mutant phenotype is controlled by a single recessive gene (sg-10). The position of the locus (Sg-10) was mapped to 1.3 Mb region using bulk segregation and SNP array analyses. Further, the fine mapping will be carried out using SNP marker analysis to identify the gene which is responsible for low saponin concentration in PE1653 mutant.

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Characterization and Genetic Analysis of a spotted leaf sheath Mutant Involved in ROS homeostasis in Rice

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Lesion mimic mutants (LMMs) commonly exhibit spontaneous cell death similar to the hypersensitive defense response that occurs in plants in response to pathogen infection. Several lesion mimic mutants have been isolated and characterized, but their molecular mechanisms remain largely unknown. Here, a spotted leaf sheath (SLES) mutant derived from japonica cultivar Koshihikari is described. The SLES phenotype differed from that of other LMMs in that lesion mimic spots were observed on the leaf sheath rather than on leaves. The SLES mutant displayed early senescence, as shown, by color loss in the mesophyll cells, a decrease in chlorophyll content, and upregulation of chlorophyll degradation-related and senescence-associated genes. ROS content was also elevated, corresponding to increased expression of genes encoding ROS-generating enzymes. Pathogenesis-related genes were also activated and showed improved resistance to pathogen infection on the leaf sheath. Genetic analysis revealed that the mutant phenotype was controlled by a single recessive nuclear gene. Genetic mapping and sequence analysis showed that a single nucleotide substitution in the sixth exon of LOC Os07g25680 was responsible for the SLES mutant phenotype and this was confirmed by T-DNA insertion line. Taken together, our results revealed that SLES was associated with the formation of lesion mimic spots on the leaf sheath resulting early senescence and defense responses. Further examination of SLES will facilitate a better understanding of the molecular mechanisms involved in ROS homeostasis and may also provide opportunities to improve pathogen resistance in rice.

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Genetic analysis of giant embryo mutants and identification of LARGE EMBRYO(LE) controlling embryo size in rice

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Rice hulls consist of two bract-like structures, the lemma and palea. The hull is an important organ that helps to protect seeds from environmental stress, determines seed shape, and ensures grain filling. Achieving optimal hull size and morphology is beneficial for seed development. We characterized the split-hull (sph) mutant in rice, which exhibits hull splitting in the interlocking part between lemma and palea and/or the folded part of the lemma during the grain filling stage. Morphological and chemical analysis revealed that reduction in the width of the lemma and lignin content of the hull in the sph mutant might be the cause of hull splitting. Genetic analysis indicated that the mutant phenotype was controlled by a single recessive gene, sph (Os04g0447100), which encodes a type-2 13-lipoxygenase. SPH knockout and knockdown transgenic plants displayed the same split-hull phenotype as in the mutant. The sph mutant showed significantly higher linoleic and linolenic acid (substrates of lipoxygenase) contents in spikelets compared to the wild type. It is probably due to the genetic defect of SPH and subsequent decrease in lipoxygenase activity. In dehulling experiment, the sph mutant showed high dehulling efficiency even by a weak tearing force in a dehulling machine. Collectively, the results provide a basis for understanding of the functional role of lipoxygenase in structure and maintenance of hulls, and would facilitate breeding of easy-dehulling rice.

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A Novel Allelic Mutation in LPA1 Gene results in Low Phytic Acid in Rice (Oryza Sativa L.)

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In plants, myo-inositol-1,2,3,4,5,6-hexakisphosphate (InsP6), also known as phytic acid (PA), is a major component of organic phosphorus (P), and accounts for up to 85% of the total P in seeds. In rice (Oryza sativa L.), PA mainly accumulates in rice bran, and chelates mineral cations, resulting in mineral deficiencies among brown rice consumers. Therefore, considerable efforts have been focused on the development of low PA (LPA) rice cultivars. In this study, we performed genetic and molecular analyses of OsLpa1, a major PA biosynthesis gene, in Sanggol, a low PA mutant variety developed via chemical mutagenesis of Ilpum rice cultivar. Genetic segregation and sequencing analyses revealed that a recessive allele, lpa1-3, at the OsLpa1 locus (Os02g0819400) was responsible for a significant reduction in seed PA content in Sanggol. The lpa1-3 gene harbored a point mutation (C623T) in the fourth exon of the predicted coding region, resulting in threonine (Thr) to isoleucine (Ile) amino acid substitution at position 208 (Thr208Ile). Three-dimensional analysis of Lpa1 protein structure indicated that myo-inositol 3-monophosphate [Ins3(3)P1] could bind to the active site of Lpa1, with ATP as a cofactor for catalysis. Furthermore, the presence of Thr208 in the loop adjacent to the entry site of the binding pocket suggests that Thr208Ile substitution is involved in regulating enzyme activity via phosphorylation. Therefore, we propose that Thr208Ile substitution in lpa1-3 reduces Lpa1 enzyme activity in Sanggol, resulting in reduced PA biosynthesis.

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Genetic Diversity and Relationship in Soybean MDP (Mutant Diversity Pool) Revealed by TRAP and TE–TRAP Markers

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In this study, we evaluated the 11 agronomic traits in 528 soybean mutant lines for selecting elite mutants with acquisition of the various genetic pools. As a result, 210 soybean mutants with their original cultivars were selection based on the investigated traits and we named 210 selected lines as Mutant Diversity Pool (MDP). To investigate genetic diversity and relationship among MDP, we confirmed total of the 551 amplified fragments derived from 16 primer combination in TRAP marker. The highest (84.0%) and the lowest (32.35%) polymorphism levels were showed in MIR157B+Ga5 and B14G14B+Ga3, respectively. Based on the phylogenetic tree and population structure analysis, the MDP lines divided into four groups and highest genetic diversity observed between ‘Paldal’ and 523-7 (FST=0.409) lines, whereas the lowest genetic diversity exhibited between KAS360-22 and 94seori (FST=0.065) lines. AMOVA analysis revealed that a percentage of variations was 11.583 (21.0%) and 43.532 (79.0%), inter and intra mutant population, respectively. Overall, the genetic similarity of each intra mutant populations was closer than inter mutant population. In TE-TRAP marker analysis, a total of 408 fragments were amplified derived from 12 primer combinations that was obtained from a combination of 3 TIR sequence of transposable elements (MITE-stowaway; Ms, MITE-tourist; M4, PONG). The polymorphism levels ranged from PONG+Sa4 (77.42%) to PONG+Sa12 (56.0%). Compared genetic variation within and among populations, M+ and M4 showed similar level at 2.209 (20%) and 8.957 (80%), 2.766 (18%) and 12.385 (82%) variations of inter and intra mutant population, respectively. However, PONG was revealed 3.151 (29%) and 7.646 (71%), these results indicating that an aspect of radiation sensitivity, M+ and M4 showed higher mobility than that of PONG. Our TRAP and TE-TRAP markers results may be useful for assessing the genetic diversity and relationship among soybean mutants.

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Transcriptome Analysis of Differentially Expressed Unigenes Involved in Anthocyanins and Kaempferitrin Biosynthesis in Kenaf (Hibiscus cannabinus L.) Based on De Novo RNA-Seq

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Kenaf (Hibiscus cannabinus) is a valuable fiber and medicinal crop. In this study, we performed an RNA sequencing-based transcriptome analysis of kenaf leaves from six kenaf cultivars/mutants. A total of 396,030,664 base pairs were generated by paired-end sequencing from a merged representative unigene set. De novo assembly yielded 299,880 unigenes having an average length of 1,217 bp, of which 231,825 (77.3%) were annotated against various databases, such as UniProt, NCBI NR, TAIR, InterPro, PlantCyc, COG and KEGG. To identify genes potentially related to flavonoid biosynthesis in kenaf, we compared the transcriptomes of kenaf cultivar C-14 and two of its mutant lines, Jeokbong (purple leaves and stems) and Backma (light-green leaves and stems). In addition to their altered coloration, leaves of these two mutants had significantly different anthocyanin and kaempferitrin contents. We therefore reconstructed anthocyanin and kaempferitrin biosynthetic pathways based on four KEGG pathways and identified 671 unigenes mapping to the entire flavonoid biosynthetic pathway.

Furthermore, a differentially expressed gene (DEG) enrichment analysis of the anthocyanin-accumulating mutant Jeokbong identified 29 DEGs assigned to eight structural genes (4CL, CHS, CHI, F3H, DFR, ANS, FLS, and 3GT) and 41 DEGs related to MYB, bHLH, and WD40 transcription factors. Our results provide a large transcriptome library pool for understanding gene functions and should also be useful in further studies of flavonoid biosynthesis in kenaf.

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Development of high linolenic acid soybean mutants and measuring expression of fatty acid related genes in development stages

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Soybean oil is one of the most widely consumed cooking oil, is interesting for its richness in polyunsaturated fatty acid. Linoleic and linolenic acid, essential polyunsaturated fatty acids, found mostly in plant oil and can not produced within human body and animals. Linoleic acid are considered for good health and can be used for the prevention of many diseases. Health benefits and biological equivalency of linolenic acid is a topic of strong interest. Seed of two soybean cultivars Danback (DB) and Daepung (DP) were irradiated with gamma rays. Linolenic acid content of 78 and 154 M9 mutant lines from above two cultivars were evaluated from M9 generation and four elite lines with the highest fatty acid proportion in seed were selected through 2 years of investigation. Seed linolenic acid proportions were determined and compared in M10 generation. The expression level of linolenic acid synthesis genes during seed development were detected using quantitative RT-PCR (qRT-PCR) and FATTY ACID DESATURASE (FADs) genetic variation were compared. Four selected mutant lines had increased linolenic acid contents, 33.9% and 69% higher compared to the original cultivars. FADs gene showed common up-regulated gene expression in the mutant selected lines compared to their original cultivars during seed development. The increased expression levels of FAD3D and FAD3C gene in selected mutant lines probably varied in promoter region or regulation transcription factors (TFs). Increased levels of linolenic acid content was closely associated with increased expression levels of FAD3C and FAD3D genes in the endoplasmic reticulum, which was uncovered by radiation mutation breeding of soybean.

Keywords: Linolenic acid, gamma ray, soybean, fatty acid desaturase, mutation breeding

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Development of EST-SSR markers through de novo RNA seq and application of genetic diversity and relationship in *Perilla* germplasms

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**Chemical contents of novel *Dendrobium* mutants developed by mutation breeding techniques**

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Dendrobium plants are the most important orchids used in oriental medicine East Asia. This study quantified the functional compounds among 7 Dendrobium mutant genotypes using HPLC-MS. Recently, several Dendrobium mutant genotypes with improved horticultural traits have been developed using various mutagens such as gamma irradiation (*D. loddigesii*), somaclonal variation (*D. candidum*), and aerospace mutagenesis (*D. moniliforme*). The highest total phenolic content (TPC) and total flavonoid content (TFC) were observed in the *D. loddigesii* and the lowest content in the *D. moniliforme*. Among the solvents studied, the highest content of TPC and TFC contents were observed for the water extract in all genotypes. HPLC-MS analyses identified 28 different phenolic compounds in the *Dendrobium* genotypes. Rutin, apigenin-6,8-di-c-b-D-glucoside, Diosmetin-6,8-di-C-glucoside were major phenolic compounds in the *D. candidum* genotypes. The most abundant phenolic compounds were Apigenin-6,8-di-C-b-D-glucoside, quercetin-acetyhexoside and unknown compound (347 m/z) in *D. loddigesii* genotype: rutin, narirutin, nariginin and didymin were the principal phenolic compounds in *D. moniliforme*. These results may help determine the optimal genotypes for breeding new cultivars of *Dendrobium* with potentially greater health benefits.

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Analysis of Volatile Oil Compositions of Gamma Irradiated Mutant Rose (Rosa hybrid Hortorum) Cultivars

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Roses (Rosa hybrid Hortorum) are important ornamental crops and they also are economically important as a source of essential oils for perfumes industry. In this research, we investigated the volatile compound compositions of five rose mutant lines and their original cultivars. The rose mutant lines were developed through the treatment of 70 Gy gamma-ray (60Co) source on stem cuttings of the commercials cultivar (Lovelydia). The Lovelydia cultivar has red petal and middle open flower types. Five mutant lines have novel characteristics that distinguish from these original cultivar, such as pink petal (CR-S10), light-pink petal (CR-S11) increase of petal numbers (CR-S12), wide open flower types (CR-S8) and round flower shape (CR-S9). Essential oils from full bloom flower were analyzed by gas chromatography- mass spectrometry (GC-MS). Fifty-five volatile compounds were detected and the abundant volatiles were hydrocarbons and terpenoids in the all rose genotypes. The results showed that the corolla types changed lines, CR-S8 and CR-S9 showed higher contents of hydrocarbon compounds than did the respective original cultivars. The pink petal mutant line (CR-S12) contained more than two-times higher oil yield compared to their original cultivars. These findings suggested the potentials of using the selected radiation mutant rose cultivars as a functional source, related to the abundant of aroma beneficial components.

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Variations in Phenolic compounds and chemical fingerprints from the leaves of Roselle (Hibiscus sabdariffa L.) accessions

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The leaves of roselle (Hibiscus sabdariffa L.) have been used as traditional folk medicines for diuretic and mild laxative. Roselle is cultivated throughout much of the world for medicines and food. However, study on the variation of functional compounds in different accessions are relatively limited. This study investigated the phenolic compound contents to assess the pharmacological properties and chemical classification of 49 different roselle accessions from worldwide collection by ultra-high performance liquid chromatography mass spectrometry. The phenolic compounds were identified as neochlorogenic acid, cryptochlorogenic acid, rutin, rutin isomer, isoquercitin, kaempferol-3-O-rutinoside, kaempferol-3-O-glucoside, quercetin, quercetin isomer and kaempferol. We found significant differences in the phenolic compound levels of leaves from all accessions. The most abundant phenolic compound was rutin in 45 accessions. The total phenolic compound contents (TPC) ranged from 18.75 to 46.51 mg/g with average contents of 31.52 mg/g. The two accessions showing the highest TPC contents were from Ghana (PI286316) and Senegal (PI275413). The cluster analysis of the showed that all the Roselle accessions could be classified into three category based on phenolic compound contents. These results could be used for the selection of Roselle genotypes with improved functional compounds.

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Selection of Mutant with Fatty Acid Compositions in Rapeseed (*Brassica napus*)

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Rapeseed (*Brassica napus* L.) is one of the most important oil crop worldwide. Mutation breeding techniques have been used for modify fatty acid composition in oil crops. This study was conducted to evaluate the fatty acid composition among 56 rapeseed mutants derived from commercial rapeseed cultivar ("Tammi"). The 56 mutant lines were obtained through gamma irradiation. Mutant selections were carried out to altered crude fat content and fatty acid composition in seed oil from M₄ generations. The crude fat content was 33.98% for the original cultivar. Whereas the crude fat content of 56 mutant lines varied from 26.85 to 42.32%. The palmitic, stearic, oleic, linoleic, linolenic and erucic acid content of the original cultivar was 3.82%, 0.00%, 66.28%, 19.30%, 6.19% and 0.4%, respectively. The fatty acid composition of the mutant lines ranged from 3.35 to 5.59% for palmitic acid, 0 to 14.72% for stearic acid, 37.26 to 73.45% for oleic acid, 12.04 to 22.32% for linoleic acid, 1.44% to 8.62% for linolenic acid and 0.01 to 21.61% for erucic acid. This material can be used to get more information about the biochemistry and regulation of lipid metabolism. The mutant lines are also most valuable for rapeseed breeding programs directed on the development of cultivars with specific seed oil qualities.

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Evaluation of sensitivity to DNA methyltransferase inhibitors and gamma rays in rice

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Mutation breeding is a useful technique for crop improvement. Chemical mutagens, such as ethyl methane sulphonate and ethyleneimine, and physical mutagens, such as gamma rays, X-rays and ion beams, have mainly been used to induce mutations. DNA methyltransferase inhibitor (DNMTi) reduces catalytic activity and reduces total DNA methylation through covalent binding with methyltransferases. It is involved in transcriptional regulation, formation and maintenance of (hetero-)chromatin. This study was performed to evaluate sensitivity to DNMTi, gamma rays, and their combined treatments in rice. Rice seeds were treated with two types of DNMTi, 5-azacytidine and zebularine (20, 40, and 80 μM), and were irradiated using a ⁶₀Co gamma irradiator (100, 150, 200, 250, and 300 Gy). Steady reduction in germination rate, survival rate, root and shoot length was observed in M₄ plants. Combination treatment of DNMTi and gamma rays caused more damage than single treatment of DNMTi or gamma rays. The LD₅₀ and RD₅₀ estimated by analyzing the survival rate and the growth of four-week-old seedlings were 60 to 80 μM for DNMTi and 250 to 300 Gy for gamma rays, respectively. To induce mutations with combination treatment, doses from 40 to 80 μM for DNMTi and from 100 to 150 Gy for gamma rays seem to be proper.

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Studies on Change of Some Agricultural traits of Colored Rice by Gamma-ray Treatment

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Pigmented rice varieties contain various natural pigments such as reddish red, dark red, dark brown and black purple. The black color of rice contains a large amount of anthocyanin pigments. It enhances antioxidant, anti-cancer function, human immune function, and it is known that it is highly useful as a functional food material. Recently, rice breeding has become an important goal not only in terms of increasing the yield, improving the quality and stability of cultivation, but also cultivating varieties for special use and purpose.

In this study, mutagenicity of gamma ray was induced in C3G-rich functional varieties of Korea National Open University to investigate the agricultural traits of in M\textsubscript{2} generation and to breed for market needs.

The test varieties were irradiated with 100 Gy, 200 Gy and 300 Gy of gamma ray. In M\textsubscript{2} generation some agricultural traits were examined and C3G contents were analyzed.

As a result of investigation of the germination rate of the next group after irradiation with gamma rays, the germination rate of ‘Superhongmi’ was 83\% in 100 Gy. However, as the radiation dose increased, it was rapidly decreased to 52\% and 32\%.

To develop the lines with waxy and semi-dwarf, the plants selected by Iodine test and phenotype investigate with C3G contents analysis.

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Identification of genomic region controlling \(\omega\)-linolenic acid concentration for a mutant soybean line ‘PE2166’

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Soybean seed has about 20\% oil content at maturity with the oil being the world’s most widely used vegetable oil. Soybeans contain five predominant fatty acids, 12\% palmitic acid, 4\% stearic acid, 23\% oleic acid (\(\omega\)-9), 54\% linoleic acid (\(\omega\)-6, LA) and 8\% \(\omega\)-linolenic acid (\(\omega\)-3, ALA). ALA or \(\omega\)-3 was reported to have anticancer and anti-inflammatory effects and a role in preventing cardiovascular diseases. Several studies have shown that minimizing the \(\omega\)-6/\(\omega\)-3 ratio in edible oils could have human health benefits. Therefore, increasing \(\omega\)-3 concentration in seed oil has become a goal in breeding programs. Normal soybeans contain \(~8\%\) \(\omega\)-3 in seed oil, wherever ‘PE2166’ produced by ethyl methyl sulfonate (EMS) mutation of ‘Pungnamannul’ have \(~14\%\). A cross between ‘Daepung’ with \(~8\%\) \(\omega\)-3 concentration was made with EMS mutant soybean ‘PE2166’, with \(~14\%\) \(\omega\)-3. There was large variation in ALA content in F\textsubscript{3} RIL population range from 5.1 to 18.1\%. ICIMapping and GWAS analyzes were conducted and high LOD score were confirmed on chromosome 5, the analysis was made in 2 locations of 2 years data. Through NGS analysis, SNP changes in the candidate region was investigated and finally 2 candidate genes were identified.

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Response of Embryogenic Calli of Arabica Coffee Var. Kartika against Gamma Irradiation

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Arabica coffee (Coffea arabica) is a self-pollinating plant that has narrow genetic diversity. Mutation induction using gamma rays is expected to increase its genetic diversity, so that it can support Arabica coffee plant breeding programs. This study aimed to obtain lethal dose value (LD_{20}-LD_{30}) which will be used as the basis for mutations induction of embryogenic calli, and to observe the effect of gamma irradiation on the growth and development of somatic embryos of Arabica coffee var. Kartika. The study was conducted at the Tissue Culture Laboratory, Indonesian Industrial and Beverage Crops Research Institute, from July 2017 to April 2019. The embryogenic calli of Arabica coffee var. Kartika was used as research material. The treatments tested were gamma irradiation doses at 0, 10, 20, 30, 40 and 50 Gy. The calli treated with gamma irradiation was weighed 0.2 grams, then sub cultured on Murashige and Skoog (MS) media at half salt solution concentrations, 35% sucrose, kinetin 9.30 μM, Caseine hydrolyzate and Malt extract each 400 mg L^{-1} and phytagel 2.5 gram L^{-1}. Torpedo phase somatic embryos were sub cultured to MS media given 1.33 μM BAP, 40% sucrose and phytagel 2.5 gram L^{-1}. The results showed the values of LD_{20} and LD_{30} of Kartika Arabica coffee are 17.21 and 26.45 Gy, respectively. The treatment of more than 20 Gy dose of gamma irradiation decreased calli fresh weight, while doses of more than 10 Gy decreased the number of torpedo phase somatic embryos produced. The higher gamma irradiation dose can inhibit the germination of Arabica coffee that caused the number of produced plantlets decreases.

Keywords: Coffea arabica, embryo somatic, genetic diversity, lethal dose, mutation

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Transcriptome analysis of cowpea in response to gamma-ray and proton-beam irradiation

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In this study, we investigated transcripational responses of cowpea plants exposed to two different types of radiations, the proton-beam and the gamma-ray. Seeds of Okdang cultivar were irradiated to 100, 200 and 300 Gy of gamma-ray and proton-beam, respectively. RNA was extracted from fresh leaf tissues at 4 weeks after planting and RNA-seq was performed using the Illumina HiSeq 2000. We identified 32, 75 and 69 differentially expressed genes (DEGs) per each dosage (100Gy, 200Gy, 300Gy) of gamma-ray irradiation compared with control. In contrast, 168, 434 and 387 DEGs were selected for each dose of proton beam irradiation compared with control. A total of 61 DEGs were commonly up-regulated at all doses of proton beam. The functions of DEGs were involved in heat shock transcription factor A6B, chaperone DnaJ-domain superfamily protein, nitrate reductase 1, NAC transcription factor-like 9 and beta glucosidase 15. In addition, one down-regulated gene is involved in nodulin MNN21 / EmA-like transporter family protein 1. In all doses of gamma-rays, a total of 8 genes were up-regulated. These DEGs were involved in Subtilisin-like serine endopeptidase family protein, NAD(P)-binding Rossmann-fold superfamily protein, Peroxidase superfamily protein and cytochrome P450, family 78, subfamily A, polypeptide 6. However, there is no down-regulated gene. Our research provides important information on the mechanism for gene regulation in responses to two ionizing radiations in cowpea.

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**Characterizing alleles for early maturity at two heading date loci derived from “Baegilmi”, a “Koshihikari” mutant rice cultivar**

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“Baegilmi” is an extremely early-maturing Korean rice cultivar developed by the ethyl methanesulfonate (EMS) mutagenesis of a Japanese premium quality cultivar “Koshihikari”. To detect chromosomal locations responsible for the early maturity of Baegilmi, we developed a mapping population composed of 142 recombinant inbred lines (RILs) derived from a cross between Koshihikari and Baegilmi. A total of 125 single nucleotide polymorphism (SNP) markers selected from the genotyping-by-sequencing (GBS) of the RIL population were used for the genetic map construction and linkage mapping for days to heading (DH). Two major loci for DH, qDH6 and qDH7, were identified on the short arms of chromosomes 6 and 7, respectively, each explaining over 20% of the phenotypic variances. When the homozygous Baegilmi alleles replace the homozygous Koshihikari alleles at qDH6, DH was expected to be advanced by 9.5-9.9 days. Similarly, DH advance of 10.2-10.5 days was expected when the homozygous Baegilmi alleles replace the homozygous Koshihikari alleles at qDH7. Two-way ANOVA revealed no significant interaction between qDH6 and qDH7 on DH. Further study on identifying the causal induced mutations underlying qDH6 and qDH7 in Baegilmi is on-going. The two induced alleles of qDH6 and qDH7 from Baegilmi would provide useful sources for developing early maturing rice cultivars that can be utilized in diversifying cropping system in rice paddies to increase farmers’ income.

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**PCS11-21**

**A Large Sized Sweet Persimmon (Diospyros kaki Thunb.) Cultivar, 'Dannuri' with High Sugar Content**

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'Dannuri' is a new persimmon cultivar with high quality. It has been bred in 2018 by Sweet Persimmon Research Institute from a crossing between 'Danyeon 104' and 'Taishu'. It is safe for late frost damage in spring due to its late bud break. Fruits ripen around October 12 in Gimhae, which is 29 days faster than those of 'Fuyu' (standard cultivar), and their average weight is 320 g, 45% larger than that of 'Fuyu'. Fruit shape index (diameter/length) is lower than the standard cultivar. De-astringency character of the flesh shows pollination constant non-astringent type. This cultivar is characterized by high sugar content of 18.4 °Brix in the flesh, about 2.2 °Brix higher than that of 'Fuyu'. The flesh tends to fast soften after harvest, compared with 'Fuyu'. Although 'Taishu', having a lot of stain in the skin, was crossed for this cultivar, the occurrence of stains is rare in 'Dannuri'. The fruit contains 2 seeds in average, reflecting higher eating convenience than 'Fuyu' fruit (4 seeds/fruit). Since the tree bears large sized fruits in general, adjusting leaf-to-fruit ratio to 15-20 by flower bud and fruitlet thinning is required to prevent the tree vigor from weakness.

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Assessment of Kenaf (Hibiscus cannabinus L.) Mutants Induced by Gamma-Ray

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Kenaf (Hibiscus cannabinus L.) is known as a multipurpose crop producing biomass for energy thus, the study was conducted to select the elite mutants with higher biomass and salt tolerance produced through mutation. Obtained from the National Agricultural Genetic Resources Center (NAGRC) in Korea, the seeds of the original natural resource named IT202801 (Control) were irradiated with 250 Gy gamma-ray. It was possible to select the elite mutant lines based on the agronomic performances, genetic variation and histological analysis at M4 generation in comparison with to the Control. The leaf shape of the Control was entire, while the leaf shape of the mutant was palmate. Of many lines, IT20-5 showed better performance in regard to diameter, dry weight and seed weight per plant. At the M5 generation, this line presented tolerance for anthracnose at the germination stage. Its survival rate was 57.1%, however, its Control showed the survival rate of 28.6%. Also, IT20-5 line presented better growth condition than the Control at reclaimed soil. The Control bloomed earlier than the IT20-5, so the plant height of the Control was decreased sharply compared to the IT20-5. For SPAD value, the Control and IT20-5 showed 46 and 38.3 respectively at soil without salt. However, 39.8 and 38 in 15 days at reclaimed soil. It demonstrated differentiation between the Control and IT20-5 mutant. Taken together, the mutant line, T20-5, can be useful resource so as to respond to reclaimed land.

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Breeding efforts to reduce the immunogenic potential of wheat flour: omega gliadins encoded by the D genome of hexaploid wheat may also harbor epitopes for the serious food allergy WDEIA

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Omega-5 gliadins are a group of highly repetitive gluten proteins in wheat flour encoded on the 1B chromosome of hexaploid wheat. These proteins are the major sensitizing allergens in a severe form of food allergy called wheat-dependent exercise-induced anaphylaxis (WDEIA). The elimination of omega-5 gliadins from wheat flour through biotechnology or breeding approaches could reduce the immunogenic potential and adverse health effects of the flour. A mutant line missing low-molecular weight glutenin subunits encoded at the Glu-B3 locus was selected previously from a doubled haploid population generated from two Korean wheat cultivars. Analysis of flour from the mutant line by 2-dimensional gel electrophoresis coupled with tandem mass spectrometry revealed that the omega-5 gliadins and several gamma gliadins encoded by the closely linked Glu-B1 locus were also missing as a result of a deletion of at least 5.8 Mb of chromosome 1B. Two-dimensional immunoblot analysis of flour proteins using sera from WDEIA patients showed reduced IgE reactivity in the mutant relative to the parental lines due to the absence of the major omega-5 gliadins. However, two minor proteins showed strong reactivity to patient sera in both the parental and the mutant lines and also reacted with a monoclonal antibody against omega-5 gliadin. Analysis of the two minor reactive proteins by mass spectrometry revealed that both proteins correspond to omega-5 gliadin genes encoded on chromosome 1D that were thought previously to be pseudogenes. The work illustrates the importance of detailed knowledge about the genomic regions harboring the major gluten protein genes in individual wheat cultivars for future efforts aimed at reducing the immunogenic potential of wheat flour.

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Associate analysis for grain size in rice using large grain mutant induced by EMS

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Grain size is one of major determinant of grain yield in rice. Large grain mutant (LGM) was developed from ‘Hyowon 6’, high quality japonica variety, by EMS (Ethyle Methanesulfonate). Length and width of LGM are 4% and 11% longer than ‘Hyowon 6’. 1000 grain weight of LGM is 114% of ‘Hyowon 6’. To detect the gene caused LGM, 117 F2 population was developed from a cross LGM and ‘Hanareum’, a tongil-type variety. The length of ‘Hanareum’ and LGM were 8.02 cm and 8.55 cm, the width were 3.0 cm and 3.72 cm and the thickness were 2.0 cm and 2.31 cm, respectively. The length of F2 seeds derived from each F2 individuals were from 6.89cm to 8.92cm. The Width and thickness of F2 seeds were from 2.79 cm to 3.62 cm and from 1.85 cm to 2.37 cm, respectively. To detect Gene associated with grain size, we will perform Fluidigm analysis on parent plants and F2 population.

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Analysis of genetic variations in gamma radiation-induced salt-tolerant silage maize mutants

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Salt stress is a significant factor limiting growth and productivity of crops. However, little is known about the response and resistance mechanism to salt stress in maize. The objective of this research is to develop an enhanced salt-tolerant silage maize by mutagenesis with gamma radiation. To generate gamma radiation-induced salt-tolerant silage maize, we irradiated 100 gray (Gy) gamma rays to KS140 inbred line. Salt tolerance was evaluated by the plant growth, morphological changes, and gene expression under NaCl stress. We screened 10 salt-tolerant maize inbred lines from 2,248 M2 mutant populations and selected one of them. The selected mutant 140RS516 exhibited improved seed germination and plant growth compared with wild-type under salt stress conditions. Enhanced salt tolerance of the 140RS516 mutant was attributed to higher stomatal conductance and proline contents. In re-sequencing analysis, total 384 of single nucleotide polymorphisms (SNPs) were identified in 140RS516 mutant. We found that the expression of ABP9, CIPK21, and CIPK31 genes, which are involved in salt stress tolerance, were increased by salt stress in 140RS516 mutant. Our results suggest that genetic variations in 140RS516 mutant caused by gamma rays might be associated with higher salt tolerance in maize.

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Development of Glucoraphanin-rich Broccoli Inbreeding Lines

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To date, over 120 kinds of glucosinolate have been found in Brassicaceae family. It is known that glucosinolate is decomposed into isothiocyanate, glucose, acid sulphate and so on by enzymatic action called myrosinase. Among them, isothiocyanate is known to health beneficial effects such as strong anti-cancer, anti-bacterial and insecticidal action. Broccoli (Brassica oleracea var. italica) is one of Brassicaceae that is known to have a variety of health beneficial effects including anti-cancer, hypertension prevention, and cardiovascular disease prevention, etc. Therefore, domestic consumption of broccoli in Korea has been rapidly increasing since 2000. A representative functional compound of broccoli is known as sulforaphane (S-methylsulfinylbutyl isothiocyanate). Broccoli synthesis glucoraphanin, a precursor of sulforaphane, and is known to be produced by sulforaphane and sulforaphane nitrile as they are degraded by myrosinase when the tissue is mechanically wounded. Therefore, the various health beneficial effects of broccoli are thought to be proportional to the content of glucoraphanin, and attempts have been made to increase the content of glucoraphanin. However, there are many constraints to make high content of glucoraphanin through traditional breeding program. Therefore, we intend to breed broccoli cultivars with increased glucoraphanin content by applying the latest genome editing technology called CRISPR / Cas9 directly to the current inbreeding lines. Here we present the current status of genome edited-broccoli lines using the genes encoding MYB transcription factor protein.

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Development of Environmental Stress Stable Non-pungent Pepper Inbreeding Lines

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Consumers and growers of peppers (C. annuum) are demanding a low pungent green pepper varieties that are stable to environmental stress. However, the pungent taste of green pepper sold in Korea market is highly dependent on environmental stress (temperature, moisture, nutrients, etc.). However, there is a considerable difficulty in breeding low-pungent cultivars by applying traditional breeding techniques, as well as need a long time and huge amount of investment. Therefore, in this project, we select the genes involved in the capsaicin biosynthetic pathway by environmental stress. We applied genome editing techniques (CRISPR / Cas9) to knock the genes involved the pathway. In this conference, we present the current status of the project.

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Screening efficient CRISPR-RNPs in protoplasts of two pepper cultivars

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DNA-free, targeted genome editing is a vital trial for precision crop editing in GMO concerns. RNA-guided programmable nuclease, such as a CRISPR/Cas9 or a CRISPR/Cpf1 is the representative molecular scissors for precision genome editing, which can be delivered by preassembled CRISPR-Cas9 or Cpf1 ribonucleoproteins (CRISPR-RNPs) as a DNA-free tool. We had successfully applied CRISPR-RNP tools to various plants; Arabidopsis, soybean, cabbage, rapeseed, wild tobacco, and rice. Although pepper is one of the most economically essential vegetables of the Solanaceae, precision breeding application in pepper is still far from a market. To employ versatile genome-editing tools for precision pepper improvement, we have developed a stable source of pepper protoplasts from soil-grown, leaf-derived cali in both hot pepper CM334 and bell pepper Dempsey. Additionally, we successfully obtained stable pepper protoplasts and edited a target gene with both CRISPR-Cas9 RNP and CRISPR-Cpf1 RNP.

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Functions and molecular mechanism of NF-Y members with an ERF transcription factor in developing endosperm and grain filling using CRISPR/Cas9 system

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Rice endosperm consists of starchy endosperm and the aleurone layer. During grain filling, nutrients are transported into the developing caryopsis through the dorsal vascular bundle, then into the nucellar projection and finally to the endosperm. Grain yield and quality of rice mainly depend on grain filling and endosperm development. Here we report that rice NUCLEAR FACTOR Y (NF-Y) members with an ERF transcription factor, were specifically expressed in the aleurone layer of developing endosperm and regulates grain filling and endosperm development. Knockout genes encoding OsNF-Y members using CRISPR/Cas9 system significantly retarded grain filling, leading to small grains with chalky endosperm as well as altered starch quality. Phenotypic observations showed that compared with Dongjin, there were no obvious growth differences of knockout mutants, including height, flowering timing, panicle numbers per plant, and grain numbers per panicle, while brown grains were smaller, resulting in a reduced 1000-brown-grain weight. Detailed measurement showed that smaller brown grain was mainly due to reduced grain width and thickness, and grain length was not altered. Further comparison revealed the decreased grain-filling rate of knockout mutants during grain development. Interestingly, compared with those of Dongjin, knockout plants grains displayed higher chalkiness, including a higher percentage of grain with chalkiness (PGWC) and degree of endosperm chalkiness (DEC). The apparent amylose content (AAC) of knockout plants grain endosperm was reduced, and analysis of the structural changes of amylopectin showed that the proportion of chains with degree of polymerization (DP) in the range of 6-7 was increased, whereas the proportion of chains with DP in the range of 8-17 was significantly decreased. The Rapid Visco Analyzer (RVA) profile provides a comprehensive evaluation of starch quality and further analyses showed that knockout plants grains had a different RVA profile, indicating the obviously altered physicochemical characteristics of starch under suppressed genes encoding OsNF-Y members. Therefore these results provide direct evidence of aleurone layer function in endosperm development and provide clues to the molecular mechanisms of the NF-Y family.

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287
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Improvement of grain yield by editing gene related to amino acid transporter using CRISPR / cas9 system in rice

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Amino acid transporters are the major mediators of N distribution and are important regulators of resource allocation in plants. Inorganic nitrogen (N) is mainly absorbed by plants in the form of nitrate and ammonium and then converted directly into amino acids at the roots or after conversion to leaves. Amino acids are then transported to roots, leaves, flowers, pollen and embryos (Fischer et al., 1998). Amino acids require transporter proteins to transfer them from source to sink organs (Coruzzi and Bash, 2001; Tegeder, 2012). These amino acid transporters (AATs) are cellular membrane proteins that transport specific amino acids. Transporters play an important role in the development of seeds and in various processes in plants such as abiotic and pathogen stresses. Although the functions of AtAATs have been extensively studied in Arabidopsis, the roles of OsAATs in rice are much less well understood (Zhao et al., 2012). Whole genome analyses have suggested the presence of 79-85 AAT homologous genes in rice (Lu et al., 2012; Zhao et al., 2012). It has been shown that biomass and yield of rice are altered significantly when OsAAT genes are knocked out (Lu et al., 2012; Peng et al., 2014). In these studies, Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)-associated (Cas) systems have been successfully used as efficient tools for genome editing in a variety of species. We used the CRISPR/Cas9 system to mutate the AAT5 (Os08g0506000), AAT7 (Os08g0506600), AAT24 (Os08g0506600), AAT49 (Os08g0506000), AAT60 (Os08g0506600) of Dongjin cultivar, these genes which have been reported to function as regulators of the grain number, panicle architecture, grain size and plant architecture, respectively. Analysis of the phenotypes and frequencies of edited genes in the first generation of transformed plants (T0) showed that the CRISPR/Cas9 system was highly efficient in inducing targeted gene editing, with the desired genes being edited in 47.5% (AAT5), 77.5% (AAT7), 57.5% (AAT24), 53.7% (AAT49) and 57.5% (AAT60) of the transformed plants. The T1 generation of the AAT7, AAT49, and AAT60 mutants featured enhanced grain number and grain size, respectively. In addition, we found that the deletion mutants obtained by AAT gene editing rarely off-target in similar target sequences. These results proved that multiple regulators of important traits can be modified in a single cultivar by CRISPR/Cas9, and thus facilitate the dissection of complex gene regulatory networks in the same genomic background and the stacking of important traits in cultivated varieties. These results suggest that manipulation of AAT gene expression could be used to increase grain yield in rice.

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PCS12-06

Improvement of Grain Quality through Application of CRISPR/Cas9 System in Rice

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Grain quality improvement is a key target for rice breeders, along with yield. It is a multigenic trait that is simultaneously influenced by many factors. Over decades, breeding for semi-dwarf cultivars and hybrids has significantly contributed to the attainment of high yield. Meanwhile, grain quality has also been improved along with increasing yield. However, consumers have continuously required the better quality of cereal grain. Since the rice genome sequence has been decoded, it has been facilitated to discover useful genes and to induce target mutations, and has succeeded in revealing the function of quality related genes. In recent years, with the development of gene editing technology, knockout techniques of target genes have been improved and successfully applied in many crops. Genome modification using CRISPR/Cas9 not only improves the quality of rice but also enables new researches in various life science fields. In this presentation, we would like to report the successful compilation of many genes related to various aspects of rice grain quality through CRISPR/Cas9 technology. Especially, we analyzed 23 starch synthesis related genes such as Wx, SBE1, SBE1b, ISA1, FLO2, FLO5/ALK and PHO1, and transcription factors regulating Waxy genes. Currently, T2 and T3 generations of null segregants selected from T1 generation are being cultivated and analyzed. Interestingly, studies on functional genomics at larger scales have become possible because of the availability of gene editing technology. Therefore, we discuss the progress made in rice by employing the CRISPR/Cas9 gene editing system and its eminent applications. We also elaborate possible future avenues of research with this system, and our understanding regarding the biological mechanism of rice grain quality improvement. The rapid shift of research toward the utilization of CRISPR/Cas9 systems for targeted mutagenesis could be a promising approach for overcome barriers to breeding improved quality rice.

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Knockout of abscisic acid (ABA)-dependent transcription factor gene OsVP1 using CRISPR/Cas9 system improves germination velocity and pre-harvest sprouting in rice (Oryza sativa L.)

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Seed dormancy is a condition that has not germinated during a specific period, even in environmental conditions that are prone to sprouting. These phenomena vary in proportion to the dry storage (after ripening) of the seeds and are genetically controlled by the genotypes of both mother plant and embryo. The dormancy imposed by the coat is enhanced by the tissue that covers the seed, i.e., glue and pale (or crust), pericarp and testis, and optionally endosperm. Embryonic dormancy of the endosperm is finely controlled during development. In cultivated rice, seed dormancy is commonly removed with dry after-ripening to achieve rapid and uniform germination on seed sowing. In this report, Pre-harvest sprouting is a phenomenon that seeds germinate while still attached onto the maternal plants in the condition of cloudy and rainy weather, and is also a restrictive factor of rice production and seed propagation. The phenotype of rice pre-harvest sprouting is very similar to that of maize seed-specific vp1 mutant. VP1 gene is essential for seeds maturation and dormancy, and is also a key transcription factor of ABA signal transduction pathway. Thus, it is of great significance to effectively control the occurrence and hazard of rice pre-harvest sprouting. The aim of the current investigation is to dissect the biological function of homologous gene OsVP1 by using CRISPR/Cas9 system in rice. Germination experiment showed that the percentage of germinated seeds from T1 knockout lines was higher than that of wild-type plants. Under the different concentrations of abscisic acid (ABA) treatment, the inhibition of germination ratio of OsVp1 gene knockout seeds was not significantly different when comparing with wild-type plants. Therefore, knockout lines of OsVP1 gene using CRISPR/Cas9 system can increase germination velocity of seeds and also lead to pre-harvest sprouting.

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Strategy for Editing Genes Encoding Seed Storage Proteins in Rice via CRISPR-Cas9 System

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Seed Storage Proteins (SSPs) are consists of mainly glutelins, prolamins and globulins. Glutelins are major rice storage proteins, accounting for 60%-80% of the total seed protein content. They are encoded by 15 gene copies in the genome, classified into four sub-families such as GluA, GluB, GluC, and GluD based on the similarity of their amino acid sequence. Rice prolamins, which accounting for 20-30% of seed storage proteins, are encoded by 34 genes and classified into 10, 13, and 16-kDa prolamins depending on their relative molecular weights. The 13-kDa prolamins are sub-grouped to pro13a and pro13b according to the number of cysteines. It has been known that rice SSPs are indigestible to patients with kidney problems and older people, and their contents limit the yield of a valuable foreign protein in seeds. Prolamin has been reported to be indigestible, resulting in decreasing in the nutritional value. To challenge these issues, we have tried to develop SSP knockout rice lines using CRISPR-Cas9 technique. CRISPR-Cas9 Technique has recently emerged as an efficient and easy to handle genome editing tool. Here we have designed nine sgRNAs targeting more than one SSP gene. We have checked that the sgRNAs activate the cleavage of the targeted genes in vitro and in vivo (Rice protoplast system). We have constructed different sgRNA-Cas9 vectors for Agrobacterium-mediated rice transformation. Also we mined potential SSP transcription factors by using gene co-expression network analysis, including C2C2(Zn)-GATA type, OsICE1, S1FA, RISBZ1, OsGZF1 & Zf-HD. Their effect on glutelin expression level has been checked in rice protoplast system.

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Homology-directed repair (HDR)-based gene targeting in tomato

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Genome editing (GE) based on CRISPR technology, a technique coined as plant breeding innovation (PBI), is expected to open a new era of crop breeding. GE takes place usually through the DNA repair pathways. DNA double strand breaks (DSBs) occurred in cells are a serious threat to survival and all living organisms have developed mechanisms to treat DSB rapidly. Among them, cells rapidly ligate the ends of the truncated DNA through the non-homologous end joining (NHEJ) repair pathway, where some nucleotides can be deleted or inserted, resulting in mutations. On the other hand, homology-directed repair pathway can occur when homologous DNA templates are present, which is very inefficient compared to the NHEJ pathway in plant somatic cells and is not well utilized as a tool in plant GE. Unlike the NHEJ repair pathway, which mainly produces knock-out, the HDR pathway can replace long DNA fragments as well as SNP mutations, allowing replacement of alleles or pyramidal integration of multiple genes in a specific locus of a chromosome. The latter is very advantageous to crop breeding. We report our approaches and results to improve HDR efficiency through various approaches using geminivirus - based plant replicon in tomato model crops.

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Agrobacterium- and virus-mediated CRISPR/Cas9 genome editing in tomato for viral resistance

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Plants with favorable alleles are important for crop improvement through plant breeding. Current breeding approaches mainly have been relied on random mutagenesis and recombination to create novel genetic variations. Targeted genome editing has great promise for functional genomics research and is becoming an increasingly popular tool for precise plant breeding. In the present study, two approaches, Agrobacterium-mediated stable expression and virus mediated transient expression of CRISPR/Cas9 systems are being standardized for efficient genome editing in tomato. As a proof of principle, the PDS gene from the carotenoid biosynthetic pathway was chosen as a target for genome editing due to their easily detectable phenotype change. For developing potyvirus resistant tomato lines, eIF4E and eFiso4E genes, which are known to be involved in recessive resistance of potyvirus are chosen as targets of targeted genome editing. Transgenic shoots of PDS, eIF4E and eFiso4E targeted plants were regenerated through Agrobacterium-mediated transformation. Mutated sequences were detected in PDS, eIF4E targeted regions by sequencing. Tomato lines overexpressing the Cas9 gene have been regenerated for virus mediated CRISPR/Cas9 genome editing. To deliver gRNA, Tobacco Rattle virus (TRV) and Potato virus X (PVX) mediated transient expression of gRNA will be used. We expect additional ongoing optimization of stable and transient expression of CRISPR/Cas9 systems have the potential for the development of an efficient and simple procedure for targeted genome editing, and may provide insights into sophisticated targeted genome editing in other crop species.

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Construction of Siderophore producing *Agaricus bisporus* transformants

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The button mushroom *Agaricus bisporus* is an edible mushroom native to grasslands in Europe and North America. It is one of the most commonly and widely consumed mushroom species throughout the world. However, in Korea, *A. bisporus* is urgent mushroom that have to be develop the new strain due to low usage and lack of domestic strain. In this study, we produce transformants inserting siderophore biosynthesis gene that is known to absorb ferric ion and have anti carcinogenic effect, and make it as the bio-factory. hapX gene that regulates siderophore biosynthesis was inserted to binary vector pBGgHg. For constitutive expression of hapX, promoter was replaced to *A. bispora* GPD promoter. Then pBGgHg-hapX was transformed to four hundred of *A. bispora* gill tissue fragments through *Agrobacterium tumefaciens*-mediated Transformation(ATMT). Obtained transformants were then confirmed by nucleotide sequencing and mRNA expression. After then, stability was checked with serial subculture. Finally selected 3 transformants were cultured on compost PDB and siderophore in culture medium was analyzed by HPLC and LC/MS.

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Genome editing effect of phytoene desaturase gene using CRISPR–Cas9 in hybrid poplar

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The CRISPR-Cas9 system has been successfully applied to genome editing in several plant species; however, there are a few reports on tree genome editing. In this study, we used the CRISPR-Cas9 system to induce the mutation of a target gene in a hybrid poplar (*Populus alba × P. glandulosa*). To easily screen genome-edited plants, we selected guide RNA-binding sites in the *PagPDS3* (phytoene desaturase 3) genes, which are followed by the protospacer adjacent motif sequence. After *Agrobacterium*-mediated transformation, the mutants were classified into three groups according to the albino patterns of transformed leaves. Eighty-two of the 110 mutants had an albino or pale-green phenotype, and 28 of the 110 mutants had green leaves. Therefore, the mutation rate of the *PagPDS3* gene was 74.55% in the hybrid poplar. The albino phenotype appeared when the mutation occurred in bi-alleles in the hybrid poplar. These results clearly show that the CRISPR-Cas9 system can effectively induce the targeted mutation in hybrid poplar. We expect that this technique will be used to improve tree quality such as environmental stress tolerance and biomass in a hybrid poplar.

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The *Arabidopsis* ATXR2 inhibits de novo shoot regeneration by controlling cytokinin signaling

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Plants have remarkable cellular plasticity. Differentiated cells revert pluripotent cells called calli on high-auxin medium, and the calli can regenerate shoots on high-cytokinin medium. Callus tissue resembles lateral root primordium (LRP), thus tissue identity conversion is key biological process underlying plant regeneration.

Accumulating evidence has demonstrated that changes in genome-wide chromatin landscape accompanies the cell fate transition. However, chromatin modifiers responsible for plant regeneration remain to be elucidated. Here, we demonstrated the roles of two TrxG proteins, *ARABIDOPSIS TRITHORAX* TRITHORAX 4 (ATX4) and *ARABIDOPSIS TRITHORAX-RELATED* 2 (ATXR2). ATX4 is essential for maintaining of shoot identity. The ATX4 protein globally deposits histone H3 lysine 4 trimethylation (H3K4me3) to shoot identity genes to promote their expression. Whereas, ATXR2 is important for acquisition of root identity. It was recruited to promoters of *LATERAL ORGAN BOUNDARIES-DOMAIN* (LBD) genes by *AUXIN RESPONSE FACTOR* 7 (ARF7) and ARF19 to deposit H3K36me3. However, ATXR2 has an independent role in de novo shoot regeneration. During shoot regeneration, ATXR2 positively regulates type-A *ARABIDOPSIS RESPONSE REGULATORS* (ARRs), *ARR5* and *ARR7*, which repress cytokinin signaling, and it was dependent on a type-B ARR, *ARR1*. Then, it ultimately repressed the *WUSCHEL (WUS)* expression to inhibit shoot regeneration.

Taken together, we provide that organ identity conversion is crucial for plant regeneration and two chromatin remodeling enzymes, ATX4 and ATXR2 underlie this process. Considering the conservation of these enzymes in crops, they would be valuable resources for improving crop regeneration.

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Systemic gene editing of *AtRabA1* subfamily

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AtRabA1 subfamily has nine gene members of the Ras superfamily of small GTPase (RabGTPase), which is the most divergent subfamily among RabA1-RabA6 in *Arabidopsis*. Although a couple of T-DNA mutants of AtRabA1 subfamily were released, the mutants are not currently available for further analysis. Here we present individually targeted mutants of 9 members of RabA1, RabA1a to RabA1i. Previously we reported a simple, flexible binary vector system, pHIBATC vectors. We devised the vector for harnessing two sgRNAs linked by the endogenous tRNA processing system, pHATRC. Using PCR based two guide RNA cloning procedures, we successfully generated individual binary vectors for *AtRabA1* subfamily with simultaneously targeted two sgRNAs to RabA1a-RabA1i each. We obtained edited mutants and subsequently analyzed the mutation ratio and insertion/deletion (Indel) patterns via targeted deep sequencing. Of the edited mutants, a couple of members showed differential editing efficiency, especially *AtRabA1h*. These pHATRC-mediated rabA1a-rabA1i mutants will be useful to characterize the distinct role of the RabA1 subfamily not only for cellular responses in *Arabidopsis* but also for Arabidopsis-environmental stresses.

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292
**PCS12-15**

*Agrobacterium* mediated transformation and genome edition in *Solanum nigrum*

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Numerous research activities have been carried out on Solanaceae species such as *Solanum tuberosum*, *Solanum lycopersicum*, *Solanum melongana* but still, molecular breeding activity on *Solanum nigrum* is necessary, it is an important medicinal plant that has the effect of antioxidant, anticancer, diuretic, antidiabetic, anti-inflammatory, hepatoprotective, and antipyretic. In the present work, genetic engineering study ranging from gene transformation to gene editing technique has been carried out on *Solanum nigrum*. We optimized the preincubation and regeneration method, resulted in shortening the *Agrobacterium* mediated transformation period to 8 weeks in *S. nigrum*. *S. nigrum* T1 plants having 35s:GUS transgene were strongly stained in whole plant tissues by GUS staining. To apply this method for genome edition in *S. nigrum*, *SnLAZY1*, ortholog of *LAZY1* known as shoot gravitropism controller in Arabidopsis, was edited by CRISPR/Cas9 system using our transformation system. T1 plants were inherited the deletion in *SnLAZY1* and showed reduced upright shoot growth like vine type stem. Currently our results showed that recombinant gene transformation and genome edition is applicable for breeding of a medicinal species of *Solanum nigrum*.

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**PCS13-01**

Plan for High Throughput Phenotyping Approach to Screen Drought Resistance in Soybean

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Soybean is one of the major crops worldwide. Its annual production is about 90,000 tons in Korea, which is the second largest amount of domestic crop productions. Recently, there are huge yield reduction due to the rapid and various change of climate, particularly frequent drought. However, most soybean cultivars do not have drought resistance. Consequently, it is crucial to develop drought resistant cultivar as soon as possible under current circumstance. To achieve this, high-throughput phenotyping (HTP) is the best option for accelerating the development of new cultivars because it can handle massive data in an automatic, accurate, and precise manner. Currently, various image data such as multi-spectral and RGB images would be used to be analyzed to screen drought resistance in 28 parents of nested association mapping (NAM) population of soybean. Based on the results, the best candidate individuals among those would be selected to breed further as drought resistance donors. Fast and accurate selection here will shorten the whole breeding process, which can help to ensure the soybean yield under the drought condition which will occur more frequently in a near future due to drastic climate changes.

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Rice basic Helix-Loop-Helix 79 (OsbHLH079) determines leaf angle and grain shape by upregulating brassinosteroid signaling-associated genes

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Plant architecture has been a major improvable trait for crop yield, such as leaf size, leaf shape, leaf angle, plant height, and floral organs. Among the basic Helix-Loop-Helix (bHLH) transcription factor family in rice (Oryza sativa), we found a T-DNA insertion activation-tagged mutant of OsbHLH079 (termed osblhlh079-D). osblhlh079-D mutant showed wide leaf angle and produced long slender grains, similar to the phenotypes with increased brassinosteroid (BR) levels or enhanced BR signaling. By qRT-PCR, we found that BR signaling-associated genes are largely upregulated in osblhlh079-D, but not BR biosynthesis-associated genes, compared with its wild-type parent ‘Dongjin (DJ)’. Consistently, osblhlh079-D showed a hypersensitive phenotype to exogenous BR treatment compared with DJ. Histological analysis of osblhlh079-D suggested that increased cell length in adaxial surface of lamina joint is responsible for increased leaf inclination. Moreover, expression of cell elongation-associated genes encoding expansins and xyloglucan endotransglycosylase/hydrolases increased in osblhlh079-D. The regulatory function of OsbHLH079 was further examined by analyzing both 3SS::OsbHLH079 and 3SS::RNAi-OsbHLH079 transgenic rice; the 3SS::OsbHLH079 transgenics showed similar phenotypes to osblhlh079-D, while the 3SS::RNAi-OsbHLH079 transgenics displayed opposite phenotypes to osblhlh079-D. Taking together, we propose that OsbHLH079 functions as a positive regulator of BR signaling in the rice development.

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CONSTITUTIVE PHOTOMORPHOGENIC 1 (COP1) promotes gibberellic acid-mediated seed germination by destabilizing REPRESSOR OF ga1-3-LIKE 2 (RGL2) in Arabidopsis thaliana

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The crosstalk between GA and abscisic acid (ABA) has a pivotal role in seed germination, in which GA hormone is a major regulator in induction of seed germination. Many genes involved in the seed germination regulatory pathway have been identified. RGL2 (REPRESSOR OF GA1-3-LIKE2) is one of the major factors that negatively regulates seed germination by repressing of germination-associated genes. Here, we show that COP1 (CONSTITUTIVE PHOTOMORPHOGENIC1) is closely involved in the GA-mediated germination pathway. In germination analysis, the 3SS::COP1-GFP/cop1-4 seeds showed a paclobutrazol (PAC) insensitive phenotype similar to rgl2 mutant seeds, while cop1-4 mutant seeds showed a PAC hypersensitive phenotype. COP1 protein is more stabilized by GA3 and directly interacts with RGL2. In genetic analysis, COP1 acts as an upstream negative regulator of RGL2, in which cop1-4 rgl2 double mutant seeds showed a PAC insensitive germination phenotype like rgl2 mutant seeds. Furthermore, COP1 is involved in the regulation of RGL2 protein stability, leading the promoting seed germination by upregulation of germination-associated gene. Taking together, we suggest that COP1 destabilizes RGL2 to promote GA-mediated germination during seed inhibition.

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Ultrafast PCR assays to detect approved genetically modified (GM) cotton

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As the number of approved items for genetically modified (GM) cotton worldwide increases, ongoing monitoring of unauthorized GM cotton events is needed against the possibility of their inflow. In addition, there is a need for the detection method of GM cotton that can be quickly and efficiently confirmed on the spot. In this study, we tried to develop a detection method of GM cotton using ultrafast PCR which is easy to perform the PCR in about 20 minutes. The detection targets, a total of twelve approved GM cotton events (MON531, MON1445, MON15985, MON88701, MON88913, GHB119, GHB614, COT102, LLcotton25, 281/3006, DAS81910, and T304-40 x GHB119), were selected. The specificity of the ultra PCR was confirmed to amplify specifically among each target event for 21 GM events including genetically modified cotton, canola, maize, and soybean. The sensitivity of each primer set showed detection value ranging from 0.005% to 0.5%. This result demonstrated that the LOD of the ultrafast PCR is lower than 3% threshold of the unintentional limit of GM events in Korea.

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Abiotic stress-specific cis-regulatory element assembling approach to increase response in drought

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Abiotic stresses such as drought, heat, cold, and high salinity hinder the growth and productivity of crop plants. Coping with abiotic stress, it necessary to understand the molecular regulatory networks that make organisms to respond to adverse environmental conditions. In the present study, we screened 5 stress-inducible promoters that are expressed only under stress conditions using RT-PCR, thereby founding 40 cis-element in stress-inducible promoters using bioinformatics tool. We designed 4 synthetic promoters (1.seq, 2.seq, 3.seq, 4.seq) for tightly-controlled regulation under abiotic stress such as drought. This is achieved by assembling cis-elements from the native promoters which are expressed only under abiotic stress. To verify that synthetic promoters respond to abiotic stress, each synthetic promoter was independently linked to a β-glucuronidase (GUS) reporter gene and GUS activity was analyzed using histochemical staining method. Analysis of the transgenic plant (1.seq:GUS, 2.seq:GUS, 3.seq:GUS, 4.seq:GUS) showed that the synthetic promoters are increased the expression of GUS in transgenic plants upon treatment with PEG. Overall, control of the transcriptional networks is an efficient and powerful strategy to be resistant to stress without causing growth retardation. Furthermore, this approach facilitated us to provide as an enabling tool for the application of future synthetic biology that seek to exploit stress-resistance within a plant.

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**PCS13-06**

**AtCBX2-OX decreases lignin content and increases biomass in plant**

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Alfalfa (*Medicago sativa*) has been regarded as a useful forage for animals as it contains high nutrient. However, its lignin content reduces the digestibility and utilization of alfalfa in livestock industry. Lignin is a cell wall component along with cellulose and hemicellulose constituents that accumulates in the plant tissues, particularly in the stem. While a certain amount of lignin is essential for healthy plants to be stand upright, lignin is an indigestible component of plants and reduces the fiber digestibility of forages in the rumen of livestock. Therefore, forage producers and commodity purchasers desire alfalfa with lower lignin levels but without loss of nutritional components such as protein and fiber (also called as “high-quality alfalfa”). In this study, we used *CBSX2* (Cystathionine-β-synthase Domain-Containing Protein 2) and novel promoters, which were screened from our previous studies with *Arabidopsis thaliana*, to develop biotechnology-derived high-quality alfalfa with reduced lignin and increased biomass. Intensive phenotype analyses indicate *AtCBSX2-OX* plants showed reduced lignin deposition in the stem as well as delayed senescence and abscissions, resulting in the elevated biomass production when compared to the wild-type plant at the same growth stage. Reproducibility of these phenotypes is going to be re-evaluated with *CBSX2-OX* alfalfa plants that are currently under construction.

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**PCS13-07**

**Identification of OsPAPs responsible for chloroplast development in rice**

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Transcription of chloroplast genes is a key step determining chloroplast development, and plastid-encoded RNA polymerase (PEP) is a major RNA polymerase governing the transcription of chloroplast genes. Recent studies reported that establishment of PEP complex through interaction with PEP-associated proteins (PAPs) is a key to controlling the transcription activity of PEP. These suggest that PAP proteins are essential in the regulation of PEP activity and chloroplast gene expression. To understand PAPs-mediated chloroplast development in rice, we attempted to identify rice homologs of arabidopsis PAPs responsible for rice chloroplast development. To explore OsPAPs in chloroplast development, light-dependent expression patterns were analyzed, and it was shown that expressions of OsPAPs were activated by light, which promotes chloroplast development. To further understand their function in rice chloroplast development, it was attempted to generate CRISPR/Cas9-mediated rice mutants of the 12 OsPAP genes. Total 24 guide RNAs were designed for 12 OsPAPs mutagenesis (2 independent guide RNAs X 12 OsPAPs), and recombined into pRGEB31, a CRISPR/Cas9 binary plasmid. These recombinant DNAs were introduced into rice by rice callus transformation using *Agrobacterium tumefaciens* LBA4404. We found that some T0 plants expressing OsPAP3, OsPAP4 and OsPAP9 guide RNA showed abnormal whitening phenotype, indicating that the OsPAPs are key PAPs governing rice chloroplast development.

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Overexpression of two glutathione biosynthesis genes increased productivity via enhanced stress tolerance in rice plant

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Abiotic stresses cause accumulation of reactive oxygen species (ROS) and various antioxidants exist in plant defense system to prevent cell damages from ROS. Glutathione (GSH) is one of the effective antioxidant molecules and synthesized by two enzymes, γ-glutamylcysteine synthetase (ECS) and glutathione synthetase (GS). We established the transgenic rice plants which overexpress either the ECS or GS gene. Also transgenic rice plants with simultaneously overexpression of the ECS and GS genes were constructed (C1, C3). The C1 and C3 rice plants showed higher GSH contents which resulted in reduced malondialdehyde (MDA) than WT rice plants under salt stress condition. In the natural paddy field, plant growth indicators such as root length, total weight, water content, tiller number, and chlorophyll content were increased in C1 and C3 rice plants than those of other control rice plants. Additionally, C1 and C3 rice plants exhibited decreased ROS accumulation, ion leakage, and MDA content by maintaining higher GSH concentration in the system. Total biomass of transgenic rice plants was increased and grain yield was the highest in C1 and C3 rice plants for years of 2017 and 2018. Taken together, we conclude that higher GSH contents in rice plants contributed in improvement of salt stress tolerance and grain yield.

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A Heat Shock Protein Gene Increased Tolerance to Salinity and High Temperature in Oryza sativa

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High temperature and salinity stress are among the two most important environmental factors influencing plant development and growth which eventually determine the final yield of the crop. Recent studies have shown that transgenic plants overexpressing the HSP genes prevent protein denaturation and enhance tolerance under controlled stress conditions in laboratories and greenhouses. However, there were only few studies reported on the role of the HSP gene in stress tolerance or crop yield in natural paddy fields which possess simultaneously and combinational environmental stresses. In the present study, we cloned a rice (Oryza sativa) HSP gene, OsHSP, and characterized its function in rice plants growing in various conditions. The OsHSP overexpressing transgenic rice plants exhibited improved antioxidant capability, and the antioxidant enzyme activities were increased under high temperature and salinity stresses. Also adaptability of the transgenic rice plants after the transplantation from greenhouses to natural paddy fields increased significantly. Overall agronomic traits and grain yields of transgenic rice plants were improved in natural paddy fields. Our findings indicate that the stress-resistant OsHSP transgenic rice plants may be used for cultivation under harsh environmental conditions for enhanced grain yields.

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Autophagy interacts with the plant immune receptor

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Autophagy is a cellular pathway facilitating damaged protein degradations and elimination of pathogens. Given these two important roles, autophagy could be one of the important mechanisms in the plant immunity regulation. Interestingly, it has been reported that the autophagy-related protein ATG8 interacts with Arabidopsis orosomucoid (ORM) protein which acts as a selective autophagy receptor of Flagellin-sensing 2 (FLS2). Thus, protein accumulation of FLS2 immune receptor is regulated by selective autophagy. In our research, we found that ATG8 and ATG6 associated with the RPS4/RRS1 immune receptor in coIP. Using the iLIR autophagy database, we found some of the putative autophagy interacting motifs (AIM) in the RRS1 and RPS4. If coexpressed ATG8 with RPS4/RRS1 in the non-recognized or recognized condition, ATG8 strongly suppressed HR response. These data indicate that the immune receptors seem to be regulated by autophagy pathway. This study may be useful tools to regulate plant immune receptor in crop development.

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Pathogen effector PopP2 acetylates the plant autophagy-related protein 8

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Autophagy is involved in maintaining cellular homeostasis and regulates biotic/abiotic stresses in eukaryotes. Furthermore, autophagy contributes with both pro-death and pro-survival functions to specific pathogen infections. Several pathogens have evolved strategies to manipulate host autophagy pathways to suppress plant immunity. In this study, the plant autophagy-related gene 8 (ATG8) is colPed and acetylated by Ralstonia solanacearum effector PopP2 which has an acetyltransferase activity. PopP2 is partial relocalized in the autophagosome when coexpressed SIATG8. We further identify a putative ATG8 acetylation amino acid residue via a protein sequence analysis. PopP2 acetylates clade-specific ATG8 proteins but still is able to interact with other clade ATG8 proteins. Together, we demonstrate that autophagy ATG8 might be targeted by bacterial pathogen effector to manipulate host autophagy pathway. Regulation of ATG8 acetylation will provide new approaches in crop engineering.

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Common cis-elements regulated by ABA and JA in *Oryza sativa*

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The phytohormone abscisic acid (ABA) enables plants to adapt to adverse environmental conditions through the modulation of metabolic pathways and of growth and developmental programs. We used comparative microarray analysis to identify genes exhibiting ABA-dependent expression and other hormone-dependent expression among them in *Oryza sativa* shoot and root. We identified 854 genes as significantly up- or down-regulated in root or shoot under ABA treatment condition. Most of these genes had expression profiles in root and shoot under ABA treatment condition, whereas 86 genes displayed opposite expression responses in root and shoot. To examine the crosstalk between ABA and other hormones, we compared the expression profiles of the ABA-dependently regulated genes under several different hormone treatment conditions. Interestingly, Transcriptome analysis of ABA and JA showed that many genes are commonly regulated by both hormones. We searched the promoter regions of these genes for cis-elements that could be responsible for their responsiveness to both hormones, and found that ABRE and MYC2 elements, among others, were common to the promoters of genes that were regulated by both ABA and JA. These results show that ABA and JA might have common gene expression regulation system and might explain why the JA could function for both abiotic and biotic stress tolerance.

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Overexpression of OsDREB1G gene, a Member of the OsDREB1 Subfamily, increases low temperature tolerance in rice

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Plants have evolved effective ways to avoid or reduce possible damages from adverse environment, such as cold, drought, salt, etc. Altered gene expression is one of the key responses to abiotic stress in plants. Several transcription factors function as master switches to induce the expression of stress-tolerance genes. To find out a major regulator for the cold stress tolerance in rice, we focused on functionally identifying DREB subfamily which plays important roles in cold stress tolerance of plants. Here, we characterized OsDREB1G (LOC_Os02g45450), a functionally unidentified member of the DREB1 subgroup. OsDREB1G is dominantly expressed in leaf sheath, blade, node, and root, and specifically induced under cold stress conditions among several abiotic stresses examined. Transgenic rice overexpressing this gene exhibited strong cold tolerance and growth retardation, like transgenic rice overexpressing other OsDREB1 genes. However, not similar to these rice lines, transgenic rice overexpressing OsDREB1G did not exhibit significant increases in drought or salt tolerance. Cold-responsive genes were extremely induced in transgenic rice overexpressing DREB1G compared to wild type. In addition, OsDREB1G overexpression directly induced the expression of a reporter gene fused to the promoters of cold-induced genes in rice protoplasts. Therefore, OsDREB1G is a particular CBF/DREB1 transcription factor that specifically functions in the low temperature stress condition and OsDREB1G could be useful for developing transgenic rice with enhanced cold-stress tolerance.

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Stepwise Strategy for the Practical Development of Carotenoids-Enriched Transgenic Rice

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The β-carotene-enriched golden rice, PAC (Psy-F2A-CrtI) and codon-optimized stPAC (stPsy-F2A-stCrtI), was developed via a bicistronic expression of phytoene synthase (Psy) and bacterial carotene desaturase (CrtI) involving the ribosomal pausing 2A peptide (F2A) from mammalian virus. To generate rice varieties producing diverse carotenoids beyond β-carotene, a β-carotene hydroxylase gene, B (Bch) and a codon optimized stB (stBch) were used to increase zeaxanthin synthesis. A recombinant BAK gene (Bch-F2A-Bkt), consisting of the Bch and a β-carotene ketolase gene (Bkt) linked by F2A sequence, as well as a codon optimized stBAK gene (stBch-F2A-stBkt) were used to create astaxanthin synthesis. The B, stB, BAK and stBAK genes were combined with a PAC gene, and as results, B-PAC, stB-PAC, BAK-PAC and stBAK-PAC rice accumulated zeaxanthin and astaxanthin in the endosperm. Meanwhile, to overcome the limitation of a mammalian pathogenic viral origin, two recombinant genes of stPTAC (stPsy-T2A-stCrtI) and stPTAC (stPsy-I2A2-stCrtI) with replacement of F2A with either non-mammalian viral 2A peptides T2A or I2A, also generated the β-carotene enriched rice, suggesting their bicistronic expression activities with even better ribosomal pausing efficiency than F2A. To establish polycistronic expression in rice plants, stBch or stBkt were linked alone or in combination with stPTAC for tri-, tri- and tetra-cistronic expression, generating stPTAC-IABc (stPsy-F2A-stBch), stPTAC-IABk (stPTAC-I2A1-stBkt), and stPTAC-IABc-IABk (stPTAC-I2A1-stBch-I2A2-stBkt) vectors, and resulted in the accumulation of zeaxanthin, astaxanthin and astacanthan. To develop β-carotene enriched rice events being able to be commercialized, patent-free vector, endosperm-specific promoters and chloroplast targeting transit peptides (Tp) were found, leading selection of pFZP200 vector, globulin (GB) promoter and PTpR3Tp, as most efficient components on β-carotene production in rice endosperm. Collectively, GB:stPTAC (GB:stPsy-T2A-PTp-stCrtI) and GB:stPTAC (GB:stPsy-T2A-R3Tp-stCrtI) rice were generated. Among these rice transformants, 1 copy, intergenic gene insertion lines with the highest transgenic protein levels and carotenoids content were selected as GMO event.

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Influence of gene flow from GM to non-GM soybeans by the size of the pollen donor

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The use of genetically modified (GM) crops has increased continuously over the world, and concerns about the potential risks of GM crops have also risen. Although, until now, GM crops have not been cultivated commercially in Korea, it is necessary to develop technology for the safe evaluation of GM crops. In this study, we investigated the influence of gene flow from GM to non-GM soybeans by the size of the pollen donor. In the experimental design, GM soybeans were placed in the center as a pollen donor and non-GM soybeans were placed in four directions as the pollen receivers. Three sizes of pollen donor were designed as 90 cm × 90 cm, 180 cm × 180 cm, and 360 cm × 360 cm. A total 22,719 seeds were collected from non-GM soybeans, and 14 hybrids were finally obtained through herbicide resistance screening and PCR analysis. The highest hybridization rate was 0.78% at a distance of 15 cm from a 360 cm × 360 cm GM pollen donor, and the farthest distance of hybridization was 180 cm from a GM pollen donor which was 360 cm × 360 cm in size. Ten hybrids were found among the 14 hybrids at the 360 cm × 360 cm pollen donor size, 3 hybrids at 180 cm × 180 cm, 1 hybrid at 90 cm × 90 cm. From these results, it could be concluded that with the larger pollen donor size, more hybridization occurred in soybeans.

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Influences of Insect-Resistant Genetically Modified Rice (Bt-T) on the Diversity of Non-Target Insects in an LMO Quarantine Field

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This study was conducted to develop environmental risk assessments and biosafety guides for insect-resistant genetically modified rice in an LMO (Living Modified Organism) isolation field. In the LMO quarantine area of Kyungpook National University, the species diversities and population densities of non-target insects found on insect-resistant genetically modified rice (Bt-T), rice resistant to Chrobroccoris medalis, and non-GM rice (Dongjin-byeo and Ilmi-byeo) were investigated. The Bt-T plants were, therefore, evaluated under field conditions to detect possible impacts on above-ground insects and spiders. In 2016 and 2017, the study compared transgenic rice and two non-GM reference rice, namely Dongjin-byeo and Ilmi-byeo, at Gunwi. A total of 9,552 individuals from 51 families and 11 orders were collected from the LMO isolation field. From the three types of rice fields, a total of 3,042; 3,212; and 3,297 individuals from the Bt-T, Dongjin-byeo, and Ilmi-byeo were collected, respectively. There was no difference between the population densities of the non-target insect pests, natural enemies, and other insects on the Bt-T compared to non-GM rice. The data on insect species population densities were subjected to principal component analysis (PCA) without distinguishing between the three varieties, namely GM, non-GM, and reference cultivar, in all cultivation years. However, the PCA clearly separated the samples based on the cultivation years. These results suggest that insect species diversities and population densities during plant cultivation are determined by environmental factors (growing condition and seasons) rather than by genetic factors.

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Influence of Vitamin A enhanced transgenic soybean cultivation on above-ground arthropods in Korea

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This study was carried out to develop environmental risk assessments of potential effects on the non-target above-ground insects and spiders within agroecosystems for Vitamin A enhanced transgenic soybean with tolerance to the herbicide glufosinate (PPT) at LMO (Living Modified Organism) isolation field. In LMO quarantine areas of National Institute of Agricultural Sciences (Jeonju) and Kyungpook National University (Gunwi), insect species diversities and population densities on Vitamin A enhanced transgenic soybean and non-GM soybean, Gwangan were investigated. A total of 93,419 individuals of 64 families from 11 orders were collected in LMO isolation field. In Gunwi, total of 17,110 individuals in Vitamin A enhanced transgenic soybean and 17,627 individuals in Gwangan were collected, respectively. In Jeonju, total of 28,621 individuals in Vitamin A enhanced transgenic soybean and 30,061 individuals in Gwangan were collected, respectively. There was no difference between the population densities of insect pests, natural enemies and other insects on Vitamin E enhanced transgenic soybean and Gwangan within same field, while the population densities of insect pests, natural enemies and other insects in Jeonju was higher than those in Gunwi, respectively. Throughout the study, analysis of variance indicated no significant differences (P<0.05), and multivariate analysis showed that the abundance and diversity of plant dwelling insects was similar within same filed.

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PCS13-18

Selection of essential genes for ingestion RNA interference against western flower thrips using leaf disc-mediated dsRNA delivery

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Frankliniella occidentalis is a major pest that damage wide varieties of crops and vegetables. Following extensive use of insecticides to control this pest, high levels of resistance to almost all groups of insecticides have developed due to its high reproduction rate and short generation time. Therefore, alternative pest control strategy, such as RNA interference (RNAi)-based control, is essential for managing this insect. To establish the ingestion RNAi-based control, a total of 57 genes involved in various biological processes were selected, and their double-stranded RNAs (dsRNA) were delivered to insecticide-susceptible strain via the leaf disc-feeding method following the optimization of bioassay chamber by 3D printing. The mortality of dsRNA-ingested thrips was examined every 24 h until 120 h post-treatment. Out of the 57 genes screened, the dsRNAs of Toll-like receptor 6, apolipophorin, coatomer protein subunit epsilon and sorting and assembly machinery component resulted in the highest lethality when ingested by thrips. The dsRNA-fed thrips showed substantially reduced transcription levels target genes, demonstrating that the observed mortality of thrips following dsRNA ingestion was likely due to RNAi. When these selected genes were tested for ingestion RNAi against an insecticide-resistant strain of F. occidentalis, similar results were obtained as well. In conclusion, this study provides the first proof of concept that ingestion RNAi can be lethal to F. occidentalis, a mesophyll sucking pest, and transgenic plants expressing hairpin RNA of essential genes can be employed as a practical tool to control insecticide-resistant thrips in the field.

Keywords: RNAi interference, Ingestion delivery, Frankliniella occidentalis, Lethal dsRNA

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PCS13-19

Nutritional composition profiles and natural variation of commercial soybean cultivars cultivated in the different locations during two years

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This study was to evaluate the nutritional profiles of 14 kinds of soybeans cultivated in the three locations which were Daegu, Suwon, and Iksan of south Korea. All of these soybeans were cultivated by standard and conventional agricultural practice. Commercial varieties of soybeans were analyzed to compare the nutritional profiles according to the different environmental conditions. The pH of soil, annual rainfall, and weather temperature were investigated for the environment differences. The proximates, amino acids, minerals, fatty acids, vitamins, and isoflavones were investigated for the environmental effects. The contents of proximates and minerals were not different among three locations but the contents of amino acid and lipid were different significantly (p<0.05) among three locations. Micronutrients were affected more by the environment conditions such as cultivated locations than kinds of varieties. The fatty acid profile showed that linoleic acid, (10.2–12.5% of total) was the most abundant fatty acids followed oleic acid, palmitic acid, linolenic acid and stearic acid. Analyses of mineral content indicated that the most abundant mineral was potassium, followed by magnesium, calcium, iron, zinc, sodium and manganese. The result of % variability for proximates from R statistics according to the environmental effects showed that the natural variation of proximates was mainly contributed by the location (30.56%), and next by the year (22.15%) and variety (12.23%), in order. Our findings demonstrate that the natural variation of soybean nutrient composition can be explained and compared by various statistical approach method (linear mixed model by R program et al.). The results may offer reasonable and scientific assessment for further new plants developed by the biological techniques. Furthermore, these data can be used in the safety assessment of new plants developed by the biotechnology by comparing the substantial equivalence.

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**PCS13-20**

**GPM1** encodes a male gametophyte-specific R2R3 MYB transcription factor required for polarized microspores to undergo pollen mitosis I in Arabidopsis

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Correct development of gametophytes is pivotal for sexual reproduction in flowering plants. Male gametophyte consists of two sperm cells and a vegetative cell that are formed through an elaborately coordinated genetic program. To explore genetic regulation underlying pollen development, we morphologically screened DAPI-stained mature pollen grains from a mutant population. As a result we isolated mutant line named *gene-for-pollen mitoses 1* (*gpm1*) on the basis of mutant pollen phenotypes displaying complete abortion and various numbers of nuclei. In *gpm1* mutants microspores develop normally until polarized microspore stage but fail to divide at pollen mitosis I. Typically, the mutant microspores continue to grow in size with the single vacuole extremely enlarged and subsequently degenerate to complete abortion at later stages. Only occasionally mutant microspores undergo pollen mitosis I at delayed stages, reflecting a small fraction of mutant pollen grains that contain various numbers of nuclei. However, even in this type of mutant pollen grains, the cell fates are not correctly established. Genetic transmission of the *gpm1* allele was found to be normal through the female but highly limited through the male, showing that *GPM1* function is specifically required for the male gametophyte development. Through a map-based cloning approach, we identified the *GPM1* to encode a R2R3 MYB transcription factor. Gene expression analyses revealed that the *GPM1* gene is expressed in a male-specific manner and *GPM1* protein is transiently accumulated only in microspore nuclei before pollen mitosis I. Ectopic expressions of *GPM1* driven by constitutive or cell type-specific promoters cause severe developmental defects, demonstrating that the *GPM1* expression needs to be tightly controlled for normal plant development. Taken together we report *GPM1* to be a microspore-specific MYB transcription factor required for polarized microspores to undergo pollen mitosis I in Arabidopsis.

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**PCS13-21**

Increasing resistant starch content in legumes for higher nutritional prospect

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Starch is an essential component of human and animal diets and has various applications in food industries. Although cereal grains form a major source of starch, the legume is an excellent source of resistant starch which has various advantages over cereal starch and therefore has become an important topic of research in the past two decades. However, no effort has been made in recent time to assess the present status of the seed starch composition in legume crops. The legume starch imparts several advantages when directly used in food preparations. For instance, little increases in the starch amylose content of legume seeds leads to increase the slow digestibility and lower the glycemic index which impact the release of blood glucose. High amylose starch also alter the texture and softness of the end food product. Hence, genetic improvement of starch content in legumes have become essential, especially due to its commercial applications and consumer demand. Here we review the research in key areas. We have addressed factors influencing starch digestibility, environmental influence on starch composition, and showed how improved resistant starch content is beneficial for the nutritional prospect. In addition, we have also discussed means to improve resistant starch content and total starch composition through genetic and genomic technologies. This improved legume with high resistant starch may give better option to protect form lifestyle related diseases. Further, the present literature investigation forms a resource of information useful to the farmers and breeders who are interested in developing cultivars for improved starch content.

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**Preservation for GMO crops and Bio-Information developed by Agricultural Biotechnology Research Center**

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This project aims to provide available summarized information on the status of genetic management of materials and information of genetically modified organism (GMO) in South Korea and to lay the foundations on the preservation of GMO materials for the medium and long term. It is necessary to utilize the existing information and materials of GMO in order to increase efficiency in future projects. First, a yearly collection of material of GMO and genetic information with assigned format are organized to facilitate searching the information on database of Agricultural Biotech Research Group. The establishment of database can help future researches efficiency, reduce overlapping investment and prevent losing developed GMO materials. Secondly, to preserve, propagate and use GMO materials in medium and long term (10 to 30 years), genetic management on database can ensure that the deposited materials of GMO is to monitor seed viability and the regeneration of seeds are carried out when they are damaged or lose viability. Thirdly, it is our responsibility in this project to regenerate and increase the collections of GMO seed in permitted research field (Gunwi, Korea). GMO materials can be shared in another research project to develop an economical crop. This project can help collect the GMO resources which is not on the database or deposited to utilize those materials in the future. Finally, these materials and information of GMO could be used to develop new global crops through material or technology transfer to industry.

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**Development of useful transgenic Chinese cabbage for the future-proof breeding resources**

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In order to maintain the international competitiveness of Korean Chinese cabbage seeds in the rapidly changing world vegetable seed market, it is necessary to breed the new varieties. In addition, the domestic industry of Chinese cabbage has reached to the limit to increase its productivity and to add useful values, and it is required to recreate values by developing new and various varieties. In this study, we have developed transgenic Chinese cabbage lines with various characters such as *Tetranychus urticae* resistance, drought resistance or self-compatibility. Generation progress of developed lines is being made to fix the acquired traits and to perform the equivalence analysis at Hankook Seed Co. (Pyungtaek, Korea). Observation and characterization were assessed following the guidelines for surveying characteristics issued by the Korea Seed & Variety Service. As the result of observation, no difference was found in 26 characteristics between non-transgenic and transgenic lines. Also, we constructed gene editing vectors for self-compatibility and drought resistance. We examined the efficiency of constructed vectors through HRM analysis using transgenic callus. Consequently, CRISPR-Cas9 vector showed accurate genetic editing process and its own gene rearrangement in target site.

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**Embryo transmission of Alternanthera mosaic potexvirus enables CRISPR editing of GFP-transgenic Nicotiana benthamiana through combined expression of split Cas 9 and guide RNA**

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CRISPR/Cas9 has been used for gene editing in animals and plants. However, in plant applications delivery of a high concentration of stable guide RNA to the target has been an obstacle. Agroinfiltration delivery of Cas 9, and stable guide RNA expression in plant cells using a Tobacco mosaic virus vector has been demonstrated for GFP-transgenic *N. benthamiana*. Fully functional guide RNAs were produced by an unknown host processing mechanism (Cody et al., 2017; Plant Physiology, 175:23-35). In our newly introduced CRISPR/Cas9 plant application system, two split Cas9 constructs of 1.6 kb and 1.3 kb were expressed from an Alternanthera mosaic virus (AltMV; genus Potexvirus) vector, and GFP guide RNA[TGAGTTTGTAACAGCCT(AlwNI)CTGG] including the Protospacer Adjacent Motif (PAM) sequence also produced from AltMV, were introduced together to GFP-transgenic *N. benthamiana*. Among about three thousand harvested seeds we detected twenty-five non-GFP-expressing germinated seedlings. *AlwNI* cut purified DNA which was amplified using GFP-specific primers from non-GFP-expressing plants. The PCR amplified DNA was cloned to a TOPO vector to determine the sequences, and genomic DNAs of two plants lacking GFP expression were shown to have deletions in the guide RNA target sequence. Our newly developed system could become a potentially powerful tool without requirement for tissue culture; however increased efficiency is required to allow gene editing through seed not only for visual markers such as GFP but also for non-phenotypically characterized genes. Optimization for coordinated expression of the guide RNA and Cas 9 enzyme during plant embryo development is also required.

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**MULTISEEDED1 and 2 affects sorghum grain yield regulating at pedicellate spikelet fertility**

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Inflorescence architecture mainly contributes to final grain yield and grain number per panicle (GNP) and is a major determinant of grain yield in cereals. Sorghum *Sorghum bicolor* (L.) Moench) inflorescence is basically composed of one fertile sessile spikelet (SS) and two infertile pedicellate spikelets (PS). To identify regulatory factors involved in the inflorescence architecture, we screened an EMS mutagenesis population from the pedigreed sorghum mutant library. We found inflorescence architecture mutants, named as *multiseeded* mutants, *msd1,2,3,4*, with gained fertile ability in PS and also an increased number of floral branches. A detailed dissection of developmental stages of wild type and *msd1* and *msd2* described that the PS in wild type do not have floral organs, including ovary, stigma, filament and anther, while the *msd1* and *msd2* generate intact floral organ in the sessile spikelet. We found *MSD1* encoded a TCP (Teosinte branched/Cycloidea/PCF) transcription factor, and lipoxigenase (LOX) domain-containing gene *MSD2* encoded lipoxigenase (LOX) domain-containing protein which plays a role in the jasmonic acid (JA) biosynthetic pathway. *MSD1* and *MSD2* were a strongly enriched expression during inflorescence developmental stages. We proposed that *MSD1* and *MSD2* functions to suppress floral organ maintenance at PS during inflorescence development in Sorghum. To explore the regulatory network associated with PS fertility, whole genome expression profiling was performed at 4 different developmental stages in 6 various tissue types among wild type, *msd1* and *msd2*. Whole-genome expression profiling reveals that jasmonic acid (JA) biosynthetic enzymes are transiently activated in pedicellate spikelets. Young *msd1* panicles have 50% less JA than wild-type (WT) panicles, and application of exogenous JA can rescue the *msd1* and *msd2* phenotype. Recent results reveal a new mechanism for increasing GNP, with the potential to boost grain yield, and provide insight into association of JA pathway with sorghum panicle development and spikelet fertility.

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Epigenetic regulation by microRNA820 in *Oryza sativa*

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Epigenetic regulation has been implicated in plant development and stress responses. The underlying mechanisms of epigenetic regulation include DNA methylation, histone modification, and non-coding RNA-mediated regulation of gene expression. Of these, non-coding small RNAs, including microRNAs and small interfering RNAs, play a crucial role in negative regulation of gene expression at both transcriptional and posttranscriptional levels. microRNA820 is a small RNA produced from transcripts originated from a region inside CACTA DNA transposons in rice. It targets OsDRM2, which is involved in de novo DNA methylation of CG and non-CG sequences in the rice genome through a RNA-dependent DNA methylation mechanism to suppress transposon activity. Interestingly, both miR820 and OsDRM2 are down-regulated by drought stress treatment. To explore the function of miR820, transgenic rice plants over-expressing miR820 was generated. The transgenic plants exhibited drought-resistant phenotype compared with wild type plants. In addition, several transposable elements, including RIRE7, CACTA, and Tos17, were up-regulated in these transgenic plants. We also confirmed that those transposons were less-methylated in the miR820 over-expressing plants. These results might be due to the down-regulation of OsDRM2, which is responsible for the suppression of those transposable elements. Possible roles of this epigenetic regulation by miR820 and OsDRM2 as well as their agricultural impacts on drought stress resistance will be discussed.

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Production of soybean plants with high contents of omega-3

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α-linolenic acid, an omega-3 fatty acid, is taken as health supplement. *PfFAD3-1* gene, which is derived from *Physaria fendleri* called Lesquerella plant, strongly produces α-linolenic acid. *PfFAD3-1* gene was introduced into soybean by *Agrobacterium*-mediated transformation method. In transgenic plants (*T₃*), *PfFAD3-1* gene was identified by using PCR and Southern blot analysis of T-DNA. In addition, the content of α-linolenic acid in the transformed seeds (*T₃*) was confirmed by gas-chromatography analysis, and it was measured 6-times higher than wild type soybean seeds. Agronomic characters of 12 transgenic lines (*T₃*) with high α-linolenic acid content were investigated in the GMO field. As a result, the yield was increased in harvested *T₂* seeds. Commercial varieties of soybeans were analyzed to compare the nutritional profiles according to the different environmental conditions. The micronutrients of vitamin, minerals, and fatty acids were investigated for the environmental effects. These data could be used in the safety assessment of new plants developed by the biotechnology by comparing the substantial equivalence.

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Debunking the Claims that Glyphosate Tolerant GM Crops and the Herbicide are Responsible for Various Modern Diseases

Donghern Kim*, Yumi Choi
Future Food Resources Forum, Seoul, Korea

Series of papers published by Seneffe and Samsel together with the one by Swanson have been widely cited by Anti-GMO activists and NGOs as strong evidences supporting their view that GMOs are not safe to use. In this presentation, we summarize and critically review their arguments in order to provide balanced information to agricultural biotech society. In detail, claims reviewed here are such as glyphosate is responsible for 1) chronic illness due to its activity inhibit Cytochrome P450 and aromatic amino acid biosynthesis, 2) rise in non-celiac gluten sensitivity, 3) chronic disease due to its activity to chelate manganese and 4) rise in certain types of cancer. Swanson’s contention that the increase of glyphosate usage in the US are highly correlated with steep rise in various modern disease is also criticized in this presentation.

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Understanding of Séralini Affair: Controversy Surrounding the Research Paper Claiming the Causality between Glyphosate tolerant GM Corn and Cancer

Donghern Kim, Yumi Choi, Kyu-Hang Kyung*
Future Food Resources Forum, Seoul, Korea

The research article reported by a Gilles-Éric Séralini group in 2012 provoked immediate responses from scientists and regulatory agencies against it. Although the paper was retracted and republished without any further peer-review process in 2014, it has been widely cited by Anti-GMO activists and NGOs. In this presentation, we summarize defects in the paper and experts’ opinion on those issues in order to provide general view on the ‘Séralini Affair’ to agricultural biotech society so that the society is able to do ‘Knowledge-based Communication’ with publics and government agencies. Especially, flaws in designing the experiment and ‘cherry-picking’ type data presentation, which are most criticized issues, will be stressed in the presentation.

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국내 개발 우수 생명공학작물의 중국 및 동남아 시장 진출을 위한 국내외 육종 플랫폼 구축

이강섭

전라북도 전주시 완산구 농생명 370 농촌진흥청 국립농업과학원 농업생명자원부 생물안정성과

국내 개발 우수 생명공학작물은 유전자 지적재산권 점유, 우량 형질전환 이벤트 부족, 소비자의 사회문화적 수준을 고려하지 않은 GM작물개발 등의 문제점으로 인하여 아직까지 심화된 예가 없다. 따라서 GM작물의 개발초기부터, 품종화까지 모든 단계에 작품되는 체계적인 GM작물개발 프로토콜과 기술이 필요하다.


전라북도 농생명과 임상적 선발방법을 이용하여, 환경스트레스 내성 검정을 실시한 결과 환경스트레스 저항성 유전자를 좌우하는 역할의 품종군은 개발된 이 벡터의 생존율을 계통별로 차이가 있었으나 증가하였다.

금후 이벤트 개발을 위해 확보된 식물체는 계속적으로 세대진전을 하며, 포장에서의 표현형검정을 할 예정이다.

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Utilization and stable expressed miraculin protein to in vitro using plant suspension culture system

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Miraculin is the taste modifying protein and was isolated from red berries of Richadella dulcifica which is native to West Africa. The indigenous peoples use these berries to improve the taste of acidic maize food or for sweetening sour quencher. The active component of the berry is miraculin protein which is tasteless and has the property to make sweet taste of sour tasting product but salty, bitter and sweet tastes are not modified by it. Compared to sucrose, miraculin can induce 3000 times sweetness on the weight basis. Miraculin is very stable protein which does not change its sweetness property at 5°C (pH 4) for more than 6 months. The miraculin is consisting of 191 amino acids including seven cysteines and 3 intrachain and one interchain disulfide bonds were determined. In these studies, we have constructed a Ti-plasmid vector to express the miraculin gene with the SWPA2 and transformed it into plant cells by the Agrobacterium method. The 160 callus cells were transfected three times using callus induction medium containing 2 ppm of 2,4-D. The most rapid growth rate of callus was selected during the process. The selected callus was finely cut with tweezers and then cultured in a suspension liquid medium to investigate cell growth rate. These cell lines were confirmed by PCR analysis and checked gene expression by RT-PCR and Western blot analysis. These results demonstrate that recombinant miraculin was efficiently expressed in rice cell lines, and that we will be development of pilot-scale system to product natural sweetener.

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**PCS13-32**

Ubiquitination and decay of NMD factors triggered by pathogen infection fine tunes R transcripts during an early immune response

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NMD (nonsense-mediated mRNA decay) is one of key mRNA quality control processes and has been implicated in plant immunity. RNA-seq and expression analyses reveal that 81.2% and 65.1% of FS natural TIR-NBS-LRR (TNL) and CC-NBS-LRR (CNL) transcripts, respectively, retain characteristics of NMD regulation, by which their transcript levels are controlled post-transcriptionally. Both bacterial infection and perception of bacteria by pattern recognition receptors (PRRs) initiated the destruction of UPF1, UPF2 and UPF3 within 30 minutes of inoculation via the independent ubiquitination of UPF1 and UPF3 and the 26S proteasome pathway, and subsequently, NMD-sensitive TNL and CNL transcript levels increase. Induction of UPF1 and UPF3 ubiquitinations was delayed specifically in mpk3 or mpk6, but not in SA-signalling mutants, at an early immune response. Finally, previously uncharacterized TNL-type R transcripts accumulated in upf mutants conferred disease resistance on plants. Our findings therefore demonstrate that NMD is the control node through which PRRs can fine-tune R transcript levels to reduce fitness costs and achieve effective immunity.

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**PCS13-33**

Role of a hydrophobic residue in pyrabactin recognition by ABA receptors from Oryza sativa

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Pyrabactin is a synthetic mimicry of abscisic acid (ABA), a phytohormone related to abiotic stress. Although ABA and pyrabactin can be recognized by ABA receptors, pyrabactin induce different agonistic behavior according to each ABA receptors. Previous researches in Arabidopsis revealed that functionality of pyrabactin depends on unconserved residue in binding pocket and subfamily-specific manner. However, these studies are mainly performed in Arabidopsis thaliana. Pyrabactin effects toward Oryza sativa ABA receptors remains largely unexplored. Additionally, we observed that rice ABA receptors have different tendency to respond to pyrabactin. To identify structural determinants for pyrabactin recognition, we determined the molecular structure of OsPYL/RCAR3-pyrabactin:OsPP2C50 receptor:co-receptor complex by X-ray crystallography. Pyrabactin is located in the ligand binding pocket of OsPYL/RCAR3 as an unobserved conformation in Arabidopsis researches. Phe125, unconserved residue in binding pocket appears to be the culprit for the differential conformation of pyrabactin. Especially, this phenylalanine is only found in OsPYL/RCAR subfamily I among both Oryza and Arabidopsis. Although the gate closure essential for complex formation is preserved in the presence of pyrabactin, Phe125 apparently restricts accessibility of pyrabactin, leading to decreased affinity for OsPYL/RCAR3 in phosphatase assay. However, Phe125 does not affect conformation and accessibility of ABA. Yeast two-hybrid, germination and gene transcription analyses in rice also support that pyrabactin induces a weak effect on ABA signaling pathway. Overall, our study revealed that how does unconserved phenylalanine residue of ABA receptor affect pyrabactin recognition. Additionally, this phenylalanine substitution is also found in many other monocot crops. It may be one of considerations for ABA synthetic agonist development.

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Investigation of Root Characteristics for Evaluation of Resistance against Waterlogging Stress in Wild Soybeans

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Waterlogging stress is one of the restrict factors in yield reduction of soybean. For this reason, many scientists have tried to identify waterlogging tolerance mechanism however, clear tolerance mechanism against waterlogging have not yet been identified in soybean. Recently, our research team identified that exo-ethylene application can mitigated waterlogging condition in soybean. Furthermore, different root architecture was detected between waterlogging tolerance and waterlogging susceptible. Thus, we assumed that different root architecture would be participated in waterlogging tolerance mechanism. Base on above proof, we investigated various root phenotypes such as total root length, lateral root length, number of tips and root angle etc. using 1,334 wild soybean germplasm by WinRHIZO. Among 1,334 wild soybean genotypes, 714 wild soybean genotype were germinated thus, we analyzed root phenotype with WinRHIZO using 714 wild soybean genotype. To collect accurate result, we used PVC pipes as a pot (diameter: 6 cm, height: 40 cm). Frist, two of wild soybean seeds were propagated in each pot which was contained with horticulture soil. After two weeks, root was take off from the pot and then, root samples were carefully washed with tap water. Washed-root samples were placed on transparent plastic box which was containing with clean water and then, measured root image with scanner. Using the root images, WinRHIZO software calculated a number of root phenotypes base on pixel of each root image. Among the many root phenotype data, we focused on the root biomass such as total root length, lateral root length, number of tips and tap root length etc. According to results, most of root phenotype data showed normal distribution. Total root length showed range 30 mm to 450 mm and value of lateral total length showed between 4 mm to 108 mm. Number of tips revealed 100 to 1,200 per plant.

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Expression of Resveratrol-Dependent Glucosyltransferase Genes in the Resveratrol Rice DJ526 Germinated Seeds

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According to glycosylation process, resveratrol product can converted to piceid which is a glycoside form. During seed germination, glycosylation plays an important role to transfer sugar molecules by enzymatic process such as glucosyltransferase. Therefore, our present study purposed to find the resveratrol-dependent glucosyltransferase candidate genes in resveratrol rice DJ526 in order to improve the resveratrol production. Germinated seeds for 5 days were collected and used as tissue model for selection of candidate genes due to the level of resveratrol product. Twenty-seventh of candidate genes were selected from NCBI database which are related to glucosyltransferase in Japonica rice. From the results, we suggested 7 candidate genes including RG4, RG7, RG9, R10, RG11, RG13 and RG25 which are revealed an up-regulation expression. Furthermore, among of 7 candidate genes, RG10 showed the highest expression stability with 3.5-fold changes compared with non-transgenic germinated seed and might be used as a putative resveratrol-dependent glucosyltransferase gene to develop a new DJ526.

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Screening of Candidated Glucosyltransferase Genes in Resveratrol Rice DJ526 Callus

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DJ526 rice was established to express resveratrol production which is well-known as a powerful healthy agents. DJ526 rice callus was obtained in an optimum culture and media condition. After 10 days cultured, calli were used as sample tissues for analysis of glucosyltransferase gene. The synthesized cDNA products were evaluated the expression of candidate glucosyltransferase genes (CGs) through real-time PCR to select the appropriated resveratrol-dependent gene. Among of 27 CGs, six genes relative to glucosyltransferase in DJ526 rice callus. RG 1, 3, 4, 7, 14 and 19 gene which are expressed up-regulation in DJ526 callus based on cq value and target regulation level, whereas others CGs were showed not only down regulation but also no expression in DJ526 callus compared with control (non-transgenic callus). Within six proper genes, RG14 showed the highest 2.07-fold change level of gene expression compared with non-transgenic callus. Finally, this experiment is an attempt to improve the resveratrol yield of transgenic rice DJ526.

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Expression of recombinant Miraculin protein in transgenic carrot cell suspension culture

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Plant is an one of powerful biofactory system to produce recombinant protein. Herein we report a research progress of Miraculin, which is a taste-regulating protein, using plant cell culture system. Miraculin is a taste-regulating protein with the ability to interact with human sweet taste receptors and transform savoriness into sweet taste, extracted from the fruit ‘miracle fruit’ of Sysepalum dulcisfium. Since miracle fruit is difficult to mass-produce due to regional and seasonal limitations, there have been many efforts to express miraculin in various in-vitro culture systems like hairy root and cell suspension culture. Therefore, in order to produce miraculin from hairy roots of carrots, we induced hairy roots by infecting carrot root pieces with Agrobacterium rhizogenes. After 4 weeks of transformation, putative hairy roots induced in 5 of the 22 explants (23%). To confirm the hair roots, the presence of rol gene insertion was confirmed by PCR, and 4 lines out of 5 lines were confirmed to be hairy root. Three lines (HR1, 2, 3) except for HR4, which has a slow growth rate among four hairy root lines, were selected and used for 2 step transformation for miraculin production. The plant expression vector with SWPA promoter was introduced into carrot selected hairy roots and calli via Agrobacterium-mediated transformation methods. One miraculin transgenic hairy root and 18 transgenic cali were obtained through Agrobacterium-mediated ‘Miraculin’ transformation. The integration of the miraculin gene into the chromosome of the transgenic callus and hairy roots was verified via genomic DNA PCR amplification and miraculin expression in transgenic carrot suspension cells and hairy roots was confirmed via RT-qPCR analysis. RT-PCR was carried out using 6 transgenic calli lines (1, 7, 11, 13, 14, 18) with the best growth. It showed the highest ‘Miraculin’ gene expression in line 7. In further study, we will investigate the yield of miraculin production through protein extraction and purification in transgenic hairy roots and suspension cultured cells. This study confirmed the optimal system for efficient production of recombinant ‘Miraculin’ protein.

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Agrobacterium-mediated transformation carrot cells for the expression of recombinant Brazzein, a sweet-tasting protein

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The application of plant cell culture to recombinant protein production has focused on well-characterized plant cell lines such as carrot and rice. Recently, the importance of low-calorie sweeteners is increasing for persons who care about their health, especially the persons affected by diseases linked to the consumption of sugar. Brazzein (6.5 kDa) is the smallest naturally occurring sweet-tasting protein. The study was conducted to optimize the culture conditions of transgenic carrot cell lines as a part of study to establish stable expression system of brazzein protein from carrot cell cultures. The induced carrot cell line was transformed with Agrobacterium and transgenic cell suspension culture was induced. Brazzein expression was analyzed every 3 days during the culture period of cell suspension culture. In order to investigate the optimal light condition of brazzein expression, five different kinds of light quality were examined: white, red, blue, mixed light. By Agrobacterium-mediated transformation, three cell lines (TL1, 11, 12) were selected, line TL12 showed the highest cell proliferation. The highest gene expression was shown in transgenic cell line L11, however, considering the cell growth rate, L12 was the best, so L12 was used in the next experiment. After 4 weeks of culture under different light quality, carrot cell line showed the excellent cell biomass in all light condition. Total protein content was the highest at 1.1 mg · g⁻¹ FW in cell cultures grown under blue light. According to cell growth curve, cell cultures were reached to stationary phase around 15-18 days of suspension culture, and it was the time for subculture and harvest. After proliferating in 250-300 ml flask culture, transgenic carrot cells were transferred various type of bioreactor for mass production. Transgenic cell proliferation and gene expression were the highest in the column type air-lift bioreactor. In further study, the yield of brazzein protein by stress factor will be investigated. Based on the results obtained in this study, we intend to establish a stable brazzein protein production system using air-lift bioreactor.

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A N molecular sensor system: a breeding technique for development of high NUE rice under low N conditions

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Nitrogen (N) is an essential nutrient for plant growth and development. N supply from natural soil is insufficient for crop production and rest of N sources are inevitably supplied by N fertilizer. Although N fertilizer induces great benefits in crop yield, overdose of the fertilizer results in a negative impact on the environment. Improvement of N-use-efficiency (NUE) of crops aims to reduce N fertilizer usage while maintaining crop yield. At first, we developed an N molecular sensor system to monitor N status in a rice plants. We identified two genes for allantoin metabolism, ALLANTONASE (OaALN) and UREIDE PERMEASE 1 (OuUPS1), to be highly responsive to N status. OaALN was rapidly up-regulated under a low N condition, whereas OuUPS1 was up-regulated under a higher N condition. Taking advantage of their nature in response to N status, we generated N sensors as proALN::OaALN-LUC2 and proUPS1::OuUPS1-LUC2 in rice plants. The transgenic mimicked transcriptional regulation of the endogenous OaALN and OuUPS1 genes in response to N status. Importantly, the N sensors showed similar levels of specificity to nitrate and ammonium, inferring the sensing ability of the sensors. Transgenic rice plants with proUPS1::OuUPS1-LUC2 sensor showed strong luminescence activity under a low N condition (<0.1 mM N source). With the N sensor-integrated transgenic rice, we generated an EMS mutant population (10,000 individual lines). We are screening the high NUE rice under low N conditions based on the N sensor system and trying to identify key players in rice N metabolism based on bulk segregant analysis and next generation sequencing techniques.

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Development of Drought Tolerant Crops using noncoding RNAs

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Abiotic stresses are major constraints of agricultural productivity. Drought, the most serious stress, and its negative impacts are likely to increase worldwide. Recent studies have shown that abiotic stresses induce aberrant expression of many noncoding RNAs, including miRNAs, thus suggesting that miRNAs may be promising targets for genetically improved crops tolerance to abiotic stresses. In general, abiotic stress induces miRNAs to downregulate their target miRNAs, and their downregulation leads to accumulation and activation of positive regulators. This implies that miRNAs do not control directly plant growth and development but control indirectly plant development by mediating a miRNA-target gene network. Therefore, it is evident that endogenous miRNAs have been shown to work as developmental switches and to regulate drought-responsive genes under drought stress. Previously, we identified the rice noncoding RNAs (66 miRNAs and 98 IncRNAs), whose expressions were highly regulated by drought conditions, and whose transcript levels were negatively correlated with the putative target genes. For a further investigation of the biological functions of each miRNA, we generated 12 miRNA overexpressing and knockout lines using constitutive GOS2 promoter and CRISPR/Cas9, respectively. During cultivation, we found several phenotypes in the overexpression lines, including premature leaf senescence, increased number of tillers and grain yield along with the drought tolerance phenotype. The use of miRNA-overexpressing and knockouts and their targets will be a promising technique for determining the native functions of individual miRNAs in response to drought stresses. The identification of the specific positions of miRNAs underlying their regulatory networks represents a convincing research area to pursue in the future.

Keywords: Noncoding RNA, Drought tolerance, Grain yield, Target gene, CRISPR/Cas9

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Genome-wide analysis of radish lincRNAs and partial identification of putative target genes

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Since the radish genome analysis is completed, genetic information can be utilized for the improvement of agronomical traits. Radish shares with other Brassicaceae species a common aim of improved target characteristics such as sugar content and low temperature resistance. Because IncRNAs regulate a variety of agricultural traits including environmental resistance and seed development, their functional roles need to be identified prior to the development of value-added crops. By transcriptomic analysis from different tissues and developmental stages of radish, the 17448 IncRNA candidates were obtained. Among them, 11148 were in the antisense, 6340 were in the sense direction, and 3,230 IncRNAs were expressed in tissue- and developmental-specific manner. In addition, 309 IncRNAs were newly expressed and 77 IncRNAs were reduced upon vernalization. In order to compare the function of IncRNA in radish and Arabidopsis, we selected 30 candidate IncRNAs in Arabidopsis, and generated transgenic Arabidopsis lines overexpressing IncRNA. Four 35S:IncRNA transgenic plants showed phenotypic changes. 35S:IncRNA #1, 35S:IncRNA #2, 35S:IncRNA #3 and 35S:IncRNA #4 reduced the expression level of the their target genes and their phenotypes were similar to the T-DNA mutants defective in target genes. When IncRNA #1 was overexpressed, plants showed aberrant rosettes leaves, but other phenotypes similar with those of wild type. While IncRNA #2 was overexpressed, plants showed abnormal siliques, IncRNA #3 and IncRNA #4 showed seed abortion. We expect that the modulation of expression levels of IncRNAs could be used for increasing the content of sugar and/or secondary metabolites, suppressing bolting, and growing at low temperature in Brassicaceae plants.

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High expression of recombinant proteins in Arabidopsis protoplasts by using Gal4/UAS gene expression system and PTGS suppressor

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Various approaches have been attempted to achieve high production of recombinant proteins in plant tissues, such as strong promoter design, specific 5' untranslated region (UTR) insertion, utilization of virus RNA replication system and so on. In this study, we investigated Gal4/Upstream Activation Sequence (UAS) and post transcriptional gene silencing (PTGS) suppressor to utilize them synergistically for high production of recombinant proteins in plant tissues. Compared with the construct driven by the CaMV 35S promoter that is generally used for protein overexpression in plant tissues, coexpression of the Gal4-VP16 led to more than 2 times higher expression level increase of the target protein regulated by the UAS promoter in Arabidopsis protoplasts. However, Gal4-VP64m induced protein expression with only similar amount of the target protein driven by the 35S promoter, indicating that 4 repeats of VP16 minimal domain are not sufficient to increase protein expression significantly as reported in previous researches. The PTGS suppressor P38 coexpression also enhanced the target protein expression level effectively and combination with Gal4/UAS system accomplished much higher protein production, suggesting that the synergic effect of these independent approaches can be usefully applied for high production of recombinant proteins. Taken together these results, we concluded that each approach using Gal4/UAS system or PTGS suppressor is remarkably effective for high production of recombinant proteins in plant tissues and sophisticated utilization combining them can be the useful strategy to increase recombinant protein expression level even more dramatically.

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Natural variation of anti-nutrient compounds in soybean cultivars grown in different regions

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The rate of development and commercialization of biotech crops is steadily increasing. In addition, a safety assessment based on the concept of substantial equivalence is being conducted to evaluate the unintended and un expected impact of new biotech crops. Equivalence evaluation through nutrient and anti-nutrient analysis is performed mainly according to the standards of Codex Alimentarius Commission and OECD (Organization for Economic Cooperation and Development). In particular, the safety assessment requires analysis data for crops grown in different and climate. This is because the components of a crop are affected by biotic and abiotic factors. Therefore, this study was carried out to secure the crop value of functional GM soybean through comparative evaluation of the natural variation of anti-nutrient such as phytic acid, raffinose and stachyose in soybean varieties grown in three different regions of Korea.

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Analysis of genome evolution of naturally occurring attenuated isolates of *Burkholderia glumae*

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*Burkholderia glumae* is a casual agent of bacterial panicle blight in rice and has a single LuxI-R type quorum sensing (QS) system. N-octanoyl homoserine lactone and its cognate receptor TofR regulate production of toxoflavin in *B. glumae*. Genome information of a total 58 isolates of *B. glumae* obtained from diseased rice panicles, broken rice, and solanaceae crops was determined. Significant differences in genome structures such as inversion, rearrangement, and mergence of chromosomes were found among isolates. Most of isolates from diseased broken rice did not produce toxoflavin and were avirulent. In the toxoflavin-defective isolates, a large size of DNA fragment carrying foreign DNA was inserted in the promoter region of toxoflavin biosynthetic gene cluster. Most of toxoflavin-defective isolates were resistant to kanamycin and spectinomycin and more competent than a prototype isolate BGR1. Those isolates produced less amounts of QS signals and oxalate compared to those produced by BGR1, which caused alkaline environment due to massive generation of ammonia upon growth in Luria-Bertani medium. These results indicate that genomes of *B. glumae* isolated from different ecological niches reflect how they have evolved to affect virulence.

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Development of safety assessment methods for transgenic soybeans as cosmeceutical protein production

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Development and commercialization of domestic transgenic crops have difficulties in public consensus formation due to safety concern, despite their economic and environmental benefits to farmers and consumers. Therefore, it is necessary to develop scientific and transparent risk assessment technology and a wide range of safety verification to resolve those concern. Soybean is suitable for producing proteins for cosmetic materials because of its high protein content. With transgenic soybeans used in this study, it is expected that the cost of protein production for cosmetics are reduced by more than 90% compared to conventional method using bacteria expression systems, and it is also expected that soybean farmers can sell their crops at 6 times higher price than non-transgenic soybean price. In this study, we developed ingredient analysis method and safety assessment method for human health and environmental risk of two transgenic soybeans producing TRX and EGF protein. In detail, we establish evaluation standards by developing equivalence assessment method, single dose toxicity testing, the assessment of gene flow and weediness, the analysis of general composition of TRX transgenic soybean, and the selection of agricultural environmental species of these transgenic soybeans. The results of these studies will contribute to the development of evaluation standards for the commercialization of transgenic crops and the reduction of consumer safety concerns about transgenic crops.

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Characteristics and efficacy evaluation of transgenic rice for improving glucose metabolism as a medicinal material

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In this study, we generated and characterized the transgenic rice plant expressing a spider silk protein. Spider silks have great potential as biomaterials with extraordinary properties. Here, we report the cloning and characterization of the major ampullate silk protein gene from the spider Araneus ventricosus. A cDNA encoding the partial major ampullate silk protein (AvMaSp) was cloned from A. ventricosus. Transgenic rice plants with high contents AvMaSp protein, the GluC promoter driven AvMaSp was introduced into rice plant via Agrobacterium tumefaciens-mediated gene transformation. We generated a homozygous transgenic rice line that accumulates AvMaSp protein in seeds using by southern, northern and western blot analysis. Also, diabetic mouse used to examine the effects of diabetes treatment and to investigate molecular mechanism by tissue process and immunohistochemistry method.

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A comparative study on metabolic differences of soybean leaves from commercial cultivars and wild species

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The primary metabolite profile is closely related to phenotype. GC-MS-based metabolite profiling is useful for the rapid and highly sensitive detection of plant metabolites from the central pathways of primary metabolism and to assess the variation in polar primary metabolites in plants. In this study, low molecular weight molecules of soybean leaves from commercial cultivars (Glycine max) and wild species (Glycine soja) were identified by gas chromatography-time-of-flight mass spectrometry (GC-TOFMS) to explore metabolic differences between their genotypes. G. max is one of the most widely grown crop species in the world. G. soja is the closest extant wild relative of soybean and is generally considered to be the undomesticated progenitor of the domesticated soybean. G. max and G. soja are phenotypically disparate in many ways, but they readily cross with one another and give rise to fertile hybrids. The core metabolites comprising amino acids, organic acids, sugars, and sugar alcohols were identified in all samples. The quantitative data for all metabolites identified were subjected to Principal component analysis and partial least-squares discriminant analysis to determine phenotypic variation and relationship between metabolite contents. The identification and profiling of primary metabolites using GC-TOFMS analysis allows clear discrimination between soybean genotypes. This study determined metabolic differences between soybean leaves of G. max and G. soja and provides useful information for genetic manipulation of soybeans to influence primary and metabolism.

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Identification of a synthetic partial ABA agonist, S7

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The stress hormone abscisic acid (ABA) helps plants to survive abiotic stresses; however, its use as an agrochemical is limited by its chemical instability and expense. Here, we report the development of an in vivo screening system to isolate chemicals able to induce ABA signaling responses in rice (*Oryza sativa*) protoplasts. This system consists of an ABA-hypersensitive synthetic promoter containing ABRE and DRE motifs driving a luciferase reporter gene. After efficiently transfecting rice protoplasts with this construct, we screened 100 chemicals with a similar molecular weight and chemical structure to ABA. We identified one chemical, S7, that weakly induced ABA signaling by inefficiently mediating interactions between the group I and II OsPYL receptors and certain OsPP2CAs in a yeast two-hybrid assay. In an in vitro pull down assay, S7 was found to mediate a weak interaction between OsPYL5/8 and various OsPP2Cs. S7 treatments did not affect seedling growth or seed germination, but could reduce water loss. Rice seedlings treated with S7 exhibited transcriptome profiles that partially overlapped those treated with ABA. Taken together, we conclude that S7 is a weak and partial new ABA agonist, which has potential use in future dissections of ABA signaling and as an agrochemical.

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Establishment and utilization of scientific information service system for agricultural biotechnology

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In recent years, there has been a growing trend toward development and utilization of agricultural biotechnology across the globe. Thus, providing information objectively and transparently is absolutely crucial for supporting the public's right to know and forming social consensus on agricultural biotechnology. Furthermore, an efficient system of providing information is required to reduce the social cost of new technology development. Providing useful information from around the world in real time with respect to diversification in traits of biotechnology crops, as well as development subjects and rapid expansion of R&D on genetic modification, contributes to sharing accurate and reliable information based on research strategies and scientific knowledge. For such a purpose, establishment of a communication channel among biotechnology research scientists in the professional realm, consumers who are considered end-users, and government bodies supervising related policies is urgently needed. The main objective of this study was to improve communication regarding the study on biotechnology crops by forming and utilizing a scientific knowledge-based information service for agricultural biotechnology, and the following major outcomes were achieved. First, user-oriented efficiency methods were drawn through development and research on utilization of a program that provides information on agricultural biotechnology. Second, directions on structural improvement were proposed and methods were derived for the establishment and revitalization of an agricultural biotechnology information service system. Third, a real-time information sharing system was established for sharing and utilizing information on agricultural biotechnology from around the world, in addition to an efficient R&D information system. Fourth, trends in public awareness of biotechnology were analyzed through an awareness survey on biotechnology and a study on developing practical communication governance; a situation analysis on the communication between government officials, researchers, and consumers was conducted and effective cooperative measures were obtained as part of practical communication governance.

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Gametic Transfer Defect (GTD2), encoding WD40 domain, functions as a positive regulator of pollen tube growth in rice

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Successful delivery of sperm cells to the embryo sac is mediated by pollen tubes in higher plants. The molecular mechanisms determining pollen germination and tube growth in crop plants remain largely unknown, although it is crucial in reproduction and grain formation. Unlike Arabidopsis with many oocytes in one carpel, the carpel of grass crops only contain one ovule, therefore gametic defect of rice and maize frequently results in nonproducing homozygous mutants, which makes more difficult for functional study. Recently, genome-wide analyses specifically in rice pollen grains extend our current understanding of the regulatory components involved in pollen tube journey. We have identified the Gametic Transfer Defect2 (GTD2) by screening pollen specific genes in rice (Oryza sativa). GTD2 contains seven WD40 repeats, which is highly conserved with other plants WD repeat containing proteins. GTD2 is specifically expressed in rice pollen, analyzed by qRT-PCR and promoter-fused GUS transgenic rice, and it is localized into nucleus, cytosol, and plasma membrane. The homozygous mutant created by CRISPR-Cas9 exhibited male sterility, with the disruption of pollen tube elongation in vivo. Transcriptome analysis of GTD2-defective alleles revealed that 852 pollen-prefer genes were down-regulated, especially for cell wall modification. Yeast two hybrid screening of GTD2 identified three interacting partners function in endocytosis, suggesting that GTD2 might function as scaffold for protein interactions to regulate downstream events such as endocytosis for continuous pollen tube elongation. Taken together, GTD2 functions as a positive regulator in rice pollen tube elongation.

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유전자변형 제조제성형 돌잔디에 방사선 조사로 육성된 무추대 품종의 형질 안정성 평가

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이 연구는 유전자변형 제조제성형 돌잔디에 방사선을 조사하여 육성된 무추대성 돌잔디 품종(JG21-MS1)에 대한 무추대 형질의 안정성을 평가하기 위해 수행되었다. 재주, 서귀포, 전북 전주를 포함한 서로 다른 3 지역의 자연환경조건과 개화유도를 위한 몇몇 인위적인 조건에서 복수 년 동안 추대 회복을 조사하였다. 자연환경조건의 실험은 각 지역의 LMO 환경에 대한 대용량장에서 수행되었다. 인위적인 조건은 흙과포와 온실 내 안공조명의 장인 또는 전일 조건 하에서 시험 재료의 추대 가능성을 관찰하였다. 이러한 인위의 실험에서 어느 환경 조건에서도 무추대성 돌잔디의 추대가 회복되는 경계는 발견되지 않았다. 따라서 본 연구는 자연 환경과 온실 등의 인위적인 환경 조건 모두에서 JG21-MS1의 무추대성이 쉽게 회복되지 않는 형질로 고정되어 있음을 보여 주었다. 또한, 꽃이 피지 않는 유전자변형 제조제성형 잔디인 JG21-MS1은 꽃가루에 의한 유전자이동 가능성이 원전적으로 낮아지므로 이 LMO 잔디가 자연환경에서 방출되더라도 생태계를 교란할 가능성이 매우 낮을 것으로 사료된다.

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Overexpression of auxin biosynthetic enzyme YUCCA6 activates glucosinolate biosynthetic pathway in Arabidopsis

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YUCCA (YUC) proteins constitute a family of flavin monooxygenases (FMOs) and participate in auxin biosynthetic pathway via conversion of indole-3-pyruvic acid (IPA) to indole-3-acetic acid (IAA). Previously, it has been reported that Arabidopsis YUC6 positively regulates abiotic stress tolerances, such as oxidative and drought stresses, and negatively involved in leaf senescence via maintaining ROS homeostasis. Here, we conducted transcriptomic analysis using Arabidopsis dominant mutant yuc6-ID (activation-tagged YUC6) displaying high auxin levels. Gene Ontology (GO) enrichment analysis again pointed to the enrichment of genes involved in the response to auxin stimulus in yuc6-ID. Interestingly, genes involved in the glucosinolate biosynthetic process also up-regulated in yuc6-ID. Glucosinolates display diverse regulatory functions in inflammation, stress response, and antioxidant activities, as well as direct antimicrobial properties and is one of highly accumulated secondary metabolites under diverse stress conditions. Genes encoding 2-OXOGLUTARATE-DEPENDENT DIOXYGENASE, ACC OXIDASE, UDP/GLUCOSYL TRANSFERASE 74B1, and PRODUCTION OF METHIONINE-DERIVED GLUCOSINOLATE 1 were up-regulated in yuc6-ID. This data suggests that overexpression of YUC6 promotes the accumulations of stress-responsible secondary metabolite glucosinolates to improve defense response against diverse biotic and abiotic stresses. [Supported by a grant from the Next-Generation BioGreen 21 Program (PJ013671012019), Rural Development Administration, Republic of Korea]

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Need for FDA Approval of Transgenic Resveratrol–enriched Rice

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Resveratrol is a kind of stilbenoid found in some fruits and vegetables and has various beneficial health effects, called the ‘French paradox’. There is also research showing that resveratrol can help improve metabolic syndrome. For these reasons, many researchers have attempted to develop major crops that produce resveratrol but most have not succeeded. In previous study, production of transgenic resveratrol-enriched rice was succeeded. The efficacy of the resveratrol-enriched rice on metabolic syndrome, obesity and melanin synthesis was confirmed by animal experiments. Resveratrol-enriched rice is expected to generate high economic value because of these beneficial effects and is considered to be competitive in the global GM crops market. However, the cultivation of resveratrol-enriched rice in Republic of Korea was frustrated by opposition of public opinion, although resveratrol-enriched rice passed safety assessment of GMO. Because these hostility of GMO in Republic of Korea is difficult to solve in a short time, it is necessary to enter the abroad market to produce the economical and medical value of resveratrol-enriched rice. FDA approval is essential for entry into the Us market, which is the largest market among abroad markets. In this project (PJ0145132019) dossier preparation, GMO safety regulation review, and approval letter preparation for FDA approval of transgenic resveratrol-enriched rice will be performed.

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A Study on the Value Increase and Future Application of the Research Team

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Drought has become a serious global problem that leads to decline in food production due to climate change. In this study, rice phytochrome B mutants (osphyb) which were known to have increased drought tolerance were used to analyze drought-related traits of rice. The values of image parameters which can be measured by RGB camera, such as plant area, leaf color, object extent X and Y, compactness, and convex hull area were increased in osphyb plants compared to wild type (WT) plants under drought stress conditions. These results reflected phenotypes such as leaf discoloration and wilting of the stressed plants. Near-infrared (NIR) intensities of osphyb plants were about 3 fold higher than WT plants after recovery for 8 days following drought treatment. This result shows that the osphyb plants have higher water contents than WT plants. In addition, it was revealed that leaf temperature of WT plants was increased about 0.3°C compared to osphyb plants under drought stress conditions using infrared (IR) imaging. These results might indicate that OsPhyB regulate stomata opening and closing. Also, as drought stress progressed, the chlorophyll fluorescence of plants changed remarkably. The values of fluorescence parameters, such as Fv, Fm, Fm/F0, and Fv/Fm, and fluorescence area were reduced in WT plants while they remained normal in osphyb plants. Eventually, RGB, NIR, IR, and fluorescence imaging and their image-based parameters have been effective in selecting drought-tolerant rice plants. This study has established basis for image analysis methods for drought tolerance measurement. In the future, these results will be applied to development of efficient methods for high-throughput phenotyping.

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Development of utilization technology of rice varieties based on Indel big-data

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유전자 변형 생물체에 대한 오해 및 우기는 농업경영이 개선된 우수한 형질전환 식물체를 심화하는 데 크나큰 장벽으로 존재한다. 우리는 이를 극복하기 위해 사람이 인위적으로 변형한 형질전환 식물체가 아닌 자연적으로 변이가 일어난 비 품종을 활용하여 유용 작물을 발굴하고자 한다. 작내에 엽기생장 해독 기술을 활용하여 Nipponbare 비 품종을 기준으로 유전자 단위(Locus ID)에서 insertion/deletion (indel) 형성 여부를 확인할 수 있는 데이터베이스를 공주대학교 연구팀의 도움으로 구축하였다. 이를 토대로 기존에 보고된 논문 중 가품 스트레스에 저항성을 가지는 유전자 5개를 선발한 후, 5개 유전자 모두에서 indel 형성이 일어난 품종 5개, indel 형성이 하나도 일어나지 않은 품종 5개를 확보하였다. 이는 염분 스트레스에 저항성을 가지는 품종을 선발하는 과정에서도 동일하게 적용되었다. 현재 공주대학교 연구팀의 도움으로 비 고밀도 830K Chip 분석을 통해 indel 형성 여부를 재확인 과정에 있다. 더불어, 공동연구를 통해 관련 품종의 짝을 확보하였으며, 가품 및 염분 스트레스 실험을 수행 중에 있다. 우리는 이 과정을 통해 바이데이터를 활용한 유용 품종을 탐색 및 확보하고, 이를 활용할 수 있는 토대를 만들고자 한다.

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Transformation of maize immature embryos using Agrobacterium tumefaciens

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Maize is the most important grain crop in the world. The genetic engineering technology has been used to enhance the various agronomical traits. The maize transformation is a crucial step for application of gene technologies to improve maize. The choice of genotype and explant material influences on the transformation efficiency and the production of stable transgenic plants. In this study, plant regeneration ability of 16 maize genotypes was investigated using 9-15 day-old immature zygotic embryos. Among these genotypes tested, M1 (H1 II), M2 (H99), and M3 (A188) gave the best plant regeneration. Immature embryos were infected with Agrobacterium tumefaciens LBA4404 including superbinary vector (bar and gus or GFP genes). We obtained stable transgenic plants with herbicide resistance from only M1 genotype. The progeny analysis confirmed that the integration and expression of bar, gus, and GFP genes in T0 and T1 generations of transgenic plants.

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Construction of Siderophore producing *Agaricus bisporus* transformants

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*Agaricus bisporus*, button mushroom, is an edible mushroom native to grasslands in Europe and North America. It is one of the most commonly and widely consumed mushrooms worldwide. It produces various biological materials such as oxidative enzymes and bioactive compounds. In this study we have focused on the production of siderophore which is required for uptake of iron and is known to show anti-cancer activities. We first generated transformants that can overexpress genes related to siderophore biosynthetic pathway. For this, hapX gene, serving as key regulating transcription factor, was inserted to binary vector pBGgHg for constitutive expression of hapX with a constitutive promoter. *A. bisporus* was transformed with the binary vector through *Agrobacterium tumefaciens*-mediated transformation (ATMT). The resulting transformants were selected by serial transfer on selective medium. Obtained transformants were then confirmed by nucleotide sequencing and mRNA expression. Among the isolated transformants, 3 of stable transformants were selected as for final candidates and their ability to produce siderophore was confirmed by HPLC and MS spectrometry. The culture conditions were elaborated through the cultivation in various environmental and media compositions.

Production of male sterile tomatoes edited by CRISPR/Cas9 system

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Most domestic tomato hybrids(F₁) are produced through emasculation and cross-pollination. Worldwide, the demand for processing tomato is steadily increasing, but production of processing tomato seeds through emasculation and cross-pollination is less economical as production costs are higher than sales costs. In this study, to improve efficiency of hybrid seed production and protect breeding materials, we try to produce various tomato male sterility materials using CRISPR/Cas9 systems. Through research on the transcriptome of spontaneous male-sterile mutant (ms10⁵) and male sterility in Arabidopsis and rice, twelve putative genes associated with ms were selected. Each guide RNA targeting putative ms genes was designed and fused into Two-genes-target CRISPR vector (pAGM4723, Addgene) which could edit two target genes simultaneously. And then, the tomato M82 and Micro-tom were transformed by *Agrobacterium tumefaciens* EHA105 including the final CRISPR/Cas9 binary vector. Currently, we are investigating the genome editing of target genes and characteristics of male sterility in the transgenic M82.

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Agricultural Biotechnology Research Center Development Resources and Life Information Mid to Long Term Preservation

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This project aims to provide available summarized information on the status of genetic management of materials and information of genetically modified organism (GMO) in South Korea and to lay the foundations on the preservation of GMO materials for the medium and long term. It is necessary to utilize the existing information and materials of GMO in order to increase efficiency in future projects. First, a yearly collection of material of GMO and genetic information with assigned format are organized to facilitate searching the information on database of Agricultural Biotech Research Group (ABRG). The establishment of database can help future researches efficiency, reduce overlapping investment and prevent losing developed GMO materials. Secondly, to preserve, propagate and use GMO materials in medium and long term (10 to 30 years), genetic management on database can ensure that the deposited materials of GMO is to monitor seed viability and the regeneration of seeds are carried out when they are damaged or lose viability. Thirdly, it is our responsibility in this project to regenerate and increase the collections of GMO seed in permitted research field (Gunwi, Korea). GMO materials can be shared in another research project to develop an economical crop. This project can help collect the GMO resources which is not on the database or deposited to utilize those materials in the future. Finally, these materials and information of GMO could be used to develop new global crops through material or technology transfer to industry.

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Comparison of Isoflavones in commercial soybean cultivars with different physicochemical characteristics

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A biochemical functional compounds of 14 soybean cultivars has been analyzed. The objectives of this study were to determine the effects of Korean soybean variety, planting date, physical seed quality, planting location, and crop year on isoflavone content, as well as to analyze the relationship between seed viability grown in difference locations. Soybean cultivars represented five soybean species according to the commercial usage, which were categorized with soybean sauce, black soybean, soybean sprout, and others. Major isoflavones were daidzein, daidzin, genestein, genistin, glycitein, and glycitins. These were quantified by high performance liquid chromatography. The results showed that composition and level of metabolites in soybeans varied greatly between and was independent of species and geographical location. Isoflavone content in soybeans varied considerably depending on such factors as variety type, and planting location. Most had significantly higher isoflavone content when planted in early rather than in late date. Additionally, seed viability of different conditions seemed likely to affect isoflavone content in Korea soybean varieties. Isoflavone content in soybean seeds grown in Korea depends on multiple genetic and environmental factors. Total isoflavone content of Daepung cultivated in Suwon, total isoflavone content of Pungwon in Iksan and total isoflavone content of Daepung 2 in Miryang exhibited moderately high isoflavone content regardless of sowing date. Based on these metabolic data, five cultivar types were selected for further metabolic and molecular analysis, in order to assist future comparative analysis aimed at safety assessment for GMO and new biotechnology crops in soybean crops.

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Analysis and identification of SIHDC-A promoter elements in tomato

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The development of promoters associated with the initiation of specific temporal and spatial expression patterns is crucial for crop biotechnology. Through RNA-seq and RT-PCR analysis, we found that SIHDC-A mRNA was involved in tomato fruit ripening. To obtain the fruit-specific promoter, we isolated a SIHDC-A promoter in tomato and generated transgenic tomato transformed with SIHDC-A::GUS and 35S::GUS. Unlike 35S::GUS transgenic tomato with constitutive expression in various tissues, SIHDC-A::GUS transgenic plants showed fruit-specific expression of GUS. The intensity of GUS activity in fruits of SIHDC-A::GUS transgenic plants was approximately tenfold higher than that in fruits of 35S::GUS transgenic plants. The core region responsible for its fruit-specific expression was identified by promoter deletion analyses. Removal of the − 880 to − 577 region abolished the fruit-specific expression of SIHDC-A promoter. This suggests that the − 880 to − 577 region is the core region responsible for the fruit-specific expression of SIHDC-A. This finding was further supported by analysis of chimeric fusion promoter. Unlike 3S minimal promoter which had no activity to express GUS, the chimeric fusion promoter of the core region and 35S minimal promoter showed fruit-specific expression similar to intact SIHDC-A promoter. Collectively, these findings indicate that the promoter of SIHDC-A is fruit-specific and the − 880 to − 577 region is the core region of SIHDC-A promoter.

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Development of Novel Rice Producing Ginseng Protopanaxadiol

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Panax ginseng produces triterpene saponins called ginsenosides, which are classified into two groups by the skeleton of aglycones, namely dammarane type and oleanane type. Dammarenediol-II (DD) is biologically active tetracyclic triterpenoid, which is basic triterpene skeleton of ginsenoside sapogenin in Panax species. Protopanaxadiol (PPD) is converted from DD triterpene. PPD, an aglycone of ginsenosides, has apoptotic effects in various cancer cells and is cytotoxic to multidrug resistance in tumor cells. This study was conducted to develop transgenic rice plants that produce DD and PPD by overexpression of the Panax ginseng dammarenediol-II synthase gene (PyDDS) and protopanaxadiol synthase gene (CYP716A47). Through A. tumefaciens-mediated transformation of rice callus, more than 60 transgenic plants were obtained. The introduction of the genes in T1 transgenic plants was confirmed by genomic PCR and Southern analysis. The expression of the introduced genes in T1 plants was real-time PCR. The productions of DD and PPD were identified by LC/MS in the T1 seeds of transgenic rice plants. Interestingly transgenic rice plants produced not only DD but also PPD. The mean concentrations of DD and PPD in rice grains were 4.5 and 16.4 ug/g, respectively.

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**PCS13-64**

Study of rubber biosynthesis and rubber content increase in Taraxacum kok-saghyz

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Para rubber tree (*Hevea brasiliensis*) is an important rubber-producing plant to produce commercially valuable natural rubber. As the rubber demand has been increased, it is important to identify alternative source of natural rubber production and to elevate rubber content in rubber-producing plant using molecular biology techniques. Recently, Russian dandelion (*Taraxacum kok-saghyz*) is coming to the fore as the alternative rubber-producing plant species. Especially, the rubber quality of *T. kok-saghyz* is similar to that of Para rubber tree. *T. kok-saghyz* contains more than 4-5% latex in the root. They have high quality rubber with over 10⁵ Da in their latices. In addition, *T. kok-saghyz* is the most suitable to produce natural rubber, because it is an annual plant, which shows fast-growth and produces large amounts of biomass. First of all, *T. kok-saghyz* is very adaptable in Korean climate because that can grow all temperate regions. Therefore, we aim to produce natural rubber on a large scale using *T. kok-saghyz* by characterization of rubber biosynthesis related genes and increasing of rubber contents in *T. kok-saghyz* plants

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**PCS13-65**

Analysis of sticky germ cell mutant reveals a critical role of a conserved DUF707 family member for the germ cell migration after pollen mitosis I in Arabidopsis

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For sexual reproduction in flowering plants, the male gametophyte provides two sperm cells to the female gametes through a pollen tube. Although seemingly simple structure, the male gametophyte (pollen) develops under a highly coordinated genetic regulation. To further dissect the genetic control underlying pollen development, we screened DAPI-stained mature pollen grains from a mutant pool. As a result, we isolated a mutant line and termed sticky germ cell (sgc) based on its signature phenotype in which the mutant germ cell remains on the pollen wall. Ontogeny analysis revealed that pollen development in the sgc mutant occurs normally until pollen mitosis I and produces a typical form of highly asymmetric daughter cells, a larger vegetative cell and a smaller germ cell attached to the pollen wall. At later stages, however, the germ cell migration inwards the vegetative cytoplasm is blocked due to an ectopic deposition of callose in the vicinity of the sgc mutant germ cell. We also found that cell fates are compromised in the sgc mutant pollen grains. We positionally identified the SGC gene to encode a conserved Domain of Unknown Function 707 (DUF707). Expression analysis showed that the SGC gene is broadly expressed in somatic tissues and male gametophytic cells. More interestingly, the SGC protein is specifically detected in the cytoplasm of male germ line cells after pollen mitosis I. Genetic analysis also showed that transmission of the sgc mutant allele is normal through the female but highly reduced through the male, suggesting that the SGC function is critically required for the male gametophyte development. In conclusion, we report that the SGC gene, a member of DUF707 family, functions for the germ cell migration after pollen mitosis I in Arabidopsis, probably in a manner related to callose metabolism in the germ cell.

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Impaired plastid ribosomal protein L3 and L13 cause an albino seedling lethal phenotype in rice

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Chloroplast, the semi-autonomous photosynthetic organelle plays an essential role in plant growth and development particularly in crops through manipulating the photosynthetic capacity and biosynthesis of carbon skeletons. Plastid ribosomal proteins (PRPs) are crucial for the establishment of the transcription/translation apparatus during the chloroplast differentiation. Here, we isolated and characterized T-DNA-tagged rice mutants with defective chloroplasts, named prpl3 and prpl13, which exhibit a distinct albino seedling lethality. Transmission electronic microscopy (TEM) observation showed that the stacks of grana were not properly formed with disrupted structure of thylakoids in the chloroplast of those mutants. Chlorophyll content was also significantly reduced in the leaves of prpl3 and prpl13 mutant seedlings. PRPL3 and PRPL13 are nuclear genes encoding PRPs, which are localized in chloroplasts. prpl13 mutants are functionally stronger alleles of white leaf and panicles 1 (wdp1) and prpl3 is a novel mutant impaired in PRPL3 gene. We further demonstrated that PRPL3 is responsible for the phenotypic alterations by generating additional mutant alleles with the aid of CRISPR/Cas9 systems. Moreover, expression level of genes involved in photosynthesis and chloroplast development (plastidial transcription/translation and in photosynthesis) was altered in the mutants, prpl3 and prpl13. These results collectively show that nuclear-encoded PRPL3 and PRPL13 are indispensable for proper development of chloroplasts in rice.

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Identification of genes important for male gametophytic development in Arabidopsis

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School of Applied Biosciences, Kyungpook National University, Korea

The male gametophyte (pollen grain) development is a critical step for successful proliferation in flowering plants. The pollen grain consists of two sperm cells and a vegetative cell which are formed by two rounds of pollen mitoses under the elaborate genetic control. In order to identify genes important for the pollen development, we adopted a forward genetic approach. First, we generated a mutant population using an activation tagging vector in Arabidopsis. We morphologically screened DAPI-stained mature pollen grains from 1,500 BASTA-resistant transgenic lines at T1 generation. As a result, we isolated 5 putative mutant lines which exhibit high levels of abnormal pollen phenotypes including aborted, binucleate or single nucleate pollen grains. From the second round of morphological screen, we observed that 3 mutant lines, AL4-34, AL26-3 and AL31-8, show reproducible phenotypes at T2 generation and are being used for further analyses. We carry out pollen developmental analysis in order to determine which stage of pollen development the mutant defects start to appear. In addition, we perform genetic transmission analysis by reciprocal crosses between mutant and wild type plants to investigate whether the mutant plants display male- and/or female-gametophytic defects. Moreover, Identification of genes that might be responsible for mutant phenotypes is in progress by the Thermal asymmetric interlaced polymerase chain reaction (TAIL) PCR. So far, T-DNA flanking regions were detected from the AL4-34 and AL31-8 mutant lines, which are located in genes encoding the AUGMIN complex that plays an essential role for dynamic microtubule organization. Currently we test cosegregation between the T-DNA insertions and the mutant pollen phenotypes in both lines.

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Evaluation of heat tolerance using CBF1 and Hsp101 overexpression in Arabidopsis

Sang Dae Yun1, Jinwon Lee1, Sung Aeong Oh1, Moon-Soo Soh2, Soon Ki Park1*

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2Department of Molecular Biology, Sejong University, Korea

As the world population and grain demand have increased, food security is the most urgent challenge we face. In addition, environments of the plant growth are predicted to be changed due to global climate changes in the coming decades, which will seriously affect sufficient crop yield. Pollen grains are known to be most vulnerable to high temperature condition. There have been significant efforts to improve plant fitness that can withstand various stress conditions. Hsp101 gene is well known for a molecular chaperone that is required for the development of heat tolerance in plants. On the other hand, there have been reports that overexpression of CBF1(C-repeat-binding factors)/DREB(dehydration-responsive element-binding protein1) genes increases freezing tolerance by inducing expression of cold-responsive genes. In this study, we ask whether these two representative stress-related genes, Hsp101 and CBF1, can confer heat tolerance during both sporophytic and reproductive stages in Arabidopsis. To this end, we generated Arabidopsis transgenic lines which overexpress Hsp101 and CBF1 under the various promoters, proUBQ14, proTDF1, proRMP1 and proOsLPS1. The proUBQ14 is used for constitutive, proTDF1 for anther-specific, and proRMP1 and proOsLPS1 for pollen-specific expressions. First, we tested 10-day-old seedlings from transgenic lines containing UBQ14 promoter under the heat stress conditions and then calculated their survival rates. Our preliminary results suggest that both Hsp101 and CBF1 overexpression increase heat tolerance in seedlings with higher survival rates from the CBF1 than Hsp101. Based on this result, we will continue to investigate Hsp101- and CBF1-overexpression lines from the other promoters at heat stress conditions during reproductive stages.

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Optimization of growth rate by regulating chloroplast movement in lettuce

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2Department of Agricultural Engineering, National Institute of Agricultural Sciences, RDA, Jeonju 54875, Korea

Chloroplasts change their intracellular positions to optimize photosynthetic efficiency and/or to reduce photodamage in response to the intensity and position of light. Chloroplast movement is mediated by two phototropins, phot1 and phot2. Chloroplasts are arranged along the pericinal walls of the cell to maximize light capture under low intensity light (accumulation response), while they move to the place along the anticlinal walls of the cell under high intensity light (avoidance response). The accumulation response is redundantly mediated by phot1 and phot2, but the avoidance response is only mediated by phot2 in Arabidopsis. In this study, we analyzed the relationship between plant growth and chloroplast movement in different blue and red light-emitting diode (LED) lighting in plant factory. Green leaf lettuce showed efficient chloroplast movements like Arabidopsis. The physiological parameters of green leaf lettuces were significantly increased in fresh weight by ~1.6 times and dry weight by ~2 times when lettuces were grown in the light condition for accumulation response compared to that for avoidance response. Furthermore, the SPAD value (chlorophyll content) of green leaf lettuce were significantly increased in the light condition for accumulation response rather than for avoidance response at the same total light intensity. Therefore, modification of chloroplast movement is a good challenge to lead to improved vegetable crop yields in plant factor.

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**PCS13-70**

N-Glycan analysis of glycosylation-modified lines in Rice

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N-linked glycosylation is one of post-translational modifications in eukaryotes. In general, the glycosylation patterns are known to be somewhat different between animals and plants, which becomes a serious problem when plant is used as a platform producing pharmaceutical proteins (ex. antibodies). Therefore, glyco-engineering is a prerequisite for using plants to produce pharmaceutical proteins. α 1,3-fucosyltransferase (FucT) functions in transferring α 1,3-linked fucose residues to N-glycan of glycoprotein, which is unique in plants. In case of mammals, a fucose is transferred to α 1,6-residue. To make the rice line that attaches fucose to α 1,6-residue instead of α 1,3-residue, we introduced human α 1,6-fucosyltransferase (HsFucT) gene driven by rice α 1,3-FucT gene promoter into α 1,3-FucT gene knock-out mutant (Osfuct), and then obtained 3 independent lines (HsFucT OX/Osfuct). To investigate the change of glycosylation, N-glycan pattern was analyzed and compared among WT (DJ), Osfuct, and HsFucT OX/Osfuct.

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**PCS13-71**

THRUMIN1 is the bundling factor of cp–actin filaments for chloroplast photorelocation movement in Arabidopsis

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Chloroplast movement is an essential physiological response for plant survival in fluctuating light environments. Under weak light conditions, chloroplasts accumulate along the periclinal cell walls for efficient photosynthesis (accumulation response), while under strong light conditions chloroplasts move to anticlinal cell walls to avoid photodamage (avoidance response). These responses are regulated by two blue light receptors, phototropin 1 (phot1) and phot2 in Arabidopsis. Both phot1 and phot2 mediate the accumulation response, while phot2 alone regulates the avoidance response. During the movements, cp–actin filaments are dynamically reorganized on moving chloroplasts according to the intensity and position of incident light. THRUMIN1 functions as a plant-specific actin bundling factor in chloroplast movement. To address the functions of THRUMIN1 in the regulation of cp–actin filaments, THRUMIN1-GFP (TH1-G) was transformed into the chapl, phot1, phot2, and phot1phot2 mutants, named as TH1-GWT, TH1-Gchapl, TH1-Gipl, TH1-Gp2 and TH1-Giplp2, respectively. Blue-light-induced asymmetric organizations of THRUMIN1 were regulated mainly by phot2 but partially by phot1 as previously observed in cp–actin filaments. In addition, THRUMIN1 probed cortical actin filaments in chapl mutant cells with no cp–actin filaments. Taken together, our results suggest that THRUMIN1 plays as the bundling factor of cp–actin filaments for chloroplast photorelocation movement.

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phot2 as a light switch to regulate CHUP1–CHIP1 interaction for chloroplast photorelocation movement in Arabidopsis

Jae-Woo Han¹, Gyeong-Hoon Lee², Koji Okajima³, Aino Komatsu³, Fumio Takahashi⁴, Takayuki Kohchi³, Masamitsu Wada⁵, Sam-Geun Kong¹*

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⁴College of Life Sciences, Ritsumeikan University, Japan
⁵School of Science and Engineering, Tokyo Metropolitan University, Japan

Chloroplast photorelocation movement is essential to optimize photosynthetic ability and/or to prevent photodamage under various light conditions. Chloroplasts accumulate at the cell surface under weak light conditions (accumulation response) and move to the anticlinal walls parallel to the direction of incident light under strong light conditions (avoidance response). Chloroplasts attach to the plasma membrane via chloroplast actin (cp-actin) filaments. During the movement, cp-actin filaments are reorganized dynamically according to light intensity and direction. CHLOROPLAST UNUSUAL POSITIONING1 (CHUP1) plays pivotal roles as the cp-actin nucleator not only in chloroplast movement but also in chloroplast anchoring. To investigate the molecular mechanism underlying chloroplast anchoring, we carried out yeast two-hybrid assays and identified a CHUP1-INTERACTING PROTEIN 1 (CHIP1) that is a novel plant-specific gene found only in land plant. E. coli protein expression systems further revealed that CHUP1 interacts with CHIP1, CHIP1-LIKE 1 (CHIL1) and CHIL2 as well as CHIP1 interacts with CHIL1 and CHIL2. In order to examine the possibility whether phot2-dependent phosphorylation could be involved in blue light-dependent chloroplast de-anchoring, phot2 and CHIP1 were co-expressed in E. coli and binding assay was performed with CHUP1. CHUP1 preferentially interacted with unphosphorylated CHIP1. These data suggest that phot2-dependent phosphorylation of CHIP1 plays as a light switch to regulate chloroplast de-anchoring in Arabidopsis.

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Special Session
(Green-bio Forum & ILSI Korea)
**Special Session : Science-based Policy for Gene Edited Crops**

유전자교정 작물의 합리적 정책방향

- **Date**: 2019.7.4.(Thur) 13:00 ~ 16:30
- **Place**: C3 Room (308-309) in Kimdaejung Convention Center
- **Organizer**: Green-bio Forum / ILSI Korea

### 2019. 7. 4. (Thursday)

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
</tr>
</thead>
<tbody>
<tr>
<td>13:00~13:30</td>
<td>Registration</td>
</tr>
<tr>
<td></td>
<td><strong>Chair</strong> Soo-Chul Park (Seoul National University) Ho-Min Jang (Korea Biosafety Clearing House)</td>
</tr>
</tbody>
</table>
| 13:30~14:10| USDA regulatory experience in plant biotechnology, including gene editing  
Ibrahim Shaqir (USDA-APHIS) |
| 14:10~15:00| The regulatory frameworks of genome editing organisms and foods in Japan  
Yutaka Tabei (NARO) |
| 15:00~15:30| Science-based policies for genome edited crops in EU & Latin American countries  
CHA Jin (CORTEVA) |
| 15:30~16:00| Science-based Policy for genome editing crops in Korea  
JANG Ho Min (KBCH) |
| 16:00~16:30| Discussion                                                            |

### 2019년 7월 4일, 목요일

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
</tr>
</thead>
<tbody>
<tr>
<td>13:00~13:30</td>
<td>등록</td>
</tr>
</tbody>
</table>
|            | 좌장 박수철 (서울대학교 그린바이오과학기술연구원)  
장호민 (한국생명공학연구원 바이오안전성정보센터) |
| 13:30~14:10| 미국 농무부의 유전자교정 작물 정책  
Ibrahim Shaqir (USDA-APHIS) |
| 14:10~15:00| 일본의 유전자교정 작물 정책  
Yutaka Tabei (NARO) |
| 15:00~15:30| 유럽과 남미의 유전자교정 작물 정책  
CHA Jin (CORTEVA) |
| 15:30~16:00| 한국의 유전자교정 작물 정책  
장호민 (KBCH) |
| 16:00~16:30| 종합토론                                                             |
USDA regulatory experience in plant biotechnology, including gene editing

Ibrahim M Shaqir, Associate Deputy Administrator
USDA-APHIS, Biotechnology Regulatory Services

In 1986 the Executive Office of the President published the Coordinated Framework for the Regulation of Biotechnology, which described the existing laws and agencies relevant for regulating the safe use of biotechnology. For biotech plants, the three main agencies are the United States Department of Agriculture’s Animal and Plant Health Inspection Service (USDA-APHIS), the U.S. Environmental Protection Agency (EPA), and the U.S. Food and Drug Administration (FDA). Depending on its characteristics, a plant product may be subject to the jurisdiction of one or more of these agencies. This presentation will focus on the regulatory experience of USDA over the past 32 year, from the early days when the focus was on regulating field tests of experimental GE plants to the most recent proposal published on just last month on June 6 to amend the regulations to take into consideration how gene-edited plants might be treated under the revised APHIS biotechnology regulations.

Under the current APHIS biotechnology regulations, importation, interstate movement, and release into the environment require prior authorization from APHIS by either permit or notification when the activity involves a “regulated article.” The definition of a regulated article is described in the regulations as a living organism that meets two criteria: (1) it is derived by genetic engineering, and (2) that a plant pest was involved in the engineering, either as the donor organism, recipient organism, or vector agent. From the earliest days, the APHIS program had to answer questions from researchers who were unsure if their organism met this definition of regulated article. In 2011, APHIS started a process called “Am I Regulated” to streamline inquiries and provide information to other researchers and the general public about which organisms met the definition of regulated article and which did not. To date APHIS has posted over 65 inquiries and responses, many of which are focused on plant breeding innovations using techniques of gene editing.

APHIS has been working on revising its biotechnology regulations for over a decade, and in the March 2018 USDA Secretary Perdue issued a statement on the regulation of plant breeding innovations, including the gene-editing techniques that have been developed over the past decade. This 2018 statement noted that USDA doesn’t currently regulate and did not intend to regulate in the future genetically engineered plants that could otherwise have been developed through traditional breeding techniques, as long as the plants not plant pests or developed using plant pests.

Just last month APHIS published a proposal for updating our current USDA biotechnology regulations consistent with the Secretary’s 2018 statement and with a goal to have the regulations meet both current and future needs to protect against risks posed by plant pests.

USDA’s proposed rule is available for public review, and comments will be accepted from June 6, 2019, through August 5, 2019. After the public comment period closes, USDA will review the comments and decide on next steps. Additionally, USDA published a draft programmatic Environmental Impact Statement (EIS), which is also available for public comment and we look forward to stakeholder input on that document. The public can view the proposed rule, supporting documents, and submit comments online at: http://www.regulations.gov/#/d/APHIS-2018-0034.

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The regulatory frameworks of genome editing organisms and foods in Japan

Yutaka Tabei

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The Japanese government has considered the handling of organisms and foods produced by genome editing. In Japan, organisms with foreign genes are regulated as genetically modified organisms (GMOs). GMOs are evaluated their influence on biodiversity under the Cartagena domestic Act, and genetically modified foods are also confirmed their safety under the Food Sanitary Law prior to commercialization.

Regulatory framework has been examined by relevant Ministries based on different genome editing types (SDN-1, SDN-2 and SDN-3). The Ministry of Environment (MoE) has reported framework of genome editing organisms, which described the organisms produced by SDN-2 and SDN-3 are regulated as GMO, however, those by SDN-1, if those were null segregant, are not regulated under Cartagena domestic Act.

In regulatory framework of genome editing foods, according to report of Ministry of Health, Labor and Welfare (MHLW), the products developed by SDN-3 are regulated as genetically modified foods and those were regulated under the Food Sanitary Law. On the other hand, although being null segregant is major premise, it was concluded the foods produced by SDN-1 and SDN-2 should be evaluated by the modified DNA sequence as a result (product-base), rather than by the difference of genome editing types (process-base). As a product-based evaluation, this report stated that genome editing foods will not be regulated as genetically modified foods if modified DNA sequences were indistinguishable from natural or artificial mutations. Meanwhile, MoE and MHLW request developers to provide information for genome editing organisms and foods prior to commercialization on voluntary basis.

Each regulatory policy was reported in February and March 2019 by MoE and MHLW respectively and the relevant Ministries are examining the details of the guidelines including information to be submitted.

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Science-based policies for genome edited crops in Latin American countries

Jin Cha*

Regulatory & Stewardship for Korea, Corteva Agriscience

Agriculture constitutes a large sector of economy of Latin America. Argentina and Brazil represent well known examples of Latin American countries that have emerged as key suppliers of agricultural products, such as corn and soybean, to feed global food needs. Countries in this continent also have established governance on agricultural biotechnology which is consistent with the principles and concepts established in the Cartagena Protocol on Biosafety (CPB) although most of the countries in Latin America are not parties to CPB. With the advance of agriculture in the geography, countries in Latin America became very open to technological innovations, such as genome edited crops. Argentina became the first country to develop and publish the policy for gene edited crops and other new breeding techniques (NBTs) in 2015. In the Argentinian policy developed for NBTs, absence of novel combination genetic material in the final product is the criteria to differentiate NBT products from GMO crops. New combination of genetic material is defined as a stable and joint insertion of one of more genes or DNA sequences that are a part of a defined genetic construct. Following Argentina, Chile, Brazil, Colombia, and Paraguay have also published respective policies with criteria similar among Latin American countries. Policies in Honduras, Panama and Uruguay are expected to be finalized in the near future as well. Adopted regulatory policies for NBTs in Latin American countries include a case-by-case consultation process to confirm absence of the novel combination of genetic material exempting such NBT products from the regulatory scope of GMO crops.

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The Korean Society of Breeding Science’s Award
The Korean Society of Breeding Science’s Award

- 시상일: 2019년 7월 2일, 17:40~18:20
- 장소: 광주 김대중컨벤션 센터 4층 컨벤션홀 3홀

- 시상내용
  1. 농우육종학회상
     - 수상자: 고희종 (서울대학교 농업생명과학대학)
     - 선정사유: 다수성, 품질과 기능성에 관여하는 다수의 유용 유전자를 발굴하고 이들의 유전진화학적 의의를 밝히며, 20여 개의 우수 버섯종을 육성함과 더불어 후학 양성에 진력하여, 국내외 식량작물 육종학의 발전에 크게 기여
  2. 한국육종학회-연구상
     - 수상자: 이현숙 (충남대학교 농업생명과학대학)
     - 논문제목: Genetic Analysis of Seedling Traits Regulated by Light in Weedy Rice (Plant Breeding and Biotechnology 2018;6:257-266)
  3. 코레곤품종상
     - 수상자: 송석보 (농촌진흥청 국립식량과학원 남부작물부)
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  4. 한국육종학회-품종상
     - 수상자: 남정권 (농촌진흥청 국립식량과학원 상주출장소)
     - 품종명: 조평 (벼), 품종번호 제4063호
  5. 우수논문상 (다다인용부문)
     - 한국육종학회지: 김홍식 (충북대학교 농업생명환경대학)
     - PBB: 정영수 (동아대학교 생명자원과학대학)
  6. 우수논문상(다수논문게재부문)
     - 한국육종학회지: 박현수 (국립식량과학원)
     - PBB: 이정동 (경북대학교 농업생명과학대학)
  7. 공로상
     - 박순기 (경북대학교, 31대 한국육종학회장)
Index
<table>
<thead>
<tr>
<th>Name</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td></td>
</tr>
<tr>
<td>A-hyeon Kang</td>
<td>295</td>
</tr>
<tr>
<td>A. J. Nagano</td>
<td>220</td>
</tr>
<tr>
<td>Abdul Hakim</td>
<td>242, 243</td>
</tr>
<tr>
<td>Abdullah Taufiq</td>
<td>91</td>
</tr>
<tr>
<td>Abel Teshome</td>
<td>249</td>
</tr>
<tr>
<td>Abhinandan S. Patil</td>
<td>230</td>
</tr>
<tr>
<td>Abil Dermail</td>
<td>59</td>
</tr>
<tr>
<td>Acnad</td>
<td>182</td>
</tr>
<tr>
<td>Ae Jin Hwang</td>
<td>249</td>
</tr>
<tr>
<td>Aejin Hwang</td>
<td>171</td>
</tr>
<tr>
<td>Agry Pradipita</td>
<td>61</td>
</tr>
<tr>
<td>Ah-Keum Han</td>
<td>274</td>
</tr>
<tr>
<td>Ahn Euk-Keun</td>
<td>114</td>
</tr>
<tr>
<td>Aino Komatsu</td>
<td>329</td>
</tr>
<tr>
<td>Akira Endo</td>
<td>67</td>
</tr>
<tr>
<td>AlMahmnur Alam</td>
<td>104</td>
</tr>
<tr>
<td>Alebel Mekuriw Abebe</td>
<td>176</td>
</tr>
<tr>
<td>Alemayehu T. Negaewo</td>
<td>249</td>
</tr>
<tr>
<td>Alemayehu T. Negewo</td>
<td>99</td>
</tr>
<tr>
<td>Ali Liaiat</td>
<td>100</td>
</tr>
<tr>
<td>Aluana Abreu</td>
<td>226</td>
</tr>
<tr>
<td>Alvin Palanog</td>
<td>51</td>
</tr>
<tr>
<td>Amery Amparado</td>
<td>51</td>
</tr>
<tr>
<td>Amika Yawichai</td>
<td>54</td>
</tr>
<tr>
<td>Amin Nur</td>
<td>112</td>
</tr>
<tr>
<td>Amy B. Emerman</td>
<td>53</td>
</tr>
<tr>
<td>Amy Emerman</td>
<td>226</td>
</tr>
<tr>
<td>Ancheol Chang</td>
<td>300, 301, 317</td>
</tr>
<tr>
<td>Andi Sauleka</td>
<td>182</td>
</tr>
<tr>
<td>Andre Silvanovich</td>
<td>190</td>
</tr>
<tr>
<td>Andrew Barry</td>
<td>53, 226</td>
</tr>
<tr>
<td>Andrew H. Paterson</td>
<td>5</td>
</tr>
<tr>
<td>Ani Kurniawati</td>
<td>217</td>
</tr>
<tr>
<td>Anil Kumar Nalini Chandran</td>
<td>161, 165, 321</td>
</tr>
<tr>
<td>Ayako Nishizawa-Yokoi</td>
<td>67</td>
</tr>
<tr>
<td>Ayasha Akter</td>
<td>144</td>
</tr>
<tr>
<td>Ayoung Jung</td>
<td>202</td>
</tr>
<tr>
<td>B</td>
<td></td>
</tr>
<tr>
<td>B.P. MallikarjunaSwamy</td>
<td>51</td>
</tr>
<tr>
<td>B.S Purwoko</td>
<td>102</td>
</tr>
<tr>
<td>B.S Purwoko2</td>
<td>31</td>
</tr>
<tr>
<td>Baekki Kim</td>
<td>275</td>
</tr>
<tr>
<td>Badri Anarjan Mahdi</td>
<td>219</td>
</tr>
<tr>
<td>Baek Hie Nahm</td>
<td>125, 149</td>
</tr>
<tr>
<td>Bai Jianjiang</td>
<td>194</td>
</tr>
<tr>
<td>Benildo G. de los Reyes</td>
<td>27, 29</td>
</tr>
<tr>
<td>Beom-Kyu Kang</td>
<td>98, 220, 250</td>
</tr>
<tr>
<td>Beom-Gi Kim</td>
<td>299, 309, 317</td>
</tr>
<tr>
<td>Beom-Kyu Kang</td>
<td>74</td>
</tr>
<tr>
<td>Beom-Soon Choi</td>
<td>130, 131</td>
</tr>
<tr>
<td>Beom-young Son</td>
<td>105</td>
</tr>
<tr>
<td>Bettina Berger</td>
<td>46</td>
</tr>
<tr>
<td>Bhulang Suriharn</td>
<td>59</td>
</tr>
<tr>
<td>Bin Ha</td>
<td>259</td>
</tr>
<tr>
<td>Bishnu Adhikari</td>
<td>97</td>
</tr>
<tr>
<td>Bjoern Textor</td>
<td>226</td>
</tr>
<tr>
<td>Bo Ram Choi</td>
<td>260</td>
</tr>
<tr>
<td>Bo-Keonyong Kim</td>
<td>120, 178</td>
</tr>
<tr>
<td>Bo-Keun Ha</td>
<td>202, 225, 245,</td>
</tr>
<tr>
<td>Bo-Kyeong Kim</td>
<td>175</td>
</tr>
<tr>
<td>Bo-Kyeong Kim</td>
<td>64, 103, 105,</td>
</tr>
<tr>
<td>Bo-Keun Ha</td>
<td>106, 110, 254, 266, 283</td>
</tr>
<tr>
<td>Bo-Ra Park</td>
<td>138, 184, 185</td>
</tr>
<tr>
<td>Bo-Ram Kim</td>
<td>274</td>
</tr>
<tr>
<td>Bomi Nam</td>
<td>274</td>
</tr>
<tr>
<td>Bon-Cheol Koo</td>
<td>136, 226, 256</td>
</tr>
<tr>
<td>Bong Choon Lee</td>
<td>136</td>
</tr>
<tr>
<td>Boonrat Jongdee</td>
<td>93</td>
</tr>
<tr>
<td>Boram Choi</td>
<td>137</td>
</tr>
<tr>
<td>Brendon Desmond</td>
<td>226</td>
</tr>
<tr>
<td>Brendan S. Desmond</td>
<td>53</td>
</tr>
<tr>
<td>Brooke Bruning</td>
<td>46</td>
</tr>
<tr>
<td>Budi Wahyono</td>
<td>61</td>
</tr>
<tr>
<td>BudiSetiadi Daryono</td>
<td>41</td>
</tr>
<tr>
<td>Burn-Soo Hahn</td>
<td>184, 238, 328</td>
</tr>
<tr>
<td>Bumkyu Lee</td>
<td>300, 317</td>
</tr>
<tr>
<td>Bue Chi Bau</td>
<td>89</td>
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<tr>
<td>Byeong Cheol Moon</td>
<td>35</td>
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<td>Byeong Ho Moon</td>
<td>167</td>
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<td>Byeong Sam Kim</td>
<td>62</td>
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<td>Byeong-Gyu Min</td>
<td>268</td>
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<td>Byeong-Hoon Kim</td>
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<td>135</td>
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<td>Byoung Il Je</td>
<td>113</td>
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<tr>
<td>Byoung-Cheol Kang</td>
<td>36, 143, 147,</td>
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<tr>
<td>Chang-deok Han</td>
<td>113, 186</td>
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<tr>
<td>C. Park</td>
<td>220</td>
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<td>Caixia Gao</td>
<td>11</td>
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<tr>
<td>Carl Garnaat</td>
<td>190</td>
</tr>
<tr>
<td>Chae Soo Young</td>
<td>191, 214</td>
</tr>
<tr>
<td>Chae Won Byoung</td>
<td>191, 214</td>
</tr>
<tr>
<td>Chae-In Na</td>
<td>310</td>
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<tr>
<td>Chan Kyu Lim</td>
<td>251</td>
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<td>Chan Seop Ko</td>
<td>117</td>
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<td>Chan-Ho Kang</td>
<td>284</td>
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<td>Chan-Sung Oh</td>
<td>92</td>
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<td>274</td>
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<td>Chang-Woo Lee</td>
<td>293</td>
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<tr>
<td>Chang-Kug Kim</td>
<td>35, 130, 148</td>
</tr>
<tr>
<td>Chang-Min Lee</td>
<td>99, 103, 106, 132, 208</td>
</tr>
<tr>
<td>Chang-Mak Lee</td>
<td>184, 238</td>
</tr>
<tr>
<td>Chang-Sik Oh</td>
<td>176</td>
</tr>
<tr>
<td>Chang-Soo Kim</td>
<td>235</td>
</tr>
<tr>
<td>Changsoo Kim</td>
<td>32, 224</td>
</tr>
<tr>
<td>Changwak Eun</td>
<td>301</td>
</tr>
<tr>
<td>Chanhoo An</td>
<td>180</td>
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<tr>
<td>Chanon Lapjit</td>
<td>169</td>
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<tr>
<td>Chapsee Shin</td>
<td>164, 175</td>
</tr>
<tr>
<td>Name</td>
<td>Page</td>
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<tr>
<td>-------------------------------</td>
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</tr>
<tr>
<td>Charles D. Elfe</td>
<td>53</td>
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<tr>
<td>Chau ThanhNha</td>
<td>51</td>
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<tr>
<td>Chen Chen</td>
<td>171</td>
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<td>Chen Xin</td>
<td>168</td>
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<tr>
<td>Chenchen Xue</td>
<td>90</td>
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<tr>
<td>Cheol Seong Jang</td>
<td>107</td>
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<td>Cheol Soo kim</td>
<td>302</td>
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<td>Cheol Woo Min</td>
<td>37</td>
</tr>
<tr>
<td>Cheol-Won Yoon</td>
<td>291</td>
</tr>
<tr>
<td>Cheol-Woo Choi</td>
<td>191</td>
</tr>
<tr>
<td>Cheryl Adeva</td>
<td>110</td>
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<tr>
<td>Chetan Kaur Bhogal</td>
<td>144</td>
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<td>Chi Eun Hong</td>
<td>113</td>
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<td>Chi-Hwan Kim</td>
<td>140</td>
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<td>141</td>
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<tr>
<td>Chinreddy Subramanyam Reddy</td>
<td>184</td>
</tr>
<tr>
<td>Cho Hui Joo</td>
<td>134</td>
</tr>
<tr>
<td>Choi MG</td>
<td>90, 91</td>
</tr>
<tr>
<td>Choi SB</td>
<td>90, 91</td>
</tr>
<tr>
<td>Chon-Sik Kang</td>
<td>32</td>
</tr>
<tr>
<td>Choon-Song Kim</td>
<td>99</td>
</tr>
<tr>
<td>Choon-Tak Kwon</td>
<td>228</td>
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<tr>
<td>Choong-Il Cheon</td>
<td>109</td>
</tr>
<tr>
<td>Choonkyun Jung</td>
<td>124</td>
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<tr>
<td>Choonsok Lee</td>
<td>276</td>
</tr>
<tr>
<td>Chris S. Jones</td>
<td>99</td>
</tr>
<tr>
<td>Christos Michailidis</td>
<td>17</td>
</tr>
<tr>
<td>Chul Soo Park</td>
<td>207</td>
</tr>
<tr>
<td>Chuloh Cho</td>
<td>126</td>
</tr>
<tr>
<td>Chulunatsetseg Jadamba</td>
<td>127</td>
</tr>
<tr>
<td>Chun Hwan Kim</td>
<td>251</td>
</tr>
<tr>
<td>Chun Woo Nam</td>
<td>118</td>
</tr>
<tr>
<td>Chun-Huai Cheng</td>
<td>39</td>
</tr>
<tr>
<td>Chun-Song Kim</td>
<td>110</td>
</tr>
<tr>
<td>Chung Ryl Jung</td>
<td>269</td>
</tr>
<tr>
<td>Chung-Gen Lee</td>
<td>133</td>
</tr>
<tr>
<td>Chunying Zhang</td>
<td>219</td>
</tr>
<tr>
<td>Chutirittorn Yundaeng</td>
<td>168</td>
</tr>
<tr>
<td>Cici Tresniwati</td>
<td>183</td>
</tr>
<tr>
<td>Cindy Gresyllia Permadi</td>
<td>41</td>
</tr>
<tr>
<td>Colton Kessenich</td>
<td>190</td>
</tr>
<tr>
<td>Cuc Thi Nguyen</td>
<td>94</td>
</tr>
<tr>
<td>Cui Xiaoyan</td>
<td>168</td>
</tr>
<tr>
<td>Cynthia Hendrickson</td>
<td>226</td>
</tr>
<tr>
<td>Cynthia L. Hendrickson</td>
<td>53</td>
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<tr>
<td>D</td>
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<tr>
<td>D. S. Kishor</td>
<td>276</td>
</tr>
<tr>
<td>D. Wirmas</td>
<td>31</td>
</tr>
<tr>
<td>Da Eun Im</td>
<td>267</td>
</tr>
<tr>
<td>Da-Eun Kwon</td>
<td>104</td>
</tr>
<tr>
<td>Da-Hye Jeon</td>
<td>166</td>
</tr>
<tr>
<td>Da-Hye Kim</td>
<td>138, 184</td>
</tr>
<tr>
<td>Dae Young Baek</td>
<td>302, 323</td>
</tr>
<tr>
<td>Dae Hyun Park</td>
<td>246, 247</td>
</tr>
<tr>
<td>Dae Seon Kim</td>
<td>196</td>
</tr>
<tr>
<td>Dae Yeon Kim</td>
<td>118, 186, 268</td>
</tr>
<tr>
<td>Dae Young Kim</td>
<td>261</td>
</tr>
<tr>
<td>Dae-Gyu Kim</td>
<td>230</td>
</tr>
<tr>
<td>Daesuke Tsugama</td>
<td>100</td>
</tr>
<tr>
<td>Dan Bi Lee</td>
<td>206</td>
</tr>
<tr>
<td>Dan-Be Park</td>
<td>123</td>
</tr>
<tr>
<td>Daniel F. Klessig</td>
<td>40</td>
</tr>
<tr>
<td>Daeheon Jang</td>
<td>124, 150</td>
</tr>
<tr>
<td>Danim Jo</td>
<td>304, 323</td>
</tr>
<tr>
<td>Darren Plett</td>
<td>46</td>
</tr>
<tr>
<td>Darush Struss</td>
<td>54</td>
</tr>
<tr>
<td>David Honyks</td>
<td>17, 30</td>
</tr>
<tr>
<td>David PotSil</td>
<td>17</td>
</tr>
<tr>
<td>David Twell</td>
<td>303</td>
</tr>
<tr>
<td>Dawood Dedekule</td>
<td>141</td>
</tr>
<tr>
<td>Dechudom Pamuta</td>
<td>89</td>
</tr>
<tr>
<td>Deek Ho Kwon</td>
<td>173</td>
</tr>
<tr>
<td>Deok Hyun Soo</td>
<td>95, 296</td>
</tr>
<tr>
<td>Depika Prasad</td>
<td>216</td>
</tr>
<tr>
<td>Derek Barchenger</td>
<td>169</td>
</tr>
<tr>
<td>Derek W. Barchenger</td>
<td>57</td>
</tr>
<tr>
<td>Desta Wirmas</td>
<td>59, 247</td>
</tr>
<tr>
<td>Dewi Sukma</td>
<td>66, 243</td>
</tr>
<tr>
<td>Dho hoon kim</td>
<td>316</td>
</tr>
<tr>
<td>Dian Rahkmad</td>
<td>244</td>
</tr>
<tr>
<td>Dibyajyoti Pramanik</td>
<td>67, 290</td>
</tr>
<tr>
<td>Didah Nur Faridah</td>
<td>217</td>
</tr>
<tr>
<td>Didy Sopandie</td>
<td>59, 247</td>
</tr>
<tr>
<td>Do Won Yun</td>
<td>324</td>
</tr>
<tr>
<td>Do Yeon Kwak</td>
<td>98, 220, 250</td>
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<tr>
<td>Do-Yeon Kwak</td>
<td>98, 220, 250</td>
</tr>
<tr>
<td>Do-Gyeong Lee</td>
<td>209, 211</td>
</tr>
<tr>
<td>Do-Gyu Lee</td>
<td>128</td>
</tr>
<tr>
<td>Do-Hak Lee</td>
<td>158</td>
</tr>
<tr>
<td>Dong-Hoon Jeong</td>
<td>306</td>
</tr>
<tr>
<td>Dong-Keun Lee</td>
<td>166</td>
</tr>
<tr>
<td>Dong-Kwan Kim</td>
<td>225, 282</td>
</tr>
<tr>
<td>Dong-Min Kim</td>
<td>52</td>
</tr>
<tr>
<td>Dong-So Park</td>
<td>122, 172</td>
</tr>
<tr>
<td>Dongern Kim</td>
<td>307</td>
</tr>
<tr>
<td>Dongho Lee</td>
<td>129, 141</td>
</tr>
<tr>
<td>Donghwan Shim</td>
<td>137, 228</td>
</tr>
<tr>
<td>Dongyun Lee</td>
<td>275</td>
</tr>
<tr>
<td>Doo Gyung Moon</td>
<td>251</td>
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<tr>
<td>Dool Yi Kim</td>
<td>299</td>
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<tr>
<td>Dooeyeon Hung</td>
<td>200</td>
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<tr>
<td>Dooeyon Kwak</td>
<td>199, 205, 254</td>
</tr>
<tr>
<td>Dr. HarkamalWalia</td>
<td>36</td>
</tr>
</tbody>
</table>

57, 252, 262, 263, 271
<table>
<thead>
<tr>
<th>Name</th>
<th>Page</th>
<th>Name</th>
<th>Page</th>
<th>Name</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>Duk-Ju Hwang</td>
<td>149, 180, 194</td>
<td>Eunju Seo</td>
<td>225</td>
<td>Guk Jin Lee</td>
<td>206</td>
</tr>
<tr>
<td>Duong Thi Hai Doan</td>
<td>67</td>
<td>Eunsuk Sim</td>
<td>195</td>
<td>Gun Ho Jung</td>
<td>255</td>
</tr>
<tr>
<td>Dwi Asmono</td>
<td>61, 241</td>
<td>EunYoung Oh</td>
<td>201</td>
<td>Gung Pyo Lee</td>
<td>134</td>
</tr>
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<td></td>
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<td>Eunyoung Oh</td>
<td>97, 199, 205, 231</td>
<td>Gwag-Hwan Ahn</td>
<td>283</td>
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<tr>
<td></td>
<td></td>
<td>Eunyoung Seo</td>
<td>175</td>
<td>Gwen Iris Descalsota-Empelo</td>
<td>51</td>
</tr>
<tr>
<td>Eun-Ju</td>
<td>53, 226</td>
<td>Eun Mauzeli</td>
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<td>Gyeong Dan Yu</td>
<td>176</td>
</tr>
<tr>
<td>Eun-Kee Ahn</td>
<td>27, 126</td>
<td>Fahmi Wendra S</td>
<td>61</td>
<td>Gyeong-Dan Yu</td>
<td>177, 209, 256</td>
</tr>
<tr>
<td>Erin Puspirita Rini</td>
<td>59</td>
<td>Fang Jun</td>
<td>194</td>
<td>Gyeong-Hoon Lee</td>
<td>329</td>
</tr>
<tr>
<td>Ermias H. Haile</td>
<td>99</td>
<td>Felix Vera</td>
<td>61</td>
<td>Gyeong-Jin Kim</td>
<td>229</td>
</tr>
<tr>
<td>Ermias Habte</td>
<td>249</td>
<td>Francisco Orellana</td>
<td>61</td>
<td>Gyeong-Rok Yang</td>
<td>191</td>
</tr>
<tr>
<td>Eun-Jung Kim</td>
<td>318</td>
<td>Franz M. Ngoy</td>
<td>179, 213</td>
<td>Gyeongnam Nam</td>
<td>215</td>
</tr>
<tr>
<td>Eun-Juung Rha</td>
<td>310, 311</td>
<td>Fumio Takahashi</td>
<td>329</td>
<td>Gyeongnam Nam</td>
<td>121, 178</td>
</tr>
<tr>
<td>Eun Keun Ahn</td>
<td>261</td>
<td></td>
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<td>Gynheung An</td>
<td>111, 326</td>
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<tr>
<td>Eun Jeong Kim</td>
<td>104</td>
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<td>Gyoungiu Nah</td>
<td>129, 140, 141</td>
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<td>Eun Joo Park</td>
<td>309</td>
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<td>Gy Dong Oh</td>
<td>55</td>
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<td>Eun Ju Byeon</td>
<td>145, 147</td>
<td>Ga Ram Kim</td>
<td>271</td>
<td>Gy Tu Park</td>
<td>94, 245, 274</td>
</tr>
<tr>
<td>Eun Jung Suh</td>
<td>180, 321, 322</td>
<td>Ga-Hyeon Kim</td>
<td>310, 311</td>
<td>Gy Tu-Ka Cho</td>
<td>57, 252, 262, 263</td>
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<td>Gahyeon Kim</td>
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<td>Gyuta Kim</td>
<td>202</td>
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<td>Eun Young Yang</td>
<td>118, 191, 214</td>
<td>Ganesh Kumar Agrawal</td>
<td>215</td>
<td>Ha Cheol Hong</td>
<td>108</td>
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<tr>
<td>Eun-A Lim</td>
<td>204</td>
<td>Gang-Seeob Lee</td>
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<td>Ha Kyung Oh</td>
<td>270</td>
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<tr>
<td>Eun-Cheon Lim</td>
<td>187</td>
<td>Geon Hui Son</td>
<td>67, 290</td>
<td>Hae Keun Yun</td>
<td>206</td>
</tr>
<tr>
<td>Eun-Gyeong Kim</td>
<td>283</td>
<td>Geon Hee Lee</td>
<td>114</td>
<td>Hae Koo Kim</td>
<td>31, 135, 170</td>
</tr>
<tr>
<td>Eun-Ha kim</td>
<td>203</td>
<td>Geon Hui Son</td>
<td>67, 290</td>
<td>Hae Ri Kim</td>
<td>247</td>
</tr>
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<td>Eun-Jeong Kim</td>
<td>198</td>
<td>Geun-Hyoung Choi</td>
<td>229</td>
<td>Hae-Yeong Kim</td>
<td>295</td>
</tr>
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<td>Eun-Ji Ga</td>
<td>299</td>
<td>Geupil Jang</td>
<td>95, 296</td>
<td>Haelim Park</td>
<td>240</td>
</tr>
<tr>
<td>Eun-Jo Shin</td>
<td>52</td>
<td>Gi Ho Sung</td>
<td>137</td>
<td>Haeng-Hoon Kim</td>
<td>240</td>
</tr>
<tr>
<td>Eun-Ju Sohn</td>
<td>43</td>
<td>Gi Hyun Lee</td>
<td>215</td>
<td>Haerim Park</td>
<td>141</td>
</tr>
<tr>
<td>Eun-Jun Kim</td>
<td>187</td>
<td>Gi Jun Choi</td>
<td>189, 260</td>
<td>Hai Anh Tran</td>
<td>94</td>
</tr>
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<td>Eun-Jung Kim</td>
<td>67</td>
<td>Gi Jun Kim</td>
<td>48</td>
<td>Hak Soo Seo</td>
<td>94, 245, 274</td>
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<td>Eun-Kyung Bae</td>
<td>123, 291</td>
<td>Gi-Won Cho</td>
<td>222</td>
<td>Han Bal-Kum</td>
<td>134</td>
</tr>
<tr>
<td>Eun-sung Lee</td>
<td>293</td>
<td>Gibum Yi</td>
<td>50, 265</td>
<td>Han Kyum Choi</td>
<td>163</td>
</tr>
<tr>
<td>Eun-Taek Woo</td>
<td>304</td>
<td>Gideon V. Torpollo</td>
<td>183</td>
<td>Han-Bin Oh</td>
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<td>Eun-Young Oh</td>
<td>259</td>
<td>Gil Dong Hong</td>
<td>302</td>
<td>Han-Yong Um</td>
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<td>Eunbyeol Koh</td>
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<td>Gil Soo Han</td>
<td>237</td>
<td>Hana Ahmed Labri</td>
<td>129</td>
</tr>
<tr>
<td>Eung Gi Jeong</td>
<td>101, 261</td>
<td>Gileung Lee</td>
<td>275</td>
<td>Hana Nur Rahmi</td>
<td>59</td>
</tr>
<tr>
<td>Eung-Gi Jeong</td>
<td>108, 109</td>
<td>Goon-Bo Kim</td>
<td>69</td>
<td>Hana Yoo</td>
<td>139, 145</td>
</tr>
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<td>Eungyeong Lee</td>
<td>35, 44, 195, 232, 320</td>
<td>Green Jhang</td>
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<td>Hanhong Bae</td>
<td>305</td>
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<td>Eunhye Goo</td>
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<td>Grienggrai Pantuwan</td>
<td>93</td>
<td>Hanna Shin</td>
<td>272</td>
</tr>
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<td>301</td>
<td>Gu Kang</td>
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<td>Haris Wijaya</td>
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<td>261</td>
<td>Haruyasu Hamada</td>
<td>42</td>
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<td>Hasan Mehraj</td>
<td>143</td>
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<td>243</td>
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<td>216</td>
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<td>Hayan Lee</td>
<td>150</td>
<td>Hwan-Hee Bae</td>
<td>105</td>
<td>Hyeon-Chung Chun</td>
<td>127, 128</td>
</tr>
<tr>
<td>He-ping Gu</td>
<td>130</td>
<td>Hwang-Bae Sohn</td>
<td></td>
<td>Hyo Chul Kim</td>
<td>258</td>
</tr>
<tr>
<td>Hea-Young Lee</td>
<td>36, 211, 227, 230, 264, 273</td>
<td>Hwang-ween Jeong</td>
<td>196</td>
<td>Hyo Ja Oh</td>
<td>140</td>
</tr>
<tr>
<td>Hee Chung Ji</td>
<td>189, 204</td>
<td>Hwangweon Jeong</td>
<td>322</td>
<td>Hyo joong Gim</td>
<td>62</td>
</tr>
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<td>Hee Jeong Jeong</td>
<td>266, 270</td>
<td>Hwi-Young Park</td>
<td>314</td>
<td>Hyo Ju Lee</td>
<td>287, 288, 289</td>
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<tr>
<td>Hee Kyoung Kim</td>
<td>287, 288, 289, 308</td>
<td>Hyang Sook Chun</td>
<td>129, 141</td>
<td>Hyo-Jin Kim</td>
<td>270</td>
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<tr>
<td>Hee-Jin Kim</td>
<td>297</td>
<td>Hyang-Mi Park</td>
<td>126</td>
<td>Hyo-Jin Park</td>
<td>303, 325</td>
</tr>
<tr>
<td>Hee-Jong Koh</td>
<td>73, 155, 158, 275, 276</td>
<td>Hye Joon Joo</td>
<td>167</td>
<td>Hyeon Lee</td>
<td>138, 174</td>
</tr>
<tr>
<td>Hee-Ju Yu</td>
<td>69</td>
<td>Hye Ju Seong</td>
<td>115</td>
<td>Hyeon Lee</td>
<td>229</td>
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<td>Hye Jung Hyun</td>
<td>190</td>
<td>Hyeon Lee</td>
<td>170</td>
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<td>Heera Jeon</td>
<td>158</td>
<td>Hye Ryun Ahn</td>
<td>321</td>
<td>Hyeon Lee</td>
<td>318</td>
</tr>
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<td>67</td>
<td>Hye Ryun An</td>
<td>257</td>
<td>Hyeon Lee</td>
<td>240</td>
</tr>
<tr>
<td>Hiroaki Saika</td>
<td>67</td>
<td>Hye Sik Kim</td>
<td>130, 131</td>
<td>Hyoja Oh</td>
<td>35, 232</td>
</tr>
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<td>Hiroyuki Fukuoka</td>
<td>55</td>
<td>Hye Sun Choi</td>
<td>200</td>
<td>Hyong Woo Choi</td>
<td>40</td>
</tr>
<tr>
<td>Hiroyuki Ichida</td>
<td>63</td>
<td>Hye Sun Cho</td>
<td>62</td>
<td>Hyongsuk Kim</td>
<td>45</td>
</tr>
<tr>
<td>Ho Bang Kim</td>
<td>191, 221, 268</td>
<td>Hye Young Kwon</td>
<td>62</td>
<td>Hyoseob Seo</td>
<td>294</td>
</tr>
<tr>
<td>Ho Hwi Jeon</td>
<td>32</td>
<td>Hye-eun Lee</td>
<td>290</td>
<td>Hyeoseon Choi</td>
<td>102</td>
</tr>
<tr>
<td>Ho Jun Joh</td>
<td>35, 151</td>
<td>Hye-In Kang</td>
<td>112, 212</td>
<td>Hyoshin Lee</td>
<td>123, 291</td>
</tr>
<tr>
<td>Ho Sun Lee</td>
<td>249</td>
<td>Hye-Jin Lee</td>
<td>166</td>
<td>Hyoun-Sub Lim</td>
<td>305</td>
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<td>Ho-Cheol Ko</td>
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<td>Hye-Jin Yoon</td>
<td>194</td>
<td>Hyoung Seok Kim</td>
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<td>Ho-Sun Lee</td>
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<td>Hye-Myeong Yoon</td>
<td>268</td>
<td>HyoungSeok Kim</td>
<td>47</td>
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<td>Ho-sun Lee</td>
<td>255</td>
<td>Hye-Yeon Kim</td>
<td>43</td>
<td>Hyuk Sung Yoon</td>
<td>100</td>
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<td>Ho-Sung Yoon</td>
<td>297</td>
<td>Hye-Young Lee</td>
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<td>Hyun A Jang</td>
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<td>265</td>
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<td>Hon-Ming Lam</td>
<td>15</td>
<td>Hyejin An</td>
<td>137, 241</td>
<td>Hyun Jo</td>
<td>58, 100, 126, 291, 303, 304, 323</td>
</tr>
<tr>
<td>Hong Gil Lee</td>
<td>120</td>
<td>Hyejin Hyeon</td>
<td>215</td>
<td>281, 303, 304, 323</td>
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<td>Hong Sik Kim</td>
<td>98, 220, 250</td>
<td>Hyemin Lim</td>
<td>121</td>
<td>Hyun Jo Koo</td>
<td>141</td>
</tr>
<tr>
<td>Hong Tae Yun</td>
<td>200</td>
<td>Hyemyeong Yoon</td>
<td>252, 257</td>
<td>Hyun Jun Kim</td>
<td>269</td>
</tr>
<tr>
<td>Hong Woo Park</td>
<td>269</td>
<td>Hyenso Ji</td>
<td>195</td>
<td>Hyun Kyeng Min</td>
<td>124</td>
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<td>Hong-Gyu Kang</td>
<td>318</td>
<td>Hyeon Ju Jeong</td>
<td>62</td>
<td>Hyun Mi Kim</td>
<td>274</td>
</tr>
<tr>
<td>Hong-II Ahn</td>
<td>132, 142, 146</td>
<td>Hyeon Jung Lee</td>
<td>235, 236, 320</td>
<td>Hyun Min Kim</td>
<td>324</td>
</tr>
<tr>
<td>Hong-II Choi</td>
<td>64, 164, 186, 277, 280</td>
<td>Hyeon-Jin Kim</td>
<td>319</td>
<td>Hyun Namgung</td>
<td>158</td>
</tr>
<tr>
<td>Hong-Kyu Choi</td>
<td>37, 162, 163</td>
<td>Hyeon-Jin Sun</td>
<td>318</td>
<td>Hyun Oh Lee</td>
<td>130, 131</td>
</tr>
<tr>
<td>Hong-Kyu Park</td>
<td>110</td>
<td>Hyeon-Jung Kang</td>
<td>192, 314</td>
<td>Hyun Sook Lee</td>
<td>233</td>
</tr>
<tr>
<td>Hong-Sig Kim</td>
<td>128</td>
<td>Hyeon-So Ji</td>
<td>158</td>
<td>Hyun Suk Cho</td>
<td>306</td>
</tr>
<tr>
<td>Hong-Sik Kim</td>
<td>74</td>
<td>Hyeon-Su Ro</td>
<td>291, 322</td>
<td>Hyeon Tae Kim</td>
<td>98, 220, 250</td>
</tr>
<tr>
<td>Hong-Tae Yun</td>
<td>222, 223</td>
<td>Hyeonah Shim</td>
<td>149, 151, 152</td>
<td>Hyun Uk Kim</td>
<td>68, 203, 306</td>
</tr>
<tr>
<td>Hongseock Lee</td>
<td>44</td>
<td>Hyeong Joong Kang</td>
<td>188</td>
<td>Hyun Ung-Jo</td>
<td>114</td>
</tr>
<tr>
<td>Hongseok Lee</td>
<td>320</td>
<td>Hyeong-Un Lee</td>
<td>176, 177, 209, 256</td>
<td>Hyun-Jin Jung</td>
<td>127</td>
</tr>
<tr>
<td>Hosub Shin</td>
<td>265</td>
<td>Hyeonjung Jung</td>
<td>295</td>
<td>Hyun-Jin Koo</td>
<td>151</td>
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<td>46</td>
<td>320</td>
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<td>Hyun-Jung Kang</td>
<td>302, 323</td>
</tr>
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<td>Hugo Carvajal</td>
<td>61</td>
<td>Hyeran Kim</td>
<td>287, 292</td>
<td>Hyun-Oh Lee</td>
<td>35, 151</td>
</tr>
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<td>Huh Jin Hyuck</td>
<td>134</td>
<td>Hyeri Lee</td>
<td>118</td>
<td>Hyun-Seung Park</td>
<td>35, 149, 151</td>
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<tr>
<th>Name</th>
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<tbody>
<tr>
<td>Ingyu Hwang</td>
<td>315</td>
</tr>
<tr>
<td>Indah Sulistiyorini</td>
<td>253</td>
</tr>
<tr>
<td>Indeok Hwang</td>
<td>173</td>
</tr>
<tr>
<td>Inho Seo</td>
<td>198</td>
</tr>
<tr>
<td>Indhwa Yeam</td>
<td>176</td>
</tr>
<tr>
<td>Inhwan Hwang</td>
<td>43, 314</td>
</tr>
<tr>
<td>Inkyu Park</td>
<td>28</td>
</tr>
<tr>
<td>Inseok Seo</td>
<td>121, 178, 215</td>
</tr>
<tr>
<td>Insk Kim</td>
<td>112, 265</td>
</tr>
<tr>
<td>Inyoung Kim</td>
<td>203</td>
</tr>
<tr>
<td>Ines Yacoubi</td>
<td>118</td>
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<td>Izzatul Muhallilin</td>
<td>66</td>
</tr>
<tr>
<td>J. Abe</td>
<td>220</td>
</tr>
<tr>
<td>Ja-Hong Lee</td>
<td>125, 285</td>
</tr>
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<td>Ja-Hwan Ku</td>
<td>223, 251</td>
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<tr>
<td>Jae A Jung</td>
<td>271</td>
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<tr>
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<td>54</td>
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<td>Jae Bok Lee</td>
<td>270</td>
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<td>Jae Bok Yoon</td>
<td>180, 236</td>
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<td>Jae Eun Lee</td>
<td>249, 255</td>
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<td>Jae Eun Park</td>
<td>201, 205</td>
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<tr>
<td>Jae Ho Kim</td>
<td>268, 269</td>
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<td>45</td>
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<tr>
<td>Jae Hyeon Oh</td>
<td>220</td>
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<td>Jae Hyun Oh</td>
<td>98, 250</td>
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<td>Jae Hyun Park</td>
<td>167</td>
</tr>
<tr>
<td>Jae Il Lyu</td>
<td>273, 277</td>
</tr>
<tr>
<td>Jae Il Ryu</td>
<td>245</td>
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<tr>
<td>Jae Jung Noh</td>
<td>249</td>
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<tr>
<td>Jae Ki Chang</td>
<td>108</td>
</tr>
<tr>
<td>Jae Kwang Kim</td>
<td>215, 315</td>
</tr>
<tr>
<td>Jae Seo Lee</td>
<td>45</td>
</tr>
<tr>
<td>Jae Sung Shim</td>
<td>312</td>
</tr>
<tr>
<td>Jae Sung Shim</td>
<td>116, 258</td>
</tr>
<tr>
<td>Jae Ung Yang</td>
<td>259</td>
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<tr>
<td>Jae Yoon Kim</td>
<td>293</td>
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<td>315</td>
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<td>293</td>
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<td>Jae-Do Song</td>
<td>92</td>
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<td>171</td>
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<td>207</td>
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<td>291</td>
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<td>133</td>
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<td>232</td>
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<td>Jae-II Lyu</td>
<td>276, 277</td>
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<td>Jae-In Chun</td>
<td>39</td>
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<td>Jae-Keun Choi</td>
<td>211</td>
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<tr>
<td>Jae-Woo Han</td>
<td>329</td>
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<tr>
<td>Jae-Yeon Kim</td>
<td>67, 290</td>
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<td>Jae-Yoon Kim</td>
<td>134, 161, 221</td>
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<td>Jaebok Lee</td>
<td>266, 268, 270</td>
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<tr>
<td>Jaebuhm Chun</td>
<td>126, 219, 248, 285</td>
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<tr>
<td>Jaceun Song</td>
<td>238</td>
</tr>
<tr>
<td>Jael, Kim</td>
<td>187</td>
</tr>
<tr>
<td>Jaeilong Noh</td>
<td>171, 255</td>
</tr>
<tr>
<td>JaekEun Choi</td>
<td>215</td>
</tr>
<tr>
<td>Jaekkeun Choi</td>
<td>121, 178</td>
</tr>
<tr>
<td>Jaeki Chang</td>
<td>141</td>
</tr>
<tr>
<td>Jagadeesh Sundaramorthy</td>
<td>94, 245, 274</td>
</tr>
<tr>
<td>Jahee Ryu</td>
<td>292</td>
</tr>
<tr>
<td>Jai Il Lyu</td>
<td>278</td>
</tr>
<tr>
<td>Jaihyunk Ryu</td>
<td>277, 278, 279, 280</td>
</tr>
<tr>
<td>Jan Fila</td>
<td>17</td>
</tr>
<tr>
<td>Jana Jeevan Rameneni</td>
<td>47, 163</td>
</tr>
<tr>
<td>Jang Uk Kim</td>
<td>113</td>
</tr>
<tr>
<td>Jang-Hwan Yoo</td>
<td>127</td>
</tr>
<tr>
<td>Janghwon Park</td>
<td>254</td>
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<tr>
<td>Jaquie H. Mitchell</td>
<td>93</td>
</tr>
<tr>
<td>Jarunjit Pongrat</td>
<td>89</td>
</tr>
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<td>Javier Hererro</td>
<td>241</td>
</tr>
<tr>
<td>Jaw Fen Wang</td>
<td>218</td>
</tr>
<tr>
<td>Jaw Rong Chen</td>
<td>218</td>
</tr>
<tr>
<td>Je Min Lee</td>
<td>49, 176</td>
</tr>
<tr>
<td>Jean Hanson</td>
<td>249</td>
</tr>
<tr>
<td>Jean-Baka Domelevo Entfeller</td>
<td>249</td>
</tr>
<tr>
<td>Je Young Park</td>
<td>35, 151</td>
</tr>
<tr>
<td>Jee-Hye Kim</td>
<td>222</td>
</tr>
<tr>
<td>Jee-Soo Park</td>
<td>304</td>
</tr>
<tr>
<td>Jee-Hyeon Ko</td>
<td>254</td>
</tr>
<tr>
<td>Jeli Venkatesh</td>
<td>230, 290</td>
</tr>
<tr>
<td>Jemin Kim</td>
<td>164</td>
</tr>
<tr>
<td>Jeniffer Silva</td>
<td>318</td>
</tr>
<tr>
<td>Jeom Ho Lee</td>
<td>108</td>
</tr>
<tr>
<td>Jeom-Ho Lee</td>
<td>103, 110, 254</td>
</tr>
<tr>
<td>Jeom-Sig Lee</td>
<td>183</td>
</tr>
<tr>
<td>Jeong Eun Lee</td>
<td>123</td>
</tr>
<tr>
<td>Jeong Eun Park</td>
<td>265</td>
</tr>
<tr>
<td>Jeong Eung-Gi</td>
<td>114</td>
</tr>
</tbody>
</table>

**J**
<table>
<thead>
<tr>
<th>Name</th>
<th>Page</th>
<th>Name</th>
<th>Page</th>
<th>Name</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>Jeong Guk-Hyun</td>
<td>114</td>
<td>Ji-Young Son</td>
<td>283</td>
<td>JingbinChen</td>
<td>65</td>
</tr>
<tr>
<td>Jeong Heo Kim</td>
<td>303</td>
<td>Jiah Kim</td>
<td>112</td>
<td>Jinhee Jeong</td>
<td>186</td>
</tr>
<tr>
<td>Jeong Heui Lee</td>
<td>108</td>
<td>Jihae Kim</td>
<td>67, 290</td>
<td>Jinhee Kim</td>
<td>64, 105, 106, 147, 261, 266, 283</td>
</tr>
<tr>
<td>Jeong Hlwan Ahn</td>
<td>135</td>
<td>Jihee Park</td>
<td>180, 196, 322</td>
<td>Jinho Ho</td>
<td>30, 53</td>
</tr>
<tr>
<td>Jeong Ho Kim</td>
<td>118</td>
<td>Jiho Chu</td>
<td>248, 254</td>
<td>Jinho Yung Kim</td>
<td>140</td>
</tr>
<tr>
<td>Jeong Ho Song</td>
<td>272</td>
<td>Jihye Park</td>
<td>187</td>
<td>Jinho Jeong</td>
<td>140</td>
</tr>
<tr>
<td>Jeong Hyun Baek</td>
<td>45</td>
<td>Ji Hyun F. Kim</td>
<td>13</td>
<td>Jinhoong Kim</td>
<td>112, 212, 265</td>
</tr>
<tr>
<td>Jeong Hyun Seo</td>
<td>98, 220, 250</td>
<td>Jimin Lee</td>
<td>124, 150</td>
<td>Jinho Jung Kim</td>
<td>167</td>
</tr>
<tr>
<td>Jeong Im Kim</td>
<td>319</td>
<td>Jin A Kim</td>
<td>102, 170, 197, 205</td>
<td>Jinkwan Ham</td>
<td>215</td>
</tr>
<tr>
<td>Jeong Ju Kim</td>
<td>107, 261</td>
<td>Jin Cheon Park</td>
<td>176, 209, 256</td>
<td>Jinkwan Ham</td>
<td>121, 178</td>
</tr>
<tr>
<td>Jeong O-Young</td>
<td>114</td>
<td>Jin Cui</td>
<td>130</td>
<td>Jinkwank Jo</td>
<td>36, 147, 264</td>
</tr>
<tr>
<td>Jeong Sheop Shin</td>
<td>296</td>
<td>Jin Hee Kim</td>
<td>175</td>
<td>Jin Su Gil</td>
<td>266, 268, 270</td>
</tr>
<tr>
<td>Jeong Sung Jung</td>
<td>260</td>
<td>Jin Hee Shin</td>
<td>55</td>
<td>Jin Tae Kim</td>
<td>149</td>
</tr>
<tr>
<td>Jeong SW</td>
<td>90, 91</td>
<td>Jin Hoe Huh</td>
<td>265</td>
<td>Jinwun Lee</td>
<td>326, 327</td>
</tr>
<tr>
<td>Jeong Wook Heo</td>
<td>327</td>
<td>Jin Hoon Jung</td>
<td>44, 189, 190</td>
<td>Jinwoo Choi</td>
<td>176</td>
</tr>
<tr>
<td>Jeong-Dong Lee</td>
<td>53, 58, 94, 100, 126, 274, 281, 303, 304, 310, 323</td>
<td>Jin Kwan Ham</td>
<td>211</td>
<td>Jinwoo Kim</td>
<td>315</td>
</tr>
<tr>
<td>Jeong-Hee Lee</td>
<td>132, 142, 282</td>
<td>Jin Man Lee</td>
<td>56</td>
<td>Jinxia Shi</td>
<td>171</td>
</tr>
<tr>
<td>Jeong-Hwan Mun</td>
<td>69, 313</td>
<td>Jin Seok Yoon</td>
<td>117</td>
<td>Jiong Zhang</td>
<td>90</td>
</tr>
<tr>
<td>Jeong-Hyun Seo</td>
<td>74</td>
<td>Jin Su Gil</td>
<td>270</td>
<td>Jirawat Sanitchon</td>
<td>59, 89, 92, 93</td>
</tr>
<tr>
<td>Jeong-Ju Kim</td>
<td>103, 254</td>
<td>Jin Young Kim</td>
<td>306</td>
<td>Jiyeong Jung</td>
<td>30, 53</td>
</tr>
<tr>
<td>Jeong-Kwon Nam</td>
<td>103, 110, 254</td>
<td>Jin Young Y. Barnaby</td>
<td>107</td>
<td>Jiyoung Lee</td>
<td>58</td>
</tr>
<tr>
<td>Jeongheon Han</td>
<td>121, 178</td>
<td>Jin Young Yoon</td>
<td>84</td>
<td>Jo-yi Yen</td>
<td>60</td>
</tr>
<tr>
<td>JeongHo BAEK</td>
<td>195</td>
<td>Jin-Ae Kim</td>
<td>299, 317</td>
<td>Jodi Humann</td>
<td>39</td>
</tr>
<tr>
<td>JeongHo Baek</td>
<td>195, 320</td>
<td>Jin-Baek Kim</td>
<td>64, 117, 164, 245, 267, 280</td>
<td>John Anderson</td>
<td>46</td>
</tr>
<tr>
<td>Jeongho Baek</td>
<td>35, 44, 140, 232, 273, 274, 276, 277, 278, 279, 280</td>
<td>John Hammond</td>
<td>305</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Jeonghoon Lee</td>
<td>141</td>
<td>Jin-Baek Kim, 280</td>
<td>Jonaliza L. Siangliw</td>
<td>89</td>
<td></td>
</tr>
<tr>
<td>Jeonghwan Seo</td>
<td>222, 275</td>
<td>Jin-Beak Kim</td>
<td>47, 186</td>
<td>Jonathon Dunn</td>
<td>226</td>
</tr>
<tr>
<td>Jeongsu Ahn</td>
<td>328</td>
<td>Jin-Dong Seo</td>
<td>100</td>
<td>Jonathon S. Dunn</td>
<td>53</td>
</tr>
<tr>
<td>JeongYeon Yoon</td>
<td>175</td>
<td>Jin-Hee Park</td>
<td>207</td>
<td>Jong Hee Kim</td>
<td>287, 288, 289</td>
</tr>
<tr>
<td>Jeongyoon Yi</td>
<td>257</td>
<td>Jin-Ho Kang</td>
<td>39</td>
<td>Jong Hee Lee</td>
<td>207</td>
</tr>
<tr>
<td>Ji Hee Park</td>
<td>187</td>
<td>Jin-hyuk Kim</td>
<td>129</td>
<td>Jong Ho Kim</td>
<td>108</td>
</tr>
<tr>
<td>Ji Hwan Im</td>
<td>276</td>
<td>Jin-Hyun Kim</td>
<td>37, 162, 163</td>
<td>Jong Kook Kim</td>
<td>43</td>
</tr>
<tr>
<td>Ji Hye Heo</td>
<td>115</td>
<td>Jin-Ju Kim</td>
<td>297</td>
<td>Jong Mi Kim</td>
<td>317</td>
</tr>
<tr>
<td>Ji Hye Kim</td>
<td>204</td>
<td>Jin-Kee Jung</td>
<td>52</td>
<td>Jong Min Jeong</td>
<td>107, 175</td>
</tr>
<tr>
<td>Ji Ung Jeong</td>
<td>175</td>
<td>Jin-Ki Park</td>
<td>237</td>
<td>Jong Min Ko</td>
<td>207</td>
</tr>
<tr>
<td>Ji Yoon Lee</td>
<td>98, 207</td>
<td>Jin-Kyoung Kwon</td>
<td>173</td>
<td>Jong Tae Song</td>
<td>94, 100, 126, 245, 274, 281</td>
</tr>
<tr>
<td>Ji Yun Ko</td>
<td>308</td>
<td>Jin-Kyu Woo</td>
<td>221</td>
<td>Jong Taek Park</td>
<td>271</td>
</tr>
<tr>
<td>Ji-Eun Lee</td>
<td>104</td>
<td>Jin-Kyung Kwon</td>
<td>202, 227, 230, 290</td>
<td>Jong Won Han</td>
<td>272</td>
</tr>
<tr>
<td>Ji-Eun Park</td>
<td>295</td>
<td>Jin-Soo Kim</td>
<td>9</td>
<td>Jong Wook Chung</td>
<td>242</td>
</tr>
<tr>
<td>Ji-Hye Moon</td>
<td>261</td>
<td>Jin-Suk Kim</td>
<td>310, 311, 324</td>
<td>Jong-Bo Kim</td>
<td>188</td>
</tr>
<tr>
<td>Ji-Mi Kim</td>
<td>188</td>
<td>Jin-Won Lee</td>
<td>318</td>
<td>Jong-Eun Han</td>
<td>311, 312</td>
</tr>
<tr>
<td>Ji-Min Kim</td>
<td>30, 53</td>
<td>Jin-Woo Bae</td>
<td>237</td>
<td>Jong-Hee Lee</td>
<td>110, 122, 172</td>
</tr>
<tr>
<td>Ji-Min Yoo</td>
<td>153, 155, 157, 1158</td>
<td>Jin-Woo Han</td>
<td>272</td>
<td>Jong-Ho Lee</td>
<td>26</td>
</tr>
<tr>
<td>Ji-Nam Kang</td>
<td>146</td>
<td>Jin-Woo Young</td>
<td>207</td>
<td>Jong-Ho Park</td>
<td>74</td>
</tr>
<tr>
<td>Ji-Ung Jeong</td>
<td>103, 254</td>
<td>Jin-Young Choi</td>
<td>295</td>
<td>Jong-Min Jeong</td>
<td>64, 103, 105, 106, 283</td>
</tr>
<tr>
<td>Ji-Yoon Lee</td>
<td>110, 122, 172</td>
<td>Jing Yu</td>
<td>39</td>
<td>Jong-Min Jeong</td>
<td>64, 103, 105, 106, 283</td>
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<td>Jong-Min Ko</td>
<td>122, 172</td>
<td>Ju-ko Kim</td>
<td>312</td>
<td>Jung-Woo Lee</td>
<td>111</td>
</tr>
<tr>
<td>Jong-Sung Lim</td>
<td>141</td>
<td>Ju-Pyo Hong</td>
<td>227</td>
<td>Jung-Wook Yang</td>
<td>176, 177</td>
</tr>
<tr>
<td>Jong-sun Lim</td>
<td>129</td>
<td>Ju-Seok Seo</td>
<td>315</td>
<td>Jungeol Yeum</td>
<td>147</td>
</tr>
<tr>
<td>Jong-Wook Ahn</td>
<td>264</td>
<td>Ju-Won Kang</td>
<td>172</td>
<td>JungHeon Han</td>
<td>215</td>
</tr>
<tr>
<td>Jong-Wook Chung</td>
<td>137, 241, 263</td>
<td>Ju-Won Kong</td>
<td>122</td>
<td>Jungheon Han</td>
<td>180, 322</td>
</tr>
<tr>
<td>Jong-Woong Ahn</td>
<td>223, 251</td>
<td>Ju-Young Choi</td>
<td>128</td>
<td>JungHo BAEK</td>
<td>196</td>
</tr>
<tr>
<td>Jong-Yeo Lee</td>
<td>138, 184, 185, 210, 284</td>
<td>Juhyun Kim</td>
<td>187</td>
<td>Junghyun Shim</td>
<td>29</td>
</tr>
<tr>
<td>Jong-Yeol Park</td>
<td>211</td>
<td>Jun Gu Lee</td>
<td>173</td>
<td>Jungin Kim</td>
<td>254</td>
</tr>
<tr>
<td>Jonghyun Kwon</td>
<td>190</td>
<td>Jun Hee Jung</td>
<td>54</td>
<td>Jungkyu Kim</td>
<td>305</td>
</tr>
<tr>
<td>Jongtaek Kim</td>
<td>320</td>
<td>Jun Hyeon Cho</td>
<td>98, 207</td>
<td>Jungmin Ha</td>
<td>32, 33, 54, 139, 142, 227</td>
</tr>
<tr>
<td>Jongyeol Park</td>
<td>215</td>
<td>Jun Hyoung Bang</td>
<td>242</td>
<td>Jungrye Nam</td>
<td>152, 153, 154, 155, 156, 157, 158, 159, 160</td>
</tr>
<tr>
<td>Joo Yeol Kim</td>
<td>121, 178</td>
<td>Jun Oh</td>
<td>35, 140, 232</td>
<td>Junho Lee</td>
<td>314</td>
</tr>
<tr>
<td>Joo-hyun Lee</td>
<td>170, 197, 205</td>
<td>Jun-Cheol Moon</td>
<td>107</td>
<td>Junhyung Park</td>
<td>141</td>
</tr>
<tr>
<td>Joo-Sook Park</td>
<td>37, 162, 163</td>
<td>Jun-Dae Lee</td>
<td>267</td>
<td>Junki Lee</td>
<td>152</td>
</tr>
<tr>
<td>Joo-seung Lee</td>
<td>295</td>
<td>Jun-Hye Shin</td>
<td>328</td>
<td>Juyoung Choi</td>
<td>328</td>
</tr>
<tr>
<td>Joohee Choi</td>
<td>313</td>
<td>Jun-Hyeon Cho</td>
<td>122</td>
<td>Jwa-Kyung Sung</td>
<td>241</td>
</tr>
<tr>
<td>Joohyeong Lee</td>
<td>32</td>
<td>Jun-Yong Jeong</td>
<td>297</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Joohyun Lee</td>
<td>200, 222</td>
<td>Jundae Lee</td>
<td>132, 197, 212, 214</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Joon Ki Hong</td>
<td>321, 322</td>
<td>Jung Ching Hsu</td>
<td>217, 218</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Joon Ki Hong</td>
<td>187</td>
<td>Jung Heo</td>
<td>113, 228, 293</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Joon-Soo Sim</td>
<td>184, 238</td>
<td>Jung Heon Han</td>
<td>211</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Joon-Woo Ahn</td>
<td>64, 186, 245, 277, 279, 280</td>
<td>Jung Hwan Nam</td>
<td>136, 226, 256</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Joon-Yung Cha</td>
<td>319</td>
<td>Jung Kyung Moon</td>
<td>195</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Joong Hyoun Chin</td>
<td>101, 111</td>
<td>Jung Min Kim</td>
<td>245, 273, 276, 277, 278, 279</td>
<td>Jung-Heum Cho</td>
<td>139, 142</td>
</tr>
<tr>
<td>Joong-Hyoun Chin</td>
<td>158</td>
<td></td>
<td></td>
<td>Jung-Mo Ku</td>
<td>49</td>
</tr>
<tr>
<td>Jooneum Park</td>
<td>326</td>
<td>Jung Nam Suh</td>
<td>182</td>
<td>Karel Müller</td>
<td>17</td>
</tr>
<tr>
<td>Joonwhan Lee</td>
<td>45</td>
<td>Jung Sook Sung</td>
<td>249</td>
<td>Karel Raabe</td>
<td>30</td>
</tr>
<tr>
<td>Jooyeon Bae</td>
<td>313</td>
<td>Jung Sun Kim</td>
<td>34, 137, 145, 146, 147, 148</td>
<td>Katarina Kulichová</td>
<td>17</td>
</tr>
<tr>
<td>Jooyeong Choi</td>
<td>202</td>
<td></td>
<td></td>
<td>Katsuya Negishi</td>
<td>67</td>
</tr>
<tr>
<td>Joseph Noble Amoah</td>
<td>116</td>
<td>Jung Woo Lee</td>
<td>113</td>
<td>Kawin Krupeu</td>
<td>169</td>
</tr>
<tr>
<td>Joung Sug Kim</td>
<td>38, 125, 149</td>
<td>Jung Yeon Han</td>
<td>324</td>
<td>Keon-Mi Lee</td>
<td>99, 103, 106, 132</td>
</tr>
<tr>
<td>Joung-Ho Lee</td>
<td>143, 173, 200, 211</td>
<td>Jung-Du Shin</td>
<td>229</td>
<td>Kesavan Markkandan</td>
<td>226</td>
</tr>
<tr>
<td>Ju Hee Kim</td>
<td>119</td>
<td>Jung-Heon Han</td>
<td>35, 232</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ju Hee Rhee</td>
<td>249</td>
<td>Jung-Ho Kwak</td>
<td>181</td>
<td>Keunpyo Lee</td>
<td>31, 132, 135, 142, 146, 170</td>
</tr>
<tr>
<td>Ju Hui Do</td>
<td>324</td>
<td>Jung-Ho Park</td>
<td>315</td>
<td>Kevin Cushman</td>
<td>29</td>
</tr>
<tr>
<td>Ju Hyeon Kim</td>
<td>302</td>
<td>Jung-Hwan Nam</td>
<td>206, 258</td>
<td>Khuat Thi Mai Luong</td>
<td>234</td>
</tr>
<tr>
<td>Ju Kyong Lee</td>
<td>97, 246, 247</td>
<td>Jung-In Kim</td>
<td>199</td>
<td>Ki Hong Nam</td>
<td>287, 288, 289</td>
</tr>
<tr>
<td>Ju Seok Lee</td>
<td>267</td>
<td>Jung-Kyung Moon</td>
<td>134, 158, 225</td>
<td>Ki Hun Shin</td>
<td>309</td>
</tr>
<tr>
<td>Ju Won Kang</td>
<td>207</td>
<td>Jung-Kyung Moon</td>
<td>30</td>
<td>Ki Jin Park</td>
<td>321</td>
</tr>
<tr>
<td>Ju Yeon Jung</td>
<td>55</td>
<td>Jung-Pil Lee</td>
<td>208</td>
<td>Ki Yoon Kim</td>
<td>269</td>
</tr>
<tr>
<td>Ju-Hee Rhee</td>
<td>171, 255</td>
<td>Jung-Pil Suh</td>
<td>99, 106, 110, 132, 254</td>
<td>Ki-Deuk Bae</td>
<td>192</td>
</tr>
<tr>
<td>Ju-Hee Yang</td>
<td>184, 185</td>
<td>Jung-Ro Lee</td>
<td>57, 262, 263</td>
<td>Ki-Hong Jung</td>
<td>158, 161, 165, 318, 320, 321</td>
</tr>
<tr>
<td>Ju-hee Yang</td>
<td>185</td>
<td>Jung-Ro Lee</td>
<td>252</td>
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</tr>
<tr>
<td>Ju-Hyeon Lee</td>
<td>328</td>
<td>Jung-Sook Sung</td>
<td>171, 255</td>
<td>Ki-Won Lee</td>
<td>99, 189, 204, 249, 260</td>
</tr>
<tr>
<td>Ju-Kon Kim</td>
<td>21, 313, 321</td>
<td>Jung-Tae Kim</td>
<td>105</td>
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<td>Ki-Yong Kim</td>
<td>189, 260</td>
<td>Kyeonglim Min</td>
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<td>Lawrence Kenyon</td>
<td>169</td>
</tr>
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<td>Ki-Yong Kim</td>
<td>103</td>
<td>Kyong Hwan Bang</td>
<td>113</td>
<td>Le Hung Linh</td>
<td>234</td>
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<tr>
<td>Kieatisak Pakdeekaew</td>
<td>92</td>
<td>Kyong Mi Jun</td>
<td>38, 125, 149</td>
<td>Le Van Trang</td>
<td>213, 214</td>
</tr>
<tr>
<td>Kihun Ha</td>
<td>301</td>
<td>Kyong Sil Lee</td>
<td>180</td>
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<td>194</td>
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<td>Kihwan Kim</td>
<td>295</td>
<td>Kyong-Cheul Park</td>
<td>122, 139, 234</td>
<td>Lee Sae Hyun</td>
<td>149</td>
</tr>
<tr>
<td>Kihwan Lim</td>
<td>295</td>
<td>Kyong Dae Kang</td>
<td>130, 131</td>
<td>Lenka Steinbachová</td>
<td>17</td>
</tr>
<tr>
<td>Kihwan Song</td>
<td>264, 273</td>
<td>Kyong Hyoun Kim</td>
<td>134, 221</td>
<td>Leslie L Domier</td>
<td>305</td>
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<td>270</td>
<td>Libo Shan</td>
<td>40</td>
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<td>Kim EJ</td>
<td>90, 91</td>
<td>Kyong Rok Geum</td>
<td>314</td>
<td>Lin Cheng</td>
<td>152, 153, 154, 155, 156, 157, 158</td>
</tr>
<tr>
<td>Kitya Ankul</td>
<td>131, 133</td>
<td>Kyounghhee Lee</td>
<td>292</td>
<td>Lixia Wang</td>
<td>131</td>
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<tr>
<td>Kiyomi Abe</td>
<td>67</td>
<td>Kyoungho Cho</td>
<td>289</td>
<td>Lori Hinze</td>
<td>29</td>
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<tr>
<td>Kiyoo Kang</td>
<td>28, 216</td>
<td>Kyu Chan Shim</td>
<td>233</td>
<td>Luong Ngoc Ha</td>
<td>110, 233, 234, 235</td>
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<td>Kodai Matsuoka</td>
<td>143</td>
<td>Kyu Hong Cho</td>
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<td>Koeun Han</td>
<td>211, 230</td>
<td>Kyu JIn Sa</td>
<td>97, 246, 247</td>
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<td>329</td>
<td>Kyu Num An</td>
<td>124</td>
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<td>Kotaro Ishii</td>
<td>63</td>
<td>Kyu Whan Choi</td>
<td>235, 236, 320</td>
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<td>Kruti M. Patel</td>
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<td>Kyu-Chan Shim</td>
<td>110, 233, 235</td>
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<td>Kruti Patel</td>
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<td>101, 108, 109</td>
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<td>Kyung Hae-Kim</td>
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<td>Kun Cho</td>
<td>127, 128</td>
<td>Kyung Hwa Kim</td>
<td>126, 285</td>
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<td>Kyung Jun Lee57, 252, 262, 263, 271</td>
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<td>Kyoung-Hye Kim</td>
<td>30, 53</td>
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<td>112, 212, 265</td>
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<td>179, 213, 214</td>
<td>Minsu Park</td>
<td>164</td>
<td>Myoung-Hee Lee</td>
<td>132, 142, 199, 201, 205</td>
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<tr>
<td>Media Fitri Isma Nugraha</td>
<td>253</td>
<td>Minwook Kim</td>
<td>301</td>
<td>Myoung-Jae Shin</td>
<td>57, 252, 262, 263</td>
</tr>
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<td>Meechau Siangliw</td>
<td>89</td>
<td>Mirjalol Akhtamov</td>
<td>233</td>
<td>Myoungjae Shin</td>
<td>257</td>
</tr>
<tr>
<td>Megan Sweeney</td>
<td>29</td>
<td>Mirjalol Axtamov</td>
<td>235</td>
<td>Myung Hee Lee</td>
<td>199</td>
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<td>Meki S. Muktar</td>
<td>99, 249</td>
<td>Mita Dianasari</td>
<td>66</td>
<td>Myung Ju Shin</td>
<td>130, 131</td>
</tr>
<tr>
<td>Mercy Samia</td>
<td>51</td>
<td>Miyeon Son</td>
<td>150</td>
<td>Myung Ki Min</td>
<td>299, 309, 317</td>
</tr>
<tr>
<td>Merry Gloria Meliala</td>
<td>247</td>
<td>Myoung Kim</td>
<td>43</td>
<td>Myung Ok Byun</td>
<td>299</td>
</tr>
<tr>
<td>Meynarti Sari Dewi Ibrahim</td>
<td>282</td>
<td>MK Hossain</td>
<td>218</td>
<td>Myung Suk Ahn</td>
<td>271</td>
</tr>
<tr>
<td>Meyong-Eun Choe</td>
<td>259</td>
<td>MM Hossain</td>
<td>218</td>
<td>Myung-Chul Lee</td>
<td>252, 257</td>
</tr>
<tr>
<td>Mi Nam Chung</td>
<td>176, 256</td>
<td>MM Islam</td>
<td>218</td>
<td>Myung-Eun Park</td>
<td>166</td>
</tr>
<tr>
<td>Mi-Jeong Jeong</td>
<td>102, 170, 197, 205</td>
<td>MM Rashid</td>
<td>218</td>
<td>Myung-Hee Kim</td>
<td>318</td>
</tr>
<tr>
<td>Mi-Nam Jeong</td>
<td>209</td>
<td>Moch Rosyadi Adnan</td>
<td>186</td>
<td>Myung-Ho Lim</td>
<td>193</td>
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<td>Mi-Reu Kim</td>
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<td>Mohamed Rhaka</td>
<td>217</td>
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<td>Mohammad Amiruzzaman</td>
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<td>281</td>
<td>Mohammed Sameer</td>
<td>141</td>
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<td>Moon Young Kim</td>
<td>54, 139, 142, 227</td>
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<td>191</td>
<td>Moon-jong Kim</td>
<td>211</td>
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<td>Min Kang</td>
<td>95, 96</td>
<td>Moon-Joo Lee</td>
<td>124</td>
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<td>121, 178, 211, 215</td>
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<td>121, 178</td>
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<td>Min-Gyun Jeong</td>
<td>162, 163</td>
<td>Moonojo Lee</td>
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<td>Moonoong Kim</td>
<td>121, 178</td>
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<td>Min-Jeong Kang</td>
<td>138, 174</td>
<td>Muhamad Syukur</td>
<td>242, 243, 244</td>
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<tr>
<td>Min-Ju Kim</td>
<td>193</td>
<td>Muhamad Irfan Siddique</td>
<td>143, 230</td>
<td></td>
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<td>Min-Jung Seo</td>
<td>222, 223</td>
<td>Muhamad Rauf</td>
<td>252</td>
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<td>232</td>
<td>Muhamad Ridha Alfarabi Istiqal</td>
<td>247</td>
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<td>Min-Kyu Lee</td>
<td>273, 276, 277, 278</td>
<td>Muhamad Sharma</td>
<td>122, 234</td>
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<td>272</td>
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<td>229</td>
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<td>118, 173, 191, 214</td>
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<td>202, 230</td>
<td>Yamaha Hyun Min</td>
<td>152, 153, 154, 155, 156, 158</td>
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<td>126, 219, 248, 285</td>
<td>Yamaha Hyun Youu</td>
<td>161</td>
<td>Namiko Nishida</td>
<td>144</td>
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<tr>
<td>Minah Oh</td>
<td>293</td>
<td>Yamaha-Jin Kang</td>
<td>194</td>
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<td>Mingmin Zhao</td>
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<td>248</td>
<td>Namshin Kim</td>
<td>134, 161, 221</td>
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<td>Naoaki Taoka</td>
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<td>Naomi Miyaji</td>
<td>144</td>
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<td>Minjin Kim</td>
<td>320</td>
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<td>271</td>
<td>Narayana Chandra Paul</td>
<td>176, 256</td>
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<td>Yeoung Hee Lee</td>
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<td>97, 231</td>
<td>Neha Roy</td>
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<td>Yeoung Ryoul Park</td>
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<td>Nuri Oh</td>
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<td>Scott Adams</td>
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<td>Scott M. Adams</td>
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<td>Sebastin Raveendar</td>
<td>262, 263</td>
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<td>SeEun Choe</td>
<td>43</td>
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<td>Sejong Oh</td>
<td>252, 257</td>
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<td>Seo Ho Shin</td>
<td>124</td>
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<td>324</td>
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<td>132, 142, 146</td>
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<td>Seon-Kyeong Lee</td>
<td>184, 238</td>
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<td>Seon-Woo Oh</td>
<td>192, 203, 302, 324</td>
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<td>301</td>
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<td>Seong-Beom Jin</td>
<td>191, 193</td>
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<td>Seong-Gyu Jang</td>
<td>125, 285</td>
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<tr>
<td>Seong-Hoon Kim</td>
<td>57, 262, 263</td>
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<td>58</td>
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<td>223</td>
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<td>Seong-Im Park</td>
<td>297</td>
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<td>Seong-Kon Lee</td>
<td>203, 204</td>
</tr>
<tr>
<td>Seong-Ryong Kim</td>
<td>328</td>
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<td>Seong-Uk Son</td>
<td>69</td>
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<tr>
<td>Seong-Woo Cho</td>
<td>207, 224</td>
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<td>224</td>
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<tbody>
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<td>Seongman Jeong</td>
<td>134, 161, 221</td>
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<td>Seonwoo Oh</td>
<td>204</td>
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<td>Seowon Choi</td>
<td>312</td>
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<td>Serim Kim</td>
<td>266</td>
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<tr>
<td>Serry Koh</td>
<td>235, 236, 320</td>
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<td>Seuk-Bo Song</td>
<td>259</td>
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<td>248</td>
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<tr>
<td>Seul-Gi Park</td>
<td>99, 103, 106, 132, 208</td>
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<td>Seul-Ki Jung</td>
<td>109</td>
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<td>95, 96</td>
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<td>293</td>
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<td>Seung-Hyun Kim</td>
<td>155, 158</td>
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<tr>
<td>Seung-il Yoo</td>
<td>137</td>
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<tr>
<td>Seung-up Kim</td>
<td>31, 170</td>
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<td>Seungill Kim</td>
<td>36, 38</td>
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<td>Seungki Back</td>
<td>200</td>
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<td>309</td>
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<td>256</td>
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<td>Sherry Lou Hechanova</td>
<td>27</td>
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<td>Shih-wen Lin</td>
<td>57, 169</td>
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<td>Shin Hwa Kim</td>
<td>136</td>
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<td>62</td>
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<td>Shipra Kumari</td>
<td>102</td>
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<td>Shu Fukai</td>
<td>93</td>
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<td>Shu Mei Huang</td>
<td>217, 218</td>
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<td>Si Hyeock Lee</td>
<td>302</td>
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<td>211</td>
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<td>Si-Myung Lee</td>
<td>192</td>
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<td>Si-Yong Kang</td>
<td>64, 84, 277, 278, 280, 282</td>
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<td>Sichul Lee</td>
<td>326</td>
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<tr>
<td>Sihwan Ryu</td>
<td>121, 178, 215</td>
</tr>
<tr>
<td>Sin-Gi Park</td>
<td>137, 270</td>
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<td>290</td>
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<td>186</td>
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<td>43</td>
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<td>Sungtaeg Kang</td>
<td>30, 53, 225, 267</td>
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<td>97, 231</td>
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<td>43, 325</td>
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<td>177, 179</td>
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<td>186</td>
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<td>110</td>
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<td>Sunjoo Kang</td>
<td>177</td>
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<td>Sunok Moon</td>
<td>165, 318</td>
</tr>
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<td>238</td>
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<tr>
<td>Surjono Hadi Sutjahjo</td>
<td>112</td>
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<td>Susan B. Altenbach</td>
<td>210, 284</td>
</tr>
<tr>
<td>Susan E. Corbett</td>
<td>53</td>
</tr>
<tr>
<td>Swapan Kumar Roy</td>
<td>127, 128</td>
</tr>
<tr>
<td>Swati Tyagi</td>
<td>34</td>
</tr>
<tr>
<td>Syafaruddin</td>
<td>183, 253</td>
</tr>
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<td>Syarifah Is Aisyah</td>
<td>66, 243</td>
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<table>
<thead>
<tr>
<th>Name</th>
<th>Page</th>
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<tbody>
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<td>TaeJoung Ha</td>
<td>254</td>
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<td>30, 53</td>
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<td>193</td>
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<td>254</td>
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<td>164, 175</td>
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<td>164, 175</td>
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<td>329</td>
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<td>Takeshi Yasuda</td>
<td>143, 144</td>
</tr>
<tr>
<td>Tania Afroz</td>
<td>171</td>
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<tr>
<td>Tarika Yimram</td>
<td>133, 168</td>
</tr>
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<td>41</td>
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<tr>
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<td>100</td>
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<td>Tereza Borba</td>
<td>226</td>
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<td>324</td>
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<td>89</td>
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<td>94</td>
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<td>303</td>
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<td>93</td>
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<td>92</td>
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<td>214</td>
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<td>17</td>
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<td>54</td>
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<td>63</td>
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<td>Tran Dang Xuan</td>
<td>89</td>
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<td>Tran Thi Mil</td>
<td>67, 290</td>
</tr>
<tr>
<td>Trevor Garnett</td>
<td>46</td>
</tr>
<tr>
<td>Trikoesomaningtyas</td>
<td>59, 112, 247</td>
</tr>
<tr>
<td>Tsung-Han Lin</td>
<td>57</td>
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<td>Tsung-han Lin</td>
<td>169</td>
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<td>Tuan Viet Do</td>
<td>324</td>
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<td>Uk LEE</td>
<td>81</td>
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<td>Un-Sang Yeo</td>
<td>254</td>
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<td>Ung Jo Hyun</td>
<td>101, 108, 109, 261</td>
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<tr>
<td>Ung-Han Yoon</td>
<td>31, 132, 135, 142, 146, 170</td>
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<td>Unseok Lee</td>
<td>45, 47</td>
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<td>Upit Sarimana</td>
<td>241</td>
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<td>Usa Duangsong</td>
<td>41</td>
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<td>67</td>
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<td>186</td>
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<tr>
<td>Vimalraj Mani</td>
<td>184</td>
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<tr>
<td>Vipada Kantayos</td>
<td>310, 311, 324</td>
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<tr>
<td>Vo Ngoc Linh Giang</td>
<td>149</td>
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<td>Vu Van Tien</td>
<td>67</td>
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<td>102</td>
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<td>194</td>
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<td>252</td>
</tr>
<tr>
<td>Wang Ying</td>
<td>168</td>
</tr>
<tr>
<td>Waras Nurcholis</td>
<td>66, 244</td>
</tr>
<tr>
<td>Weilan Piao</td>
<td>103</td>
</tr>
<tr>
<td>Wen-Xing Hu</td>
<td>305</td>
</tr>
<tr>
<td>Wening Enggarini</td>
<td>50, 253</td>
</tr>
<tr>
<td>Weon Tai Jean</td>
<td>255</td>
</tr>
<tr>
<td>Wi-Young Lee</td>
<td>121</td>
</tr>
<tr>
<td>Will Urquhart</td>
<td>190</td>
</tr>
<tr>
<td>Winda Puspitasari</td>
<td>91</td>
</tr>
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<td>Woe-Yeon Kim</td>
<td>319</td>
</tr>
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<td>118</td>
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<td>Won Choi</td>
<td>324</td>
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<td>296</td>
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<td>114</td>
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<td>241</td>
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<td>192</td>
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<td>237</td>
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<tr>
<td>Wonwoo Cho</td>
<td>121</td>
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<tr>
<td>Woo Jae Kim</td>
<td>107, 175</td>
</tr>
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<td>Woo Jin Kim</td>
<td>233</td>
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<td>Woo Joo Jung</td>
<td>116</td>
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<td>Woo Suk Jung</td>
<td>115</td>
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<tr>
<td>Name</td>
<td>Page</td>
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<td>Yeon-Hee Lee</td>
<td>147</td>
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<td>293</td>
</tr>
<tr>
<td>Yong Weon Seo</td>
<td>116</td>
</tr>
<tr>
<td>Yong-Kil Kim                186</td>
<td>208, 216, 268, 269</td>
</tr>
<tr>
<td>Yanisa sangsodkaew</td>
<td>93</td>
</tr>
<tr>
<td>Ye Eun Cheon</td>
<td>215</td>
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<tr>
<td>Ye Eun Kang</td>
<td>170</td>
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<td>Ye Ju Ha</td>
<td>247</td>
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<td>Ye Sol Jeong</td>
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<td>132</td>
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<td>Yebin Kwon</td>
<td>222</td>
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<tr>
<td>Yedomon Ange Bovys Zoclancloun</td>
<td>156, 175, 159, 160, 199, 259, 321</td>
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<td>Yong-Min Kim</td>
<td>36</td>
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<td>Yong-Gu Cho</td>
<td>127</td>
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<td>Yong-Jin Park1</td>
<td>158</td>
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<td>Yongkuk Lee</td>
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<td>68</td>
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<td>171</td>
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<td>Yongsang Lee</td>
<td>309</td>
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<td>Young-Eun Na</td>
<td>284</td>
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<td>Name</td>
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</tr>
<tr>
<td>Young-Ho Kwon</td>
<td>122</td>
</tr>
<tr>
<td>Young-il Cho</td>
<td>35, 232</td>
</tr>
<tr>
<td>Young-Im CHOI</td>
<td>81</td>
</tr>
<tr>
<td>Young-Im Choi</td>
<td>123, 291</td>
</tr>
<tr>
<td>Young-Joo Jung</td>
<td>300</td>
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<tr>
<td>Young-Joo Seol</td>
<td>196</td>
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<td>Young-Ju Oh</td>
<td>188</td>
</tr>
<tr>
<td>Young-Jun Park</td>
<td>92, 239</td>
</tr>
<tr>
<td>Young-Keun Cheong</td>
<td>207</td>
</tr>
<tr>
<td>Young-Kun, Kim</td>
<td>301</td>
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<tr>
<td>Young-Lok Cha</td>
<td>104</td>
</tr>
<tr>
<td>Young-Mi Yoon</td>
<td>74</td>
</tr>
<tr>
<td>Young-Min Jeong</td>
<td>35, 150, 232</td>
</tr>
<tr>
<td>Young-Sang Kim</td>
<td>198</td>
</tr>
<tr>
<td>Young-Sang Lee</td>
<td>155, 158, 259</td>
</tr>
<tr>
<td>Young-Soo Chung</td>
<td>302, 306, 314, 323</td>
</tr>
<tr>
<td>YoungGeum Shin</td>
<td>301</td>
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<tr>
<td>Youngho Koh</td>
<td>141</td>
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<td>Youngin Kim</td>
<td>264</td>
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<td>YoungJin Choi</td>
<td>306</td>
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<tr>
<td>Youngjun Kim</td>
<td>176</td>
</tr>
<tr>
<td>Youngjun Mo</td>
<td>64, 105, 106, 266, 283</td>
</tr>
<tr>
<td>Youngki Park</td>
<td>272</td>
</tr>
<tr>
<td>Youngmin Park</td>
<td>43</td>
</tr>
<tr>
<td>Youngshin Kwak</td>
<td>300</td>
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<td>Youngsi Lee</td>
<td>150</td>
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<td>Yoonsung Cho</td>
<td>193</td>
</tr>
<tr>
<td>Yousoo Choi</td>
<td>197, 255</td>
</tr>
<tr>
<td>Yowook Song</td>
<td>189, 204</td>
</tr>
<tr>
<td>Yozo Nagira</td>
<td>42</td>
</tr>
<tr>
<td>Yu Jeong Kwon</td>
<td>64</td>
</tr>
<tr>
<td>Yu Jin Jung</td>
<td>287, 288, 289, 308</td>
</tr>
<tr>
<td>Yu Mi Choi</td>
<td>252, 257</td>
</tr>
<tr>
<td>Yu Na kang</td>
<td>224</td>
</tr>
<tr>
<td>Yu Young Lee</td>
<td>200</td>
</tr>
<tr>
<td>Yu-A Jeon</td>
<td>28</td>
</tr>
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<td>Yu-jeong Kwon</td>
<td>267</td>
</tr>
<tr>
<td>Yu-Ji Lee</td>
<td>229</td>
</tr>
<tr>
<td>Yu-Jin Jung</td>
<td>179, 213</td>
</tr>
<tr>
<td>Yu-Jin Kim</td>
<td>161, 318, 321</td>
</tr>
<tr>
<td>Yu-Mi Choi</td>
<td>268</td>
</tr>
<tr>
<td>Yu-Mi Lee</td>
<td>64</td>
</tr>
<tr>
<td>Yu-min Jeon</td>
<td>104, 198</td>
</tr>
<tr>
<td>Yuan Cao</td>
<td>152, 153, 154, 155, 156, 157, 158</td>
</tr>
<tr>
<td>Yuan Xingxing</td>
<td>168</td>
</tr>
<tr>
<td>Yuanhu Xuan</td>
<td>113</td>
</tr>
</tbody>
</table>

국문

마정복 | 79
모영준 | 73
문지혜 | 78
<table>
<thead>
<tr>
<th>Name</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>박영식</td>
<td>79</td>
</tr>
<tr>
<td>박영은</td>
<td>75</td>
</tr>
<tr>
<td>박원흠</td>
<td>79</td>
</tr>
<tr>
<td>박진기</td>
<td>237</td>
</tr>
<tr>
<td>박필만</td>
<td>79</td>
</tr>
<tr>
<td>박향미</td>
<td>73</td>
</tr>
<tr>
<td>박현수</td>
<td>237</td>
</tr>
<tr>
<td>박효근</td>
<td>83</td>
</tr>
<tr>
<td>박문진</td>
<td>85</td>
</tr>
<tr>
<td>배진우</td>
<td>237</td>
</tr>
<tr>
<td>배현희</td>
<td>76</td>
</tr>
<tr>
<td>배현대</td>
<td>73</td>
</tr>
<tr>
<td>배성범</td>
<td>76</td>
</tr>
<tr>
<td>배인엽</td>
<td>237</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Name</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>서정남</td>
<td>79</td>
</tr>
<tr>
<td>서정필</td>
<td>73</td>
</tr>
<tr>
<td>서혜영</td>
<td>79</td>
</tr>
<tr>
<td>손범염</td>
<td>76</td>
</tr>
<tr>
<td>송우진</td>
<td>73</td>
</tr>
<tr>
<td>신윤철</td>
<td>73</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Name</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>안익근</td>
<td>73</td>
</tr>
<tr>
<td>안혜련</td>
<td>79</td>
</tr>
<tr>
<td>양미희</td>
<td>85</td>
</tr>
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<td>양은영</td>
<td>78</td>
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<td>여수형</td>
<td>80</td>
</tr>
<tr>
<td>여운상</td>
<td>73</td>
</tr>
<tr>
<td>원욱재</td>
<td>237</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Name</th>
<th>Page</th>
</tr>
</thead>
<tbody>
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<td>장은주</td>
<td>73</td>
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<td>79</td>
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<tr>
<td>장재야</td>
<td>79</td>
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<td>장중문</td>
<td>79</td>
</tr>
<tr>
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<td>79</td>
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<tr>
<td>장태욱</td>
<td>237</td>
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<td>조규택</td>
<td>73</td>
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<td>73</td>
</tr>
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<td>신운철</td>
<td>79</td>
</tr>
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<td>이강섭</td>
<td>308</td>
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<td>이경준</td>
<td>79</td>
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<td>73</td>
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<td>262</td>
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<td>79</td>
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