2016

한국육종학회–차세대BG21사업단–GSP사업단 공동심포지엄

Gene, Genome & New Technology for Plant Breeding

일시: 2016년 6월 29(수)~7월 1(금)

장소: 청주 라마다플라자 호텔

주　　최 : 사단법인 한국육종학회

공동주관 : 차세대BG21사업단 (농생물게놈활용연구사업단, GM작물개발사업단, 식물분자육종사업단), GSP사업단 (채소종자사업단, 원예종자사업단, 식량종자사업단), 시스템합성농생명공학사업단, 동아대학교 농업생명과학연구소, 서울대학교 채소육종연구센터, 서울대학교 식물유전체육종연구소, 충북대학교 농업과학기술연구소, 제주대학교 아열대원예산업연구소

후　　원 : 농촌진흥청, 국립식량과학원, 국립산림과학원, 한국농식품생명과학협회, 한국과학기술단체총연합회

Program

2016 한국육종학회-차세대BG21사업단-GSP사업단 공동심포지엄
Gene, Genome & New Technology for Plant Breeding
2016년 6월 29일(수) ~ 7월 1일(금), 라마다플라자 청주호텔

1일째 [2016. 6. 29. 수]

19:00~	이사회의 및 조직위원회의

2일째 [2016. 6. 30. 목]

09:00~09:50	공동심포지엄 학술발표회 등록 및 포스터 부착
09:50~10:00	개회식
	개회사 – 정영수 교수 (조직위원장, 동아대학교)
	환영사 – 조용구 교수 (회장, 충북대학교)
《 1부 Plenary Session 》	
	– 좌장 : 고희종 교수 (서울대학교)
10:00~10:40	▸Doubled Haploid (DH) technology in maize breeding: Application and technology for production of DH lines – Dr. Chaikam, CIMMYT, Mexico
10:40~11:20	▸Finding mineral element transporters for better and safe production of rice – Dr. Jian Feng Ma, Okayama University, Kurashiki, Japan
11:20~12:00	▸Function of Fibrillin protein in photosynthetic metabolism – 김현욱 교수 (세종대학교)
12:00~13:20	점심시간
	– 좌장 : 오대근 교수 (한국농수산대학)
13:20~14:00	▸Revisiting domestication to revitalize crop improvement: the florigen revolution – Dr. Zach Lippman, Cold Spring Harbor Laboratory, USA
14:00~14:40	▸Manipulating Fruit and Vegetable Quality Traits – Dr. David Brummell, Plant & Food Research, New Zealand
14:40~15:20	▸Designing Crops for Global Food Security:Digitizing Plant Phenotypes – Dr. Maurice Moloney, Global Institute for Food Security, Canada
15:20~15:40	휴식

2일째 [2016. 6. 30. 목]

〈〈 2부 한국육종학회 분과발표 & 포스터 발표 〉〉	
15:40~17:40	▸분과발표 OA 수량 및 저항성육종 – 좌장 : 김용호 교수 (순천향대학교), 조영찬 박사 (국립식량과학원)
	▸분과발표 OB 품질육종 및 유전변이 – 좌장 : 김보경 과장 (국립식량과학원) 강성택 교수 (단국대학교)
	▸분과발표 OC 분자육종 및 유전공학 – 좌장 : 강권규 교수 (한경대학교), 박용진 교수 (공주대학교)
17:40~18:00	한국육종학회 정기총회
18:00~18:20	포스터 발표
18:20~	특별공연 및 간친회

3일째 [2016. 7. 1. 금]

〈〈 3부 Concurrent Session 〉〉	
	주요 작물에서 유전체 정보활용 육종가 친화형 인터페이스 연구 소개 (농생물게놈활용연구사업단)
	– 좌장 : 유의수 박사 ((주)파이젠)
09:00~09:25	▸가지과 유전체 활용을 위한 생물정보분석 파이프라인 및 데이터베이스 TGsol 현황 – 조성환 박사 ((주)씨더스)
09:25~09:50	▸두과작물 유전체정보 기반 분자육종 활용을 위한 플랫폼 개발 – 최홍규 교수 (동아대학교)
09:50~10:15	▸콩 유전체 육종 지원용 Korean Soya Base 소개 – 김남신 박사 (한국생명공학연구원)
10:15~10:40	▸벼 유전체육종 연구의 진전 및 소규모 연구실간의 Resource 공유체계 구축 : 재료 정보 프로그램 연구경험 공유 – 박용진 교수 (공주대학교)
	Genome editing and molecular farming (GM작물개발사업단 & 식물분자육종사업단)
	– 좌장 : 조현석 박사 (국립농업과학원 생물안전성과)
09:00~10:40	▸Versatile application of CRSPR/Cas9 system in plant research – 배상수 교수 (한양대학교)
	▸Transgenic plants producing green-vaccine for CSFV(classical swine fever virus) lead on plant biotechnology-based product on market – 손은주 박사 ((주)바이오앱)
10:40~11:00	휴식

3일째 [2016. 7. 1. 금]

《 3부 Concurrent Session 》	
	– GSP 채소종자사업단 & GSP 원예종자사업단
	▸좌장 : 임용표 단장 (채소종자사업단)
09:00~10:40	▸육성가 권리보호와 종자산업의 발달 – 이승인 박사 (국립종자원)
	▸종자검정서비스 확대를 위한 국립종자원의 전략 – 소은희 박사 (국립종자원)
	▸좌장 : 노일섭 단장 (원예종자사업단)
	▸Breeding for Pyramiding Target-genes and Selection of F1 Hybrids by Marker Assisted Selection in Tomato – 김명권 박사 (토마토생명공학연구소)
	▸Gene Identification, Expression Analysis and Breeding for Enhanced Glucosinolate Biosynthesis in Brassica – Dr. Arif Hasan Khan Robin (Sunchon National University)
	– GSP 식량종자사업단 –
	▸좌장 : 조영찬 박사 (국립식량과학원)
09:00~10:40	▸Specialty corn breeding at Sweet Seeds in Thailand to the tropical world – Dr. Taweesak Pulam (Sweet Seeds. Inc.)
	▸중국의 벼 육종기술 및 육종 현황 – Dr. Han Longzhi (Institute of Crop Sciences of Chinese Academy of Agricultural Sciences)
	▸Application of Biotechnology in Developing New Rice Varieties For High Temperature Tolerance in the Philippines – Dr. Norvie Manigbas (PhilRice)
	▸Rice production and the change of major diseases during the period of climate change in Vietnam – Dr. Dung Laitien (Plant Protection Research Institute, Vietnam)
10:40~11:00	휴식
《 4부 Plenary Session 》	
	▸좌장 : 서용원 교수 (고려대학교)
11:00~11:40	▸CRISPR RNA-guided Genome Editing in Human Stem Cells, Animals, and Plants – 김진수 교수 (서울대학교)
11:40~12:20	▸CRISPR Genome Editing in Outcrossing Woody Perennials – Dr. CJ Tsai, University of Georgia, USA
12:20~13:00	시상식 및 폐회

Symposium Program

2016 Annual Symposium of Korean Society of Breeding Science
Date and Place : June 29 - July 1, 2016 & Ramada Hotel at Cheongju

1st day [June 29. Wednesday]

19:00~	General Meeting of Organizing Committee

2nd day [June 30. Thursday]

09:00~09:50	Registration
09:50~10:00	Opening Ceremony ▸ Dr. Kang-Sup Lee (Secretary General, RDA, Korea)
	Opening Address – Dr. Young-soo Chung (Organizer, Dong-A University, Korea)
	Welcome Address – Dr. Yong-Gu Cho (President of KSBS, Chungbuk National University, Korea)
〈〈 Plenary Session 〉〉	
	▸Chair : Prof. Hee-Jong Koh (Seoul National University)
10:00~10:40	▸Doubled Haploid (DH) Technology in Maize Breeding: Application and Technology for Production of DH Lines – Dr. Chaikam, CIMMYT, Mexico
10:40~11:20	▸Finding Mineral Element Transporters for Better and Safe Production of Rice – Dr. Jian Feng Ma, Okayama University, Kurashiki, Japan
11:20~12:00	▸Function of Fibrillin Protein in Photosynthetic Metabolism – Dr. Hyun Wook Kim, SeJong University, Korea
12:00~13:20	Lunch & Poster
	▸Chair: Prof. Deun-Gun Oh (Korea National College of Agricultural and Fisheries)
13:20~14:00	▸Revisiting Domestication to Revitalize Crop Improvement: The Florigen Revolution – Dr. Zach Lippman, Cold Spring Harbor Laboratory, USA
14:00~14:40	▸Manipulating Fruit and Vegetable Quality Traits – Dr. David Brummell, Plant & Food Research, New Zealand
14:40~15:20	▸Designing Crops for Global Food Security: Digitizing Plant Phenotypes – Dr. Maurice Moloney, University of Saskatchewan, Canada

2nd day [June 30. Thursday]

《 Oral Presentation 》	
15:40~17:40	OA. Breeding for yield increase and resistant variety
	OB. Breeding for quality improvement and Genetic variation
	OC. Molecular breeding and biotechnology
17:40~18:00	General Meeting
18:00~18:20	Poster Presentation
18:20~	Banquet

3rd day [July 1. Friday]

《 Concurrent Session 》	
	Introduction of genomics integrated Interfaces for breeders in major crops (The Agricultural Genome Center)
	▸ Chair : Dr. Yei-Soo Yu (PHYZEN)
09:00~09:25	▸Development of Bioinformatics pipeline and web database for Solanaceae genome application – Dr. SungHwan Jo (SEEDERS)
09:25~09:50	▸Constructing a Genomics-Assisted Bioinformatic Platform for Legumes – Prof. Hong-Kyu Choi(Dong-A University)
09:50~10:15	▸Genomics Integrated Breeding Platform for Soybean: Korean Soya Base – Dr. Namshin Kim (Korea Research institute of Bioscience and Biotechnology)
10:15~10:40	▸Research Updates of Rice Breeding Activities using Genome Information, and Development of Resources-Sharing Systems: Seed Materials, Genomic Information, Software and Research Experience – Prof. Yong-Jin Park (Kongju National University)
	– The National Center for GM Crops & Plant Molecular Breeding Center –
	▸ Chair : Dr. Hyun Suk Cho (National Academy of Agricultural Science)
09:00~10:40	▸Versatile Application of CRSPR/Cas9 System in Plant Research – Prof. Sangsu Bae (Hanyang University)
	▸Transgenic Plants Producing Green-vaccine for CSFV(classical swine fever virus) Lead on Plant Biotechnology-based Product on Market – Dr. Eun-Ju Sohn (BioApp Inc.,)

3rd day [July 1. Friday]

《 Concurrent Session 》	
	– Golden Seed Project for Vegetable & Horticulture –
	▸Chair : Prof. Yong-Pyo Lim (GSP Vegetable Seed Center)
09:00~10:40	▸Seed Industry Development by Strengthening Plant Breeder's Right and Seed Market Control – Dr. Yi Seung In (Korea Seed & Variety Service)
	▸Current condition and strategy for expansion of seed testing service in KSVS – Dr. Eun Hee Soh (Korea Seed & Variety Service)
	▸ Chair : Prof. Ill-Sup Nou (GSP Horticulture Seed Center)
	▸Breeding for Pyramiding Target-genes and Selection of F1 Hybrids by Marker Assisted Selection in Tomato – Dr. Myung Kwon Kim (Tomato Life Science & Research)
	▸Gene Identification, Expression Analysis and Breeding for Enhanced Glucosinolate Biosynthesis in Brassica – Dr. Arif Hasan Khan Robin (Sunchon National University)
10:40~11:00	Coffee Break
《 4부 Plenary Session 》	
	– Golden Seed Project for Cereal –
	▸Chair : Dr. Young-Chan Cho (National Institute of Crop Science)
09:00~10:40	▸Specialty Corn Breeding at Sweet Seeds in Thailand to The Tropical World – Dr. Taweesak Pulam (Sweet Seeds Co., Ltd., Thailand)
	▸The Status of Rice Production and Breeding in China – Dr. Han Longzhi (Institute of Crop Sciences of Chinese Academy of Agricultural Sciences)
	▸Application of Biotechnology in Developing New Rice Varieties For High Temperature Tolerance in the Philippines – Dr. Norvie Manigbas (PhilRice, Philippines)
	▸Introduction of rice in rice production and the change of major diseases in rice during the period of climate change in Vietnam – Dr. Lai Tien Dung (Plant Protection Institute Research, Vietnam)
10:40~11:00	Coffee Break
《 Plenary Session 》	
	▸ Chair: Prof. Yong-Won Seo (Korea University)
11:00~11:40	▸RNA-guided genome editing in stem cells, animals, and plant – Dr. Jin Soo Kim, Seoul National University, Korea
11:40~12:20	▸CRISPR Genome Editing in Outcrossing Woody Perennials – Dr. CJ Tsai, UGA, USA
12:20~13:00	Awards Ceremony & Closing Remark

농업생명공학기술 연구개발에 대한 소신 있는 정책 추진과 국가차원의 적극적인 투자를 촉구한다

우리 농업은 녹색혁명을 통해 대한민국의 굶주림을 해결하는 등 우리나라 국민들의 식량과 건강을 지키는데 크게 기여한바 있다. 이러한 농업의 발전은 새로운 기술의 도입을 통해 이루어지고 있으며, 현재도 지속적인 새로운 농업기술 개발을 위한 노력이 진행되고 있으며 미래에도 지속되어야 할 것이다.

첨단 육종기술의 산물인 GM작물은 상용화 된지 이미 20여년이 지난 지금까지 아무 문제없이 재배되고 이용되고 있다. 다국적 기업이 개발과 상업화를 주도하는 GM종자의 시장점유율도 지속적으로 증가하여 2015년 현재 세계 종자시장의 35% 이상을 차지하고 있으며, 중국, 일본 등 우리의 경쟁국들도 GM종자 개발에 국가 차원의 대규모 투자를 시행하고 있다.

반면, 우리의 경우 과학적 근거가 없는 극단적이고 비상식적인 정보 전달로 GM농산물이 위험하다는 인식이 확산되고 있다. 더욱이, 당장의 상용화가 아닌 미래 대비 기술경쟁력 확보를 위한 GM종자 개발 연구까지 반대하는 안타까운 현상이 벌어지고 있다.

민간기업의 R&D 기반이 부족한 우리의 경우 국가 차원의 투자를 통해 우리 농업을 위한 다양한 기술 개발에 노력하고 있다. 농업생명공학 연구 개발도 이러한 차원에서 미래 기술력 확보를 위해 추진되고 있다. GM 작물의 연구 개발마저 반대하는 집단 행동은 결코 우리 농업의 발전에 도움이 되지 않을 것이다.

일부 여론에 밀려 국내 기업들이 참여를 기피하고, 국가차원의 GM종자 연구개발 마저 잘못된 여론에 밀려 중단된다면, 미래 농업기술 경쟁력 확보가 어려운 것은 물론이고 더 나아가 기술종속국으로 전락할 위험에 빠지게 될 것이라는 것이 과학계의 공통된 시각이다.

이에 우리나라 육종의 발전을 위해 설립된 한국육종학회는 현 상황이 국가농업 기술의 경쟁력 확보를 위협하는 매우 위중한 상황임을 인식하고, 정책 지도자들의 소신 있는 입장표명을 요청하며 다음과 같이 건의하는 바이다.

1. 국가기술력 확보차원의 GM작물 개발연구를 적극 보장하고 보다 과감한 연구 개발 투자를 촉구 한다

20년 전에 상용화가 시작된 GM종자는 이미 글로벌 종자시장의 35% 이상을 차지하며 종자시장의 핵심으로 자리 잡았다. 투자와 기술력을 통해 선진국의 다국적 기업이 독점하던 GM종자 시장은 이제 국가 간 첨단기술 경쟁 각축장으로 변화되고 있다.

중국은 정부 책임자가 GM종자 개발 필요성을 강조한데 이어, 다국적 종자기업인 신젠타를 인수함으로써 일약 GM종자 기술 강국으로 도약하였다. 일본도 푸른 GM장미에 이어 세계 최초로 동물치료용 GM딸기를 개발 상용화함으로서 기술력을 입증하였다.

반면, 우리의 경우 일부의 극단적 반대로 고부가 GM종자 개발 기술력 확보를 위한 노력이 위축되는 심각한 상황이 발생되고 있다. 더욱이 연구개발 경쟁에 매진하고 있는 우리 연구원들을 다국적기업의 협조자로 매도하는 어이없는 상황도 벌어지고 있다.

정부는 이러한 문제의 심각성을 인식하여 오해와 불신에 대한 적극적인 설명을 통해 정확한 사실을 알리는데 노력할 것을 촉구한다. 또한, 우리 농업의 어려움 해결에 활용될 고부가 GM종자 개발에 대한 정책적 지지와 보다 과감한 투자를 촉구한다.

2. 정부와 국회는 농업생명공학기술 개발과 활용에 대한 소신 있는 입장표명을 통해 국민들과 여론을 올바르게 선도해야 한다

현재 상용화된 GM농산물은 엄격한 평가기준에 따라 안전성이 검정된 것으로, 전 세계적으로 재배되거나 사료 또는 식품용으로 사용되고 있다. 이처럼 안전성 확인에도 불구하고 소모적 논란이 지속되는 것은 과학기술 발전에 심각한 저해요인이 되고 있다.

우리는 광우병 파동을 통해 비과학적이고 잘못된 정보가 얼마나 큰 사회적 갈등과 국력낭비를 가져왔는지 경험한 바 있다. 이제 더 이상 잘못된 정보와 막연한 우려로 국가 미래 성장 동력에 필요한 기술력 확보에 실패하는 과오를 범하지 말아야 할 것이다.

이에, 정부와 국회는 명확한 입장표명과 적극적 소통을 통해 올바른 여론 조성에 노력할 것을 촉구한다. 또한, 소비자가 공감할 고부가 GM작물의 합리적 실용화 방안을 마련하여 생명공학기술이 우리 농업 발전에 적극 활용되도록 노력할 것을 촉구한다.

3. 우리의 주곡인 쌀의 기술주권 보호를 위한 첨단기술 활용을 촉구 한다

쌀은 우리나라의 주곡인 만큼 세계 최고의 기술력을 확보해야 한다. 쌀은 세계적으로도 중요한 식량작물로서 많은 국가가 GM벼 개발을 적극 추진하고 있다. 중국은 2009년에 이미 해충저항성 GM벼를 개발하여 안전성심사를 통과시킨바 있다. 일본은 2007년에 삼나무 꽃가루 알레르기 예방백신을 생산하는 GM벼를 개발하고 현재 상용화에 필요한 임상실험을 진행하고 있다.

최근 GM벼 연구를 중단하라는 안타까운 주장이 나오고 있다. 경쟁국들과의 경쟁에서 스스로 우리의 손발을 묶는다면, 우리 주곡의 기술종속이라는 끔직한 결과를 초래할 수 있다. 이러한 문제의 심각성을 인식하여 잘못된 오해를 바로잡고 지속적인 연구개발 지원으로 미래를 대비한 우리 주곡의 기술경쟁력 확보에 적극 노력해야 한다.

4. 생명공학기술에 대한 과감한 투자로 농과계열 및 자연계열 분야의 연구 활성화를 유도하고, 첨단 육종기술 개발을 견인할 국가 인재양성에 적극 노력해야 한다.

현재 합성생물학 등 현재의 기술을 뛰어넘는 새로운 기술이 개발되고 상용화가 이루어지고 있다. 지금 같이 생명공학에 대한 이해 부족에 따른 부정적인 여론으로 연구개발 투자를 주저할 경우, 이 분야의 기술경쟁력을 상실하고 결국에는 기술종속국으로 전락하게 될 가능성이 크다.

정부는 생명산업의 소재인 농생물체를 다루는 농업이 우리나라 바이오산업을 이끌 핵심 산업임을 인지하고, 농업생명공학에 대한 과감한 투자로 농과계열 및 자연계열 대학의 연구기반 구축과 미래 국가성장동력 창출을 주도할 작물육종 및 생명공학 연구 인력 양성에 적극 노력하여야 한다.

2016년 6월

한국육종학회

Contents

연사 발표

SYMP-01 Doubled Haploid (DH) Technology in Maize Breeding: Application and Technology for Production of DH Lines ····· 3
Vijaya Vardhana Reddy. Chaikam

SYMP-02 Finding Mineral Element Transporters for Better and Safe Production of Rice ····· 4
Jian Feng Ma

SYMP-03 Function of Fibrillin Protein in Photosynthetic Metabolism ····· 5
Hyun Uk Kim

SYMP-04 Revisiting Domestication to Revitalize Crop Improvement: The Florigen Revolution ····· 6
Zach Lippman

SYMP-05 Manipulating Fruit and Vegetable Quality Traits ····· 7
David A. Brummell

SYMP-06 Designing Crops for Global Food Security: Digitizing Plant Phenotypes ····· 8
Maurice Moloney

SYMP-07 CRISPR RNA-guided Genome Editing in Human Stem Cells, Animals, and Plants ····· 9
Jin-Soo Kim

SYMP-08 CRISPR Genome Editing in Outcrossing Woody Perennials ····· 10
Chung-Jui Tsai

구두 발표

수량 및 저항성육종(Breeding for yield increase and resistant variety)

OA-01 **Genetic Analysis of Shoot Fresh Weight in Soybean Using an Interspecific Cross of PI483463 and Hutcheson** ····· 13

Krishnanand P. Kulkarni, Sovetgul Asekovaa, Minsu Kim, Cheol-Woo Park, Jae-Eun Jeong, Jong Tae Song, Jeong-Dong Lee

OA-02 **Identification of Candidate Genes Conferring to Resistance to Foxglove Aphid in Soybean** ····· 14

Sumin Park, Eunsil Kim, Mijung Cho, Kyung Hye Kim, Jin Kyo Jung, Jeong-Dong Lee, Ju Seok Lee, Sungtaeg Kang

OA-03 **침수처리에 따른 콩 생육특성 및 저항성 자원 선발** ····· 15

조미정, 박수민, 김은실, 김경혜, 문준경, 이주석, 강성택

OA-04 **한국 밀 품종 육성현황 및 발전방향** ····· 16

강천식, 정영근, 김경훈, 손재한, 김학신, 박종철, 오영진, 김경호, 이광원, 김보경, 박철수

OA-05 **벼흰잎마름병 저항성 유전자가 집적된 자포니카 벼 계통 개발** ····· 17

박현수, 김기영, 김우재, 정지웅, 이종희, 노태환, 남정권, 백만기, 신운철, 김정주, 정종민, 조영찬, 김보경, 안상낙

OA-06 **Disruption-Mediated Functional Characterization of Rice Defense-Related Genes Selected Through Genome-Wide Association Study for Core Population** ····· 18

Feng Peng Li, Won-Hee Ra, Kyu-Won Kim, Yoo-Hyun Cho, Shin-Chul Bae, Duk-Ju Hwang, Sang-Ryeol Park, Yong-Jin Park, Il-Pyung Ahn

OA-07 **Development of Cultivar-specific DNA Markers Based on Ty1-*copia*-like Retrotransposon-based Insertional Polymorphism in Pear (*Pyrus pyrifolia*)** ····· 19

Hoy-Taek Kim, Jong-In Park, Ill-Sup Nou

OA-08 **Breeding for Pyramiding Target-genes and Selection of F_1 Hybrids by Marker Assisted Selection in Tomato** ····· 20

김명권

OA-09 **Characterization and Stress-responsive Expression Profiling of *MCM* genes in *Brassica*** ····· 21

Ashokraj Shanmugam, Hoy-Taek Kim, Jong-In Park, Ill-Sup Nou

OA-10 **Classical and GBS-based QTL mapping downy mildew resistance loci in cucumber** ····· 22
Khin Thanda Win, Chunying Zhang, Sanghyeob Lee

OA-11 **Genome Wide Characterization and Expression Profiling of Aquaporin Gene Family in *Brassica rapa* for Responsiveness to Abiotic and Biotic Stresses** ····· 23
Md. Abdul Kayum, Hoy-Taek Kim, Jong-In Park, Ill-Sup Nou

품질 육종 및 유전변이(Breeding for quality improvement, Genetic variation)

OB-01 **Role of Flowering Pathway Genes on Anthocyanin Biosynthesis and Accumulation in *Brassica rapa*** ····· 24
Ujjal Kumar Nath, Md. Abdul Kayum, Rawnak Laila, Khadiza Khatun, Jong-In Park, Ill-Sup Nou

OB-02 **Leaf Developmental and Genotypic Variations in Wax Content, Composition and Expression of Wax Biosynthetic Genes in The Inbred Lines of Brassica Oleracea Var. Capitata** ····· 25
Rawnak Laila, Kiwoung Yang, Arif Hasan Khan Robin, Mi Chung Suh, Juyoung Kim, Jong-In Park and Ill-Sup Nou

OB-03 **EMS 돌연변이체 PE1905의 사포닌 특성 및 유전 연구** ····· 26
박철우, 송종태, 정규화, 이정동

OB-04 **Comparative Phylogenomics to Elucidate The Effects of Whole Genome Triplication Event on *glutathione transferases* Superfamily Genes in *Brassicaceae*** ····· 27
Harshavardhanan Vijayakumar, Senthil Kumar Thamilarasan, Jong-In Park, Ill-Sup Nou

OB-05 **Molecular Breeding for Fruit Color in Tomato** ····· 28
Indeok Hwang, Hee-Jeong Jung, Song-I Kang, Ill-Sup Nou

OB-06 **곡실발효사료 조제를 위한 사료맥종별 수확시기 및 발효품질** ····· 29
박종호, 오영진, 정영근, 송태화, 박태일, 이광원, 김경호, 김양길, 박종철

OB-07 ***In vitro* and *in vivo* Antioxidant Activity and α -glucosidase Inhibitory Potential of Major Phenolic Compound Isolated from Superhongmi (*Oryza sativa* L.) Varieties** ····· 30
Soo-In Jang, Hanna Kang, Suyeon Jang, Jung-Yun Lee, Tae-Ho Ham, Sung-Gil Hong, Su-Noh Ryu, Young-In Kwon

OB-08 **식미 간접적 평가를 위한 기기활용 및 신속한 관능평가를 위한 해석** ····· 31
전재범, 이점식, 윤미라, 이정희, 천아름, 김우재, 정지웅, 강경호, 김보경

OB-09 **Inter-subspecific Indel Variations in Wild Rice Suggesting The Early Appearance of *japonica-specific* Alleles of The *Oryza* genus** ····· 32
Joong Hyoun Chin, Jonghwa Park, Dongryung Lee, Jong Seok Heo, Hee-Jong Koh

OB-10 **Diachronic Analysis of Genetic Diversity in Rice Landraces Under On-Farm Conservation in Yunnan, China** ····· 33
Di Cui, Jinmei Li, Cuifeng Tang, Jeonghwan Seo, Zhuo Jin, Yoye Yu, Hee-Jong Koh, Longzhi Han

OB-11 **가공용 쌀 품종개발을 위한 배유변이 육종소재 개발 및 유전분석** ····· 34
정지웅, 전재범, 조성우, 김우재, 강경호, 고재권, 김현순, 김보경

분자육종 및 유전공학(Molecular breeding and biotechnology)

OC-01 **Plant Gene Targeting with Site-Specific Nucleases and Homologous Recombination** ····· 35
Yong-Ik Kwon, Woo-Nam Kim, Min-ji Hong, Hong-Kyu Kang, Hyo-Yeon Lee, Kiyomi Abe, Seiichi Toki

OC-02 **Engineering Rice to Reduce As Accumulation in Grain** ····· 36
Won-Yong Song, Youngsook Lee

OC-03 **Development of Co-Dominant *Female* (*F*) Locus Diagnosis Marker in Cucumber (*Cucumis sativus* L.)** ····· 37
Chunying Zhang, Khin Thanda Win, Sanghyeob Lee

OC-04 **Drought-Tolerant Qtls from Samgang Lead to Tiller Formation at The Vegetative Stage in Rice** ····· 38
Dongjin Shin, Tae-Heon Kim, Sang-Ik Han, Jun-HyunCho, You-Chun Song, Yeong-Up Kwon

OC-05 **Genetic Analysis of Seedling Traits Regulated by Light in Weedy Rice** ····· 39
Hyun-Sook Lee, Yun-Joo Kang, Ju-Won Kang, Sang-Nag Ahn

OC-06 **QTL Mapping of Cold Tolerance at The Seedling Stage in Rice and Development of Advanced Backcross Lines Using Marker-Assisted Selection** ····· 40
Suk-Man Kim, Kyung-Ho Kang, Bo-Kyung Kim, Jong-Min Jeong, Russell Reinke, Kshirod Jena

OC-07 **Development of Tolerant Rice Plants to High-Temperature Stress: A Way Forward to Address Unease** ····· 41
Rupesh Tayade, Tien Dung Nguyen, Sung Aeong Oh, Ki Hong Jung, Soon Ki Park

OC-08 유전체육종 기반구축을 위한 콩 핵심집단 및 돌연변이 집단 양성 현황 ····· 42
박수권, 문중경, 황사달, 김둘이, 옥현충, 이춘석, 김선림, 홍하철

OC-09 Pedigree Reconstruction of Korean Soybean [Glycine max L. Merrill] Cultivars ····· 43
Chaeyoung Lee, Jin-Hyun Kim, Joo-Seok Park, Yoram Choi, Hong-Kyu Choi

OC-10 Completion of The Mitochondrial Genome Sequence of Onion (*Allium cepa* L.) Containing The CMS-S Male-Sterile Cytoplasm and Identification of an Independent Event of the $ccmF_N$ Gene Split ····· 44
Bongju Kim, Kyunghee Kim, Tae-Jin Yang, Sunggil Kim

OC-11 Efficient QTL Mapping Strategy for Agronomical Traits in Pepper (*Capsicum annuum*) ····· 45
Koeun Han, Hee-Jin Jeong, Hee-Bum Yang, Sung-Min Kang, Seungill Kim, Doil Choi, Byoung-Cheorl Kang

OC-12 Bioinformatics Analysis for Transcription Factor Associated SSR Markers Developments and Characterization in Lilium Species ····· 46
Manosh Kumar Biswas, Jewel Howlader, Namhee Jeong, Ujjal Kumar Nath, Md Abdul Kayum, Jong-In Park, Ill-supNou

포스터 발표

수량 및 저항성육종(Breeding for yield increase and resistant variety)

PA-01 서산간척지에서 내염성 콩 계통의 생육 ····· 49
이정동, 김정화, 김민수, 박철우, 정재은, 아세코바소베툴, 한두호, 송종태

PA-02 Development of an Efficient *in vitro* Screening Methods for Lily Cultivars Resistant to *Botrytis elliptica* ····· 50
Ji-Young Jang, Jae-Heung Jeon, Geung-Joo Lee, Hyun-Soon Kim

PA-03 *Xoo* Bacteria-Mediated Rice Leaf Blight is Prevented by Human Drug Niclosamide ····· 51
Sung-Il Kim, Hak Soo Seo

PA-04 **Breeding of High Yield Leaf Lettuce 'Chunhacu' from Spring to Fall Season** ····· 52
Suk-Woo Jang, Su-Hyoung Park, Won-Byoung Chae, Jong-Nam Lee, Myeong-Hoon Seo, Min-Jeong Lee, Min-Sik Yin, Un-Ji Kim, Hee Dae Kim, Sun-Bo Ko

PA-05 **EPG를 이용한 벼멸구 저항성 계통과 감수성 품종의 흡즙 파형 차이 분석** ····· 53
김우재, 박현수, 하기용, 김현순, 조영찬, 정지웅, 전재범, 조성우, 김보경

PA-06 **분자표지를 이용한 친환경재배 적응 복합내병충성 벼 '중모1045호' 육성** ····· 53
김우재, 박현수, 신운철, 김현순, 고재권, 조영찬, 정지웅, 전재범, 조성우, 김보경

PA-07 **내한성, 내병성이 강한 식용 및 바이오디젤용 유채 1대잡종 '진애'** ····· 54
김광수, 고산, 이영화, 장영석, 최규환, 신정호, 이경보

PA-08 **고품질 조사료 최대생산을 위한 3모작 재배의 생산성 및 사료가치** ····· 55
김영진, 이상학, 정종성, 황태영, 김원호

PA-09 **국내품종과 수입품종 이탈리안 라이그라스 품종들의 생육특성과 수량성 비교** ····· 55
지희정, 김기용, 황태영, 이기원, 최기준, 이상훈

PA-10 **중생 고품질 내도복 오갈병 저항성 벼 '영보' 육성** ····· 56
박노봉, 남민희, 김상열, 여운상, 이지윤, 권오덕, 박동수, 이종희, 조준현, 송유천, 한상익, 손영보, 장재기, 권영업

PA-11 **가공용 초다수성 복합내병성 벼 신품종 "한아름3호"** ····· 57
이지윤, 조준현, 이종희, 손영보, 박노봉, 오성환, 한상익, 송유천, 박동수, 여운상, 박병명, 오인여, 남민희, 권영업, 이영희

PA-12 **온대자포니카 지역 적응 벼 우량계통 '밀양321, 322호' 육성** ····· 58
송유천, 조준현, 이지윤, 손영보, 이종희, 오성환, 박동수, 조영찬, 권영업

PA-13 **Ginseng *cis*-prenyltransferase Interacts with a Nogo-B Receptor Homolog for Dolichol Biosynthesis** ····· 59
Ngoc Quy Nguyen, Ok Ran Lee

PA-14 **Development of Molecular Marker for Screening Salt Tolerant and Sensitive Soybeans** ····· 60
Seokhyung Lee, Gyu Tae Park, Jagadeesh Sundaramoorthy, Jeong-Dong Lee, Hak Soo Seo, Jong Tae Song

PA-15 **곡우 호밀의 경엽 예취가 출수기 지연에 미치는 효과** ····· 61
오명곤, 구자환, 한옥규, 안종웅, 권순종

PA-16 중산간지 지역에 따른 미세온도변화와 벼 생육양상의 차이 II ····· 61
양창인, 김명기, 백남현, 강위금, 신운철, 김정주, 조현숙

PA-17 벼흰잎마름병 저항성 유전자 *Xa1, Xa2, Xa3, Xa4* 상호간 두 개의 유전자 집적 효과 ····· 62
박현수, 신운철, 정종민, 김우재, 김정주, 백만기, 남정권, 박슬기, 조영찬, 김보경

PA-18 극조생종 내도복 및 도열병 저항성 수수형 벼 신품종 '조품' ····· 63
김명기, 원용재, 서정필, 안억근, 정국현, 양창인, 백남현, 윤광섭, 전용희, 이점호, 윤영환, 이상복, 정종민, 정응기

PA-19 A New Large Grain and High Yielding Peanut Variety "Ahwon" ····· 64
Suk-Bok Pae, Myung-Hee Lee, Sung-Up Kim, Eun-Young Oh, Chan-Sik Jung, Deok-Young Song, In-Seok Oh, Young-Hee Lee

PA-20 Genetic Analysis of Economically Important Characters in Okra (Abelmoschus esculentus (L.) Moench) Under Peninsular Conditions of Southern India ····· 65
Kishor D S, Arya K, Yogeesh K J, Vinod Kumar, Yashoda , Hee-Jong Koh

PA-21 복합내병성 고품질 신품종 '청품'의 농업적 특성 ····· 66
원용재, 이정희, 양창인, 김명기, 장재기, 조영찬, 이상복, 이점호, 최임수, 안억근, 서정필, 정국현, 전용희, 현웅조, 정응기, 하운구, 김정주, 오세관, 최용환, 강경호, 성낙식, 김보경

PA-22 집단제정법 및 제웅 교배방법에 따른 기장 교배 효율 ····· 66
고지연, 송석보, 최명은, 곽도연, 고종철, 김기영, 최지명, 오인석

PA-23 조사료 수량이 높고 사일리지 품질이 우수한 청보리 신품종 '다청' ····· 67
오영진, 박태일, 박종호, 김양길, 박형호, 박종철, 강천식, 한옥규, 강현중, 윤건식, 홍기흥, 배정숙, 송재기, 김경호, 정영근, 이광원, 김보경

PA-24 밀 고온 및 단기등숙 유전자원 생육특성 조사 ····· 68
김경민, 김경훈, 박형호, 이상학, 이나리, 현종내, 권영업

PA-25 재래종과 육성 콩 품종의 연차별 형질 변이 분석 ····· 69
서민정, 김길현, 정건호, 박명렬, 박장환, 김병주

PA-26 저 질소 환경에 적합한 옥수수 교잡종 선발 ····· 70
류시환, 서영호, 박종열, 최재근, 박기진, 용우식, 이정훈, 이장용, 김경희

PA-27 **Variation of Soybean Sprout Characteristics in Two Breeding Populations** ····· 71
Mirwais Ghani, Akbota Makulbekova, Sovetgul Asekova, Minsu Kim, Chul-Woo Park, Jae-Eun Jeong, Dong-Ho Lee, Jong Tae Song, Jeong-Dong Lee

PA-28 **친환경 안전 조사료 생산이 가능한 다수성 사료용 벼 품종 '영우'** ····· 72
안억근, 이상복, 원용재, 이점호, 장재기, 정응기, 최임수, 정국현, 김명기, 이정희, 조영찬, 최용환, 양창인, 하운구, 정종민, 서정필, 김정주, 정오영, 전용희, 홍하철, 이규성, 김보경, 김병주

PA-29 **A New Boxthorn(*Lycium chinense* Miller) Variety with Tetradiploid and Self-compatibility 'Whasu'** ····· 73
Jung-Il Ju, Tug-Sang Yun, Bo-Hee Lee, Young-Chun Park, Su-Dong Kim, Min-Sik In, Hyun-Ho Kim

PA-30 **자포니카벼 팔공 유래 도열병 내구저항성 QTL탐색** ····· 74
백만기, 박현수, 신운철, 정종민, 남정권, 권순욱, 김보경, 조영찬

PA-31 **바이오에너지 작물 억새의 우량 억새 육종을 위한 바이오매스 수량 결정 핵심 형질 탐색** ····· 75
임수현, 육민정, 김도순

PA-32 **내재해성 및 튀김율이 높은 팝콘용 옥수수 신품종 '지팝콘'** ····· 75
최재근, 박종열, 장은하, 류시환, 서영호, 박기진, 용우식, 이정훈, 김경희

PA-33 **조숙 내도복 다수성 조사료용 겉귀리 '다조'** ····· 76
김양길, 박형호, 오영진, 박종호, 강천식, 박종철, 김경호, 최규환, 홍기흥, 박태일, 정영근, 김보경, 이광원

PA-34 **구기자나무의 비가림하우스 재배시 용도별 적합 품종선발** ····· 77
주정일, 윤덕상, 박영춘, 이보희, 인민식, 김현호

PA-35 **중부지역 적응 복합내병성 벼 신품종 '삼광1호'의 농업적 특성** ····· 78
이정희, 원용재, 조영찬, 최임수, 이점호, 양창인, 김명기, 안억근, 서정필, 이상복, 전용희, 성열규, 정응기, 하운구, 장재기, 정국현, 윤미라, 강경호, 박향미, 황기호, 노재환, 김보경

PA-36 **국내 자포니카 유전자원 이용 GWAS 분석에 의한 도열병 저항성 유전자 탐색** ····· 79
조영찬, 백만기, 권순욱, 박현수, 정종민, 남정권, 김보경

PA-37 **Protein Dynamics of Rice Seedling Leaves in Response to High Temperature Stress** ····· 80
Sang-Woo Kim, Swapan Kumar Roy, Soo-Jeong Kwon, Hyeong-Jun Park, Je-Hyeok Yu, Ki-Hyun Kim, Yong-Gu Cho, Chul-Won Lee, Sun-Hee Woo

PA-38 **Complementary Screening Method for Phytophthora Blight Resistance and Varietal Difference in Sesame(*Sesamum indicum* L.)** ····· 81
Eun-Young Oh, Sung-Up Kim, Young-Nam Yoon, Myung-Hee Lee, Suk-Bok Bae, Myung-Sik Kim, Un-Sang Yeo, Chan-Sik Jung, In-Seok Oh

PA-39 **베타글루칸 함량이 높고 흰가루병 저항성인 찰성 쌀보리 '베타원'** ····· 82
박종철, 이미자, 김양길, 강천식, 박종호, 오영진, 박태일, 김경호, 이광원, 정영근

PA-40 **항산화 성분과 품질이 우수한 흑색 종실 맥주용 보리 신품종 '흑호'** ····· 83
박종철, 김양길, 강천식, 박종호, 오영진, 박태일, 김경호, 이광원, 정영근

PA-41 **도복에 강한 소립 나물용 콩 '소연'** ····· 84
강범규, 김현태, 최만수, 고종민, 서민정, 신상욱, 서정현, 구성철, 윤홍태, 백인열, 오인석

PA-42 **탈립 개선 생육기간 100일 단기성 콩 '중모3013'** ····· 85
강범규, 김현태, 고종민, 최만수, 이병원, 신상욱, 서정현, 오은영, 백인열, 윤홍태, 오인석

PA-43 **토마토 풋마름병 저항성 검정방법 개선** ····· 86
안영은, 김상규, 고호철, Binod P. Luitel, 성정숙, 이주희, 윤문섭, 백형진, 류경열, 이준대, 허온숙

PA-44 **잎이 얇고 작은 구를 형성하는 배추 계통 '원교20042호' 육성** ····· 87
박수형, 장하영, 장석우, 채원병, 박민영

PA-45 **멜론 흰가루병 race동정 및 국·내외 시판품종의 저항성검정** ····· 88
홍예지, 김회택, 박종인, 노일섭

PA-46 **식용 고구마 신품종 '호감미'** ····· 89
이형운, 이준설, 정미남, 양정욱, 남상식, 한선경, 김재명, 안승현, 송연상, 황엄지, 이경보

PA-47 **Regional Variation of BaYMV Based on Nucleotide Sequences** ····· 90
Sang-Min Kim, Bong Choon Lee, Ji-Eun Ra

PA-48 **중북부 고랭지 적응 내병성 조생 벼 진부62호** ····· 90
현웅조, 정종민, 이상복, 이정희, 원용재, 안억근, 성열규, 김병주

PA-49 **Enhancement of Rice Resistance to Bacterial Blight by Overexpressing BrCP3 Gene of *Brassica rapa*** ····· 91
Marjohn Nino, Hye-Jung Lee, Jae-Young Song, Seon-Kyeong Song, Kwon-Kyoo Kang, Illsup Nou, Yong-Gu Cho

PA-50 **Comparative Transcription Profiles of Compatible and Incompatible Interactions of Rice with *Xanthomonas oryzae* pv. *oryzae*** ····· 92
Marjohn Nino, Joonki Kim, Franz M. Nogoy, Jae-Young Song, Shadi Rahimi, Kwon-Kyoo Kang, Ho-Jin Ryu, Yong-Gu Cho

PA-51 **수경재배(분무경)에서 특이적으로 발견되는 검은뿌리병의 원인균 규명** ····· 93
윤수영, 김보슬, 옥선

PA-52 **토마토 풋마름병 저항성 검정방법 개선** ····· 94
안영은, 김상규, 고호철, Binod P. Luitel, 성정숙, 이주희, 윤문섭, 백형진, 류경열, 이준대, 허온숙

품질 육종 및 유전변이(Breeding for quality improvement, Genetic variation)

PB-01 ***Glu-B1al* 대립유전자를 지닌 국내 재래종 밀 특성** ····· 95
윤영미, 김지은, 강천식, 이종열, 박철수

PB-02 **국내 밀 품종의 글리아딘 및 *Spa* 유전자 평가** ····· 96
김지은, 윤영미, 강천식, 이종열, 박철수

PB-03 **고경도 분자표지 개발 위한 고정계통을 이용한 딸기 F_2 집단 구축 및 경도 측정법 비교** ····· 97
김진희, 이선이, 안율균, 이은수, 김정호

PB-04 **화색이 선명한 황색 대륜화 절화용 거베라 '레모나이트' 육성** ····· 98
정용모, 황주천, 진영돈, 이병정, 이상대, 권오창

PB-05 **Genetic Analysis of Canadian Maize (*Zea mays* L.) Inbred Lines Using SSR Markers Under Cold Stress** ····· 99
Muhammad Qudrat Ullah Farooqi, Rahul Vasudeo Ramekar, Shi Jun Ma, Kyu Jin Sa, Ju Kyong Lee

PB-06 **Cold Stress Evaluation Among Maize (*Zea Mays* L.) Inbred Lines in Different Temperature Conditions** ····· 100
Muhammad Qudrat Ullah Farooqi, Ju Kyong Lee

PB-07 **Genetic Diversity and Association Analysis for Agronomic Traits in RDA-Genebank Maize Lines** ····· 101
O Gyeom Kim, Kyu Jin Sa, Ju Kyong Lee

PB-08 **교배를 통해 발생 된 미숙 종자로부터 감귤 3배체의 탐색** ····· 102
박석만, 박재호, 윤수현

PB-09 유용 유전자 도입을 위한 벼 캘러스의 고효율 형질전환 시스템 구축 ····· 103
박지선, 문기범, 하장호, 장지영, 김미진, 박상언. 전재흥, 김현순

PB-10 베이지색계 투톤 화색의 스프레이형 카네이션, 'Marble Magic ' 신품종 ····· 104
김미선, 유봉식, 정재아, 박종택, 신학기, 김도국

PB-11 A New Hardy Kiwi Cultivar, 'SH-1' with Large Fruit and High Yield ····· 105
Youngki Park, Jae-Hee Kim, Sea-Hyun Kim

PB-12 밝은 분홍색 홑꽃 절화용 스프레이국화 '허니핑크' 육성 ····· 106
황주천 진영돈, 정용모, 안동춘, 이병정, 이상대, 정병룡

PB-13 양성자빔 처리량에 따른 고추 종자의 발아율과 생존율 분석 ····· 107
이예린, 정규미, 김해인, 이준대

PB-14 소득작물 후작지 적응 단기성 벼 '단평' 육성 ····· 107
손영보, 조준현, 이지윤, 이종희, 오성환, 박동수, 송유천, 권영업

PB-15 Adaptation of Autumn-Sown Faba Bean Lines in South Korea ····· 108
Soon-Jae Kwon, Jai Hyunk Ryu, Sang Wook Jeong, Min Kyu Lee, Jin-Baek Kim, Si-Yong Kang

PB-16 중북부평야지 조생종 등숙기간 고온 경과시 쌀 품질 변화 ····· 108
조윤상 정정수, 이지우, 함진관, 김상수

PB-17 The Selection of Sweet Sorghum (*Sorghum bicolor* L. Moench) Germplasms Suitable for the Korea ····· 109
Jaihyunk Ryu, Soon-Jae Kwon, Sang-Wook Jeong, Min Kyu Lee, Hong-Il Choi, Jin-Baek Kim, Si-Yong Kang

PB-18 고추의 나출 소포자 배양 시 배양 방법 및 하층 고체배지의 charcoal 농도가 소포자배 발생에 미치는 영향 ····· 110
박은준, 양은영, 이인성, 채수영, 노미영, 김옥례, 박태성, 문지혜, 조명철

PB-19 Effects of Gamma-ray Irradiation on Radio Sensitivity in Lentil bean (*Lens culinari* L.). ····· 111
Min-kyu Lee, Jaihyunk Ryu, Sang Wook Jeong, Jin-Back Kim, Si-Yong Kang, Soon-Jae Kwon

PB-20 소나무 종자생산능력에 따른 개량효과 추정을 통한 최적 선발강도 ····· 112
김진중, 나성준, 심동환, 우관수, 한상억

PB-21 **Determination of Sulfur-containing Amino Acid Contents in a Core Collection of Wild Soybean (*Glycine soja*)** ····· 113

Woon Ji Kim, Juhyun Im, Yu Ri Kim, Soo-Kwon Park, Sungtaeg Kang, Soon-Chun Jeong, Jung-Kyung Moon, Bo-Keun Ha

PB-22 **Agronomic Trait Evaluation on European Common Wheat Germplasms** ····· 114

Jin Seok Yoon, Yong Weon Seo

PB-23 **한국 콩 품종의 isoflavone 함량의 변이와 다변량 분석에 의한 품종군 분류** ····· 115

김현명, 왕정은, 박병덕, 윤건식, 한정아 김홍식

PB-24 **Biological Responses of Soybean (*Glycine max* L.) Exposed to Proton-beam** ····· 115

Juhyun Im, Woon Ji Kim, Sin Ji Kim, Eun Ji Jeong, Yuri Kim, Bo-Keun Ha

PB-25 **Molecular Mapping of Quantitative Trait Loci for Forage Quality Traits in a Cross Between PI483463 and Hutcheson in Soybean** ····· 116

Sovetgul Asekova, Krishnanand P. Kulkarni, Minsu Kim, Jeong-Hwa Kim, Jong Tae Song, Jeong-Dong Lee

PB-26 **Selection and Characterization of Gamma Ray-induced Soybean Mutant Lines Based on Seed Coat Color** ····· 117

Young Eun Jang, Jung Eun Hwang, In Jung Jung, Soon-Jae Kwon, Joon-Woo Ahn, Jin-Baek Kim, Si-Yong Kang, Hong-Il Choi

PB-27 **Selection of Soybean Germplasm for Breeding Program Applications in Central Asia** ····· 118

Akbota Makulbekova, Sovetgul Asekova, Minsu Kim, Cheol-Woo Park, Jae-Eun Jeong, Dong-Ho Lee, Mirwais Ghani, Jong Tae Song, Jeong-Dong Lee

PB-28 **고 Oleic Acid 콩 청국장의 특성** ····· 119

이동호, 김병오, 이정동

PB-29 **Genome-wide Detection of Variations Among Three Sprouting Soybean Varieties by Resequencing** ····· 120

Hong-Il Choi, Young Eun Jang, Jung Eun Hwang, Injung Jung, Sung Min Han, Yeong Deuk Jo, Sang Hoon Kim, Soon-Jae Kwon, Joon-Woo Ahn, Jin-Baek Kim, Si-Yong Kang

PB-30 **약배양 이용 조생 거대배아 찰벼 계통 육성** ····· 121

박현수, 신운철, 정종민, 백만기, 남정권, 이건미, 조영찬, 김보경

PB-31 **Genotype by Environment Interaction(GGE) Biplot Analysis of Sesame Under Multi-Environmental Conditions** ····· 122
Kang-Bo Shim, Sung-Gook Kim, Seong-Hyu Shin, Kun-Ho Jung, Chung-Guk Kim, Sung-Gi Heu

PB-32 ***FASCICULATE* Regulates Plant Architecture Including Cluster Flowers and Plant Height in Pepper (*Capsicum annuum*)** ····· 123
Min-Young Kang, Koeun Han, Byoung-Cheorl Kang

PB-33 **Agronomic Traits of Soybean Line with Kunitz Trypsin Inhibitor and Lectin Protein-Free** ····· 124
Jin-A Kim, Sung-Jin Han, Sang-Woo Choi, Dong-Hui Kang, Su-Jin Lee, Jong-Il Chung

PB-34 **Marker-Assited Selection for Soybean Line with Low Content of Raffinose and Stachyose Using *rs2* Gene** ····· 124
Su-Jin Lee, Sung-Jin Han, Sang-Woo Choi, Dong-Hui Kang, Jin-A Kim, Jong-Il Chung

PB-35 **Identification and Quantification of Flavonoids from the Seed of Rice Mutant (*Oryza sativa* L.)** ····· 125
Backki Kim, Su Jang, Sunmin Woo, Hee-Jong Koh

PB-36 **Genetic Mapping Study of New Sugary Endosperm Mutant, *SUGARY-2* in Rice** ····· 126
Yunjoo Lee, Mi-Ok Woo, Gileung Lee, Eunbyeol Koh, Hee-jong Koh

PB-37 **벼 재조합집단을 이용한 고양식미 집단의 식미관련 특성 분석** ····· 127
정종민, 신운철, 백만기, 박현수, 남정권, 조영찬, 김보경

PB-38 **안토시아닌 고함유 알곡용 옥수수 색소2호 품종 개발** ····· 127
박기진, 박종열, 류시환, 서영호, 최재근, 용우식, 이정훈, 김경희

PB-39 **도입 감 유전자원 '흑시' 2 품종의 주요 생육특성** ····· 128
김은경, 박두상, 김성철, 최성태, 안광환, 김은석

PB-40 **유용 농업형질 탐색을 위한 EMS 처리에 의한 옥수수 돌연변이체 유도** ····· 129
김경화, 박수권, 옥현충, 홍하철, 김선림, 손범영 김둘이

PB-41 **고양식미 저아밀로스 향미 벼 신품종 "골든퀸3호"** ····· 130
이원도, 조유현, 강시용, 박용진, 권순욱

PB-42 **Performance of Mexican Wheat Gemplasms in Korean Environment for Selection Breeding** ····· 131
Jin Seok Yoon, Yong Weon Seo

PB-43 **Grain Color Segregation of a F_3 from Yellow Seed Coat x Deep Purple Seed Coat in Wheat (*Triticum aestivum* L.)** ····· 132
Paulina Calderón Flores, Jong Yeol Lee, Yong Weon Seo

PB-44 **LOX3 유전자 결핍 계통의 저장조건에 따른 이화학적 특성 변화** ····· 133
신운철, 김정주, 박현수, 정종민, 백만기, 남정권, 조영찬, 김보경

PB-45 **쓰러짐에 강하고 앙금 가공적성이 우수한 팥 신품종 '홍진'** ····· 134
송석보, 고지연, 우관식, 정태욱, 최명은, 여운상, 고종철, 김정인, 문중경, 최유미, 곽도연, 오인석

PB-46 **녹색자엽 검정콩자원의 주요형질과 SNP Marker를 이용한 Core Collection 작성** ····· 135
이은자, 최홍집, 배정숙, 김세종, 이정동

PB-47 **흑미와 적미의 기능성 성분이 집적된 유색미 "흑진미"** ····· 136
이종희, 조준현, 서우덕, 이지윤, 손영보, 오성환, 신동진, 송유천, 허연재, 박동수, 권영업

PB-48 **자생 억새의 유전적 다양성 및 유연관계** ····· 137
육민정, 임수현, 박해림, 김도순

PB-49 **흰잎마름병에 강한 조기출하용 조생찰벼 '운백찰'** ····· 138
남정권, 신운철, 김우재, 박현수, 백만기, 정종민, 조영찬, 김정주, 고재권, 김보경

PB-50 **슈퍼홍미의 유전적 특성 연구** ····· 139
함태호, 권순욱, 류수노

PB-51 **국내외 쌀귀리 유전자원의 품질 분석** ····· 140
김경훈, 김경민, 박형호, 이상학, 이나리, 현종내, 권영업

PB-52 **흑색 내도복 다수성 겉보리 신품종 '흑다향'** ····· 141
김양길, 박종철, 김경호, 이미자, 강천식, 오영진, 한옥규, 윤건식, 배정숙, 조수현, 박종호, 정영근, 김보경, 이광원, 박태일

PB-53 **Whole Genome Re-sequencing for Detecting Specific DNA Polymorphisms in *Brachypodium distachyon* Mutant Induced by Gamma Radiation** ····· 142
Man Bo Lee, Yong Weon Seo

PB-54 **벼 저아밀로스 품종 육성에 대한 연구동향 분석** ····· 143
이종희, 정태욱, 조준현, 이지윤, 손영보, 오성환, 신동진, 송유천, 허연재, 박동수

PB-55 더덕의 계통별 생육특성 검정 및 유효성분 분석 ····· 144
엄유리, 이이, 김호방, 허목, 정진태, 김연복, 차선우, 정찬식, 김성철

PB-56 초당옥수수(SweetCorn) 정역교배 후대 계통의 발아특성 ····· 145
최홍집, 오태영, 배정숙, 이은자, 김세종, 소윤섭, 이주경

PB-57 Protein Profiling from Disomic Addition Lines of Wheat Carrying *Leymus racemosus* Chromosomes ····· 146
Won-Ju Lee, Seong-Woo Cho, Hisashi Tsujimoto, Sun-Hee Woo

PB-58 The Antibacterial Effect of NOA in Watermelon Seeds. ····· 147
Dahyun Moon, Wook Kim

PB-59 쌀의 생산년도에 따른 인지질 함량의 변이 ····· 148
홍지화, 안종성, 김용경, 최경후, 이민휘, 이진호, 박영준, 김현태

PB-60 산화훈증제를 이용한 양배추종자 감염 병원균 살균효과 검증 ····· 148
권혁, 박세준, 김욱

PB-61 Composition and Content Analysis of Ginsenosides from Adventitious Roots (AR) and Callus-derived Roots (CR) Proliferated from Korean Wild Ginseng and Comparative Characteristics in Morphology ··· 149
Hong-yu Li, Hyeon-Jin Sun, Hong-Gyu Kang, Hyo-Yeon Lee

PB-62 고추 핵심집단의 원예적 특성평가 및 DB구축 ····· 150
양현천, 김상규, 고호철, Binod P. Luitel, 성정숙, 이주희, 윤문섭, 백형진, 류경열, 이준구, 허온숙

PB-63 '중모1024'의 고온등숙 내성 지배유전자위 표지를 위한 유전연관분석 ····· 151
조성우, 정지웅, 전재범, 김우재, 강경호, 고재권, 김현순, 김보경

PB-64 The Complete Chloroplast Genome of *Pennisetum glaucum* L. Using Illumina Sequencing ····· 152
Sebastin Raveendar, Jung-Ro Lee, Kyung Jun Lee, Myoung-Jae Shin, Yang-Hee Cho, Kyung-Ho Ma, Gi-An Lee,

PB-65 Genetic Diversity and Population Structure of Asian Tomato Accessions Based on SSR Marker ····· 152
Sebastin Raveendar, Gi-An Lee, Kyung Jun Lee, Myoung-Jae Shin, Yang-Hee Cho, Kyung-Ho Ma, Jung-Ro Lee

PB-66 **Flavonol and Glycoalkaoid Contents in Tomato Leaves and Their Antioxidant Activites** ····· 153
Kyung Jun Lee, Gi-An Lee, Jong-Ro Lee, Sebastin Raveendar, Myoung-Jae Shin, Yang-Hee Cho, Kyung-Ho Ma

PB-67 **A Comparative Study on Antioxidant Activities of Leaves Extracts Between Adzuki Bean and Soybean** ····· 154
Kyung Jun Lee, Gi-An Lee, Jong-Ro Lee, Myoung-Jae Shin, Sebastin Raveendar, Yang-Hee Cho, Kyung-Ho Ma

PB-68 **중만생 복합저항성 양식미 신품종 '효원 6호'** ····· 154
임다은, 왕형, 이아림, 장성규, 박소연, 송수향, 권순욱

PB-69 **일경일화 향기나는 한국 춘란 신품종 '아리향'** ····· 155
김동용, 박소연, 김용철, 권순욱

PB-70 **식용 자색고구마 신품종 '단자미'** ····· 156
이형운, 이준설, 정미남, 양정욱, 남상식, 한선경, 김재명, 안승현, 송연상, 황엄지, 이경보

PB-71 **Digital Phenotyping of *crepiastrumdenticulum* Revealed Phenotypic Variation Among Natural Populations** ····· 157
Sungyul Chang, Unseok Lee, HyoungSeok Kim

PB-72 **Improving The Grain Quality of High Tryptophan Rice** ····· 158
Franz Marielle Nogoy, Hye-Jung Lee, Marjohn Nino, Me-Sun Kim, Sothea Ouk, Yu-Jin Jung, Kwon-Kyoo Kang, Illsup Nou, Yong-Gu Cho

PB-73 **Classification of Korean Rice Varieties for Varietal Characteristics Using Morphological Description** ····· 159
Me-Sun Kim, Hye-Jung Lee, Dal-A Yu, Joonki Kim, Marjohn Nino, Franz Nogoy, Sothea Ouk, Eun-Ju Jeong, Jae-Young Song, Kwon-Kyoo Kang, Yong-Gu Cho

PB-74 **Modification of Starch Composition by Regulation of SSS1 Gene Using RNAi and Antisense Technology in Rice** ····· 160
Moo-Geun Jee, Hye-Jung Lee, Dal-A Yu, Me-Sun Kim, Marjohn Niño, Franz Nogoy, Kwon-Kyoo Kang, Illsup Nou, Yong-Gu Cho

PB-75 **Development and Characterization of Endophyte Free Tall Fescue New Variety** ····· 161
Ki-Won Lee, Md. Atikur Rahman, Sang-Hoon Lee, Ki-Yong Kim, Hee Chung Ji, Tae Young Hwang, Gi Jun Choi

PB-76 고추 핵심집단의 원예적 특성평가 및 DB구축 ····· 162
양현천, 김상규, 고호철, Binod P. Luitel, 성정숙, 이주희, 윤문섭, 백형진, 류경열, 이준구, 허온숙

분자육종 및 유전공학(Molecular breeding and biotechnology)

PC-01 Development of Antigen-antibody Fusion Protein Expression System Using Chinese Cabbage ····· 163
Jinhee Kim, Eun Su Lee, Hye-Eun Lee, Yul-Kyun Ahn, Jeong Ho Kim, Jongpil Hong

PC-02 Comparative Analysis of Complete Chloroplast Genome Sequence of *Cynanchum wilfordii* and *Cynanchum auriculatum* ····· 164
Inkyu Park, Wook-Jin Kim, Sang-Min Yeo, Yong-Min Kang, Byeong-Cheol Moon

PC-03 Development of Transposon Based Molecular Markers Useful for Construction of Linkage Map and Identification QTL Related to Agronomic Traits in Maize ····· 165
Rahul Vasudeo Ramekar, Kyong-Cheul Park, Kyu Jin Sa, Nam-il Park, Ju Kyong Lee

PC-04 The Draft Complete Mitochondria Genome Sequence of Wild Potato Relatives, *Solanum commersonii* ····· 166
Kwang-Soo Cho, Ji-Hong Cho, Ju-Seong Im, Hong-Sik Won, Yong-Ik Jin, Su-Young Hong, Hong-Seob Yoo

PC-05 AtSIZ1 Positively Controls DNA Methyltransferase CMT3 Activity by its Sumoylation in *Arabidopsis* ··· 167
Sung-Il Kim, Jun Soo Kwak, Joo Yong Kim, Hak Soo Seo

PC-06 Gibberellin Controls Plant Growth by Stimulating SLY1 Sumoylation and Activity ····· 168
Sung-Il Kim, Jun Soo Kwak, Hak Soo Seo

PC-07 AtSIZ1 Positively Controls Gibbrellin-mediated Seed Dormancy Break and Germination ····· 169
Sung-Il Kim, Joo Yong Kim, Hak Soo Seo

PC-08 Identification of Two Novel Mutant ANS Alleles Responsible for Inactivation of Anthocyanidin Synthase and Failure of Anthocyanin Production in Onion (*Allium cepa* L.) ····· 170
Eun-Young Kim, Cheol-Woo Kim, Min-Seon Choi, Sunggil Kim

PC-09 Characterization of rDNAs and Telomeric Repeats Distribution in a Tetraploid *Chrysanthemum zawadskii* ····· 171
Abigail Rubiato Cuyacot, Franklin Hinosa Mancia, Yoon-Ha Ju, Ki-Byung Lim, Yoon-Jung Hwang

PC-10 **Analysis of Differentially Expressed Genes During Root Development of Maize with RNA Sequencing** ····· 172
Jun-Cheol Moon, Sun-Goo Hwang, Byung-Moo Lee

PC-11 **The *Inquieta* Gene of Tomato is Involved in Trichome Development** ····· 173
In-Taek Hwang, Na-Rae Jeong, Jin-Ho Kang

PC-12 **Application of SNP Markers for Disease Resistance and Capsaicinoid Content in Pepper and Paprika Cultivars Using Fluidigm EP1™ System** ····· 174
Haein Kim, Ye Rin Lee, Kyumi Jeong, Jundae Lee

PC-13 **Analysis of The Genetic and Epigenetic Diversity Among Different Corn Varieties** ····· 175
Neha Roy, Min-Ji Lim, Sung-Il Lee, Nam Soo Kim

PC-14 **포도 유전체 육종 근접지원용 웹 데이터베이스 구축** ····· 176
이봉우, 이정희, 김상미, 김지은, 조강희, 조성환

PC-15 **Identification of SNP and InDel Sites in Strawberry Using a Next-generation Resequencing Approach** ····· 177
Ye Rin Lee, Haein Kim, Kyumi Jeong, Jundae Lee

PC-16 **Development of EST-SSR Markers Through *de novo* RNA Sequencing for Genetic Diversity and Association Study in Kenaf (*Hibiscus cannabinus* L.)** ····· 178
Sang Wook Jeong, Soon-Jae Kwon, Jaihyunk Ryu, Minkyu Lee, Joon-Woo Ahn, Jin-Baek Kim, Sang Hoon Kim, Hee-Bong Lee, Si-Yong Kang

PC-17 **A Bioinformatic Platform for Designing Cross-Species Intron-Spanning Genic Markers in Legumes** ····· 179
Jin-HyunKim, Chaeyoung Lee, Joo-Seok Park, Yoram Choi, Hong-Kyu Choi

PC-18 **GM 콩의 도입유전자 이동에 미치는 화분 매개충의 영향** ····· 180
이범규, 손수인, 권순종, 박기웅, 정영수, 이시명

PC-19 **Gene Transferability from Genetically Modified *Brassica napus* to B. *rapa* and Trait Analysis of F_1 Hybrids** ····· 181
Soo-In Sohn, Young-Ju Oh, Kyeong-Ryeol Lee, Ho-Cheol Ko, Ancheol Chang, Bumkyu Lee, Doh-WonYun, Gang-Seob Lee, Sung-Dug Oh, Hyun-Suk Cho, Yeon-Hee Lee

PC-20 **Genetic Diversity Analysis of Boysenberry Using SSR Markers** ····· 182
Woon Ji Kim, Juhyun Im, Sanghun Kim, Ee Yup Kim, Han Jig Jo, Si-Yong Kang, Bo-Keun Ha

PC-21 **Comparison of Anthocyanins and Antioxidant Capacity in Colored-wheat Mutant Lines** ····· 183
Min Jeong Hong, Bo Mi Nam, Sang Hoon Kim, Joon-Woo Ahn, Si-Yong Kang, Dea Yeon Kim, Yong Weon Seo, Jin-Beak Kim

PC-22 **벼 형질전환 Callus에서 돼지콜레라 항원 유전자의 발현** ····· 184
이주영, 김용호

PC-23 **Physiological Analysis of Wheat Cultivars Under Heat Stress Condition** ····· 185
Chan Seop Ko, Dae Yeon Kim, Young Up Kweon, Jong Nae Hyun, Kyung Hun Kim, Yong Weon Seo

PC-24 **Development of a HRM Marker Tightly Linked to Genic Male-sterile Gene (*ms*$_1$) in Paprika** ····· 186
Kyumi Jeong, Ye Rin Lee, Haein Kim, Jundae Lee

PC-25 **A Molecular Marker Linked to Saline Tolerance in Durum Wheat from Semi-desert** ····· 187
Sang Heon Kim, Inès Yacoubi, Yong Weon Seo

PC-26 **Transcriptome Analysis of Pre-harvest Sprouting Korean Wheat using RNAseq** ····· 188
Jae Yoon Kim, Dae Yeon Kim, Yong Weon Seo

PC-27 **Transcriptomic Dynamics of Wheat Peduncle at Different Developmental Stages** ····· 189
Cheol-Won Lee, Yong-Weon Seo

PC-28 **Identification of *CBF*s in rye and Their Expressions Under Various Abiotic Stresses** ····· 190
Woo Joo Jung, Yong Weon Seo

PC-29 **Comparison of Physiological Changes in 1BL.1RS Translocation and its NIL Under Cold Stress** ····· 191
Woo Joo Jung, Yong Weon Seo

PC-30 **한국 보급 및 특수품종의 SSR마커에 의한 유전적 유연관계와 품종판별** ····· 192
이가영, 곽상철, 김민음, 장은규, 황세구, 김홍식

PC-31 **The Development of Drought Resistance Bottle Gourd (*Lageneraria siceraria* Standl.) Using *Agrobacterium-mediated* Transformation.** ····· 192
Shin-Hwan Cho, Yul-Kyun Ahn, Jin-Hee Kim, Jong-Pil Hong, Eun-Su Lee, Jeong Ho Kim, Do-Sun Kim

PC-32 **Genome-wide Discovery of Simple Sequence Repeat Marker Based on Complete Genome Sequencing of *Capsicum baccatum* and *Capsicum annuum*** ····· 193
Sandeep Karna, Yul-Kyun Ahn, Jin-Hee Kim, Eun-Su Lee, Sena Choi, Eun-Young Yang, Jeong-Ho Kim, Tae-Hwan Jun

PC-33 **Pedigree Integration of Soybean [Glycine max L. Merrill] Cultivars in Korea** ····· 194
Chaeyoung Lee, Jin-HyunKim, Joo-SeokPark, Yoram Choi, Hong-Kyu Choi

PC-34 **Biosafety Assessment for Drought-tolerant Transgenic Rice (CaMsrB2-23) : Progeny Stability Study for Three Generations** ····· 195
Sung-dug Oh, Youngshin Kwak, Daesu Park, Doh-won Yun, Soo-in Sohn, Bumkyu Lee, Ancheol Chang

PC-35 **Identification of Tuber-Endophytic Bacteria in *Gastrodia elata* with Novelty of Soil *Proteobacteria*** ····· 196
Eung Jun Park, Muho Han, Hyo-Ryeon Lee, Mi Na Choi, Dae Bong Kang

PC-36 **Overexpression of a Novel Gene, E3 ubiquitin Ligase, Induce Coiled Branches (*cbi*) in Arabidopsis mutants** ····· 197
Gyu Tae Park, Jagadeesh Sundaramoorthy, Seokhyung Lee, Jeong-Dong Lee, Jeong Hoe Kim, Hak Soo Seo, Jong Tae Song

PC-37 **Uncovering the Role of DDMP Saponins in Soybean Through Molecular Characterization of DDMP Saponin-deficient Mutants** ····· 198
Jagadeesh Sundaramoorthy, Gyu Tae Park, Seokhyung Lee, Jeong-Dong Lee, Hak Soo Seo, Jong Tae Song

PC-38 **The AT-hook Motif-containing Proteins AHL27 and AHL29 Regulate Hypocotyl Elongation by Enhancing Auxin Biosynthesis in *Arabidopsis*** ····· 199
Kyounghee Lee, Pil Joon Seo

PC-39 **Expression of Antimicrobial Peptides Thanatin(S) in Transgenic Rice Enhanced Resistance to Phytopathogenic Fungi and Bacteria** ····· 200
Yeo Jin Jung, Jong Hee Kim, Yu Jin Jung,Yong Gu Cho, Ill Sup Nou, Kwon Kyoo Kang

PC-40 **Recurrent Parent Genome Recovery Analysis in a Marker Assisted Backcrossing (MAB) System of Tomato (*Solanum lycopersicum* L.)** ····· 201
Yu Jin Jung, Jong Hee Kim, Heo Ju Lee, Myoung Kwon Kim, Ill Sup Nou, Kwon Kyoo Kang

PC-41 **Identification of an SNP Variation of Elite Tomato (*Solanum lycopersicum* L.)Lines using Genome Resequencing Analysis** ····· 202
Yu Jin Jung, Hyo Ju Lee, Ill Sup Nou, Yong Gu Cho, Myong Kwon Kim, Hoy-Taek Kim, Kwon Kyoo Kang

PC-42 **The *Arabidopsis* RING Finger E3 Ligase MIEL1 Negatively Regulates Abscisic Acid Signaling by Promoting Protein Turnover of MYB96** ····· 203
Hong Gil Lee, Pil Joon Seo

PC-43 **Reducing the Expression of *SSIVa* via ZFN Results in Dwarf Phenotype in Rice and Increased Level of Starch Content** ····· 204
Yu-Jin Jung, Franz Marielle Nogoy, Ill-Sup Nou, Jong-Seong Jeon, Yong-Gu Cho, Kwon-Kyoo Kang

PC-44 **Expression Analysis of Abiotic Stress Responsive Novel Genes in *Brachypodium distachyon* L.** ····· 205
Jin Seok Yoon, Jae Yoon Kim, Yong Weon Seo

PC-45 **Expression Analysis of Five *Arabidopsis* PDLP5 Homologous Genes in Watermelon During Biotic and Abiotic Stresses** ····· 206
Jong-Pil Hong, Hye-Young Suh, Jeong-Ho Kim, Yul-Kyun Ahn, Jinhee Kim, Eun Su Lee, Hye-Eun Lee

PC-46 **Expression Analysis of Pepper Esterase (PepEST) Homologous Genes in Watermelon During Biotic and Abiotic Stresses** ····· 207
Jong-Pil Hong, Jeong-Ho Kim, Jinhee Kim, Yul-Kyun Ahn, Eun Su Lee, Hye-Eun Lee

PC-47 **Genome-wide Identification and Analysis of Rice Genes Preferentially Expressed in Pollen at an Early Developmental Stage** ····· 208
Tien Dung Nguyen, Sunok Moon, Van Ngoc Tuyet Nguyen, Yunsil Gho, Moon-Soo Soh, Jong Tae Song, Gynheung An, Sung Aeong Oh, Soon Ki Park, Ki-Hong Jung

PC-48 **Application of Rice Microspore-preferred Promoters to Manipulate Early Pollen Development Through a Heterologous System** ····· 209
Tien Dung Nguyen, Sunok Moon, Moe Moe Oo, Rupesh Tayade, Moon-Soo Soh, Jong Tae Song, Sung Aeong Oh, Ki Hong Jung, Soon Ki Park

PC-49 **A Conserved Oligomeric Golgi Complex Component-Related Protein is Essential for Pollen Development in Arabidopsis** ····· 210
Tien Dung Nguyen, Binbin Li, Sung Aeong Oh, Soon Ki Park

PC-50 **Analysis of Genome-wide Transcripts in Colored-grain Wheat Under Stress Condition** ····· 211
Dae Yeon Kim, Min Jeoug Hong, Woo Joo Jung, Chan-Seop Ko, Yong Weon Seo

PC-51 **Genome-wide Detection of Single Nucleotide Polymorphisms (SNPs) Between Two Korean Tongil Type Rice Varieties** ····· 212
Hyun-Ju Kang, Eokkeun Ahn, Inchan Choi, Hye-Jin Yoon, Kyung-Hwan Kim, Hyeonso Ji

PC-52 **The high-density Genetic Map of Perilla F2 Population by Genotyping-by-Sequencing (GBS)** ····· 213
Ji-Eun Kim, Bo Mi Lee, Bong-woo Lee, Moon Nam, Myoung Hee Lee, Tae-Ho Kim, Sung-Hwan Jo, Jeong-Hee Lee

PC-53 **Characterization of Cytochrome P450 (CYP) Genes Related to Saponin Biosynthesis in *Platycodon grandiflorum*** ····· 214
Sohyeon Park, Jemin Yoo, Yurry Um, Ok Tae Kim, Chang Pyo Hong, Seong-Cheol Kim, Yi Lee

PC-54 **Analysis of Genetic Diversity in 5 *Codonopsis* Species Based on SSR Markers** ····· 215
Sohyeon Park, Serim Kim, Jinsu Gil, Yurry Um, Hee Chung, Ok Tae Kim, Ho Bang Kim, Seong-Cheol Kim, Yi Lee

PC-55 **The CRISPR/Cas9-mediated Genome Editing in Banana Cells** ····· 216
Youjin Shin, Jin-Soo Kim, Jae-Young Yun

PC-56 **Development of Chloroplast InDel Markers to Distinguish *Angelica* Species** ····· 217
Sohyeon Park, Sangik Park, Jinsu Gil, Yurry Um, Hee Chung, Seong-Cheol Kim, Yi Lee

PC-57 **High-throughput transcriptome analysis for identifying genes determining flowering time** ····· 217
Cheol-Won Lee, Yong Weon Seo

PC-58 **Candidate Gene Analysis for the Genes Controlling the Yellow Color in *Capsicum annuum* Cultivar Micropep** ····· 218
Ayoung Jung, Juhun Lee, Jin-Kyung Kwon, Suna Kim, Byoung-Cheorl Kang

PC-59 **Identification of New Resistance Sources for *Cucumber mosaic virus* New Isolate-P1 (CMV-P1) in the Germplasm Collection of Capsicum spp.** ····· 219
Seula Choi, Myeong-Sook Han, Jin-Kwan Jo, Joung-Ho Lee, Eun-Ho Son, Byoung-Cheorl Kang

PC-60 **Genetic Mapping of Resistance Sources Against ChiVMV (*Chili veinal mottle virus*) in Hot Pepper** ··· 220
Joung-Ho Lee, Jeong-Tak An, Koeun Han, Seula Choi, Muhammad Irfan Siddique, Byoung-Cheorl Kang

PC-61 **Correcting Population Stratification in Pepper Core Collection for Genome-wide Association Studies (GWAS)** ····· 221
Hea-Young Lee, Koeun Han, Jin-Kyung Kwon, Byoung-Cheorl Kang

PC-62 **Hormone Related Transcriptome Analysis of Wheat During Pre-harvest Sprouting and Exogenous ABA Treatment** ····· 222
Yong Jin Lee, Jae Yoon Kim, Yong Weon Seo

PC-63 **Probing High-yield Traits of Soybean by Transforming Senescence-delay Genes** ····· 223
Hyun Suk Cho, Jin Ho Yang, Jin Sol Park, Hye Jeong Kim, Yoon Jeong Lee, Jae Seong Kim, Hyun Hee Im, Ki Jung Lee, Dong Hee Lee, Young Soo Chung

PC-64 **Transformation of Soybean with Improved Agricultural Traits of Insect Resistance and Drought Tolerance** ····· 224

Jae Seong Kim, Hyun Suk Cho, Hye Jeong Kim, Yoon Jeong Lee, Jin Ho Yang, Jin Sol Park, Hyun Hee Im, Ki Jung Lee, Jeong Il Kim, Soon Chun Jeong,Dong Hee Lee, Young Soo Chung

PC-65 **An Interspecific Genetic Linkage Map Based on RAPD and SSR in Citrus** ····· 225

Yali Chang, Eun-Ui Oh, Kyunguk Yi, Ho Bang Kim, Kwan Jeong Song

PC-66 **Molecular Characterization of Transgenic Plants Using Next Generation Sequencing and Bioinformatics.** ····· 226

Ji Hye Ohn, Andre Silvanovich, Carl Garnaat, Colton Kessenich, Qing Tian

PC-67 **A Simple, Rapid and Systematic Method for the Developed T-DNA Insertion Population Rice** ····· 227

Hyemin Lim, A-Ram Kim, Hyun-Ju Hwang, Jung-Il Cho, Hyeonso Ji, Chang-Kug Kim, Soo-Chul Park, Gang-Seob Lee

PC-68 **Expression of a Putatively Stress-related Gene *BrTSR53* Isolated from Chinese Cabbage (*Brassica rapa*)** ····· 228

A-Ram Kim, Hyemin Lim, Hyun-Ju Hwang, Sung Han Park, Chang-Kug Kim, Hyeonso Ji, Jung-Il Cho, Soo-Chul Park, Gang-Seob Lee

PC-69 **환경 스트레스 내성 유전자 *ABF3* 도입 국화 형질전환체 개발 및 특성 분석** ····· 229

박진선, 윤여진, 형남인

PC-70 **Genome-wide Characterization of Transcription Factors and Transcriptional Regulators in *P. ginseng*** ····· 230

Sang-Choon Lee, Murukarthick Jayakodi, Beom-Soon Choi, Nam-Hoon Kim, Junki Lee, Woojong Jang, Nomar Espinosa Waminal, Yun Sun Lee, Hyun-Seung Park, Ho Jun Joh, Jee Young Park, Sampath Perumal, Nguyen Binh, Hana Lee, Jinkyung Kim, Inseo Kim, Yeisoo Yu, Hyun Jo Koo, Tae-Jin Yang

PC-71 **DNA Fingerprinting Analysis of Rice Varieties Using a Core Set of Simple Sequence Repeats(SSR) Markers** ····· 231

Jee-Hwa Hong, Yong-Sham Kwon

PC-72 **들잔디 CIGR 유전자의 분리 및 특성분석** ····· 232

김양지, 양대화, 송필순, 이효연

PC-73 **Pyramiding of Two Rice Bacterial Blight Resistance Genes, *Xa3* and *Xa4*, and a Closely Linked Cold Tolerance QTL on Chromosome 11** ····· 233

Yeon-Jae Hur, Jun-Hyeon Cho, Hyun-Su Park, Tae-Hwan Noh, Dong-Soo Park, Ji Yun Lee, Young-Bo Sohn, Dongjin Shin, You Chun Song, Young-Up Kwon, Jong-Hee Lee

PC-74 **Genome-wide Transcript Analysis of Colored-grain Wheat During Grain Development** ····· 234
Dae Yeon Kim, Min Jeoug Hong, Yong Weon Seo

PC-75 **국화흰녹병균 검출용 특이 프라이머 개발** ····· 235
배신철, 전푸름, 안호근, 안일평, 박상렬, 황덕주, 김정구

PC-76 **Sequencing Analysis Can Demonstrate the Presence and Intactness of Transgenic Events in the Biotechnology Stack Product** ····· 236
Andre Silvanovich, Bradley Comstock, Marianne Malven, Will Urquhart1, Hye Jung Hyun

PC-77 **Identification and Characterization of the Causal Agent of Gummy Stem Blight (GSB) from Melon, Watermelon and Cucumber in Korea** ····· 237
Md. Zahid Hassan, Hoy-Taek Kim, Jong-In Park, Ill-Sup Nou

PC-78 **Molecular Dissection of a Rice Nucleus-associated RING Finger Protein and its Potential Role in Salt Stress in *Arabidopsis*** ····· 238
Yong chan Park, Sandeep Chapagain, Dae Gyeom Oh, Cheol Seong Jang

PC-79 **Tomato Fruit Ripening has been Delayed through The Regulation of Ethylene Biosynthesis Transcription Factors Under Sound Wave Treatment** ····· 239
Joo Yeol Kim, Hye Ryun Ahn, Soo In Lee, Jin A Kim and Mi Jeong Jeong

PC-80 **Identification of Genes Involved in Cucurbitacin E Biosynthesis** ····· 240
Young Cheon Kim, Sanghyeob Lee

PC-81 **Exploring Resistance Against *PHYTOPHTHORA CAPSICI* in Pepper** ····· 241
Muhammad Irfan Siddique, Koeun Han, Byoung-Cheorl Kang

PC-82 **The Regulation of *Brassica rapa* GIGANTEA Gene Expression is Available to Improvement of Salt Tolerance in Chinese Cabbage** ····· 242
Ha-eun Jung, Mi Jeong Jeong, Soo In Lee, Jin A Kim

PC-83 **Diurnal Expression of Glucosinolate Genes in Brassica rapa Under Various Light Quality Conditions** ····· 243
Jin A Kim, Ha-eun Jung, Soo In Lee, Mi Jeong Jeong

PC-84 **Identification of Drought and Salt Stress-responsive Genes in Poplar (*Populus alba* × *P. glandulosa*)** ····· 244
Seo-Kyung Yoon, Eung-Jun Park, Eun-Kyung Bae, Young-Im Choi, Kyu-Suk Kang, Hyoshin Lee

PC-85 **Fine Mapping of the Root-Knot Nematode (*Meloidogyne incognita*) Resistance Gene *Me7* in Pepper (*Capsicum annuum*)** ····· 245
Amornrat Changkwian, Ji-Woong Han, Joung-Ho Lee, Gyung-Ja Choi, Byoung-Cheorl Kang

PC-86 **The Construct of Backcross Inbred Line for *qSTV11*^{Z} Fine-mapping.** ····· 246
Sais-Beul Lee, Yeon-Jae Hur, Tae Heon Kim, Dongjin Shin, Jun-Hyeon Cho, Sang-Ik Han, Un-Sang Yeo, You-Chun Song, Jong-Hee Lee, Yeong-Up Kwon, Kyung-Min Kim, Dong-Soo Park

PC-87 **Analysis of QTL Markers for Drought Tolerance in Maize** ····· 247
Hyochul Kim, Kitae Song, Seungho Shin, Kyung-Hee Kim, Jun-Cheol Moon, Jae Yoon Kim, Byung-Moo Lee

PC-88 **Development of Potyvirus Resistance in Non-transgenic Tomato Plants Using CRISPR/Cas9 Technology** ····· 248
Saminathan Subburaj, Luhua Tu, Yong-Tae Jin, Sangsu Bae, Geung-Joo Lee

PC-89 **Fine Mapping and Identification of Candidate Genes for the *sy-2* Locus in a Temperature-sensitive Chili Pepper (*Capsicum chinense*)** ····· 249
Li Liu, Jelli Venkatesh, Yeong Deuk Jo, Sota Koeda, Munetaka Hosokawa, Jin-Ho Kang, Byoung-Cheorl Kang

PC-90 **Identification and Molecular Characterization of Novel Genes Under Abiotic Stresses from *Triticum aestivum* L.** ····· 250
Jin Seok Yoon, Jae Yoon Kim, Yong Weon Seo

PC-91 **황기의 계통분류를 위한 유전체기반 분자마커 개발** ····· 251
허목, 엄유리, 길진수, 박소현, 이이, 정진태, 김연복, 김성철, 정찬식

PC-92 **Development of Genetic Map and QTLs for Stem Diameter Using New CAPS Markers in MGRIL Population** ····· 252
Ye Ji Lee, Eun Ju Byeon, Seon-Hwa Bae, Hyeonso Ji, Gang-Seob Lee, Ung-Han Yoon, Tae-Ho Kim

PC-93 ***Perilla* Genome Sequencing** ····· 253
Seon-Hwa Bae, Myoung-Hee Lee, Jeong-Hee Lee, Ye-Ji Lee, Eun-Ju Byeon, Ung-Han Yoon, Tae-Ho Kim

PC-94 **Development of Functional Molecular Markers for Cabbage Breeding** ····· 254
Hayoung Song, Ill-Sup Nou, Yoonkang Hur

PC-95 **Classification of Flowering Time and Maturity Locus Genotyping of Elite Soybean Cultivars in Korea** ····· 255
Kil-Hyun Kim, Min-Jung Seo, Myoung-Ryoul Park, Chang-Hwan Park, Jung-Kyung Moon, Byung Joo Kim

PC-96 **Construction of DNA Marker Sets for Korean Wheat Cultivar Identification** ····· 256

Jae-Han Son, Chon-Sik Kang, Young-Keun Cheong, Jong-Chul Park, Tae-Il Park, Yang-Kil Kim, Jong-Ho Park, Young-Jin Oh, Bo-Kyeoung Kim

PC-97 **Expression of Pepper Cytoplasmic Male Sterility-associated Open Reading Frame, *orf507* in Transgenic Tobacco Plants** ····· 257

Yeaseong Ha, Min-Young Kang, Yeong Deuk Jo, Byoung-Cheorl Kang

PC-98 **Identification, Molecular Cloning and Characterization of Stress-Induced Genes in *Lilium formolongi*** ····· 258

Jewel Howlader, Nasar Uddin Ahmed, Namhee Jeong, Kanij Rukshana Sumi, Jong-In Park, Ill-Sup Nou

PC-99 **Resistance of transgenic zoysiagrass overexpressed zoysiagrass class II chitinase gene *Zjchi2* against *Rhizoctonia solani* AG2-2 (IV)** ····· 259

Ji-Nam kang, Mi-Young Park, Hong-Gyu Kang, Hyeon-Jin Sun, Yong-Ik Kwon, Suk-Min Ko, Hyo-Yeon Lee

PC-100 **Use of High Performance Liquid Chromatography to Determine Genetic Factors of Fruit Colors in Tomato** ····· 260

Hee Ju Yoo, Gyu Myung Lee, Inhwa Yeam, Chang-Sik Oh, Je Min Lee

PC-101 **Genome-wide Characterization of AP2/ERF Superfamily in *Panax Ginseng*** ····· 261

Hyun-Seung Park, Sang-Choon Lee, Murukarthick Jayakodi, Junki Lee, Tae-Jin Yang

PC-102 **Proteome Analysis of the Roots of Sorghum in Response to Copper** ····· 262

Swapan Kumar Roy, Soo-Jeong Kwon, Kabita Sarker, Hyun-Jin Jung, Min-Heon Yun, Sun-Hee Woo

PC-103 **Identification of Physiological and Transcriptomal Analysis in Rice Plant (*Oryza sativa* L.) after acute and chronic γ -irradiation** ····· 263

Sung Min Han, Jung Eun Hwang, In Jung Jung, Hong-Il Choi, Soon-Jae Kwon, Si-Young Kang, Jin-Baek Kim

PC-104 **Genetic Dissection of Immature Fruit Color in Pepper** ····· 264

Gyu Myung Lee, Hee Ju Yoo, Doil Choi, Je Min Lee

PC-105 **Genetic Mapping and Marker Development for the *Powdery Mildew Resistance* Gene PMR1 in Pepper (*Capsicum annuum*)** ····· 265

Jinkwan Jo, Jelli Venkatesh, KoeunHan, Byoung-Cheorl Kang

PC-106 **Structure of Genetic Diversity in the Apple Germplasm with Genome-wide SNPs Using Genotyping by Sequencing** ····· 266
Youngjae Oh, Keumsun Kim, Sewon Oh, Jungyeon Won, Hyeondae Han, Yoon-Kyeong Kim, Daeil Kim

PC-107 **Development of SNP Set for Genetic Linkage Mapping in Interspecific Asian Pear (*Pyrus* spp.)** ····· 267
Hyeondae Han, Youngjae Oh, Keumsun Kim, Sewon Oh, Jungyeon Won, Yoon-Kyeong Kim, Daeil Kim

PC-108 **Genetic linkage Maps Using GBS Based SNPs in Interspecific Asian Pear (*Pyrus* spp.)** ····· 268
Hyeondae Han, Youngjae Oh, Keumsun Kim, Sewon Oh, Jungyeon Won, Yoon-Kyeong Kim, Daeil Kim

PC-109 **Identification of Flowering-Related Genes Responsible for Differential Expression Between Two Radish Inbred Lines Exhibiting Disparate Bolting Time Through Comparative Transcriptome Analysis** ····· 269
Won Yong Jung, Hyun Ji Park, Sang Sook Lee, Areum Lee, Youn-Sung Kim, Hye Sun Cho

PC-110 **Genome-wide Identification and Analysis of Rice Endosperm Preferred Genes Conserved in Various Rice Verities** ····· 270
Woo-Jong Hong, Yo-Han Yun, Sun-A Park, Sung-Ruyl Kim, Ki-Hong Jung

PC-111 **Improving and Sharing Computing Algorithms of Genome Analysis, and System Development of Bioinformatics Tools** ····· 271
Kyu-Won Kim, Ji-Hye Hwang, Jung-Kyung Moon, Yong-Jin Park

PC-112 **Population Genomics Identifies the Origin and Signatures of Selection of Korean Weedy Rice** ····· 272
Qiang He, Kyu-Won Kim, Yong-Jin Park

PC-113 **Identification of Octoploid Strawberry Cultivar Using High-throughput SNP Genotyping** ····· 273
Hee-Jeong Jung, Karpagam Veerappan, Sathishkumar Natarajan, Namhee Jeong, Indeok Hwang, Soichiro Nagano, Kenta Shirasawa, Sachiko Isobe, Ill-Sup Nou

PC-114 **Genome-wide Association Study of Cold Stress During Seedling Stage Using Rice (*Oryza sativa* L.) Core Set** ····· 274
Mijeong Kim, Yoonjung Lee, Giwon Cho, Jisu Choi, Joohyun Lee

PC-115 **Genome-Wide Association Study of Vitamin E Using Genotyping-By-Sequencing in Sesame (*Sesamum indicum*)** ····· 275
Qiang He, Feifei Xu, Jie Yu, Tae-Sung Kim, Yong-Jin Park

PC-116 **Rice Chloroplast Genome Variation Architecture and Phylogenetic Dissection in Diverse Oryza Species Assessed by Whole-genome Resequencing** ····· 276
Wei Tong, Tae-Sung Kim, Yong-Jin Park

PC-117 **Development of Primer Sets for the Detection and Identification of the *Epimedium* and *Thalictrum* Using Real-time PCR** ····· 277
Jae-Woo Lee, Ju-Hee Kim, Cheol Seong Jang

PC-118 **Genetic Variation Architecture of mitochondrial Genome Reveals the Differentiation in Korean Landrace and Weedy Rice** ····· 278
Wei Tong, Yong-Jin Park

PC-119 **양배추 시들음병 저항성 및 감수성 품종 구별용 분자마커 개발** ····· 279
강송이, 정희정, 황인덕, 노일섭

PC-120 **Implementation of Rapid Haplotyping Software in Personal Computers for Standalone Users** ····· 280
Kyu-Won Kim, Yong-JinPark

PC-121 **Quiescence Vs Elongation Strategy for Direct Seeding Approach in Korean Rice Core Set** ····· 281
Win Htet Oo, Tae-Sung Kim, Yong-Jin Park

PC-122 **Genome-wide Association Study and Gene Sets Analysis Reveals Candidate Genes Involved in Salt Tolerance at The Rice Seedling Stage** ····· 282
Jie Yu, Tae-Sung Kim, Yong-Jin Park

PC-123 **Orthologous and Evolutionarily Accelerated Genes Identified in Sesame (Sesamum indicum) by Deep Resequencing** ····· 283
Jie Yu, Kyu-Won Kim, Yong-Jin Park

PC-124 **Gene Expression Profiling Through de novo Transciptome Sequencing Provide Insights for the Mechanisms Underlying Side Branch Suppressions That Enhance The Production Quality of The Standard Chrysanthemum Cultivars (Dendranthema grandiflorum Ramat.)** ····· 284
Tae-Sung Kim, Jie Yu, Ha-Seung Park, Chang-Pyo Hong, Hojin Ryu, Yong-Jin Park

PC-125 **Genome-wide Association Studies(GWAS) of Related Genes for Flowering Time in Rice Core Set** ····· 285
Min-Young Yoon, Yong-Jin Park

PC-126 **유전체 기반 분자육종시스템 구축** ····· 286
이현오, 최범순, 이승욱, 최아영, 신지언, 박미소, 강경대, 유의수

PC-127 **The Complete Mitochondrial Genome Sequence of *Senna tora* L.** ····· 287
Choi Ah Young, Hyun Oh Lee, Ji Eon Shin, Mi So Park, Yeisoo Yu, SeungWook Lee, Kyoung Dae Kang, Sang-Ho Kang, Beom-Soon Choi

PC-128 산초나무(*Zanthoxylum schinifolium* S. et Z.) Microsatellite 표지 개발 및 유전변이 분석 ····· 288
김영미, 조아르나, 신유승, 정지희, 김호방

PC-129 이미지 센싱 기반으로 한 벼 생육 표현형 분석 ····· 289
이홍석, 김송림, 이은경, 최인찬, 지현소, 윤혜진, 김경환

PC-130 Identification and Characterization of Grain Weight Trait Candidate Genes in a Cross between *Oryza sativa* and *O. rufipogon* ····· 290
Yun-A Jeon, Dong-Min Kim, Hyun-Sook Lee, Ju-Won Kang, Yun-Joo Kang, Sang-Nag Ahn

PC-131 Genetic Diversity and Barcodes of Taraxacum Species Based on Complete Chloroplast Genome Sequences ····· 291
Jin-Kyung Kim, Jee Young Park, Yun Sun Lee, Hyun Oh Lee, Hyun-Seung Park, Sang-Choon Lee, Shin-Jae Kang, Jung Hwa Kang, Taek Joo Lee, Tae-Jin Yang

PC-132 식물표현체 기술을 통한 벼 생육 시 질소원이 생장에 미치는 영향 분석 ····· 292
김송림, 이홍석, 이은경, 임철희, 최인찬, 윤혜진, 지현소, 김경환

PC-133 Identification of QTL Associated with Low-temperature Germinability in NILs Derived from an Interspecific Cross in Rice ····· 293
Quynh Anh Le, Yun-Joo Kang, Kyu-Chan Shim, Yun-A Jeon, Yeo-Tae Yun, Ju-Won Kang, Hyun-Sook Lee, Sang-Nag Ahn

PC-134 The Grain Shape QTL, *GW2* is Associated with Chlorophyll Content and First Internode Diameter in Rice ····· 294
Lu Xin, Kyu-Chan Shim, Ju-Won Kang, Hyun-Sook Lee, Sang-Nag Ahn

PC-135 PagBEE3L 형질전환 포플러의 바이오매스 증대 효과 ····· 295
최현모, 최영임, 노설아, 박응준, 윤서경, 신주희, 배은경, 이효신

PC-136 Cloning of WRKY Genes, Induced by Stresses in Zoysia japonica Steud. ····· 296
Woo-Nam Kim, Yong-Ik Kwon, In-Ja song, Bo-Hwa Hwang, Dong-Sun Lee, HyoYeon Lee

PC-137 작물육종 효율 극대화를 위한 식물표현체 플랫폼 구축 ····· 297
이은경, 이홍석, 임철희, 김송림, 최인찬, 윤혜진, 지현소, 김경환

PC-138 $F_{2:3}$ 집단을 이용한 '대립벼 1호' 종자 형태를 조절하는 유전자 탐색 ····· 298
심규찬, 강주원, 이현숙, 안상낙

PC-139 **Characterization of Grain Weight QTL, *gw8*** ····· 299
Yun-Joo Kang, Yun-A Jeon, Ju-Won Kang, Hyun-Sook Lee, Sang-Nag Ahn

PC-140 **Principal Component Analysis of Primary Pears and Korean Native Pears (*Pyrus* spp.) Using a Set of Microsatellite Reference Alleles** ····· 300
Keumsun Kim, Youngjae Oh, Sewon Oh, Jungyeon Won, Hyeondae Han, Yoon-Kyeong Kim, Seolah Kim, Daeil Kim

PC-141 **Identification of Changes in Cold Hardiness and Soluble Sugars on Response to Experimental Deacclimation in Peachs (*Prunus persica*)** ····· 301
Keumsun Kim, Sewon Oh, Hyunsuk Shin, Youngjae Oh, Jungyeon Won, Hyeondae Han, Daeil Kim

PC-142 **배추과 작물의 엽록체 유전체 서열을 활용한 종간 구분 InDel 마커 개발** ····· 302
양기웅, 정지윤, 정남희, 박종인, 노일섭

PC-143 **Development of Molecular Marker for Characterizing Early and Late Bolting Genotypes of *Brassica oleracea* var. *capitata*** ····· 303
Md. Abuyusuf, Ujjal Kumar Nath, Jong-In Park, Mi-Young Chung, Ill-Sup Nou

PC-144 **Identification and Expression Profiling of Rapeseed (*Brassica napus*) Genes Involved in Lipid Metabolism During Silique Development** ····· 304
Hankuil Yi, Eunyoung Cho, Kyung Hee Roh, Ho Bang Kim

PC-145 ***BrPATL4* gene from *Brassica rapa* Expresses Small Seed and Erect Panicle in Transgenic *japonica* Rice** ····· 305
Joonki Kim, Hye-Jung Lee, Franz Marielle Nogoy, Dal-AYu, Me-Sun Kim, Kwon-Kyoo Kang, Illsup Nou, Yong-Gu Cho

PC-146 **Functional Characterization of Two NAC Transcription Factors of *OsNAC300* and *OsNAC75* in Rice (*Oryza sativa*)** ····· 306
Shadi Rahimi, Yu-Jin Jung, Me-Sun Kim, Eun-Ju eung, Kwon Kyoo Kang, Illsup Nou, Yong-Gu Cho

PC-148 **GM Cabbage Resistant to Diamondback Moth** ····· 308
Yi Re Lee, Min Jung, Jong Sup Shin, Soon-Chun Jeong, Chee Hark Harn

PC-149 **Genome-wide Identification of Sequence and Structural Variations from The Bacterial Canker of Kiwifruit *Pseudomonas syringae* pv. *actinidiae* (PSA) Pathovars and Their Application to Pathovar Genotyping** ····· 309

Chang Jae Oh, Jin-Kyu Woo, Ji-Hyeon Kim, Hye-Young Lee, Mee Hyang Hong, Gyoung Hee Kim, Young Sun Lee, Jae Sung Jung, Young Jin Koh, Ho Bang Kim

PC-150 **Functional Characterization of Alfalfa (*Medicago sativa* L.) DNAJ Gene (MsDNAJ) Involved in Abiotic Stress Defense** ····· 310

Ki-Won Lee, Md. Atikur Rahman, Sang-Hoon Lee, Ki-Yong Kim, Hee Chung Ji, Tae Young Hwang

PC-151 **Study About Gene Flow and Stability Assessment in GM Rice (*Oryza sativa* L.)** ····· 311

Jun-Hoi Kim, Jin-Hee Kim, Kyung-Min Kim

PC-152 **해충저항성 Bt벼의 개발과 안전성평가** ····· 312

임명호, 박순기, 조현석

PC-153 **CRISPR/Cas9-mediated Multiplex Genome Editing in Plants** ····· 313

Hyeran Kim, Sang-Tae Kim, Min Kyung Choi, Jahee Ryu, Jin-Soo Kim, Sang-Gyu Kim

PC-154 **Allelic Analysis of Low-molecular-weight Glutenin Subunits Using 2-DGE in Korean Wheat Cultivars** ····· 313

Hye-Rang Beom, You-Ran Jang, Susan B Altenbach, Sun-Hyung Lim, Young-Mi Kim, Jong-Yeol Lee

PC-155 **Comprehensive Characterization of Low-Molecular-Weight Glutenin Subunit Genes and Their Protein Products in Common Wheat** ····· 314

Jong-Yeol Lee, Hye-RangBeom, Susan B Altenbach, Sun-Hyung Lim, Young-Mi Kim

PC-156 **Simultaneous Suppression of Seed Storage Proteins in Rice Seed Using RNA Interference Induces ER-Stress Responses and Germination Delay** ····· 316

Kyoungwon Cho, Hye-Jung Lee, Yeong-Min Jo, Jong-Yeol Lee, Young-Mi Kim

PC-157 **Identification of a Novel Rice B-box Zinc Finger Protein Involved in Regulation of Anthocyanin Biosynthesis** ····· 316

Da-Hye Kim, SangKyu Park, MinJi Choi, Sun-Hwa Ha, Jong-Yeol Lee, Sun-Hyung Lim

PC-158 **Cloning and Characterizations of Flavonol Synthases Isolated from Yellow and Red Onion** ····· 317

SangKyu Park, MinJi Choi, Da-Hye Kim, Sun-Hwa Ha, Jong-Yeol Lee, Sun-Hyung Lim

차세대BG21사업단

농생물게놈활용연구사업단

OD-01 **가지과 유전체 활용을 위한 생물정보분석 파이프라인 및 데이터베이스 TGsol 현황** ····· 321
이봉우, 김지은, 오재은, 최준경, 이정희, 조성환

OD-02 **Constructing a Genomics-Assisted Bioinformatic Platform for Legumes** ····· 322
Jin-Hyun Kim, Joo-Seok Park, Chaeyoung Lee, Hong-Kyu Choi

OD-03 **Genomics Integrated Breeding Platform for Soybean: Korean Soya Base** ····· 323
Namshin Kim

OD-04 **Research Updates of Rice Breeding Activities using Genome Information, and Development of Resources-Sharing Systems: Seed Materials, Genomic Information, Software and Research Experience** ····· 324
Yong-Jin Park, Tae-Sung Kim, Kyu-Won Kim, Min-Young Yoon, Il-Pyung Ahn, Yong-Soo Choi, Won-Il Kim, Jung-Kyung Moon

GM작물개발사업단 & 식물분자육종사업단

OE-01 **식물연구에서 크리스퍼 유전자가위의 다양한 적용** ····· 327
배상수

OE-02 **Transgenic Plants Producing Green-vaccine for CSFV(classical swine fever virus) Lead on Plant Biotechnology-based Product on Market** ····· 328
Minhee Park, Kyungmin Min, Sungmin Gu, Soo-Hong Park, Nam-Hyung Kim, Hyunsook Lee, Hyewon Kim, Yongjik Lee, Seong-In Lim, Hye-Young Jeong, Dong-Jun An, Jaeyoung Song, Inhwan Hwang, Eun-Ju Sohn

GSP 사업단

GSP 채소종자사업단 & GSP 원예종자사업단

OF-01 **육성가 권리보호와 종자산업의 발달** ····· 331
이승인

OF-02 **Current condition and strategy for expansion of seed testing service in KSVS** ····· 332
Eun Hee Soh

OF-03 **Breeding for Pyramiding Target-genes and Selection of F_1 Hybrids by Marker Assisted Selection in Tomato** ····· 332
김명권

OF-04 **Gene Identification, Expression Analysis and Breeding for Enhanced Glucosinolate Biosynthesis in *Brassica*** ····· 333
Arif Hasan Khan Robin, Go-eun Yi, Rawnak Laila, Kiwoung Yang, Jong-In Park, Ill-Sup Nou

GSP 식량종자사업단

OG-01 **Specialty Corn Breeding at Sweet Seeds in Thailand to The Tropical World** ····· 337
Tweesak Pulam

OG-02 **The Status of Rice Production and Breeding in China** ····· 338
Longzhi Han

OG-03 **Application of Biotechnology in Developing New Rice Varieties For High Temperature Tolerance in the Philippines** ····· 340
Norvie L. Manigbas, LuvinaB.Madrid, Jupiter L. Grospe, Young-Chan Cho

OG-04 **Introduction of rice in rice production and the change of major diseases in rice during the period of climate change in Vietnam** ····· 341
Lai Tien Dung

2016 한국육종학회상

2016 한국육종학회상 ····· 345

색인

색인 ····· 349

연사 발표

SYMP-01

Doubled Haploid (DH) Technology in Maize Breeding: Application and Technology for Production of DH Lines

Vijaya Vardhana Reddy. Chaikam

International Maize and wheat improvement center (CIMMYT), Mexico

Doubled haploid technology enables rapid development of 100% homozygous inbred lines. Production of DH lines in maize involves induction of haploids using special genotypes called haploid inducers, haploid identification preferably at seed or seedling stage using anthocyanin markers, chromosomal doubling with antimitotic chemicals in haploid seedlings and self-fertilization of fertile doubled haploid plants to generate seed for DH lines. Use of DH lines in maize breeding results in increased selection gains, simplified logistics and possibly reduced costs. DH lines are also valuable in exploring and uncovering the diversity present in the landraces and open pollinated verities as fixed homozygous inbred lines. Hence, most multinational breeding companies routinely use Doubled Haploid technology in maize breeding programs. However, adoption of DH technology is lagging behind in the maize breeding programs of the developing world. Limitations include lack of adapted haploid inducers, difficulties associated with haploid identification and lack of technical knowhow on chromosomal doubling procedures. At CIMMYT, research is being conducted to address some of these limitations. CIMMYT in collaboration with University of Hohenheim developed first publicly available tropically adapted haploid inducers which were distributed to several organizations throughout the world. Further breeding for improved inducers led to development of second generation tropicalized haploid inducers with high haploid induction rates and better agronomic performance. Analysis of several tropical breeding populations and inbred lines revealed that the commonly used *R1-nj* phenotypic marker is completely or partially inhibited in significant proportion of tropical germplasm making it ineffective for haploid identification. To address this problem, we have developed haploid inducers expressing anthocyanin coloration in roots, which aid in haploid identification at seedling stage when *R1-nj* is inhibited. Also, inducers with high oil trait are also being developed which can facilitate automation of haploid identification. Different chromosomal doubling methods are being tested for improving the efficiency of doubling. In addition, the influence of source germplasm on haploid induction and chromosomal doubling has been studied which revealed a very strong influence of source germplasm. In this talk topics like advantages of using DH lines in maize breeding, different steps involved in maize DH line production, limitations at each step and new developments to address these limitations will be presented.

Corresponding author: E-mail: V.Chaikam@cgiar.org

SYMP-02

Finding Mineral Element Transporters for Better and Safe Production of Rice

Jian Feng Ma

Institute of Plant Science and Resources, Okayama University, Kurashiki, Japan

Crop productivity largely relies on mineral nutrients in soils. These mineral nutrients are taken up by the roots, translocated to the shoots and then distributed to different tissues for their growth. On the other hand, harmful mineral elements are also present in soils. Transfer of these toxic elements from soils to edible parts will affect our health through food chain. Tremendous transporters are involved in the transport of these essential and toxic mineral elements in plants, but most of them are unidentified. Therefore, identification and manipulation of these transporters will be required for better and safe production of crops. At this symposium, I will show some results on transporters of two elements (Si and Cd) in rice, which is a staple food for half population of the world. Silicon (Si) is required for high and sustainable production of rice, a high Si-accumulating species (Ma and Yamaji, 2015). We identified two transporters (Lsi1 and Lsi2) for Si uptake in rice. Lsi1 is a Si-permeable channel (Ma et al. 2006), while Lsi2 is an active efflux transporter of Si (Ma et al. 2007). Both Lsi1 and Lsi2 are localized at the exodermis and endodermis of the roots, but they show different polar localization. Lsi1 is localized at the distal side of both exodermis and endodermis, while Lsi2 is localized at the proximal side of the same cell layers. Knockout of either Lsi1 or Lsi2 results in loss of Si uptake. At next step, Si in the xylem sap is unloaded by Lsi6, a homolog of Lsi1 in rice (Yamaji et al., 2008). At reproductive stage, three transporters (Lsi2, Lsi3 and Lis6) localized at different cell layers of the node I are responsible for preferential distribution of Si to the panicles. Knockout of either of them resulted in increased distribution of Si to the flag leaf, but decreased distribution to the panicle (Yamaji and Ma, 2009; Yamaji et al., 2015). Furthermore, our recent mathematical modelling study showed that an apoplastic barrier and development of enlarged vascular bundles of the node are also required for the preferential distribution of Si to the panicles (Yamaji et al., 2015).

On the other hand, rice is a major source of Cd intake. We have identified three transporters (OsNramp5, OsHMA2 and OsHMA3) involved in Cd accumulation in rice. OsNramp5 is a major transporter for Cd uptake in the roots (Sasaki et al., 2012). It is localized in the distal side of both exodermal and endodermal cells. OsHMA3 is localized to the tonoplast of root cells (Ueno et al., 2010), which is responsible for sequestration of Cd into the vacuoles in the roots. On the other hand, OsHMA2 is a plasma membrane-localized transporter and localized in the pericycle of the root and the phloem of enlarged and diffuse vascular bundles in the nodes (Yamaji et al., 2013). OsHMA2 is responsible for translocation of Cd from the roots to the shoots and distribution of Cd into the grain. Knockout of *OsNramp5* and *OsHMA2* resulted in significant reduction of Cd accumulation in the grain, but also caused decreased yield because they are also transporters of Mn and Zn, respectively. By contrast, overexpression of functional *OsHMA3* selectively decreased accumulation of Cd in the grains without growth penalty and enhanced tolerance to Cd toxicity (Ueno et al., 2010; Sasaki et al., 2014).

Corresponding author: E-mail: maj@rib.okayama-u.ac.jp

SYMP-03

Function of Fibrillin Protein in Photosynthetic Metabolism

Hyun Uk Kim

Department of Bioindustry and Bioresource Engineering, Plant Engineering Research Institute, Sejong University, Korea

Fibrillins are lipid-associated proteins in plastids and are ubiquitous in plants. They accumulate in chromoplasts and sequester carotenoids during the development of flowers and fruits. However, little is known about the functions of fi brillins in leaf tissues. Here, we identified fibrillin 5 (FBN5), which is essential for plastoquinone-9 (PQ-9) biosynthesis in Arabidopsis thaliana. Homozygous *fbn5-1* mutations were seedling-lethal, and XVE:FBN5-B transgenic plants expressing low levels of FBN5-B had a slower growth rate and were smaller than wild-type plants. In chloroplasts, FBN5-B specifi cally interacted with solanesyl diphosphate synthases (SPSs) 1 and 2, which biosynthesize the solanesyl moiety of PQ-9. Plants containing defective FBN5-B accumulated less PQ-9 and its cyclized product, plastochromanol-8, but the levels of tocopherols were not affected. The reduced PQ-9 content of XVE:FBN5-B transgenic plants was consistent with their lower photosynthetic performance and higher levels of hydrogen peroxide under cold stress. These results indicate that FBN5-B is required for PQ-9 biosynthesis through its interaction with SPS. Our study adds FBN5 as a structural component involved in the biosynthesis of PQ-9. FBN5 binding to the hydrophobic solanesyl moiety, which is generated by SPS1 and SPS2, in FBN5-B/SPS homodimeric complexes stimulates the enzyme activity of SPS1 and SPS2. Identification of interacting partners to fibrillins will contribute to better understanding of mechanism of photosynthetic metabolism under stress conditions.

Corresponding author: E-mail: hukim64@sejong.ac.kr

SYMP-04

Revisiting Domestication to Revitalize Crop Improvement: The Florigen Revolution

Zach Lippman

Cold Spring Harbor Laboratory, USA

A major challenge in modern agriculture is to develop new approaches that can expedite breeding and make its outcomes more predictable. The last decade of studies on crop domestication has pointed to a recurring theme: selection of genetic variation in the universal florigen flowering system, which includes the flower-promoting hormone florigen and antagonistic family members. Prominent examples include perpetual flowering in strawberries and roses, biennial flowering in sugar beet, adapted flowering in barley, and the introduction of a bushy determinate growth habit for common bean, soybean, and tomato, which enabled large-scale field production. Yet, these successes are all based on rare naturally occurring florigen pathway mutations that may not be providing optimal agronomic performance. I will discuss our recent work on translating molecular mechanisms underlying florigen-dependent flowering in tomato to develop a genetic toolkit that has allowed us to fine-tune and optimize shoot architecture, flower production, and yield. I will also present a new CRISPR-based approach that we are developing to create novel quantitative variation that has the potential to invigorate breeding in all crops.

Corresponding author: E-mail: lippman@cshl.edu

SYMP-05

Manipulating Fruit and Vegetable Quality Traits

David A. Brummell

The New Zealand Institute for Plant & Food Research Limited, Private Bag 11600, Palmerston North, 4442, New Zealand

Fruit and vegetable quality aspects important to the consumer include nutritional content, texture (eating quality) and the absence of harmful compounds. Metabolic engineering of plant pathways to enhance quality aspects, including the concentrations of phytochemicals with human health benefits, is a focus of many current plant biotechnology programmes. Fruit carotenoid or anthocyanin contents have been increased by genetic manipulation of enzymes or transcription factors, but not both at the same time. However, both pathways are affected by light. We achieved fruit-specific suppression of *DET1*, a regulatory gene that represses several signal transduction pathways controlled by light, resulting in significant increases in the contents of the carotenoids lycopene and β -carotene, as well as various flavonoids. Fruit softening and texture are controlled by a range of cell wall-modifying enzymes. Historically, polygalacturonase (PG) has been accorded a minor role in the softening process. Nevertheless, silencing the *PG1* gene in apple reduced softening, and aspects of texture were altered. Interestingly, fruit water loss was also reduced, apparently due to alterations in the structure of the hypodermal layers. These observations suggest that PG may exert part of its effects on softening through altering transpirational water loss, and indicate that the function of PG in fruit ripening is more complex than previously reported. For potato tubers, storage at cold temperatures for many months is essential in order provide a constant supply of material to industry for processing. However, low temperature storage can cause the breakdown of starch to sucrose and the accumulation of the reducing sugars glucose and fructose (a process called cold-induced sweetening) due to the activity of vacuolar acid invertase. Processing these susceptible cultivars by frying or roasting results in the Maillard reaction and the generation of acrylamide, a suspected human carcinogen. We cloned two invertase inhibitors from potato tubers, and showed that overexpression of the vacuolar form reduced vacuolar invertase activity, cold-induced sweetening and the generation of acrylamide after frying.

Corresponding author: E-mail: david.brummell@plantandfood.co.nz

SYMP-06

Designing Crops for Global Food Security: Digitizing Plant Phenotypes

Maurice Moloney

Global Institute for Food Security, Canada

Information and communications technology pervades all aspects of human activity from healthcare, finance, and education to recreation. Agriculture and food production are no exceptions. Large-scale integrated data acquisition and management systems are emerging that will affect everything from plant breeding and soil science to automated farm practices. Critical technologies include genomics and bioinformatics, GIS/GPS, and high-precision satellite imaging. These are just the beginnings of a digital revolution in agriculture. Agricultural research will be profoundly affected by the development of digitized image analysis for crop phenotyping. Sophisticated imaging acquisition technologies will provide a digital signature for plant phenotypes. Advanced image analysis software utilising high-performance computation will convert the science of plant breeding from an analogue-to-digital activity to a digital-to-digital activity, allowing genotypes to be linked to phenotypes computationally. By analogy to current use of genomic bioinformatics to identify genes and functions, optimised breeding strategies will be determined by algorithms, which streamline the process of building elite germplasm. This transition will depend on advances in photonics, tomography, image recognition, and computational analytics much more than it will depend upon plant biology, but its effects on plant breeding will be profound. At a field level, the acquisition of data through imaging, sensing, and agrimetrics will result in large databases from which trends and correlations will emerge. These will be useful to individual farmers planning an optimal (and sustainable) cultivation strategy over several years. However, they will also be vital for national and international efforts to adapt crops to a changing climate.

Corresponding author: E-mail: gifs.director@usask.ca

SYMP-07

CRISPR RNA-guided Genome Editing in Human Stem Cells, Animals, and Plants

Jin-Soo Kim

Center for Genome Engineering, Institute for Basic Science, Seoul, Korea
Department of Chemistry, Seoul National University, Seoul, Korea

Genome editing that allows targeted mutagenesis in higher eukaryotic cells and organisms is broadly useful in biology, biotechnology, and medicine. We have developed ZFNs, TALENs, and Cas9 RNA-guided endonucleases (RGENs), derived from the type II CRISPR-Cas prokaryotic adaptive immune system, to modify chromosomal DNA in a targeted manner. In particular, we used purified Cas9 protein and in vitro transcribed guide RNAs rather than plasmids encoding these components to correct large chromosomal inversions in the blood coagulation factor VIII gene that cause hemophilia A in patient-derived induced pluripotent stem cells (iPSCs) and to modify diverse genes in large animals and plants. The resulting animals and plants contained small insertions or deletions (indels) at target sites, which are indistinguishable from naturally-occurring variations, possibly bypassing regulatory requirements associated with use of recombinant DNA.
Despite broad interest in RNA-guided genome editing, RGENs are limited by off-target mutations. We developed Cas9 nuclease-digested whole genome (digenome) sequencing (Digenome-seq) to profile genome-wide specificities of Cas9 nucleases in an unbiased manner. Digenome-seq captured nuclease cleavage sites at single nucleotide resolution and identified off-target sites at which indels were induced with frequencies below 0.1%. We also showed that these off-target effects could be avoided by using modified guide RNAs that contain two extra guanine nucleotides at the 5' end. Digenome-seq is a robust, sensitive, unbiased, and cost-effective method for profiling genome-wide off-target effects of programmable nucleases including Cas9.

Corresponding author: E-mail: jskim01@snu.ac.kr

SYMP-08

CRISPR Genome Editing in Outcrossing Woody Perennials

Chung-Jui Tsai

University of Georgia, USA

The CRISPR/Cas9 technology is revolutionizing all facets of biology from medicine to agriculture, owing to its precision, efficiency, versatility and ease of adoption. We recently reported the first application of CRISPR/Cas9 in stably transformed *Populus*, extending the species range of this powerful technology to woody perennials. We achieved 100% mutational efficiency in two 4-coumarate:CoA ligase (*4CL*) genes tested—all stably transformed plants contain bi-allelic DNA modifications. The primary transformants exhibited strikingly uniform phenotypes among independent transgenic lines, a consistency that is unmatched by previous gene silencing methods. With its specificity, CRISPR/Cas9 offers a less equivocal means than previous approaches for discerning functional redundancy of paralogous genes that are prevalent in plant genomes. For instance, CRISPR mutation of the Class I, lignin-associated *4CL1* resulted in reduced lignin content and S/G monolignol ratio, with a reddish-brown discoloration throughout the stem wood. Its genome duplicate *4CL5*, however, was unaffected. Class II *4CL* has been associated with flavonoid biosynthesis based on its expression pattern, but this function has not been confirmed by reverse genetics. CRISPR mutation of *Populus 4CL2* resulted in significantly reduced levels of condensed tannins in roots without affecting stem lignin. An underappreciated obstacle in genome editing of outcrossing species is the frequent occurrence of sequence polymorphisms that can render CRISPR/Cas9 unproductive. However, current genomic resources and CRISPR gRNA design tools do not support exploration of sequence variations. We present experimental evidence as well as genome-wide computational analysis to demonstrate the sensitivity of CRISPR/Cas9 to allelic heterozygosity, and discuss tools and strategies that can help deal with such sequence polymorphisms. The ability to generate "instant-nulls" by the CRISPR/Cas9 system is highly desirable for woody perennials with long generation cycles. When used in conjunction with early flowering strategies, transgene-free progenies can be obtained in one breeding generation. Elite clones carrying targeted gene mutation(s) without foreign DNA may ultimately help increase public acceptance of bioengineered agricultural products.

Corresponding author: E-mail: cjtsai@uga.edu

구두 발표

OA-01

Genetic Analysis of Shoot Fresh Weight in Soybean Using an Interspecific Cross of PI483463 and Hutcheson

Krishnanand P. Kulkarni, Sovetgul Asekovaa, Minsu Kim, Cheol-Woo Park, Jae-Eun Jeong, Jong Tae Song, Jeong-Dong Lee*

School of Applied Biosciences, Kyungpook National University, Daegu 41566, Korea

Shoot fresh weight (SFW) is one of the parameters, used to assess the total plant biomass yield in soybean. In this study, a total of 188 F5:8 recombinant inbred line (RILs) derived from an interspecific cross of PI483463 (*Glycine soja*) and Hutcheson (*Glycine max*) were investigated for SFW variation for three consecutive years. The parental lines along with RILs were phenotyped in the field at the R6 stage by measuring total biomass in kg/plot. The phenotypic variation (PV) was exploited to identify SFW QTLs. Three QTLs qSFW6_1, qSFW15_1, and qSFW19_1 for SFW were identified on chromosome 6, 15 and 19 respectively. The QTL qSFW19_1 flanked within the markers BARC-044913-08839 - BARC-029975-06765, was the consistent QTL expressed in all the three environments. The PV explained by the QTLs across all environments ranged from 6.56 to 21.32%. The negative additive effects by the consistent QTL indicated contribution of SFW from wild parent. Additive x environment interaction effects affected the expression of SFW QTL. Screening of the RIL population with additional SSRs from the qSFW19_1 region delimited the QTL within the markers SSR19-1329 - BARC-29975-06765. QTL mapping using bin map detected two QTLs, qSFW19_1A and qSFW19_1B. The QTL qSFW19_1A mapped close to the Dt1 gene locus, which affects stem termination, plant height and floral initiation in soybean. Prospective candidate genes for SFW were pinpointed and sequence variations within their sequences were detected using high quality whole genome resequencing data. The findings in the present study could be valuable in understanding genetic and molecular basis of SFW in forage soybean.

Corresponding author: Tel. 053-950-5709, E-mail: jdlee@knu.ac.kr

OA-02

Identification of Candidate Genes Conferring to Resistance to Foxglove Aphid in Soybean

Sumin Park[1], Eunsil Kim[1], Mijung Cho[1], Kyung Hye Kim, Jin Kyo Jung[2], Jeong-Dong Lee[3], Ju Seok Lee, Sungtaeg Kang[1*]

[1]Department of Crop Science and Biotechnology, Dankook University, Cheonan 330-714, Korea
[2]National Institute of Crop Science, RDA, 151 Seodun-dong, 441-857, Korea
[3]Division of Plant Bioscience, Kyungpook National Univ, Daegu 702-701, Korea

The sap-sucking insects infect a wide of plants worldwide and causes serious yield losses in soybean, especially. The objective of this study was to identify the putative genes to foxglove aphid resistance in wild soybean, PI 366121 (*Glycine soja* Sieb. and Zucc.). One hundred and forty-one F4:8 recombinant inbred lines developed from a cross between susceptible variety, Williams 82 and foxglove aphid resistance wild soybean, PI 366121 were used. The two type of resistance response, antibiosis and antixenosis resistance were evaluated through choice and no-choice test, graded by the degree of total plant damage and primary infestation leaf damage; a genome-wide molecular linkage map was constructed with 29,898 single-nucleotide polymorphism markers utilizing a Axiom® 180K soyaSNP array. Using inclusive composite interval mapping analysis for foxglove aphid resistance, one major candidate QTL on chromosome 7 was identified. The major QTL on chromosome 7 showed both antixenosis and antibiosis resistance responses. The newly identified major QTL was consistent with previously reported QTL, *Raso2*, which showed around 5 times narrow down interval range with 8 candidate genes. This result could contribute to breeding for new foxglove aphid resistant soybean cultivar.

Corresponding author: Tel. 010-3551-0534, E-mail: kangst@dankook.ac.kr

OA-03

침수처리에 따른 콩 생육특성 및 저항성 자원 선발

조미정[1], 박수민[1], 김은실[1], 김경혜[1], 문준경[2], 이주석[1], 강성택[1*]

[1]충청남도 천안시 단대로 119 단국대학교 생명자원과학대학 식량생명공학과
[2]전북 완주군 농생명로 370 농업생명자원부 농생물게놈활용연구사업단

최근 전세계적 환경변화에 따른 장기간의 계절적 강우나 배수불량으로 인한 침수 피해는 작물의 생장과 수확량에 영향을 미쳐 심각한 문제가 되고 있다. 현재까지 이러한 문제를 해결하기 위해서 내습성 품종개발 등에 대한 연구는 일부 있지만 생육특성에 대한 정확한 유전자 관련 연구는 거의 없는 실정이다. 따라서 본 연구는 콩에서 침수저항성 자원을 선발하고 선발자원의 생육특성을 규명하며 간이선발방법을 개발하여 침수피해 경감기술 개발에 도움을 주고자 실시하였다. 콩 유전자원 약4,000종을 침수처리 및 식물체 반응을 조사 하였고, 식물체 반응 조사 결과에 따라 저항성자원을 선발하고, 선발된 저항성자원을 정밀검정 하였다. 또한 포장처리는 명확하게 저항성자원을 선발 할 수 있으나 시간이 오래 걸리고 노력이 많이 들어 육종 등에 쉽게 이용 할 수 없기 때문에 간이 검정법 개발이 필요하게 되어 간이 검정법을 개발했다. 약 4,000종의 콩 유전자원에서 식물체 반응 조사 결과를 바탕으로 16종의 저항성자원을 선발하였고 이 중 줄기와 뿌리의 부패정도가 현저히 낮은 저항성자원 3점을 최종 선발하여 생육특성을 정밀검정한 결과 부정근수와 제1복엽의 엽색 변화정도가 침수처리에 따른 저항성 및 감수성자원을 구분 짓는 우수한 지표임이 확인되었다. 개발된 간이 검정법으로 검정한 결과 부정근수가 침수처리에 따른 저항성 및 감수성자원을 구분 짓는 우수한 지표임을 확인하였다.

Corresponding author: Tel. 041-550-3621, E-mail: kangst@dankook.ac.kr

OA-04

한국 밀 품종 육성현황 및 발전방향

강천식[1*], 정영근[1], 김경훈[2], 손재한[1], 김학신[3], 박종철[1], 오영진[1], 김경호[1], 이광원[1], 김보경[1], 박철수[4]

[1]전라북도 완주군 이서면 혁신로 국립식량과학원 작물육종과
[2]경상남도 밀양시 점필재로 국립식량과학원 논이용작물과
[3]전라북도 완주군 이서면 혁신로 국립식량과학원 작물재배생리과
[4]전라북도 전주시 덕진구 백제대로 농업생명과학대학 작물생명과학과

밀은 세계 3대 작물 중 하나이며 약 126개국에서 2억 2,427만ha를 재배하여 7억 만 톤가량을 생산하고 있다. 국내에서도 약 10천ha 정도를 재배하여 4만 2천 톤을 생산하고 있다. 국내 밀 품종은 1970년 이후 답리작 적응 조숙 다수성 밀 품종개발을 목표로 진행한 결과 현재까지 38품종이 개발되었다. 정부보급종은 2009년 금강밀 1품종, 162톤을 공급하기 시작하여 2016년은 금강밀 등 4품종을 농가에 보급할 예정이다. 38품종 중 금강을 포함한 30품종이 중력분용으로 이용되고 있으며, 강력분용으로 조경과 백강 2품종, 박력분으로 고소, 조아와 우리 3품종, 취반용으로 백찰, 신미찰과 신미찰1호 3품종이 개발되었다. 육종성과 중 성숙기의 경우 1970년대는 6월 13일에서 2010년대 6월 3일로 10일 단축되었고, 수량은 1970년대 408kg/10a에서 2010년대 532kg/10a로 124kg 증수하였다. 2010년 이후에는 용도별 다양한 밀 품종을 개발하였는데, 과자용, 케이크용, 국수용, 빵용, 백립계 찰밀 등 용도의 다양화가 이루어졌다. 재해안정성 부분에서는 수발아와 붉은곰팡이병 저항성인 새금강이 개발되었다. 최근 이상기후로 인하여 기존에 보고되지 않았던 생리장애와 병 등이 발생되어 생산량과 품질을 떨어뜨리고 있다. 이러한 시점에서현재까지의 답리작 적응 조숙 다수성 용도별 품종 개발을 지속적으로 진행하고, 생산안정성과 품질유지를 위한 생리장애와 병에 저항성을 증진시키기 위해 더욱더 노력하여 국산 밀 자급률 향상에 이바지해야 할 것으로 판단된다.

Corresponding author: Tel. 063-238-5227, E-mail: kcs1209@korea.kr

OA-05

벼흰잎마름병 저항성 유전자가 집적된 자포니카 벼 계통 개발

박현수[1*], 김기영[2], 김우재[1], 정지웅[1], 이종희[2], 노태환[1], 남정권[1], 백만기[1], 신운철[1], 김정주[1], 정종민[1], 조영찬[1], 김보경[1], 안상낙[3]

[1]전라북도 완주군 이서면 혁신로 181 농촌진흥청 국립식량과학원
[2]전라북도 전주시 완산구 농생명로 300 농촌진흥청 연구정책국
[3]대전광역시 유성구 대학로 99 충남대학교 농업생명과학대학

우리나라 자포니카 벼 품종의 벼흰잎마름병 저항성 증진을 위하여 네 개의 저항성 유전자 *Xa1, Xa3, xa5* 및 *Xa21*이 집적된 우량 계통을 개발하였다. *Xa1* 저항성 유전자를 보유한 '일미벼'와 *Xa3*+*xa5*+*Xa21*이 집적된 '익산575호'간 인공교배를 하였다. 분리세대에서 저항성 유전자 연관 분자표지 선발, 벼흰잎마름병 저항성 생물검정 및 농업형질에 대한 표현형 선발을 함께 적용하여 네 개의 저항성 유전자가 집적된 약배양 유래 7 계통과 계통육종 유래 10 계통을 각각 개발하였다. F2 집단에서 *Xa1*+*Xa3*+*xa5*+*Xa21* 저항성 유전자가 집적된 조합이 가장 강한 저항성 반응을 나타냈다. 이 조합은 *Xa3*+*xa5*+*Xa21*에 비해 향상된 저항성 반응을 나타내 저항성 유전자 집적에 따른 저항성 증진 효과를 확인하였다. 네 개의 저항성 유전자 집적 계통들은 국내 수집 벼흰잎마름병 균주 16개에 대해서 광범위 저항성을 나타냈으며, 병원성이 강한 K3a 균계 접종 시에도 수량성 감소 및 품질 저하가 관찰되지 않았다. 이들 계통들은 초형이 양호하고 '진백' 등 이전의 저항성 품종들에 비해서 수량성이 증가하였다. 네 개의 저항성 유전자 집적 조합 *Xa1*+*Xa3*+*xa5*+*Xa21*은 효율적이고 유망한 저항성 유전자 집적 조합으로 판단되었고, 개발된 저항성 유전자 집적 계통들은 자포니카 벼의 흰잎마름병 저항성 증진을 위한 유용한 육종소재로서 활용될 것으로 생각된다.

Corresponding author: Tel. 063-238-5216, E-mail: mayoe@korea.kr

OA-06

Disruption-Mediated Functional Characterization of Rice Defense-Related Genes Selected Through Genome-Wide Association Study for Core Population

Feng Peng Li[1], Won-Hee Ra[1], Kyu-Won Kim[1], Yoo-Hyun Cho[2], Shin-Chul Bae[3], Duk-Ju Hwang[3], Sang-Ryeol Park[3], Yong-Jin Park[1], Il-Pyung Ahn[3*]

[1]Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 32439, Korea
[2]Seedpia Corporation, Suwon 16395, Korea
[3]National Institute of Agricultural Sciences, Rural Development Administration, Jeonju 54874, Korea

Rice blast is one of the most notorious diseases and breeding employing resistant germplasms have been intensively performed during the last four decades, however, frequent resistance breakdown by domination of new or endemic races still causes serious problems worldwide and available germplasms are practically limited. To find resistant resources more efficiently, genome-wide association study (GWAS) was applied for comparative analysis of the relationship between nucleotide polymorphisms (NPs) and responses induced by infections of rice blast pathogen, KI197 and KJ401, in the Korean rice core set (KRICE_CORE) composed of 295 accessions. Nipponbare genome was used as a reference. Disease responses were also enumerated in the near-isogenic lines each containing single blast resistance gene to reveal effector spectrum of both races. GWAS analysis revealed significant relationships between variations of blast disease responses and NPs located on the chromosomes Ⅰ, Ⅱ, Ⅲ, Ⅳ, Ⅵ, Ⅸ, and Ⅻ. As most of the reported qualitative disease resistance genes have nucleotide-binding site-leucine rich repeat (NBS-LRR) motif, NBS-LRR genes were analyzed within 200 kb regions harboring meaningful NPs. Finally, eleven potent candidates were further found as novel blast resistance-conferring NBS-LRRs. For functional characterization of these candidates, genome editing methods such as Transcription Activator-Like Effector Nucleases (TALEN) and Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)/CRISPR-associated protein 9 were established. A hub gene for rice defense signaling, *OsNPR1/NH1*, and a structural gene mediating gibberellin biosynthesis, *GERANYL GERANYL PYROPHOSPHATE SYNTHASE* (*OsGGPPS1*), were chosen for these experiments. TALEN-mediated *OsNPR1/NH1* and *OsGGPPS1* disruptions resulted in the genes' disruption and loss of basic resistance and stunting in the transgenic plants, respectively. More accurate GWAS and haplotyping is under progress, and characterization of candidate genes will be performed.

Corresponding author: Tel. 063-238-4668, E-mail: jinhyung@korea.kr

OA-07

Development of Cultivar-specific DNA Markers Based on Ty1-*copia*-like Retrotransposon-based Insertional Polymorphism in Pear (*Pyrus pyrifolia*)

Hoy-Taek Kim, Jong-In Park, Ill-Sup Nou*

Department of Horticulture, Sunchon National University, 255, Jungang-ro, Suncheon, Jeonam 57922, Korea

Retrotransposons are present in all plant genomes and play important roles in genome size, genome structure remodeling, gene function, and genome evolution. Eight novel long terminal repeat retrotransposons were identified from a bacterial artificial chromosome library of Japanese pear (*Pyrus pyrifolia*). These newly identified retrotransposons appear to be closely related to Ty1-*copia* retrotransposons. *Ppcrt*1-8 were grouped with the *copia*-like retrotransposons *RIRE1* and *BARE-1* by phylogenetic analysis based on the amino acid sequences encoded by the *gag* and *pol* domains. Fluorescence in situ hybridization analysis showed that sequences homologous to *Ppcrt*4 were dispersed throughout more than half of the pear chromosomes.

We also developed retrotransposon-based insertional polymorphism (RBIP) markers based on the long terminal repeat (LTR) sequences of *copia*-like retrotransposon *Ppcrt*4 and flanking genome sequences, which were derived from 454 sequencing data from Japanese pear (*Pyrus pyrifolia*) 'Hosui'. Out of 40 sequences including both LTR and flanking genome regions, we developed 22 RBIP markers and used them for DNA profiling of 80 pear cultivars: 64 Japanese, 10 Chinese (*Pyrus ussuriensis*) and 6 European (*Pyrus communis*).

Three RBIP markers were enough to differentiate 'Hosui' from the other Japanese pear cultivars. The 22 RBIP markers could also distinguish 61 of the 64 Japanese pear cultivars. European pears showed almost no amplification of the 22 RBIP markers, which might suggest that retrotransposons had transposed during Asian pear evolution or reflect the genetic relationship between Asian and European pears. Sixteen of the RBIP markers could be positioned on a genetic linkage map of 'Hosui'. The RBIP loci were distributed in 10 linkage groups, and some loci were very closely located within the same linkage group. The information obtained will be applicable to developing cultivar-specific RBIP marker sets in plants.

Acknowledgements: This research was supported by Golden Seed Project (Center for Horticultural Seed Development, No. 213003-04-4-SB110) Ministry of Agriculture, Food and Rural Affairs (MAFRA), Ministry of Oceans and Fisheries (MOF), RDA and Korea Forest Service (KFS).

Corresponding author: Tel. 061-750-3249, E-mail: nis@sunchon.ac.kr

OA-08

Breeding for Pyramiding Target-genes and Selection of F_1 Hybrids by Marker Assisted Selection in Tomato

김명권

충북 청주시 흥덕구 강내면 월곡길, 토마토생명과학연구소

토마토 육종에서 과품질과 내병성이 중요한 요소이다. 내병성, 과품질, 과색 관련 유전자를 분자마커로 계통선발과 F_1 Hybrid 선발에 활용하였다. 내병성 마커로 토마토황화잎말림바이러스(Ty1, Ty2, Ty3), 토마토모자이크바이러스(Tm2a), 토마토반점시들음바이러스(Sw5), 시들음병(I2, I3), 반신위조병(V), 근부위조병(Forl), 역병(Ph3), 잎곰팡이병(Cf9), 선충(Mi1) 등을 검정하였고, 저장성 마커로 Rin gene, 과색 마커로 Orange, Yellow, Brown, Pink color 등을 검정하여 유묘기에 1차로 선발하고, 정식포장에서 최종선발된 계통과 F_1 hybrid를 다시 확인하였다. Marker Assisted Selection으로 육성한 토마토 6품종을 개발하여 농가에 보급 판매하고 있다.

Corresponding author: Tel. 043-235-3368, Fax. 043-235-3369, E-mail: mkkim207@naver.com

OA-09

Characterization and Stress-responsive Expression Profiling of *MCM* genes in *Brassica*

Ashokraj Shanmugam, Hoy-Taek Kim, Jong-In Park, Ill-Sup Nou*

Department of Horticulture, Sunchon National University, 255, Jungang-ro, Suncheon, Jeonam 57922, Korea

Minichromosome maintenance protein complex [MCM(2-7)] is an important replication factor which is activated at S-phase of cell cycle. This hexamer possesses helicase activity, which are regulated by various replication factor that forms the replication fork over double stranded DNA to process replication. Apart from MCM(2-7) complex, other *MCM* genes are also present which regulates the helicase activity of the hexamer. In yeast and mammalian cells, subunits of MCM(2-7) are regulated during replication stress, that has suggested to plants as well. Hexamer complex are also positively regulated during cold and salinity stresses in plants. In this study, we identified, characterized and modelled the tertiary structure of 12 *MCM* genes each from *B. oleracea* and *B. rapa* which possess two functional domains namely MCM_N and AAA (ATPases Associated) domain. Evolutionary relationship between these *MCM* genes are deduced using syntenic and phylogenetic analysis in *B. oleracea* and *B. rapa*. Expression profiling of MCM(2-7) complex genes and other *MCM* genes showed slight variation between *B. oleracea* and *B. rapa* during different stresses (replication stress, cold and salinity). Likewise, within the species, *MCM* gene expression exhibited differentially response when exposed to replication stress, cold and salinity stresses with variation in subunit genes of the complex. Overall study showed that *MCM* genes are conserved and closely related in *B. oleracea* and *B. rapa* for the proper normal DNA replication fork formation. Our expression profiling supported that *MCM* complex genes are significantly responding under replication stress, cold and salinity stresses. Therefore, we proposed that *MCM* are tolerance related genes during the respective abiotic stresses and the extension of structural, functional and molecular studies will be helpful for implication of *MCM* genes in stress biology in plants.

Acknowledgements: This research was supported by Golden Seed Project (Center for Horticultural Seed Development, No. 213003-04-4-SB110) Ministry of Agriculture, Food and Rural Affairs (MAFRA), Ministry of Oceans and Fisheries (MOF), RDA and Korea Forest Service (KFS).

Corresponding author: Tel. 061-750-3249, E-mail: nis@sunchon.ac.kr

OA-10

Classical and GBS-based QTL mapping downy mildew resistance loci in cucumber

Khin Thanda Win[1], Chunying Zhang[1], Sanghyeob Lee[1,2*]

[1]Plant Genomics Laboratory, Department of Plant Biotechnology, College of Life Sciences, Sejong University, 209 Neungdong-ro, Gwanjing-gu, Seoul 143-747, Korea
[2]Plant Biotechnology Research Institute, Sejong University, 209 Neungdong-ro, Gwanjing-gu, Seoul 143-747, Korea

Downy mildew (DM) 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 DM resistance in cucumber are not well understood. A QTL mapping study of DM resistance was conducted with 149 F2 population derived from two cucumber inbred lines R (resistant) and S (susceptible). A genetic map covering 811.7 cM in seven linkage groups was developed with 100 SSR marker loci. The 18 F2 individuals showed significant resistance and susceptible phenotype were applied GBS-based QTL analysis. Both QTL mapping analysis revealed four QTLs on chromosome 2, 4, 5 and 6. Detail information will be presented

Acknowledgements: This work was supported by grants from Bio-industry Technology Development Program (111057-5) of iPET (Korea Institute of Planning and Evaluation for Technology in Food, Agriculture and Forestry) and Korea-China Collaborative Research Program (NRF-2015K2A2A2001928) of NRF (National Research Foundation of Korea).

Corresponding author: Tel. 82-2-3408-4375, E-mail: sanglee@sejong.ac.kr

OA-11

Genome Wide Characterization and Expression Profiling of Aquaporin Gene Family in *Brassica rapa* for Responsiveness to Abiotic and Biotic Stresses

Md. Abdul Kayum, Hoy-Taek Kim, Jong-In Park, Ill-Sup Nou*

Department of Horticulture, Sunchon National University, 255 Jungang-ro, Suncheon, Jeonnam 540-950, Korea

Aquaporin (AQP) genes are those which have been so far reported as responsive for water transportation in plants. The aquaporin proteins are present in diverse forms in plants, where they function in transport of water and other nutrient molecules through living membranes, and might be essential for survival under salt and drought stresses. In this study, we have explored and identified 59 *BrAQP* genes from genome sequence data of *B. rapa* database and Br135K microarray dataset. Phylogenetic analysis of *BrAQPs* with *AQPs* from tomato (*Solanum lycopersicum*) and *Arabidopsis thaliana* revealed four distinct subfamilies, including plasma membrane intrinsic proteins (PIPs), tonoplast intrinsic proteins (TIPs), NOD26-like intrinsic proteins (NIPs), and small basic intrinsic proteins (SIPs). Here, we have selected PIP subfamily genes for detailed expression analysis through differential expression in microarray data and to find their homology to stress related *AQPs* in *B. rapa*. All *BrPIP* genes showed organ-specific expression. Eventually, we have also analyzed the expression of PIP subfamily genes in response to cold, salt, drought, and water logging conditions as well as ABA (abscisic acid) treatment and *Fusarium oxysporum* f. sp. *conglutinans* infection. Twelve out of 22 *BrPIP* genes were differentially expressed upon cold treatment in two *B. rapa* inbred lines (Chiifu and Kenshin). Seven *BrPIP* genes showed up-regulation under drought stress and 17 *BrPIP* genes were responsive to salt stress. Whereas, 18 *BrPIP* genes were up-regulated by ABA treatment, and all *BrPIP* genes showed down-regulation under water logged condition stress. Four *BrPIP* genes were found responsive to *F. oxysporum* f. sp. *conglutinans* infection. Therefore, this study gives a comprehensive report of *AQPs* in *B. rapa* on expression profile 22 members of the *BrPIP* subfamily, which could be provided a basis to elucidate the stress-related biological functions of specific PIP gene.

Acknowledgements: This research was supported by Golden Seed Project (Center for Horticultural Seed Development, No. 213003-04-4-SB110) Ministry of Agriculture, Food and Rural Affairs (MAFRA), Ministry of Oceans and Fisheries (MOF), RDA and Korea Forest Service (KFS).

Corresponding author: Tel. 061-750-3249, E-mail: nis@sunchon.ac.kr

OB-01

Role of Flowering Pathway Genes on Anthocyanin Biosynthesis and Accumulation in *Brassica rapa*

Ujjal Kumar Nath[1], Md. Abdul Kayum[1], Rawnak Laila[1], Khadiza Khatun[1], Jong-In Park[1], Ill-Sup Nou[1*]

Department of Horticulture, Sunchon National University, 255 Jungang-ro, Suncheon, Jeonnam 540-950, Korea

Anthocyanins are secondary metabolites in plants responsible for various colour formations in plant parts and their products. It is marked as potential source of antioxidant and plays a pivotal role in overcome stresses. Recent report on potential health benefits of anthocyanins brings attention to develop Brassica vegetables with high anthocyanins accumulations in different vegetative parts for consumption. The mechanisms of anthocyanins accumulation, deposition and its physiological functions are poorly understood in Brassica. In the purple Chinese cabbage (*Brassica rapa*) the anthocyanins production and accumulation remain as usual up to vegetative phase. However, the leaf pigmentation becomes fade-out when plants enter into reproductive phase with blooming of flowers. This observation creates interest to know the role of flowering pathway genes on anthocyanins biosynthesis and accumulation. To confirm this hypothesis, a Chinese cabbage inbred line Re20 (green leaf with coloured mid-rib) was crossed with another inbred line of Asia seed (designated as Asia: coloured leaf with green mid-rib). F_1 plants were confirmed and selected with the presence of coloured pigmentation both in leaf and mid-rib. Fifty eight F_2 progenies were produced by selfing from one of the best F_1 plant. RNA was extracted from all of the plant leaf blade and mid-rib separately. 7 F_2 plants were selected based on relative expression of anthocyanin biosynthesis genes and they were selfed for producing F_3 progenies. F_3 lines were grown in 5 replicates and leaf samples were collected from all the plants before put into vernalization and at first week after six weeks of vernalization. Complementary DNA (cDNA) was synthesized using SuperScript®III First Strand cDNA kit from invitrogen. Real time quantitative PCR (qRT) was performed using 12 anthocyanins biosynthesis pathway genes including phenylpropanoid pathway(*PAL, C4H, 4CL*), early biosynthesis pathway (*CHS, CHI, F3H, F3'H*), late biosynthesis pathway (*DFR, ANS, UFGT, MYB, TT*) and five flower regulatory genes including *VRN*, *FRIGIDA* and *FLC*. Relative expression was calculated following $2^{-\Delta\Delta C_T}$ method using cq value. The correlations, multiple regressions and path-coefficient analysis results of F_2 revealed that flower integrator genes had negative effect on anthocyanin accumulation during flowering in *B. rapa.* This result will be confirmed by the expression profiling and estimating anthocyanins in F_3 progeny. Meanwhile, genes involved in flower pathway and anthocyanin pathway were also found co-up or co-down regulated accompanied with the accumulation of anthocyanin in leaves which indicated the possible interaction between anthocyanin and flowering genes.

Acknowledgements: This research was supported by Golden Seed Project (Center for Horticultural Seed Development, No. 213003-04-4-SB110) Ministry of Agriculture, Food and Rural Affairs (MAFRA), Ministry of Oceans and Fisheries (MOF), RDA and Korea Forest Service (KFS).

Corresponding author: Tel. +82 61 750 3249, Fax: +82-61-750-3208, E-mail: nis@sunchon.ac.kr

OB-02

Leaf Developmental and Genotypic Variations in Wax Content, Composition and Expression of Wax Biosynthetic Genes in The Inbred Lines of Brassica Oleracea Var. Capitata

Rawnak Laila, Kiwoung Yang, Arif Hasan Khan Robin, Mi Chung Suh, Juyoung Kim, Jong-In Park and Ill-Sup Nou*

Department of Horticulture, Sunchon National University, Suncheon, Korea
Department of Bioenergy Science and Technology, Chonnam National University, Gwangju, Korea

Cuticular waxes act as a protective barrier against environmental stresses. The present study was conducted to investigate the leaf developmental and genotypic variations in cuticular wax content, composition and expression level of wax biosynthetic genes in two high-wax depositing and two low-wax depositing cabbage lines. Wax deposition analyzed cuticular wax composition for the leaves of 20 days of age collected from the 10 week old plants. The waxy compounds in all cabbage lines were predominated by C_{29}-alkanes, -secondary alcohols and-ketones. Relative expression level of wax biosynthetic genes was measured at three different growth stages. Gene expression level at the first-formed leaf of the highest wax depositing line accounted consistently higher at three sampling points collected weekly interval but that decreased in other genotypes with increasing leaf age. In 10 weeks old plants, expression level of genes generally increased from the youngest leaf to leaves at position 3-4 at the stem axis but that greatly declined at the leaf positions 8 and 12. Overall, expression level of wax biosynthesis genes decreased at the older leaves. Principal component analysis revealed that higher level of relative expression level of *LTP2* genes in the lowest wax depositing line and higher level of relative expression of *CER3* gene in the highest wax depositing line probably determined comparatively lower and higher wax content in those two lines. Results of this study might be useful in modelling wax development pattern in cabbage plants and also to develop cabbage varieties with desired level wax contents. This study was supported by the Golden Seed Project (Center for Horticultural Seed Development, No. 213003-04-4-SB110) of the Ministry of Agriculture, Food and Rural Affairs in the Republic of Korea (MAFRA).

Corresponding author: E-Mail: nis@sunchon.ac.kr

OB-03

EMS 돌연변이체 PE1905의 사포닌 특성 및 유전 연구

박철우[1], 송종태[1], 정규화[2], 이정동[1*]

[1]대구광역시 북구 산격동 경북대학교 농업생명과학대학
[2]전라남도 여수시 대학로 50 전남대학교 여수캠퍼스 생명화학 공학부

풍산나물콩을 EMS 처리하여 얻은 돌연변이체 892라인을 TLC 분석하여 사포닌 변이개체인 PE1905를 선발하였다. PE1905와 풍산나물콩의 하배축을 LC-MS 분석한 결과 돌연변이체인 PE1905에서는 wild type인 풍산나물콩 보다 Af 사포닌이 3배 이상 증가하였고 Ac 사포닌 또한 1.5 배 증가하였다. 반면에 Ab 사포닌은 10% 감소하였고, DDMP 사포닌 α g와 β g또한 감소하는 것을 알 수 있었다(각각 75%, 37% 감소). 또한 PE1905에서 새로운 물질이 생성되는 것을 확인하였고 분석결과 지금까지 발견되지 않은 Af 사포닌과 Ab 사포닌의 전구체로 추정된다.
변이체의 유전특성 연구를 위해 wild type인 풍산나물콩과 교배하여 F_1 종자를 얻었고 이를 다시 파종하여 얻은 F_2 종자를 TLC 해본 결과 wild type과 mutant type의 비가 3:1로 나타났으며 F_2 종자를 파종하여 얻은 $F_{2:3}$ 계통을 수확하여 TLC 분석을 해본 결과 wild type 동형접합 개체와, 이형접합 개체, mutant type 동형접합 개체가 1:2:1 로 분리되는 것을 확인 했고 이를 통해 PE1905 돌연변이체의 표현형은 단일열성유전자에 의해 나타나는 것으로 평가되었다. 새롭게 발견된 사포닌 변이체는 사포닌의 생합성 경로를 연구하는데 중요한 재료가 될 것으로 평가된다.

Corresponding author: Tel. 053-950-5709, E-mail: jdlee@knu.ac.kr

OB-04

Comparative Phylogenomics to Elucidate The Effects of Whole Genome Triplication Event on *glutathione transferases* Superfamily Genes in *Brassicaceae*

Harshavardhanan Vijayakumar, Senthil Kumar Thamilarasan, Jong-In Park, Ill-Sup Nou*

Department of Horticulture, Sunchon National University, 255, Jungang-ro, Suncheon, Jeollanam-do 57922, Korea

Glutathione *S*-Transferases (GSTs) are a group of multigenic enzyme family, which catalyze the addition of glutathione to the broad range of substrates for ubiquitination. Plant GSTs are mainly known for their degradation mechanism, however, they are involved in other secondary metabolite pathways which aid plant growth development and tolerance against various biotic and abiotic stresses. These superfamily enzymes are divided into 14 classes in green plants based on conserved motifs and catalytic sites (Ser/Cys), of which Tau, Phi, DHAR (dehydroascorbate reductases) and Lambda are plant specific GSTs. In this study, 431 GSTs were identified in *Arabidopsis thaliana* (70), *Brassica oleracea* (91), *Brassica rapa (*89) and *Brassica napus (*181) by a strategic computational *in silico* analysis. Based on catalytic sites and phylogenetic analysis, 431 GSTs were grouped into 11 classes and also evolutionary analysis showed that iota, hemerythrin and Ure2p are absent in Brassicaceae family. By macro- and micro-synteny analysis, we found that the duplicated regions were more conserved between *Brassica* species than *Arabidopsis*. Our data show that tandem duplication has been regarded as the major expansion mechanism in this superfamily. Non-synonymous substitutions per site (Ka) and synonymous substitutions per site (Ks) analyses showed that N- and C-terminal functional domains of GSTs (GST_N and GST_C) seem to have evolved under a strong purifying selection (Ka/Ks < 1). *Brassica* and *Arabidopsis* divergence occurred before 20-24 mya (million years ago), based on this *B. oleracea* GST genes were evolved rapidly after the *Brassica* split than other two *Brassica* species. Also, the evolution led to the formation of new genes with non-typical GST domains alone with GST domains. Our survey provides additional annotation of the GST gene family and there evolutionary divergence with *Brassicaceae*.

Acknowledgements: This research was supported by Golden Seed Project (Center for Horticultural Seed Development, No. 213003-04-4-SB110), Ministry of Agriculture, Food and Rural Affairs (MAFRA), Ministry of Oceans and Fisheries (MOF), Rural Development Administration (RDA) and Korea Forest Service (KFS).

Corresponding author: Tel. 061-750-3249, Email: nis@sunchon.ac.kr

OB-05

Molecular Breeding for Fruit Color in Tomato

Indeok Hwang, Hee-Jeong Jung, Song-I Kang, Ill-Sup Nou*

Department of Horticulture, Sunchon National University, 255 Jungangro, Suncheon, Jeonnam 57922, Korea

It is well known that color changes in tomato occur according to the amount of carotenoids, flavonoid and the presence/absence of chrolophyll. Most fruit flesh color is significantly correlated with carotenoid content in tomato. In other case, brown color is caused by *SlSGR1* mutation, which is related to chlorophyll degradation. Chlorophyll is not degraded in *SlSGR1* mutant, which results in its remaining in the flesh of the fruit and a brown color. The peel of pink-colored tomato is transparent due to the lack of accumulation of the flavonoid naringenin chalcone during ripening. A strong correlation was found between the expression and function of SlMYB12 with naringenin chalcone accumulation. Thus, *SlMYB12* is a strong candidate gene underlying the pink phenotype. Knock-out of *SlPSY1* can cause pale carotenoids, resulting in yellow colored flesh. Accordingly the inheritance of factors associated with tomato pigmentation (carotenoid, flavonoid and chlorophyll) has been investigated. In this study, we have identified a new position of mutations in *SlPSY1*, *SlMYB12* and *SlSGR1* by combining traditional breeding and the analysis of DNA/molecular markers. The data reported herein can be used as a DNA based marker during breeding and development of new tomato varieties, and enable improved color selection within adapted breeding materials and varieties.

Acknowledgements: This research was supported by the Golden Seed Project (Center for Horticultural Seed Development, No. 213003-04-4-SB110), Ministry of Agriculture, Food and Rural Affairs (MAFRA), Ministry of Oceans and Fisheries (MOF), Rural Development Administration (RDA) and Korea Forest Service (KFS).

Corresponding author: Tel. 061-750-3249, E-mail: nis@sunchon.ac.kr

OB-06

곡실발효사료 조제를 위한 사료맥종별 수확시기 및 발효품질

박종호*, 오영진, 정영근, 송태화, 박태일, 이광원, 김경호, 김양길, 박종철

전북 완주군 이서면 국립식량과학원 작물육종과

국내 배합사료 원료곡은 대부분 수입에 의존하고 있으며, 이를 국내산 곡실사료로 대체 시 외화절감 및 사료의 안정적 공급이 가능하다. 곡실사료용으로 맥류를 재배하여 이용시에는 수확시기의 분산이 가능하며, 값비싼 기계 및 인력을 더욱 효율적으로 사용할 수 있다. 본 연구는 국내 겉보리 품종에 대해서 수확시기별로 수량 특성과 발효품질의 차이를 분석하여 곡실발효사료에 적합한 겉보리 품종을 선정하고자 수행하였다. 2013년 ~ 2015년까지 수행하여 겉보리는 광안 등 6품종을, 쌀보리는 새쌀 등 5품종, 밀은 금강 등 5품종을 선정하여, 출수후 3일간격으로 보리는 24일부터 7회, 밀은 30일부터 5회 수확하여, 수량 및 pH 등 발효품질을 조사하였다. 시험결과 겉보리는 36일차에 pH4.2로 곡실발효 적합하였으며, 이후 수확에는 발효가 일어나지 않아 곡실발효에는 부적합하였다. 수량은 564kg/10a로 39일차, 42일차와도 유의적 차이가 없었으며, 사료품질은 단백질 함량은 12.7%, 조섬유 2.3%, TDN 80.2% 로 양호하였다. 쌀보리는 36일차에 pH4.5로 곡실발효에 적합하였으며, 이후 수확에는 발효가 일어나지 않아 곡실발효에는 부적합하였다. 수량은 489kg/10a였으며 39일차, 42일차와 유의적 차이를 보이지 않으면서 사료품질은 조단백질함량 14.9%, 조섬유 2.0%, TDN 76.6%로 양호하였다. 밀은 42일차에 pH4.3으로 곡실발효에 적합하였으며, 수량은 541kg/10a였으며, 조단백질 16.0%, 조섬유 2%, TDN 78.8% 사료품질이 양호하였으며, 42일차 이후 곡실발효 정도에 대한 추가 조사가 필요하다.

Corresponding author: Tel. 063-238-5228, E-mail: ark0104@korea.kr

OB-07

In vitro and *in vivo* Antioxidant Activity and α -glucosidase Inhibitory Potential of Major Phenolic Compound Isolated from Superhongmi (*Oryza sativa* L.) Varieties

Soo-In Jang[1], Hanna Kang[1], Suyeon Jang[1], Jung-Yun Lee[1], Tae-Ho Ham[2], Sung-Gil Hong[3], Su-Noh Ryu[2], Young-In Kwon[1*]

[1]Department of Food and Nutrition, Hannam University, Daejeon, 34054, Korea
[2]Department of Agriculture Science, Korea National Open University, Seoul,03087, Korea
[3]Erom R&D Center, Sungnam-Si, 13488, Korea

In the current study, we evaluated phenolic profile and oxygen radical absorbance capacity (ORAC) of Superhongmi (*Oryza sativa*; SHM). The inhibitory activity of SHM extracts against porcine pancreatic α -amylase and rat intestinal α -glucosidase was also investigated *in vitro* and *in vivo* animal model. Ethyl alcohol extract of SHM bran had the highest α -glucosidase inhibitory activity, ORAC value and total phenolic content, followed by ethyl alcohol extract of whole SHM, and water extract of whole SHM. In rat fed on sucrose meals, SHM significantly reduced the postprandial blood glucose increment after sucrose loading in a dose dependent manner. The α -glucosidase inhibitory activity of the extracts was compared to selected specific phenolics detected in the extracts using HPLC. Taxifolin, a flavanonol, a type of flavonoid, was isolated from the extract of SHM along with three known compounds. Their structures were elucidated by extensive spectroscopic analysis, including 1D and 2D NMR, and FTICR-MS. Taxifolin, a major phenolic compound in SHM extract had high α -glucosidase inhibitory activity. The α -glucosidase inhibitory activity of the SHM extracts correlated to the Taxifolin content and antioxidant activity of the extracts. These results suggest that Superhongmi which has high Taxifolin content has the potential to contribute as a dietary supplement for controlling hyperglycemia and oxidative stress-linked diabetes complications.

Corresponding author: Tel. 010-2238-7228, E-mail: youngk@hnu.kr

OB-08

식미 간접적 평가를 위한 기기활용 및 신속한 관능평가를 위한 해석

전재범[1*], 이점식[2], 윤미라[2], 이정희[3], 천아름[2], 김우재[1], 정지웅[1], 강경호[1], 김보경[1]

농촌진흥청 국립식량과학원 [1]작물육종과, [2]수확후이용과, [3]중부작물과

벼육종에서 신속한 식미 관능평가는 고품질품종을 육성하는데 필요한 부분이다. 그러나 관능평가는 1회에 4~5점 정도의 시료를 평가하게 되어 시간과 노력이 많이 소요된다. 그러므로 식미기기를 활용한 간접식미치로 관능평가를 추정하는 노력이 요구된다. 본 연구는 식미기기를 이용하여 어느 정도로 관능평가의 결과를 추정할 수 있는 가에 목적이 있다.
공시 재료는 2013~2014년 자포니카 19품종을 국립식량과학원 벼육종포장에서 재배 수확 후 90.4%로 도정하여 백미를 조제하였다. 각 시료에 대해 임의완전배치로 관능평가를 수행하였으며, Toyometer(MA-90R2)로 간접식미치를 측정하였다. 그리고 아밀로스 함량과 단백질 함량을 측정하였고 식미관능평가에 대한 추정을 간접식미치인 토요윤기치를 이용하여 잔차분석을 하였다.
그 결과 13~14년도에 수행한 관능평가와 간접식미치는 높은 상관성이 인정되었으며 결정계수는 14년도 r^2 = 0.7263 13년도 r^2 = 0.8096로 나타났다. 잔차분석 결과 `13와 `14에 공통적으로 제외되는 품종은 대야, 미품으로 이 두 품종이 제외된 공통 요인은 관능평가정도에 비해 간접식미치가 높게 나타났다. 특히 미품의 경우 14년도 간접식미치에서 93.76을 기록하여 가장 높은 값이었으나 관능평가에서는 중간정도에 위치하였다. 그러므로 관능평가와 간접식미치가 차이가 나는 품종에 대해서는 세부적인 연구가 필요하다. 단백질 함량은 관능평가점수와 상관관계를 검토한 결과 알려진 대로 마이너스의 상관을 확인할 수 있었다. 그러나 아밀로스 함량과 관능평가점수와 유의한 점을 찾기는 어려웠으며 이는 시료로 사용된 밥쌀용 품종의 아밀로스 함량은 18~20% 내외이기 때문이다.
그러므로 간접식미치를 기반으로 관능평가의 약 70~80%로 추정이 가능하다는 점을 확인하였다. 또한 하루에 측정 가능한 샘플 수는 관능평가와 비교하여 월등히 많으므로 계통육성과정에서 스크리닝하는 데 이용할 수 있다.

Corresponding author: Tel. 063-238-5237, E-mail: jbchun01@korea.kr

OB-09

Inter-subspecific Indel Variations in Wild Rice Suggesting The Early Appearance of *japonica*-specific Alleles of The *Oryza* genus

Joong Hyoun Chin[1*], Jonghwa Park[1], Dongryung Lee[1], Jong Seok Heo[1], Hee-Jong Koh[1*]

[1]Department of Plant Science, Research Institute for Agriculture and Life Sciences, and Plant Genomics and Breeding Institute, Seoul National University, Seoul 151-921, Korea

The Indel (insertion/deletion) polymorphisms study using 67 selected STS markers showed that the conservation of *indica*- and *japonica*-specific alleles even in non-AA genome species of *Oryza* genus. Commonly Indel polymorphisms are generally irreversible and highly useful to evaluate the genetic relationship within genus *Oryza*. Even though the 67 SS-STS (subspecies specific-Sequence Tagged Site) markers were selected using an evaluation variety panel composed of 30 *indica* and *japonica* varieties, the linked loci were highly conserved in wild relatives of rice. In this study, total of 290 accessions including 61 Asian cultivated rice (*O. sativa*), 27 African cultivated rice (*O. glaberrima*), and 202 accessions of wild *Oryza* species were investigated using the SS-STS markers. The average SS allele frequency of the various *Oryza* species, from AA-genome to BB~EE, and FF~HHKK showed an increased proportion of non-*O. sativa* and null alleles in the more distantly related wild species. Most of the wild species, except the more distant EE, GG, HHJJ, and HHKK genome accessions, consisted of relatively more indica than japonica alleles of SS markers. To validate the SS-STS study, PCR products of nine markers were sequenced across 24-33 accessions. Sequencing results revealed that *Oryza* species share *indica* or *japonica*-like conserved indel regions even across the different genomes. The presence of some *japonica* alleles beyond the AA genome at some SS indel loci also suggests that *japonica*-specific alleles occurred early in the history of the *Oryza* genus.

Corresponding author: Tel. 02-880-4551, E-mail: joonghyoun.chin@gmail.com; heejkoh@snu.ac.kr

OB-10

Diachronic Analysis of Genetic Diversity in Rice Landraces Under On-Farm Conservation in Yunnan, China

Di Cui[1,3], Jinmei Li[1], Cuifeng Tang[2], Jeonghwan Seo[3], Zhuo Jin[3], Yoye Yu[3], Hee-Jong Koh[3*], Longzhi Han[1*]

[1]Institute of Crop Sciences, Chinese Academy of Agricultural Sciences, Key Laboratory of Crop Germplasm Resources and Utilization, The National Key Facility for Crop Gene Resources and Genetic Improvement, Ministry of Agriculture, No.12 Zhongguancun Nandajie, Beijing 100081, China
[2]Institute of Biotech and Germplasm Resources, Yunnan Academy of Agricultural Sciences, No.9 Xueyunlu, Kunming 650205, Yunnan, China
[3]Department of Plant Science, Plant Genomics and Breeding Institute of Agriculture and Life Science, Seoul National University, Seoul 151-921, Korea

Rice (*Oryza sativa* L.) is one of the earliest domesticated crop species. Its genetic diversity has been declining as a result of natural and artificial selection. Compared with modern cultivars, traditional rice landraces that have been preserved by indigenous farmers have retained rich genetic variation. However, with the development of modern agriculture, rice landraces are no longer planted in most provinces in China, with the exception of some ethnic minority regions in areas such as Yunnan. In this study, we performed the first analysis of the levels and patterns of nucleotide variation in rice genomes under on-farm conservation in Yunnan during a 27-year period of domestication. We performed large-scale sequencing of 600 rice accessions with high diversity, which were collected in 1980 and 2007, using ten unlinked nuclear loci. Diachronic analysis showed no significant changes in the level of genetic diversity occurring over the past 27 years'domestication, which indicated genetic diversity was successfully maintained under on-farm conservation. Population structure revealed that the rice landraces could be grouped into two subpopulations, namely the indica and japonica groups. Interestingly, the alternate distribution of indica and japonica rice landraces could be found in each ecological zone. The results of AMOVA showed that on-farm conservation provides opportunities for continued differentiation and variation of landraces. Therefore, dynamic conservation measures such as on-farm conservation (which is a backup, complementary strategy to ex situ conservation) should be encouraged and enhanced, especially in crop genetic diversity centers. The results of this study offered accurate insights into short-term evolutionary processes and provided a scientific basis for on-farm management practices.

Corresponding author: Tel. 02-880-4541, E-mail: heejkon@snu.ac.kr; Tel. +8610-6217-6784, E-mail: hanlongzhi@caas.cn

OB-11

가공용 쌀 품종개발을 위한 배유변이 육종소재 개발 및 유전분석

정지웅*, 전재범, 조성우, 김우재, 강경호, 고재권, 김현순, 김보경

전라북도 완주군 이서면 혁신로 181 국립식량과학원 작물육종과

근래 서구화, 음식소비패턴의 다양화 등으로 우리나라에서 주식으로써 쌀이 차지하는 비중은 계속 낮아져 1인당 쌀 소비량은 2015년 62.9 Kg까지 감소하였다. 현재 다양한 쌀 가공제품을 개발함으로써 소비를 촉진시켜 생산기반을 유지하려는 노력이 진행 중이다. 쌀을 이용한 다양한 식품형태를 개발하여 고부가가치 상품생산으로 연계하기 위해서는 기존의 멥쌀과 찹쌀위주로 형성된 전분의 이화학적 특성을 보다 다양화해야 할 필요성이 있다. 이에 따라 자포니카계로 조생·초다수 멥쌀 품종인 '남일'에 화학적 돌연변이원을 처리, 그 후대계통들로부터 분질, 심백, 뽀얀메, 반찰 등 다양한 배유변이 육종소재들을 확보하였다. 작물학적 특성 및 가공적성 등의 표현형자료에 의거하여 분질계통인 '수원542호'를 건식제분용으로, 심백이 강화된 '중모1042'를 양조용으로 식물특허와 신품종으로 각각 등록하였다. 유용한 전분특성을 지배하는 신규 대립인자들에 대한 지적재산권을 확보하기 위해 분리집단의 표현형 자료와 유전자형 자료간의 병합분석(association analysis)에 기반을 두는 목표유전자위 표지, 유전적 작용가 추정 및 정밀분자표지를 개발 등의 유전분석 연구를 수행하였다. 육종적 활용도가 높은 주동유전자에 의해 배유특성이 지배되는 돌연변이 계통을 선별하고자 원품종(wild type)인 '남일'과의 교잡후대의 표현형 분포가 비정규분포(abnormal distribution)를 따르는지를 우선 판단하였다. 연관지도를 이용하는 목표유전자위 표지 등의 유전분석에는 분자표지의 높은 다형성을 보장하기 위해 돌연변이계통과 통일계 품종인 '밀양23호'간의 교잡후대를 이용하였다. 소규모분리집단(N<100)을 이용하였음에도 '수원542호'의 분질특성과 'Namil(SA)- dull1'의 반찰특성을 지배하는 주동유전자위를 염색체 5번 장완중단과 염색체 6번 장완말단에서 확인하여 이들에 대한 근접분자표지를 제시하였다. 반면에 현재까지 연관분석을 통해 확보된 근접분자표지들은 돌연변이 계통과 원연인 '밀양23호' 간의 다형성에 기반을 두는 것들로 원품종(남일)에 대해서는 다형성이 대부분 상실될 뿐만 아니라, 유전분석집단 내 각 개체들은 원연교잡 후대로서 육종학적 실용성이 낮다는 한계가 있다. 이러한 문제점을 해결하기 위해 원품종과 돌연변이계통의 전장유전체정보(Re-sequencing)를 분석하여 돌연변이 고유의 SNP를 분자표지로 활용함으로써 원품종 뿐만 아니라 국내육성 우량품종들과의 교잡후대에서도 유용한 신규 대립인자를 지닌 개체를 원활히 선별할 수 있는 연구를 진행 중이다.

Corresponding author: Tel. 063-238-5236, E-mail: jrnj@korea.kr

OC-01

Plant Gene Targeting with Site-Specific Nucleases and Homologous Recombination

Yong-Ik Kwon[1*], Woo-Nam Kim[2], Min-ji Hong[2], Hong-Kyu Kang[1], Hyo-Yeon Lee[1,2], Kiyomi Abe[3], Seiichi Toki[3]

[1]Subtropical Horticulture Research Institute, Jeju National University, Jeju 63243, Korea
[2]Faculty of Biotechnology, Jeju National University, Jeju 63243, Korea
[3]Plant Genome Engineering Research Unit, National Institute of Agrobiological Sciences, Tsukuba 305-8602, Japan

Gene targeting (GT) via homologous recombination (HR) is one of the best gene editing methods available to modify specific DNA sequences in genome. GT utilizes a DNA repair pathways. During HR-mediated DNA double-strand break (DSB) repair in eukaryotes, an initial step is the creation of a 3' single-stranded DNA (ssDNA) overhang via resection of a 5' end. Rad51 polymerizes on this ssDNA to search for a homologous sequence, and the gapped sequence is then repaired using an undamaged homologous DNA strand as template. Recent studies in eukaryotes indicate that resection of the DSB site is promoted by the cooperative action of RecQ helicase family proteins and exonuclease 1 (Exo1). Here, we demonstrate that overexpression of rice proteins OsRecQl4 and/or OsExo1 can enhance DSB repair processing, as evaluated by recombination substrate reporter lines in rice. Furthermore, we respect that the frequency of HR was evaluated all position of DSBs in the genome. These results could be applied to strategy of gene targeting with site-specific nucleases (ZFN/TALEN/CRISPR-Cas9) in plant.

Acknowledgements: This work was supported by Basic Science Research Program through the National Research Foundation (2009-0094059), and BioGreen 21 Program (PJ0112802016), Rural Development Administration, Republic of Korea.

Corresponding author: Tel. 064-754-3987, E-mail: yongikk@jejunu.ac.kr

OC-02

Engineering Rice to Reduce As Accumulation in Grain

Won-Yong Song*, Youngsook Lee

Department of Integrative Bioscience and Biotechnology, Pohang University of Science and Technology, Pohang 790-784, Korea

Arsenic (As) is a chronic poison that causes severe skin lesions and cancer. Rice (*Oryza sativa L.*) is a major dietary source of As; therefore, reducing As accumulation in the rice grain is critical to diminish the amount of As that enters the food chain. Previously it was found that tonoplast localized C-type ABC transporters, such as *Saccharomyces cerevisiae* yeast cadmium factor 1 (ScYCF1), *Arabidopsis thaliana* C-type ABC transporter 1 and 2 (AtABCC1 and 2) and *Oryza sativa* C-type ABC transporter 1 (OsABCC1), enhance As resistance and, especially, OsABCC1 reduces As accumulation in rice grain by facilitating the thiol-As sequestration into vacuoles in the phloem companion cells of nodes in rice. Based on these findings, we hypothesized that the enhanced vacuolar thiol-As sequestration would reduce As accumulation in rice grain. To prove the hypothesis, we developed transgenic rice plants transformed with all *ScYCF1*, *Ecγ-ECS* and *OsABCC1* and analyzed As concentrations in the roots, shoots and grains of the transgenic rice. The engineered plants exhibited reduced As translocation from root to shoot and 30% of the As concentration in brown rice compared to WT. Our result suggests that As vacuolar sequestration is one of the important steps to develop safety crop from As contamination.

Corresponding author: Tel. 053-279-8373, E-mail: songwy@postech.ac.kr

OC-03

Development of Co-Dominant *Female* (*F*) Locus Diagnosis Marker in Cucumber (*Cucumis sativus* L.)

Chunying Zhang[1], Khin Thanda Win[1], Sanghyeob Lee[1,2*]

[1]Plant Genomics Laboratory, Department of Plant Biotechnology, College of Life Sciences, Sejong University, 209 Neungdong-ro, Gwanjing-gu, Seoul 143-747, Korea
[2]Plant Biotechnology Research Institute, Sejong University, 209 Neungdong-ro, Gwanjing-gu, Seoul 143-747, Korea

Cucumber is a typical monoecious having separate male and female flowers on the same plant and sex expression in cucumber is mainly determined by three major genes: *F*/*f*, *M*/*m* and *A*/*a*. Gynoecy plays an important role in cucumber hybrid breeding and the use of gynoecious lines as maternal parents ensures high productivity. This study aimed to identify a co-dominant marker linked to *Female* (*F*) locus to distinguish homozygous and heterozygous gynoecious lines for efficient selection of gynoecy in cucumber breeding.

Acknowledgements: This work was supported by grants from Bio-industry Technology Development Program (111057-5) of iPET (Korea Institute of Planning and Evaluation for Technology in Food, Agriculture and Forestry) and Korea-China Collaborative Research Program (NRF-2015K2A2A2001928) of NRF (National Research Foundation of Korea).

Corresponding author: Tel. 82-2-3408-4375, E-mail: sanglee@sejong.ac.kr

OC-04

Drought-Tolerant Qtls from Samgang Lead to Tiller Formation at The Vegetative Stage in Rice

Dongjin Shin*, Tae-Heon Kim, Sang-Ik Han, Jun-HyunCho, You-Chun Song, Yeong-Up Kwon

Department of Southern Area Crop Science, Paddy Crop Research Division, National Institute of Crop Science, RDA, Miryang, 50424, Korea

During the past 50 years, rice varieties which are sensitive to drought stress were developed with irrigation system and the rice production was increased at two fold and more. However, recently drought caused by global climate change is seriously giving a threat to world rice production and food security in rice field. Herein, we screened 218 rice varieties to identify 32 drought-tolerant cultivars. Strongly drought-tolerant cultivar Samgang shows stable yield in rain-fed conditions and was selected for further study. To pinpoint QTLs for drought tolerance, we examined visual drought tolerance (VDT) and relative water content (RWC) phenotypes in a double haploid (DH) population of 101 individuals derived from a Samgang × Nagdong cross of a drought-tolerant and drought-sensitive variety, respectively. Three drought-tolerant QTLs for VDT derived from Samgang were identified. The phenotypic variance explained (PVE) by these QTLs was 41.8%. In particular, *qVDT11* was found to contribute 20.3% of the PVE for RWC. To determine QTL effects on drought tolerance, 7 DH lines were selected according to numbers of QTLs and tillers under non-irrigated conditions. Of the drought tolerance-associated QTLs, *qVDT2* and *qVDT6* did not affect tiller formation, but *qVDT11* increased tillers under rain-fed paddy conditions. Interestingly, tiller formation was most stable when *qVDT2* and *qVDT11* were combined. Together, these results suggest that *qVDT11* is important for drought tolerance and stable tiller formation under rain-fed paddy conditions.

OC-05

Genetic Analysis of Seedling Traits Regulated by Light in Weedy Rice

Hyun-Sook Lee[1], Yun-Joo Kang[1], Ju-Won Kang[1,2], Sang-Nag Ahn[1*]

[1]Department of Agronomy, Chungnam National University, Daejeon 34134, Korea
[2]Department of Southern Area Crop Science, National Institute of Crop Science, NICS, RDA, Milyang 50424, Korea

The Korean weedy rice, PBR (photoblastic rice) was reported to have light-inducible seed germination (photoblastism) and longer mesocotyl than cultivar rice. In previous studies, two QTL for photoblastism were mapped on chromosomes 1 and 12 using 124 F4 lines from a cross between Ilpumbyeo and PBR. Using 120 F8 lines advanced from the F4, we identified two QTL controlling mesocotyl length on chromosomes 1 and 3. The QTL for photoblastism on chromosome 1 was co-localized with the QTL for mesocotyl length near the SSR markers RM8260-RM246. To know whether these two genes regulated by light are functionally related, 110 F3 lines were developed from a cross between Ilpumbyeo and CR7124. The line, CR7124 having photoblastism and long mesocotyl was selected from 120 F8 lines. The germination rate in the dark condition and the mesocotyl length in the 110 F3 were in the range between two parents. The mesocotyl length in F3 lines showed significant correlation with germination rate in dark condition (r = 0.7, P < 0.0001). These results suggest the linkage of two QTL for two traits regulated by light in weedy rice. Fine mapping of the two QTL is underway to analyze their functional relationship.

Acknowledgements: This work was supported by a grant from the Next-Generation BioGreen 21 Program (No. PJ011048012016), Rural Development Administration, Republic of Korea.

Corresponding author: Tel. 031-821-7038, E-mail: ahnsn@cnu.ac.kr

OC-06

QTL Mapping of Cold Tolerance at The Seedling Stage in Rice and Development of Advanced Backcross Lines Using Marker-Assisted Selection

Suk-Man Kim[1,2*], Kyung-Ho Kang[3], Bo-Kyung Kim[3], Jong-Min Jeong[3], Russell Reinke[1,2], Kshirod Jena[1]

[1]Plant Breeding, Division, International Rice Research Institute, Metro Manila, Philippines
[2]C/o IRRI-Korea Office, National Institute of Crop Science, Rural Development Administration, Iseo-myeon, Wanju-gun, Jeollabuk-do 565-851, Korea
[3]Crop breeding Research Division, National Institute of Crop Science, Rural Development Administration, Iseo-myeon, Wanju-gun, Jeollabuk-do 565-851, Korea

Low temperature is a major abiotic stress for rice cultivation, causing serious yield loss in many countries. To identify QTL controlling low temperature an F_7 recombinant inbred line (RIL) population of 123 individuals derived from a cross of the cold-tolerant japonica cultivar Jinbu and the cold-susceptible indica cultivar BR29 for QTL mapping was used in this study. A total of six QTLs including two on chromosome 1 and one each on chromosomes 2, 4, 10, and 11 for seedling cold tolerance was identified with phenotypic variation (R^2) ranging from 6.1 to 16.5 %. Out of them two QTLs (*qSCT1* and *qSCT11*) on chromosomes 1 and 11, respectively, were fine mapped. To improve seedling cold tolerance of indica cultivar, BR29, Jinbu was back crossed with BR29 by MAS. Two advanced backcross population (BC_2F_4 and BC_3F_3) were developed and used for confirming QTL effects against cold stress by comparison of QTLs distribution on the lines *(qSCT1, qSCT11* and *qSCT1+qSCT11*). In the 18 DAT the average cold damage score of lines with one or two SCT QTL were included in the degree of moderated tolerance (5.63-6.83) based on the SES (standard evaluation system for seedling cold) and the score of lines without SCT showed susceptible reaction to cold stress along with BR29.

Corresponding author: Tel. 063-238-5497, E-mail: s.kim@irri.org

OC-07

Development of Tolerant Rice Plants to High-Temperature Stress: A Way Forward to Address Unease

Rupesh Tayade[1], Tien Dung Nguyen[1], Sung Aeong Oh[1], Ki Hong Jung[2], Soon Ki Park[1*]

[1]School of Applied Biosciences, Kyungpook National University, Korea
[2]Graduate School of Biotechnology & Crop Biotech Institute, Kyung Hee University, Korea

Global climate at present scenario predict that a significant increase in temperature might lead to loss of crop yield. Temperature stress regularly has effects on several physiological, biochemical and molecular pathways. High temperature during the sensitive reproductive phase of crop such as rice (*Oryza sativa*) may occur frequently in the future and also affect seriously on yield. So far, the high temperature effect has been studied widely on *indica* and *japonica* genotypes. With well-established molecular genetics maps, functional genomics resources, and other molecular tools are available in rice. In addition to these genomic tools linked with well-designed phenotyping, flowering phase study will help to develop rice varieties with higher tolerance to heat stress. However flowering phase development is important link for success in advance research of several crops which could also find a way to solve the global rice yield production. Here we highlight recent progress and studies in the response to high temperature stress during the reproductive stages of rice. In addition, pollen specific promoters and putative candidate genes availability from the microarray expression data at high temperature condition will be discussed in aspect of molecular and physiological mechanisms involved during development of reproductive stage. Understanding of the rice reproductive stage under the heat stress which could be key step towards development of heat tolerant rice cultivar to protect the yield loss and increase productivity.

Corresponding author: Tel. 053-950-7751, E-mail: psk@knu.ac.kr

OC-08

유전체육종 기반구축을 위한 콩 핵심집단 및 돌연변이 집단 양성 현황

박수권[1*], 문중경[2], 황사달[1], 김둘이[1], 옥현충,[1] 이춘석[1], 김선림[1], 홍하철[1]

[1]전북 완주군 이서면 혁신로 181, 국립식량과학원 작물기초기반과
[2]전북 전주시 완산구 농생명로 370, 국립농업과학원 기획조정과

콩은 세계적으로 가장 중요한 오일 및 단백질 공급원 작물이다. 콩은 우리나라에서 벼 다음으로 재배면적과 생산량이 많지만 국내 콩 소비량에 비해 매우 부족한 실정으로 많은 양을 수입하고 있다. 그러므로 국내 콩 수급안정을 위해 생산성 향상연구가 절실히 필요하다. 수량을 증진시킬 수 있는 주요 농업형질은 다수 유전자의 복잡한 조절과정의 산물이라 농업형질을 결정하는 유전자 및 이의 alleles의 대량발굴이 전제가 되어야 한다. 최근 콩 유전체재분석을 통한 유전체 수준의 유전정보 분석이 가능하게 되어 연구 목적별 핵심집단 양성이 무엇보다 중요하다. 본 연구는 콩 유전체 정보를 통한 유전체육종의 기반구축을 위해 재배종, 야생종 콩 핵심집단을 양성하였고 목적별 다양한 연구를 위해 방사선 돌연변이 집단을 함께 양성하였다. 콩 모집단 4,328점으로부터 기존 보유한 재배종 및 야생종 핵심집단 V_1(version 1)에서 핵심집단 재배종 및 야생종 V_2(version 2)를 개발하였다. 재배종 407점, 야생종 393점으로 개선된 핵심집단 V_2는 재배종 99%, 야생종 99.3%의 비율로 설명이 가능하다. 기존에 보유한 재배종 및 야생종 V_1 집단을 사용하여 전주, 오창, 천안의 3개 지역의 개화일수에 대한 빈도분포를 분석한 결과 전주, 천안에서만 정규분포를 따르는 것을 확인하였다. 또한 각 3개 지역의 개화일수에 대한 게놈전체연관분석(GWAS)분석을 실시한 결과 개화에 관여하는 유전자 중 E1 유전자가 지배적으로 분석되었다. 새롭게 개발된 핵심집단 V_2은 연차간 변이를 반복적으로 조사하여 유전체 육종을 위한 기반구축을 위해 사용될 것이다. 목적별 다양한 농업형질 연구를 위한 돌연변이 집단양성은 M_1 세대 5,387 개체를 확보하였고 이 중 엽색(leaf color), 왜성(dwarf), 엽표면(leaf surface), 변이 등의 다양한 변이체를 관찰할 수 있었다. 선발된 변이체들과 돌연변이 집단은 세대진전을 통한 분리양상을 파악하고 고정시킬 계획이다.

Corresponding author: Tel. 063-238-5324, E-mail: sookwonpark@korea.kr

OC-09

Pedigree Reconstruction of Korean Soybean [Glycine max L. Merrill] Cultivars

Chaeyoung Lee[1], Jin-Hyun Kim[1], Joo-Seok Park[2], Yoram Choi[2], Hong-Kyu Choi[3*]

[1]Department of Medical Bioscience, Dong-A University, Busan, Korea
[2]Department of Applied Bioscience, Dong-A University, Busan, Korea
[3]Department of Genetic Engineering, Dong-A University, Busan, Korea

Soybean [Glycine max (L.) Merrill] is one of the most important crops in the world and in Korea as well. Since the official start of soybean breeding program in Korea at which a landrace 'Jangdanbaekmok' was first released to promote cultivation in1913, approximately one century has elapsed. Currently, a total of 178 soybean varieties are registered at two representative Korean national institutes, the RDA-Genebank Information Center (http://www.genebank.go.kr) and the Korea Seed & Variety Service (http://www.seed.go.kr). Of these, 155 varieties (87.1%) have been developed through hybridization-based breeding technologies, of which most cultivars (133 varieties, 85.8%) have been released in the last twenty five years. In this review, we attempted to integrate all the information for individual cultivars and to rebuild a breeding pedigree including the entirety of registered Korean soybean varieties. The analysis has resulted in a total of four pedigrees involving 168 cultivars (94.4% out of 178 cultivars), which form the broadest network of pedigrees. Each of pedigrees highlights different key varieties within the context of progenitor networks derived from crossing of various elite parental lines as follows; pedigree I-'Kwangkyo', 'Hwangkeumkong', 'Paldalkong' and 'Sinpaldalkong2', pedigree II-'Baegunkong', 'Jangyeobkong' and 'Keunolkong', pedigree III-'Danyeob', 'Pangsa' and 'Eunhakong'. These pedigrees also reveal purpose (i.e., desirable traits)-driven development of characteristic soybean varieties during the past century of breeding history in Korea. We expect that the pedigree reconstructed in this study will provide breeders with information useful to design breeding schema and guidance towards the genomics-assisted soybean improvement in the future.

Corresponding author: E-mail: hkchoi@dau.ac.kr

OC-10

Completion of The Mitochondrial Genome Sequence of Onion (*Allium cepa* L.) Containing The CMS-S Male-Sterile Cytoplasm and Identification of an Independent Event of the *ccmF*$_N$ Gene Split

Bongju Kim[1], Kyunghee Kim[2,3], Tae-Jin Yang[2], Sunggil Kim[1*]

[1]Department of Plant Biotechnology, Biotechnology Research Institute, Chonnam National University, Gwangju 500-757, Korea
[2]Department of Plant Science, Plant Genomics and Breeding Institute, and Research Institute of Agriculture and Life Sciences, College of Agriculture and Life Sciences, Seoul National University, Seoul, 151-921, Korea
[3]Phyzen Genomics Institute, 501-1, Gwanak Century Tower, Gwanak-gu, Seoul, 151-836, Korea

Cytoplasmic male-sterility (CMS) conferred by the CMS-S cytoplasm has been most commonly used for onion (*Allium cepa* L.) F_1 hybrid seed production. We first report the complete mitochondrial genome sequence containing CMS-S cytoplasm in this study. Initially, seven contigs were *de novo* assembled from 150-bp paired-end raw reads produced from the total genomic DNA using the Illumina NextSeq500 platform. These contigs were connected into a single circular genome consisting of 316,363 bp (GenBank accession: KU318712) by PCR amplification. Although all 24 core protein-coding genes were present, no ribosomal protein-coding genes, except *rps12*, were identified in the onion mitochondrial genome. Unusual *trans*-splicing of the *cox2* gene was verified, and the *cox1* gene was identified as part of the chimeric *orf725* gene, which is a candidate gene responsible for inducing CMS. In addition to *orf725*, two small chimeric genes were identified, but no transcripts were detected for these two open reading frames. Thirteen chloroplast-derived sequences, with sizes of 126-13,986 bp, were identified in the intergenic regions. Almost 10% of the onion mitochondrial genome was composed of repeat sequences. The vast majority of repeats were short repeats of < 100 base pairs. Interestingly, the gene encoding *ccmF*$_N$ was split into two genes. The *ccmF*$_N$ gene split is first identified outside the Brassicaceae family. The breakpoint in the onion *ccmF*$_N$ gene was different from that of other Brassicaceae species. This split of the *ccmF*$_N$ gene was also present in 30 other *Allium* species. The complete onion mitochondrial genome sequence reported in this study would be fundamental information for elucidation of onion CMS evolution.

Corresponding author: Tel. 062-530-2061, E-mail: dronion@jnu.ac.kr

OC-11

Efficient QTL Mapping Strategy for Agronomical Traits in Pepper (*Capsicum annuum*)

Koeun Han[1], Hee-Jin Jeong[1], Hee-Bum Yang[1], Sung-Min Kang[2], Seungill Kim[3], Doil Choi[3], Byoung-Cheorl Kang[1*]

[1]Department of Plant Science, Plant Genomics and Breeding Institute and Vegetable Breeding Research Center, College of Agriculture and Life Sciences, Seoul National University, Seoul 151-921, Korea
[2]Department of Computer Science, College of Information Science and Technology, KAIST, Daejeon 305-701, Korea
[3]Department of Plant Science, Plant Genomics and Breeding Institute, College of Agriculture and Life Sciences, Seoul National University, Seoul 151-921, Korea

Majority of agronomical traits including plant height, fruit weight, and contents of secondary metabolites are quantitative traits. Identification of quantitative trait locus (QTL) controlling agronomical traits is important for marker-assisted breeding and understanding the mechanism for the traits. To detect the QTLs controlling agronomical traits in pepper (*Capsicum annuum*), we constructed an ultra-high-density bin map using 120 recombinant inbred lines (RILs) from intraspecific cross (*C. annuum* 'Perennial' × *C. annuum* 'Dempsey'). Reads from resequencing of RILs were aligned to the *C. annuum* 'CM334' reference genome, and single nucleotide polymorphisms (SNPs) were called. Due to the low coverage (1×) of the reads, there were large number of missing data. Therefore, linked SNPs in one window were combined as bin by sliding window approach and this method could improve the genetic map. The total map length of the bin map was 1,372 cM, and the average interval between 2,578 bins was 0.53 cM. Also for accurate QTL mapping, we evaluated the phenotype repetitively in three different environments. Using the ultra-high-density bin map and the phenotypic data from three different environments, 32 major QTLs were mapped and they controlled plant architecture, leaf, and fruit related traits. Rapid genotyping by resequencing, improvement of genetic map by sliding window approach, and repetitive phenotyping can facilitate efficient QTL mapping for agronomical traits.

Corresponding author: Tel. 82-2-880-4563, E-mail: bk54@snu.ac.kr

OC-12

Bioinformatics Analysis for Transcription Factor Associated SSR Markers Developments and Characterization in Lilium Species

Manosh Kumar Biswas, Jewel Howlader, Namhee Jeong, Ujjal Kumar Nath, Md Abdul Kayum, Jong-In Park, Ill-sup Nou*

Department of Horticulture, Sunchon National University, 255 Jungang-ro, Suncheon, Jeonnam, 540-950, Korea

Lilium species is commercially important horticultural crops widely cultivated for flower and bulbs productions. It is use as raw materials in medicine and food industry. Till to date the available SSR markers for this economically important crop is very few compare to other horticultural crops. Therefore the molecular breeding of this crop is less advances. In order to boost up the breeding programme of this valuable crops species, functional molecular markers need to be developed. Consequently, in this study we developed and in silico characterized Transcripton Factor (TF) associated Micro-Satellite Markers (TFSSR) from the large scale lily transcriptom data mining. A total 216768 unigenes were search for SSR motifs, 6966 unigenes identified with SSR motif among them 71 were potential for TFSSR markers developments. Of these markers, 15% (11) and 85% (60) TFSSR were identified as Class I and Class II, respectively, based on the length of the repeat motifs. The tri repeats were most common than other types of repeats in lily TFSSR. The GC rich TFSSR were two and 16 fold higher than AT/GC Balance and AT rich TFSSR, respectively. Further, TFSSR classified according to TF family, all these TFSSR markers distributed among the 34 transcription factor family, among them the highest number of markers associated with bHLH (10; 14%) and it was followed by MYB (8; 11%), C2H2 (5; 7%), ERF (5; 7%), C3H(3; 4%), NAC(3; 4%) and bZIP(3; 4%). So far our knowledge this is the first set of Transcripton Factor Associated Micro-Satellite Markers developed for the Lilium species. These informative TFSSR markers will be very useful in large-scale genotyping, high density mapping, understanding the population genetics, comparative mapping and functional molecular diversity studies in lily.

Corresponding author: Tel. 061-750-3249, E-mail: nis@sunchon.ac.kr

포스터 발표

PA-01

서산간척지에서 내염성 콩 계통의 생육

이정동[1*], 김정화[1], 김민수[1], 박철우[1], 정재은[1], 아세코바소베툴[1], 한두호[2], 송종태[1]

[1]대구광역시 북구 대학로 80, 경북대학교 응용생명과학부
[2]충남 서산시 부석면 천수만로, 현대서산농장

간척지는 토성이 불량하고, 염분농도가 높아 작물생육에 매우 부적합하여 작물 수량의 안정적 확보와 다양한 작물 재배를 위해서는 토양 개량과 그에 알맞은 재배기술 및 내염성 품종 개발이 시급한 실정이다. 간척지에 재배할 내염성 콩을 선발하기 위해 현대서산농장 간척지(염농도 약 0.2%)에 야생콩 PI483463(내염성) x Hutcheson(감수성) 유래 52개의 내염성 RIL, 65개의 감수성 RIL, S-100(내염성) x PI483463(내염성) 유래 106개의 RIL, Hutcheson과 우람콩(감수성)으로 여교배하여 DNA 마커로 선발한 94개의 내염성 BC1F3계통을 난괴법 2반복으로 재식하였다. 재식밀도는 70 x 15cm, 1주 2본으로 하였으며, 파종은 2015년 5월 8-9일간에 실시하였다. 간척지에서 감수성 콩 계통의 잎이 황변하고 하위엽의 경우 염해에 의해 타들어 가는 것을 관찰할 수 있었고, 내염성 계통들은 염해의 증상이 없거나 미약하게 나타났다. 내염성 유전자를 가진 계통들은 성숙기 까지 자라 종자를 생산하였으나, 감수성 계통은 정상적인 종자를 거의 생산하지 못하여 내염성과 감수성 계통간의 차이가 확연하게 나타났다. 여교잡 집단에서 간척지에 적응하는 우수한 계통을 선발할 수 있었으며, 이들 선발된 계통들은 간척지에 재배할 다양한 용도의 콩을 개발하는 자원으로 이용 될 것이다.

Corresponding author: Tel. 031-296-6898, E-mail: koreabreed@hotmail.com

PA-02

Development of an Efficient *in vitro* Screening Methods for Lily Cultivars Resistant to *Botrytis elliptica*

Ji-Young Jang[1,2], Jae-Heung Jeon[1], Geung-Joo Lee[2], Hyun-Soon Kim[1*]

[1]Molecular Biofarming Research Center, Korea Research Institute of Bioscience and Biotechnology, Daejeon 34141, Korea
[2]Department of Horticulture, Chungnam National University, Daejeon 34134, Korea

Leaf blight on lily caused by *Botrytis elliptica* and *Botrytis cinerea* is a serious threat to production of lily bulb and flower. The genetic diversity of cultivars and the reliable screening method are required for developing resistant cultivars against the leaf blight disease. Here, an efficient *in vitro* screening system for evaluating resistance to *Botrytis elliptica* in 30 *in vitro* lily cultivars was investigated. Various factors including culture condition of *Botrytis elliptica*, inoculum density, appropriate plant materials, inoculation method and duration, and incubation period of plant materials after inoculation were combined to optimize the screening method. As a result, we suggested optimal conditions of *in vitro* screening system for the selection of *Bortytis elliptica* resistant lily cultivars as follows. *Botrytis elliptica* was grown on potato dextrose agar (PDA) media for 2 weeks at 25℃ with a photoperiod of 12 h UV-A/12 h dark and used as working inoculation. Spore suspensions were prepared (inoculum density: 2.0×10^3 spores·mL^{-1}), and then leaf segments 1.5×2.0 cm^2 was inoculated by dipping for 12 hours at 25℃ in dark. Later, leaves were cultured on 0.6% agar plate at 25℃ and 50% humidity in darkness to examine the progress of leaf blight. After 7 days, disease level was divided into index 0-4, 0 = no lesions observed, 1 = 1-10% leaf area infected, 2 = 11-25% leaf area infected, 3 = 26-50% leaf area infected, and 4 = over 50% leaf area infected.

Corresponding author: Tel. 042-860-4493, E-mail: hyuns@kribb.re.kr

PA-03

Xoo Bacteria-Mediated Rice Leaf Blight is Prevented by Human Drug Niclosamide

Sung-Il Kim[1], Hak Soo Seo[1,2*]

[1]Department of Plant Science, Research Institute for Agriculture and Life Sciences, and Plant Genomics and Breeding Institute, Seoul National University, Seoul 151-921, Korea
[2]Bio-MAX Institute, Seoul National University, Seoul 151-818, Korea

A huge losses of grain yield has been reported by leaf blight of rice, which is induced by the bacterial pathogen *Xanthomonas oryzae pv. oryzae* (*Xoo*). Here, we show that leaf blight of rice induced by *Xoo* is controlled by niclosamide, an oral antihelminthic drug and molluscicide, which also functions as an anti-tumor agent. Niclosamide inhibited the growth of the three *Xoo* strains *K3a*, *10208* and *PXO99*. Niclosamide moved long distances from the site of local application to distant rice tissues. Niclosamide also increased the levels of salicylate and induced the expression of defense-related genes such as *OsPR1* and *OsWRKY45*, which suppressed *Xoo*-induced leaf wilting. Niclosamide had no side effects on vegetative/reproductive yield and growth. Taken together, these results indicate that niclosamide can be applied to block leaf blight induced by bacterial pathogen in rice with no negative side effects on plant itself.

Acknowledgements: This work was supported by a grant from the Next-Generation BioGreen 21 Program (Plant Molecular Breeding Center no. PJ01176902), Rural Development Administration, Republic of Korea.

Corresponding author: E-mail: seohs@snu.ac.kr

PA-04

Breeding of High Yield Leaf Lettuce 'Chunhacu' from Spring to Fall Season

Suk-Woo Jang[1*], Su-Hyoung Park[1], Won-Byoung Chae[1], Jong-Nam Lee[2], Myeong-Hoon Seo[3], Min-Jeong Lee[4], Min-Sik Yin[5], Un-Ji Kim[6], Hee Dae Kim[7], Sun-Bo Ko[8]

[1]Department of Horticultural Crop Research, National Institute of Horticultural & Herbal Science, Wanju 25342 55385, Korea
[2]Highland Agriculture Research Institute, National Institute of Crop Science, RDA, Pyeongchang, 25342, Korea
[3]Gyeonggi-do Agric. Res. and Extension Services, Hwaseong 18388 Korea
[4]Chungcheongbuk-do Agric. Res. and Extension Services, Cheongju, 28130, Korea
[5]Chungcheongnam-do Agric. Res. and Extension Services, Yesan, 32418, Korea
[6]Jeollabuk-do Agric. Res. and Extension Services, Iksan 54591, Korea
[7]Gyeongsangnam-do Agric. Res. and Extension Services, Jinju 52733, Korea
[8]Jeju-do Agric. Res. and Extension Services, Seogwipo 63556, Korea

A new cultivar of lettuce (*Lactuca sativa* L.) with broad elliptic and purple red leaf, 'Chuhacu' which has late bolting was developed from a cross between 'Maschima(Dark red leaf color) and 'Manchudae cheongchima(late bolting). The cross and selection for advanced lines had been done by the pedigree method during 2008-2013. The advanced lines were evaluated for yield and adaptability at several locations in Korea (Gangwon-do, Gyeonggi-do, Chungcheongbuk-do, Chungcheongnam-do, Jeollabuk-do, Gyeongnam-do, and Jeju-do) for 2 years . The 'Chuhacu' has gray seed color, leaf number of harvest is 75, and yield of per plant is 466g. So the weight of leaf is 6.2g. Expecially the 'Chuhacu' is good yeild for all season in growing period. The anthocynin content of 'Chuhacu' was lower than that of 'Yelpungjeogchima' as a 6.8 mg/100g. The BSL (Bitter Sesquiterpene Lactones, latucin+8-deoxylactucin+lactucopicrin) content of 'Chuhacu' is lower than that of 'Yelpungjeogchima' as a 38.23(ug/g, DW). Compared to 'Yelpungjeogchima' , marketable yield of 'Chuhacu' was higher by 4% as a 40.9 (ton/ha) from spring to fall cultivation. The shelf-life of 'Chuhacu' was good storage than 'Yelpungjeogchima' at 4℃. Furthermore, its taste is better, more crispy, and sweeter than those of 'Yelpungjeogchima'. So we recommend that new cultivar 'Chuhacu' can be suitable for cultivation from spring to fall season .

Corresponding author: Tel. 063-2386620, E-mail: swjang02@korea.kr

PA-05

EPG를 이용한 벼멸구 저항성 계통과 감수성 품종의 흡즙 파형 차이 분석

김우재*, 박현수, 하기용, 김현순, 조영찬, 정지웅, 전재범, 조성우, 김보경

전북 완주군 혁신로 181 농촌진흥청 국립식량과학원 작물육종과

벼 멸구저항성 품종육성 효율을 증대시킬 목적으로 EPG(electrical penetration graph) 기술을 이용 벼멸구 저항성과 감수성 벼 간 흡즙 파형의 차이를 분석하였다. 흡즙 파형분석은 감수성 품종인 남평과 저항성 유전자 *Bph1*, *bph2* 유전자를 각각 보유한 계통에 대해 벼멸구는 Biotype 1을 사용하였다. EPG 파형은 벼멸구의 주두 위치와 행동에 따라 각각 np(non-penetration), P(penetration initiation), Path(Salivation and stylet movement), X(stylet activity in xylem region), S(extracellular activity near the phloem region), sPh(intracellular activity in phloem region), Ph(Phloem sap ingestion), 7가지로 구분하였다. 감수성 품종인 남평에서는 np, P, Path, X, S 파형의 시간이 짧았으나 sPh, Ph 파형은 길었으며 전체 시간 중 77.9%로 길게 나타났다. 반대로 벼멸구 저항성 계통은 np, P, Path, X, S 파형은 길고 sPh, Ph 파형은 짧게 관찰되었다. 특히 Ph 파형은 남평에서만 관찰되고 저항성 계통에서는 관찰되지 않았다. 감수성과 저항성 계통간에는 모든 파형에서 유의한 차이가 있었으나 저항성 계통들 간에는 S 파형만 유의한 차이가 있었다. 본 실험을 통해 감수성과 저항성의 흡즙 파형차이는 지속적인 체관부 흡즙이 많은 영향을 주는 것으로 생각된다. 벼멸구 저항성 품종 육성에서 EPG 파형의 차이를 이용한 선발은 저항성 품종 육성의 효율적인 방법 중 하나로 활용 될 것으로 기대된다.

Corresponding author: Tel. 063-238-5235, E-mail: suwonman@korea.kr

PA-06

분자표지를 이용한 친환경재배 적응 복합내병충성 벼 ‘중모1045호’ 육성

김우재*, 박현수, 신운철, 김현순, 고재권, 조영찬, 정지웅, 전재범, 조성우, 김보경

전북 완주군 혁신로 181 농촌진흥청 국립식량과학원 작물육종과

친환경재배 적응 내병충저항성 품종육성을 목적으로 황금누리(벼멸구 감수성, 고품질)와 SR30071-3-7-23-6-1-1-1계통(벼멸구저항성 유전자 *Bph18* 보유)을 교배하여 계통육종법과 분자육종법을 활용하여 고품질의 벼멸구 저항성 계통을 육성하였다. 육성된 F1 20개체로부터 F2 1,200개체를 포장에 재식하여 농업형질이 유망한 23개체를 선발하였다. 이들 개체에 대해 벼멸구 유묘검정, 도열병 밭못자리검정, 흰잎마름병 K1 균계, 줄무늬잎마름병에 대해 저항성 검정 후 F5 100개체를 선발하였다. 100 개체에서 병충해 저항성 DNA 마커검정으로 *Bph18*은 92계통, *Xa3*는 96계통, *Stv-bi*는 98계통에서 저항성 유전자를 확인하였고 생물검정에서는 벼멸구 유묘검정 저항성은 94계통, 흰잎마름병 K3 균계검정에선 27계통이 저항성이고 중도저항성은 73계통이었다. F5 세대 100개체 중 주요 농업적 형질이 우수한 11계통을 생산력검정시험에 공시하였고, 이중 보통기 보비재배에서 농업형질이 양호하고 수량이 높으며 벼멸구, 흰잎마름병, 줄무늬잎마름병에 저항성을 보이는 중만생종 HR28011-1-2-3을 ‘익산562호’로 지역적응시험 계통명을 부여하였다. 이후 ‘익산562호’는 3년의 지역적응성 시험을 통해 병해충에 대한 안정적인 저항성이 확인되어 ‘중모1045호’로 명명하였고 앞으로 복합내병충성 벼 품종 육성을 위한 유전자원으로 활용할 예정이다.

Corresponding author: Tel. 063-238-5235, E-mail: suwonman@korea.kr

PA-07

내한성, 내병성이 강한 식용 및 바이오디젤용 유채 1대잡종 '진애'

김광수[1*], 고산[1], 이영화[1], 장영석[1], 최규환[2], 신정호[3], 이경보[1]

[1]농촌진흥청 국립식량과학원 바이오에너지작물연구소
[2]전라북도농업기술원
[3]경상남도농업기술원

유채(*Brassica napus* L.)는 오래 전부터 채소 및 식물성 기름으로 이용하기 위해 재배되어 왔다. 유채는 겨울작물이지만 종실 수량이 많고 종자 내의 기름함량도 매우 높아, 전 세계 기름작물중 기름작물 중 종실 생산량이 콩 다음으로 많이 생산되며, 기름 생산량은 팜오일, 콩기름에 이어 세 번째로 생산량이 많은 작물이다. 우리나라에서도 유채가 경관용, 식용 및 바이오디젤 원료 생산 작물로 관심이 증가되고 있으며 재배면적도 점진적으로 증가하고 있다. 유채의 대규모 재배를 통한 종실의 대량생산을 위해서는 기계화가 가능한 논재배가 필수적이며 이를 위해서는 벼와 작부체계가 가능한 조숙성 품종 육성과 함께, 최근 빈번하게 발생하는 이상 기상에 대비하여 내한성, 내병성 등 특징을 지닌 유채 품종육성이 필요하다. 이에 따라 국립식량과학원 바이오에너지작물연구소에서 논 재배에 적합하며 내한성과 내병성이 강한 품종육성을 목표로 2009년도에 '목포-CGMS'를 모본으로 하고 '07001-B-41-1-1-2'을 부본으로 이용하여 교배 후 우수한 특성을 나타내는 1대잡종 '단교72호'를 양성하였다. 생산력검정시험은 '선망'을 대비품종으로 하여 2011~2012년에 걸쳐 실시하였으며, 지역적응시험은 3년간(2013~2015) 전남, 전북, 경남 등 3개 지역에서 실시하였다. '단교72호'는 유채 1대잡종 대비품종인 '선망'에 비해 조숙성이며 내한성과 균핵병에 대한 내병성이 강하여 진애(Jinae)로 명명하였다. 1대잡종 '진애'는 개화기는 4월 9일이였으며 종실 숙기는 6월 3일로 '선망'에 비해 2일 정도 빠르다. 종실수량은 335kg/10a로 '선망'에 비해 1%가 증수되었다. 종자 내 기름함량(44.2%)과 불포화지방산인 올레인산 함량이 68.7%로 '선망'의 67.3%에 비해 1.4% 높았으며, 에루신산은 전혀 검출되지 않았다. 글루코시놀레이트 함량은 1.87mg/g으로 국제허용기준치인 3.0mg/g 이하이다.

Corresponding author: Tel. 061-450-0133, E-mail: ajuga@korea.kr

PA-08

고품질 조사료 최대생산을 위한 3모작 재배의 생산성 및 사료가치

김영진[1*], 이상학[2], 정종성[1], 황태영[1], 김원호[1]

[1]국립축산과학원 축산자원개발부, 충남 천안시 서북구 성환읍 신방1길 114
[2]국립식량과학원 남부작물부, 경남 밀양시 점필재로 20

본 연구는 고품질 조사료의 연중 최대생산을 위하여 하계 및 동계 사료작물의 효율적인 작부체계를 구명하고 그 생산성 및 사료가치를 비교한 것이다. 조사료 최대생산을 위해서는 하계 사료작물로 옥수수(cv. 광평옥)나 수수X수단그라스 교잡종(cv. Jumbo 등)을 5월 초, 중순에 파종하여 7월 중순~8월 중순에 수확한다. 이후 귀리(cv. 하이스피드)와 이탈리안 라이그라스(cv. 그린팜, 코윈어리)를 8월 하순에 혼파재배한 후 10월 하순에 1차 수확하고, 이듬해 5월 초, 중순에 월동하여 자라고 있는 이탈리안 라이그라스를 2차 수확하는 3모작 작부체계가 효과적이었다. 사료가치(TDN)는 옥수수가 70.6%로 가장 높았으며, 귀리+이탈리안 라이그라스가 62.9%, 수수X수단그라스 교잡종은 56.5%를 나타내었다. 건물수량은 옥수수가 24,337kg/ha, 수수X수단그라스 교잡종이 16,654kg/ha, 귀리+이탈리안 라이그라스 1차 수확이 3,466~4,510kg/ha였으며 이탈리안 라이그라스 2차 수확이 9,327~10,095kg/ha로 나타났다.

Corresponding author: Tel. 041-580-6768, E-mail: yjikim@korea.kr

PA-09

국내품종과 수입품종 이탈리안 라이그라스 품종들의 생육특성과 수량성 비교

지희정[*], 김기용, 황태영, 이기원, 최기준, 이상훈

충남 천안시 서북구 성환읍 신방1길 114 국립축산과학원 초지사료과

이탈리안 라이그라스는 지중해 연안이 원산지로 한해에는 약하지만 습해에 강한 특성을 가지는데 특히 가축 기호성 및 사료가치가 좋은 것으로 나타났다. 하지만 수입되는 대부분 품종들은 추위에 약해 이른봄 날씨가 풀리면서 많이 동사하여 수량감소가 빈번히 발생되고 있다. 따라서 본 연구는 수입되는 외국 품종과 국내 개발 품종을 파종하여 이들 품종들의 생육특성과 수량성을 알아보고자 실시하였다. 시험 결과 중부지방인 천안에서 재배하여 국내 품종과 수입품종 이탈리안 라이그라스를 비교해 볼 결과 외국 품종인 TAM 90, 플로리다 80호 등은 월동성이 약하여 이듬해 봄에 재생력이 상당히 감소함으로써 생초수량이 감소하였다. 하지만 국내 육성 품종인 그린팜, 코윈어리 품종은 월동성이 강하여 이듬해 봄에 생초수량이 안정적임을 보여 주었다. 이런 결과들로 미루어 볼 때 국내 개발 이탈리안 라이그라스 신품종들은 월동에서 많은 개체가 생존하여 안정적인 개체수를 확보하여 월동후인 봄까지 지속됨으로써 개체당 최적 분얼수를 가지게 됨으로써 안정적인 양질 조사료 생산에 기여하는 것으로 확인 되었다.
생초수량를 살펴보면 그린팜이 ha 당 51,556kg이고 코윈어리가 51,011kg인데 비하여 수입품종인 플로리다80호는 42,333kg/ha, TAM90는 ha 당 50,389kg로 작았고 건물수량에서는 그린팜은 ha당 11,018kg, 코윈어리가 ha당 10,743kg이지만 수입품종인 플로리다 80는 ha 당 8,883kg, TAM90호는 ha당 10,142kg을 보여주었다. 사료가치 측면에서 살펴보면 조단백질은 국산품종인 그린팜 8.9%, 코윈어리가 8.9%, 소화율은 그린팜이 71.4%, 코윈어리가 67.7% 이었고, 수입품종인 플로리다 80의 조단백질은 8.9%, 건물소화율은 72.2% 였고 TAM90의 건물소화율은 69.9%로 사료가치는 비슷하였다.

Corresponding author: Tel. 041-580-6749, E-mail: cornhc@korea.kr

PA-10

중생 고품질 내도복 오갈병 저항성 벼 '영보' 육성

박노봉[1*], 남민희[1], 김상열[2], 여운상[2], 이지윤[2], 권오덕[1], 박동수[2], 이종희[4], 조준현[2], 송유천[2], 한상익[2], 손영보[2], 장재기[3], 권영업[2]

[1]경북 영덕군 병곡면 원황길 44 농촌진흥청 국립식량과학원 영덕출장소
[2]경남 밀양시 내이동 점필재로 20 국립식량과학원 남부작물부
[3]경기도 수원시 권선구 수인로 126 국립식량과학원 중부작물부
[4]전북 전주시 완산구 농생명로 300 농촌진흥청 연구정책국

국립식량과학원 영덕출장소에서는 최근의 이상기상에 따른 병해충 증가에 대응하기 위해 병에 강하면서도 출수기가 적당하고 밥맛과 재배 안정성이 뛰어난 고품질 벼 품종을 육성하고자 본 연구를 수행하였다. 모본으로 초형이 양호한 '영덕35호'를, 부본으로는 다수성이면서 밥맛과 초형이 우수한 '새계화'를 2002년 하계에 인공교배하여 2003년 하계에 41개체의 F_1 식물체를 양성하여 YR24269의 교배번호를 부여하였다. 2004년 하계포장에 전개한 F_2 집단을 포장과 실내 선발하여 2005년 하계에 F_3 세대 66계통을 육성하였다. 이후 F_4~F_6 세대를 계통육종법으로 전개하면서 예비선발 시험을 실시하여 현미 외관특성이 우수하고 병해와 재해에 안정적인 계통을 선발하였다. 2010년 생산력검정 예비시험, 2010~2011년 생산력검정 본시험을 실시한 후 중생이면서 다수성이며 재배 안정성까지 갖춘 YR24269-1-2-1-2-3-3을 선발하여 '영덕57호'로 명명하였다. 2012년부터 3년간 지역적응시험을 실시한 결과, 중생종이면서 밥맛과 내병성이 양호한 것으로 평가되어 2014년 12월 농작물직무육성신품종 선정위원회에서 '영보'로 명명하게 되었다. '영보'는 보통기 재배시 출수기는 8월 8일로 중생종이며, 간장은 66cm로 작아 도복에 강하고 직립초형이다. 탈립은 잘되지 않고 이삭추출은 양호하며 까락이 거의 없다. '화성벼' 보다 수당립수는 더 많으며, 현미천립중도 23.1g으로 더 무겁다. 쌀알 모양이 단원형으로 맑고 투명하며, 도정특성은 '화성벼'와 비슷하나 밥맛은 더 우수하다. 또한 불시출수는 안되는 편이고, 위조현상에 강하고 성숙기 엽노화가 느린 편이며, 내냉성은 '화성벼' 보다 약한 중약 정도이다. 잎도열병에 중강의 저항성을 보였고, 줄무늬잎마름병, 오갈병, 흰잎마름병(K_1, K_2, K_3)에는 강하나 검은줄오갈병에는 약하고, 벼멸구 등 충해에는 감수성이다. 쌀 수량은 지역적응시험 보통기 재배 9개소에서 5.75MT/ha로 '화성벼' 보다 2% 증수 되었으며, 이모작 및 만식적응성도 높아 적응지역인 중부 및 영남평야지, 남부중산간지, 동남부해안지에 보급하게 되었다.

Corresponding author: Tel. 054-732-0385, E-mail: parknb@korea.kr

PA-11

가공용 초다수성 복합내병성 벼 신품종 “한아름3호”

이지윤[1*], 조준현[1], 이종희[2], 손영보[1], 박노봉[3], 오성환[1], 한상익[1], 송유천[1], 박동수[1], 여운상[1], 박병명[1], 오인여[1], 남민희[3], 권영업[1], 이영희[4]

[1]경남 밀양시 점필재로 20 국립식량과학원 남부작물부
[2]전라북도 전주시 완산구 농생명로 300, 농촌진흥청 연구정책국
[3]경상북도 영덕군 병곡면 원황길 44 국립식량과학원 영덕출장소
[4]전라북도 완주군 이서면 갈산리 혁신로 181 국립식량과학원

‘한아름3호’는 가공용 원료곡에 적합한 통일형 초다수성 품종을 만들기 위하여, 2006년 하계에 직립초형으로 수광태세가 우수한 밀양216호를 모본으로 하고 수량성이 높은 한아름벼를 부본으로 한 F_1에 한아름을 모본으로 인공교배를 실시하였다. 이후 계통육종법에 따라 계통을육성하여 2012년 생산력검정시험을 거쳐 밀양286호로 명명된 후 2013년부터 2015년까지 3년간의 지역적응시험 결과 수량성이 높고 가공적성의 우수성 등이 인정되어 농작물 직무육성 신품종 선정위원회에서 ‘한아름3호’로 명명되었다. ‘한아름3호’는 중부 및 영·호남평야지 보통기 재배에서 평균 출수기가 8월 14일로 다산보다 7일 늦은 중만생종이며 간장은 76cm정도이다. 까락은 거의 없는 편이며 현미외관은 심복백이 많아 약간 불투명한 중원형 메벼이고 현미천립중은 22.8g이다. 수당립수는 126개로 다산보다 많고 이삭추출은 보통이다. 정조의 길이가 8.43mm로 다산보다 조금 짧고, 심복백은 "다산"과 비슷하며, 아밀로스 함량은 18.2%로 "다산"과 비슷하다. 저온발아성과 등숙비율이 각각 각각 91.3%, 87.3%로 “다산”보다 높다. 도복에 강하고 도열병, 흰잎마름병(K1)과 바이러스병인 줄무늬잎마름병에 저항성이며, 벼멸구에 약하다.

Corresponding author: Tel. 055-350-1164, E-mail: minitia@korea.kr

PA-12

온대자포니카 지역 적응 벼 우량계통 '밀양321, 322호' 육성

송유천[1*], 조준현[1], 이지윤[1], 손영보[1], 이종희[2], 오성환[1], 박동수[1], 조영찬[3], 권영업[1]

[1]경상남도 밀양시 농촌진흥청 국립식량과학원 남부작물부 논이용작물과
[2]전라북도 전주시 농촌진흥청 연구정책국 연구운영과
[3]전라북도 전주시 농촌진흥청 국립식량과학원 작물육종과

열대지역 벼 연구 국제 컨소시엄은 국제미작연구소(IRRI)를 중심으로 연구가 활발히 이루어지고 있으나, 온대지역 벼 연구를 주관하는 국가나 연구소가 없어 농촌진흥청의 제안으로 2007년 온대 자포니카 벼 연구 및 자원교류로 생산성 향상을 위한 국가적 통합체가 필요하므로 온대벼 연구 국제컨소시엄(Temperate Rice Research Consortium ; TRRC)이 창립되었다. 2008년부터 중국에서 한국, 중국, 일본, 러시아, 이집트 등 8개국에서 제공한 회원국의 장려품종 Takanari, 일미벼, C21, Giza 177 등 25품종의 유전자원 평가와 2008～2010년 44집단을 육성하여 회원국에 분양하였다. 한국에서는 2010년 44 BC_2F_2를 분양 받아 11집단 176개체를 선발하여 계통육종법으로 2011～2014년 공시하여 2015년에 재배안전성 및 쌀 품질이 좋고 수량이 높은 중생 온대자포니카 우량계통 '밀양321, 322호'를 육성하였다.

'밀양321호'의 Takanari(일본)와 C21(중국) 품종과 여교잡으로 육성된 계통으로 출수기는 보통기 재배에서 8월 9일인 중생종으로 직립성 초형이며, 도복과 잎도열병에는 강하지만 다른 병해충에는 약하고, 천립중이 대비품종(남평벼) 보다 2g 무겁고 쌀 수량은 628kg/10a으로 9% 높았다.

'밀양322호'의 이집트 품종인 Giza177/Giza178이 여교잡으로 육성된 계통으로 출수기는 보통기 재배에서 8월 10일인 중생종으로 직립성 초형이며, 수장은 대비품종(남평벼) 보다 7cm 길지만 천립중은 3g 가볍고 도복, 잎도열병 및 흰잎마름병 K_1에는 강하지만 다른 병해충에는 약하고, 쌀 수량은 609kg/10a으로 6% 가까이 높았다.

Corresponding author: Tel. 055-350-1165, E-mail: songyc@korea.kr

PA-13

Ginseng *cis*-prenyltransferase Interacts with a Nogo-B Receptor Homolog for Dolichol Biosynthesis

Ngoc Quy Nguyen, Ok Ran Lee*

Department of Plant Biotechnology, College of Agriculture and Life Science, Chonnam National University, Gwangju 500-757, Korea

Prenyltransferases catalyze the sequential addition of IPP units to allylic prenyl diphosphate acceptors and are classified as either *trans*-prenyltransferases (TPTs) or *cis*-prenyltransferases (CPTs), depending on the stereochemistry of the polyisoprenoids. Although CPTs and TPTs share similar substrate preferences and reaction products, they can be easily distinguished by their primary amino acid sequences. The characterization of *cis*-prenyltransferases has been less studied than that of *trans*-prenyltransferases. In this present study, molecular cloning and functional characterization of a CPT gene from a medicinal plant, *Panax ginseng* Mayer are addressed. Analysis of the nature of polyisoprenoid alcohols has been reported that the levels of which are increased during the lifespan-of the plant and environmental stresses. Thus, the response of *PgCPT1* overexpressing lines to salt stress were analyzed. Partial complementation of the yeast dolichol biosynthesis mutant *rer2⊿* suggested that PgCPT1 might be involved in dolichol biosynthesis and play a role in salt stress resistance. Direct protein interaction between PgCPT1 and a human Nogo-B receptor suggests that PgCPT1 functions as a component.

Corresponding author: Tel. 062-530-2054, E-mail: mpizlee@jnu.ac.kr

PA-14

Development of Molecular Marker for Screening Salt Tolerant and Sensitive Soybeans

Seokhyung Lee[1], Gyu Tae Park[1], Jagadeesh Sundaramoorthy[1], Jeong-Dong Lee[1], Hak Soo Seo[2], Jong Tae Song[1*]

[1]School of Applied Biosciences, Kyungpook National University, Daegu, Korea
[2]Department of Plant Bioscience, Seoul National University, Seoul, Korea

Salt-affected areas are more than 6% (800 million hectares) of the world's land area. These saline soils reduce soil fertility and lead to poor crop productivity. Soybean [*Glycine max* (L.) Merr] is one of the major agricultural crops, which is widely known as a salt-sensitive crop and may result in low yield under saline condition. Therefore, it is important to develop salt tolerant soybean varieties for increasing yield in saline areas. In a previous study, a salt tolerance-related dominant gene (*GmSALT3*) was identified on chromosome 3 and nine haplotypes (H1 to H9) also detected among soybean accessions from China. The purpose of the present study is to classify genotypes depending on polymorphisms in coding regions of the *GmSALT3* gene and develop molecular markers to screen salt tolerant and sensitive lines among landraces and wild soybean accessions obtained from Korea, Japan and China. Sequence analysis for *GmSALT3* gene from a total of 92 lines of *G. max* and 110 lines of *G. soja* showed 32 novel haplotypes and four formerly reported haplotypes (H1, H2, H5, and H7). At present, we are verifying consistency with genotype and phenotype.

Acknowledgements: This work was carried out with the support of "Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ01109202)" Rural Development Administration, Republic of Korea.

Corresponding author: Tel. +82-53-950-7753, E-mail: jtsong68@knu.ac.kr

PA-15

곡우 호밀의 경엽 예취가 출수기 지연에 미치는 효과

오명곤[1*], 구자환[2], 한옥규[2], 안종웅[2], 권순종[2]

[1]경상북도 영주시 안정면 경상북도축산기술연구소
[2]경기도 수원시 서둔동 국립식량과학원 중부작물과

극조생종 곡우호밀의 월동후 경엽 예취에 의한 출수기 지연 변화를 알아보고 이에 따른 건물 생산량 차이를 알아보고자 본 연구를 수행하였다. 연구결과를 요약하면 월동후 절간신장이 시작되는 초기(3월 16일)에 지표면과 근접하여 지상부 경엽을 절단 예취한 결과 무예취(대조구)에 비해 예취한 곡우호밀의 출수기가 평균 10일이 지연되었으며, 대조구 호밀의 출수 후 9일 경(4월 23일)에 조사한 지상부 건물중은 예취처리구가 대조구에 비해 57% 감소하였다. 예취 처리구의 건물중 감소는 초장이 작아지고 유효 줄기 수가 감소한 것에서 비롯되었다. 이러한 시험결과로 볼 때 절간 신장 초기에 조생종 호밀의 경엽을 예취해줌으로써 만생종 호밀과 조생종 호밀 교배를 위한 출수기 일치를 이룰 수 있을 것으로 판단된다.

Corresponding author: Tel. 054-638-6012, E-mail: lightgon5@korea.kr

PA-16

중산간지 지역에 따른 미세온도변화와 벼 생육양상의 차이 II

양창인[*], 김명기, 백남현, 강위금, 신운철, 김정주, 조현숙

전라북도 완주군 이서면 혁신로 181 국립식량과학원

조생종 재배지역인 철원과 상주에서 벼를 재배하는 경우 재배환경과 생육양상이 어떠한 차이점이 있는 지에 관하여 오대 벼 품종을 이용하여 벼 재배기간 온도변화를 중심으로 한 미세기상과 벼 생육특성을 조사하였다. 시험지의 위치를 보면 철원은 위도가 38◦15‘ 경도 127◦15‘ 표고 192m이고 상주는 위도 36◦26‘ 경도 127◦26‘ 표고 285m에 소재하였다. 벼 식물체 주변의 온도변화를 살펴보기 위하여 생육시기를 이앙기-분얼초기, 분얼초기-분얼성기, 분얼성기-유수형성기, 유수형성기-출수기, 출수기-수확기로 구분하여 온도변화는 대기와 군락내 온도, 수온, 지온 등의 지점에서 5월20일부터 9월27일까지 조사하였다. 대기온도는 이앙기 5월20일부터 수확기 9월20일까지 상주가 철원보다 높았으며 수온은 유수형성기인 6월 하순부터 지온은 6월초 분얼초기부터 상주가 높았다. 그러나 군락내 온도는 6월하순까지 철원이 상주보다 높았다. 7월중순 출수기 이후에 대기온도에 비해 군락내온도 수온과 지온이 상주보다 철원에서 하락폭이 컸다. 초장은 생육초기부터 철원이 상주보다 큰 편이었으며 경수/수수는 생육전반기에는 상주가 많았으나 수확기에는 오히려 철원이 더 많은 편이었고 Biomass(g/m^2)는 생육초기부터 거의 비슷한 양상을 보이다가 7월초 유수형성기를 기점으로 상주가 더 무거웠다. 식물체내 질소함량은 7월 중순 출수기 이전까지 분얼기를 제외하고 상주가 높았으나 출수기 이후에는 비슷한 수준이었다. 철원에서 수당립수는 적으나 현미천립중은 무거웠으며(27.3g) 수량성은 상주보다 약간 낮은 편이었다. 전반적으로 초·중기생육은 양지역이 비슷하게 진행되었으나 출수기 이후에 점점 크게 나타나는 온도 및 일교차의 차이는 오대품종의 수량과 품질을 좌우하는 중요한 요인으로 판단되었다.

Corresponding author: Tel. 033-455-2031, E-mail: yci212@korea.kr

PA-17

벼흰잎마름병 저항성 유전자 *Xa1, Xa2, Xa3, Xa4* 상호간 두 개의 유전자 집적 효과

박현수[1*], 신운철[1], 정종민[1], 김우재[1], 김정주[2], 백만기[1], 남정권[1], 박슬기[1], 조영찬[1], 김보경[1]

[1]전라북도 완주군 이서면 혁신로 181 농촌진흥청 국립식량과학원
[2]경상북도 상주시 화서면 중화로 2161, 국립식량과학원 상주출장소

본 연구는 벼흰잎마름병 저항성 유전자 중 4번, 11번 염색체에 밀접하게 연관되어 있는 우성유전자 *Xa1*, *Xa2* (Chr. 4)와 *Xa3*, *Xa4* (Chr. 11) 상호간 두 개의 유전자 집적효과를 알아보고자 수행하였다. 단일 저항성 유전자 근동질 계통인 인디카 IRBB1, IRBB2, IRBB3, IRBB4와 자포니카 S345 Xa1, S345 Xa2, S345 Xa3, S345 Xa4를 이면교배하여 아종간 12개 조합을 작성하였다. 이형접합체 유전자형인 F_1 식물체에 대해서 국내수집 15개 벼흰잎마름병균을 접종하여 두 개의 저항성 유전자 집적효과와 생태형간의 차이를 비교 분석하였다. 인디카와 자포니카 모두 이면교배시 정역교배에 따른 병반장 차이는 없었다. 인디카와 자포니카 근동질 계통의 반복친인 IR24와 수원345호는 15개 균주 모두에 이병성 반응을 보였으며 IR24가 수원345호에 비해 이병성 정도가 컸다. 단일 저항성 유전자 중 *Xa1*, *Xa2*, *Xa4*는 아종간 병반장 차이가 없었으나 *Xa3*은 자포니카에 비해 인디카에서 이병성 정도가 컸다. 두 개의 저항성 유전자 집적 조합에서 *Xa2*+*Xa3* 조합을 제외하고는 병반장 차이는 없었다. 공시재료들은 벼흰잎마름병균에 균계 특이적 저항성 반응을 보였으며 저항성 유전자 집적시 저항성 수준이 높은 유전자가 저항성 수준이 낮거나 균계 특이적 이병성 유전자의 효과를 보완하는 질적 보완 효과와 저항성이 양적으로 상승하는 양적 상승효과를 나타냈다.

Corresponding author: Tel. 063-238-5216, E-mail: mayoe@korea.kr

PA-18

극조생종 내도복 및 도열병 저항성 수수형 벼 신품종 '조품'

김명기[1], 원용재[1], 서정필[2], 안억근[1], 정국현[1], 양창인[1], 백남현[1], 윤광섭[1], 전용희[1], 이점호[2], 윤영환[3], 이상복[1], 정종민[1], 정응기[1]

[1]전라북도 완주군 이서면 국립식량과학원
[2]전라북도 전주시 완산구 농촌진흥청
[3]충청남도 예산군 신암면 충남농업기술원

벼 신품종 '조품'은 추석전 햅쌀의 조기 단경기 출하와 벼 수확 및 쌀 출하의 분산 조절로 농가 소득 향상을 목적으로 2000년 하계에 조생종인 철원60호와 대진벼를 인공교배하여 극조생종이면서 쓰러짐과 도열병에 강하면서 쌀 외관이 양호한 SR26668-8-1-1-3-2-2-1 계통을 철원88호 계통명을 부여하여 2013~2015년 3년간 지역적응시험 실시한 결과 신품종으로서 우수성이 인정되어 2015년 12월 농촌진흥청 농작물직무육성신품종선정위원회에서 '조품'라 명명하였다.
조품의 출수기는 7월18일로 오대의 출수기 7월25일보다 7일 정도 빠르고, 엽색은 오대와 비슷한 녹색이며 길이는 약간 짧고 너비는 보통이고 반직립성으로 초형이 양호하다. 벼알에 까락이 없고 잘 떨어지지 않으면서 착립밀도는 보통이다. 밭못자리 잎도열병 검정과 쓰러짐 검정시험에서 각각 강한 반응을 보였다. 현미 천립중은 24.7g으로 오대 27.2g보다 약간 작으면서 현미 장폭비가 1.82인 단원립이고 쌀이 맑고 심복백이 약간 있으나 오대보다 쌀 외관 품위가 좋아 도정수율이 양호하다. 쌀수량은 5.65톤/ha로 오대의 5.41톤/ha보다 약간 증수되었다. 적응지역은 중북부중간지, 중·남부중산간지 및 강원 동부해안지에 적합하다. 조품 벼 신품종은 기존 오대와의 출수기를 차별화하여 벼 수확시기 분산과 쌀 출하 조절을 통하여 농가에 소득증대가 기대된다.

Corresponding author: Tel. 033-455-2031, E-mail: kimmk6690@korea.kr

PA-19

A New Large Grain and High Yielding Peanut Variety "Ahwon"

Suk-Bok Pae[1*], Myung-Hee Lee[1], Sung-Up Kim[1], Eun-Young Oh[1], Chan-Sik Jung[1], Deok-Young Song[1], In-Seok Oh[1], Young-Hee Lee[2]

[1]Department of Southern Area Crop Science, NICS, RDA, Milyang 50424, Korea
[2]National Institute of Crop Science, RDA, Wanju 55365, Korea

Korean usually like to consume large grain of peanut for the roasted or boiled. One of peanut breeding programs is also focused on developing large grain cultivar. A new peanut variety "Ahwon"(*Arachis hypogaea* ssp. hypogaea L.) with large grain and short stem was developed in the Department of Southern Area Crop Science, NICS, in Milyang 2015. This variety was developed from the crossing line between line "YG75" with large grain and erect plant type and line "YG46" with short stem Virginia plant type. "Ahwon" which is short stem and erect Virginia plant type has 40cm of main stem length and 20 branch number per plant. Each pod has two grains with ellipse shape of brown testa and its yield components are composed of 40 mature pods of per plant, 108g of 100-seed weight, 77% of pod shelling ratio in the regional yield trials(RYT). Its seed quality show 29.4% of crude protein and 47.7% of crude oil and 41.3% of oleate in fatty acid composition. This also show resistant to early leaf spot, and more resistant to web blotch, stem rot, and lodging, compared with check variety “Daekwang”. Owing to these superior growth characteristics of lodging resistance and source ability in late maturing stage, the average grain yield of "Ahwon" was more productive than reference variety by 10% with 4.74 MT/ha for grain production in 3 year regional yield trials.

Corresponding author: Tel. 055-350-1215, E-mail: paesb@korea.kr

PA-20

Genetic Analysis of Economically Important Characters in Okra (Abelmoschus esculentus (L.) Moench) Under Peninsular Conditions of Southern India

Kishor D S[1], Arya K[2*], Yogeesh K J[3], Vinod Kumar[4], Yashoda[4] , Hee-Jong Koh[1*]

[1]Department of Plant Science, Plant Genomics and Breeding Institute, Research Institute for Agriculture and Life Sciences, Seoul National University, Seoul, Korea
[2]Department of Plant Breeding and Genetics, College of Agriculture, Kerala Agricultural University, Vellayani, Trivandrum-695522, Kerala state, India
[3]Department of Farm Engineering, Banaras Hindu University, Varanasi-221005, U.P state, India
[4]International Crops Research Institute for Semi -arid Tropics (ICRISAT), patancheru, Hyderabad- 502324, Telangana state, India

Thirty six okra germplasms were grown and evaluated for yield and yield related traits at the Department of Plant Breeding and Genetics, College of Agriculture, Trivandrum, Kerala. The germplasms studied possessed sufficient variability for all the traits. High genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were noticed for almost all characters and narrow difference between GCV and PCV suggest that environmental influence is minimal for the traits studied. High estimates of heritability coupled with high to moderate genetic advance as percent over mean was recorded for all the characters considered. Yield had positive and significant association with number of fruits per plant, fruit weight, fruit girth and number of primary branches indicating that selection based on these characters may improve yield. Principal component Analysis (PCA) indicated that first three principal components contributed for sixty percent total variation among ten characters describing accessions. The cluster analysis revealed that hybridization of cluster I with cluster IV would be beneficial to develop promising varieties under diverse climatic conditions in India.

Corresponding author: Tel. +82-2-880-4551, E-mail: heejkoh@snu.ac.kr

PA-21

복합내병성 고품질 신품종 '청품'의 농업적 특성

원용재[1*], 이정희[1], 양창인[1], 김명기[1], 장재기[1], 조영찬[1], 이상복[1], 이점호[2], 최임수[1], 안억근[1], 서정필[2], 정국현[1], 전용희[1], 현웅조[1], 정응기[1], 하운구[1], 김정주[1], 오세관[1], 최용환[1], 강경호[1], 성낙식[1], 김보경[1]

[1]농촌진흥청 국립식량과학원
[2]농촌진흥청

우리 쌀 품질경쟁력을 높이기 위하여 밥맛이 우수하고 재배안정성이 높은 최고품종을 2003년 삼광을 시작으로 14품종 개발하였다. 이 중 중부지역 재배에 적합한 중생종을 다양화하고, 기상재해와 돌발병해충의 위협을 극복하고자 15번째 중생 최고품종 '청품'을 개발하였다. '청품'은 최고품종 중 재배면적이 가장 넓은 '삼광'의 복합내병성과 밥맛을 갖추고 있으면서 출수기와 내도복성을 개선한 품종이다. '청품'의 출수기는 8월10일로 삼광보다 5일 빠른 중생종이고 벼키는 79㎝로 '삼광'보다 8㎝ 작아 쓰러짐에 강하다. 이삭 당 벼알 수는 116개이고 등숙비율은 90.3%로 양호하며, 현미 천립중은 21.7g으로 작은 편이다. '청품'은 벼의 3대 병해인 도열병, 흰잎마름병, 줄무늬잎마름병에 강하여 친환경재배가 가능한 품종이다. 쌀은 심백이 일부 있지만 맑고, 단백질함량은 6.0%로 낮으며, 밥맛이 우수하다. 도정특성은 현백률, 도정률과 백미완전미율이 '화성'보다 높다. 수량성은 중부평야지에서 3년 평균 536㎏/10a로 '화성' 대비 3% 높았다. '청품'은 복합내병성이면서 밥맛이 우수하고 도정특성 또한 우수하여 생산자, 가공업자 및 소비자들이 만족할 수 있는 최고 품종으로 중부지역에서 우리 쌀의 품질을 높이고 쌀 소비를 제고할 수 있는 품종으로 역할이 기대된다.

Corresponding author: Tel. 031-695-4030, E-mail: yjwon@korea.kr

PA-22

집단제정법 및 제웅 교배방법에 따른 기장 교배 효율

고지연[1*], 송석보[1], 최명은[1], 곽도연[1], 고종철[1], 김기영[2], 최지명[1], 오인석[1]

[1]경상남도 밀양시 점필재로 20(내이동) 국립식량과학원 남부작물부 밭작물개발과
[2]전라북도 전주시 완산구 농업생명로 300 농촌진흥청

화본과 소립곡물인 기장의 효율적인 교배방법을 확립하고자 제웅 및 집단제정방법을 이용하여 교배효율을 조사하였다. 교배에 사용된 품종은 종피의 색깔 및 출수기 차이가 커 F2에서 쉽게 교배유무를 확인할 수 있는 계통인 황금기장과 밀양10호를 모본과 부본으로 이용하였다. 결실률은 교배 후 결실이 이뤄진 종실의 숫자를 조사하였고, 교배립은 F2에서 확인하였다. 처리방법으로 실시한 제웅법은 개열제웅법이고, 제정법으로는 열탕침지, 습지이용법, 저온처리법을 실시하였다. 시험 결과 처리방법에 따라 결실률은 10.3~19.3% 수준이었으며, 개열제웅법과 습지이용 제정법에서 결실률이 가장 높았다. 결실립 중 자가 수정립을 제외하고 교배가 이루어진 립수의 비율인 인공교배율은 열탕침지 45.7%, 저온처리 43.8%, 습지이용 42.1%, 개열제웅 75.7%로 나타났다. 따라서 교배 횟수에 따른 인공 교배율은 개열제웅 처리시 14.6%로 가장 높았고, 습지이용 제정 8.1%, 열탕침지 제정 7.4%, 저온처리제정시 4.5%로 나타나 개열제웅이 가장 효율적인 기장 인공교배 방법으로 판단되었다. 하지만 교배 처리수가 많을 경우 교배시행의 용이성을 고려하여 습지이용이나 열탕침지의 제정법도 바람직한 것으로 사료되었다.

Corresponding author: Tel. 055-350-1225, E-mail: kjeeyeon@korea.kr

PA-23

조사료 수량이 높고 사일리지 품질이 우수한 청보리 신품종 ‘다청’

오영진[1*], 박태일[1], 박종호[1], 김양길[1], 박형호[1], 박종철[1], 강천식[1], 한옥규[2], 강현중[1], 윤건식[3], 홍기흥[4], 배정숙[5], 송재기[6], 김경호[1], 정영근[1], 이광원[1], 김보경[1]

[1]전북 완주군 이서면 혁신로 181 농촌진흥청 국립식량과학원
[2]경기도 수원시 서둔동 국립식량과학원 중부작물부 중부작물과
[3]충청북도 청주시 청원구 오창읍 가곡길 46 충청북도농업기술원
[4]충청남도 예산군 신암면 추사로 167 충청남도농업기술원
[5]대구광역시 북구 칠곡중앙대로136길 47 경상북도농업기술원
[6]경상남도 진주시 대신로 570 경상남도농업기술원

청보리는 곡류를 포함한 사료맥류로 남부지역을 중심으로 대부분 벼+보리 작부체계로로 전통적인 이모작방식으로 재배되어왔다. 특히 청보리에 함유된 곡실은 고급육 생산에 유리하며, 배합사료를 줄일수 있어 수입곡물에 의존도가 높은 국내 축산농가의 사료비절감에 크게 기여하고 있다. 국립식량과학원에서는 우수한 청보리 품종개발에 대한 축산농가의 요구에 부응하여 2002년에 추위 및 도복에 강한 선우보리를 모본으로 하고 키가 크고 숙기가 빠른 큰알보리를 부본으로 인공교배하여 도복 및 추위에 강하고, 총체건물수량이 높으며, 사일리지 품질이 우수한 '다청'을 개발하였다. ‘다청’은 직립초형으로 초장은 99cm로 ‘영양’보다 크며, 파성은 Ⅳ정도로 가을파종에 적합하다. 답리작재배시 출수기는 4월 24일, 황숙기는 5월26일로 ‘영양’과 같다. 줄기수는 ㎡당 625개로 다얼성이며, 내한성은‘영양’보다 강하고, 호위축병은 나주(Ⅰ형), 진주(Ⅳ)에서 저항성, 익산(Ⅲ형)에서 중도저항으로‘영양’과 비슷한 내재해성 품종이다. 조사료 건물수량은 전작에서 12.8톤/ha으로 ‘영양’에 비해 5%, 답리작에서 평균 11.9 톤/ha로‘영양’에 비해 10% 높다. 조사료 품질은 조단백질 함량이 9.0%, 총가소화영양분(TDN)은 64.0%로 영양에 비해 다소 낮았으나 젖산함량이 높고 초산 및 낙산함량이 낮아 사일리지 품질이 Ⅰ등급으로 매우 양호한 품종이다. ‘다청’의 적응지역은 1월 최저평균기온 -8℃이상으로 북부 산간내륙지방을 제외한 전국에서 재배가 가능하다. ‘다청’은 추위 및 도복에도 강하고 총체수량이 높은 다수성으로 금후 축산 농가들로 부터 큰 호응을 얻을 것으로 기대되며, 금후 신품종이용촉진사업을 통한 종자 생산단계를 거쳐 2018년부터 농가에 보급될 예정이다.

Corresponding author: Tel. 063-238-5224, E-mail: ohyj5894@korea.kr

PA-24

밀 고온 및 단기등숙 유전자원 생육특성 조사

김경민[1*], 김경훈[1], 박형호[2], 이상학[1], 이나리[1], 현종내[1], 권영업[1]

[1]경상남도 밀양시 내이동 국립식량과학원 논이용작물과
[2]전라북도 완주군 국립식량과학원 기술지원과

최근 기후변화로 밀 생육기간 중 평균기온이 2016년에 평년보다 1.3℃ 높아지고 갈수록 고온으로 경과하기에 현재 보유하고 있는 밀 유전자원으로 고온 및 단기 등숙 특성을 알아보고자 본 연구를 수행하였다. 연구에 사용된 재료는 CIMMYT 추파밀 및 중국 조숙자원 등 79점으로 시험연구 포장과 온실에 각각 2014년 10월27일, 2014년 11월8일에 파종하여 간장, 수장, 출수기 및 성숙기를 조사하였다. 2015년 5월 평균기온은 19.5℃로 평년 17.8℃에 비해 1.7℃ 높았고 6월 평균기온은 22.3℃로 평년 21.9℃에 비해 0.4℃ 높았으며, 5~6월 전체 평균기온은 평년보다 1.1℃ 높게 경과하였다. 유전자원의 평균 간장은 포장의 경우 67cm로 온실 75cm에 비해 8cm 작았으며 수장은 11.4cm로 온실 11.2cm보다 0.2cm 크게 조사되었다. 출수기는 포장의 경우 평균 5월11일이었고 평균성숙기는 6월19일이며, 온실에서 평균출수기가 4월9일이었고 평균성숙기는 6월4일로써 포장보다 온실에서 평균 등숙기간이 17일 늦게 나타났다. 그 중 BERMUDE와 FLORETTO 2자원은 포장에 비해 온실에서 등숙기간 차이가 4일 늦었지만 포장과 온실간의 등숙기간 차이는 다른 자원들에 비해 가장 적었다. 조사된 유전자원의 등숙특성을 토대로 기후변화대비 안정생산이 가능한 밀 품종을 육성 및 개발하는데 활용 할 예정이다.

Corresponding author: Tel. 055-350-1174, E-mail: raiders87@korea..kr

PA-25

재래종과 육성 콩 품종의 연차별 형질 변이 분석

서민정[1*], 김길현[1], 정건호[2], 박명렬[1], 박장환[1], 김병주[1]

[1]경기도 수원시 권선구 수인로 126 국립식량과학원 중부작물부 중부작물과
[2]경기도 수원시 권선구 수인로 126 국립식량과학원 중부작물부 재배환경과

장류용, 나물용, 밥밑용 콩의 재래종과 육성종 30품종을 대상으로 형질의 연차별 변이를 알아보고자 2014년과 2015년 2년 동안 본 연구를 수행하였다. 파종기는 6월 2일, 재식밀도는 70× 15 ㎝, 1주 2개체, 시비량은 N-P_2O_5-K_2O = 3-3-3.4 (㎏/10a)의 수준으로 시용하였고 시험구는 난괴법 3반복으로 배치하였으며 경장, 마디수, 개화기, 성숙기 등 주요 농업형질을 조사하였다. 2014년도 시험 결과 평균개화일수는 51일, 평균성숙일수는 118일로 나타났는데 개화기의 분포는 7월 15일~8월 1일, 성숙기의 분포는 9월 19일~10월 15일이었다. 2015년도 시험 결과 평균개화일수는 59일, 평균성숙일수는 118일로 개화기의 분포는 7월 23일~8월 11일, 성숙기의 분포는 9월 19일~10월 18일이었다. 개화기는 2014년에 비해 2015년이 8일 가량 늦었으나 가장 빨리 개화되거나 가장 늦게 개화된 품종은 각각 신팔달콩2호와 서리태로 동일하였다. 성숙기는 2년간 거의 비슷한 시기로 나타났으며 가장 빨리 성숙한 품종과 늦게 성숙한 품종도 각각 팔달콩과 서리태로 동일하여 개화기에 비해 성숙기는 연차별 변이가 적은 것으로 나타났다. 2년 간 기상조건은 상당히 차이가 있었는데 특히 발아와 초기 입모 확보에 가장 영향이 컸을 것으로 추정되는 5월 25일~6월 30일까지의 강우량은 2014년의 경우 82.4 ㎜, 2015년은 31.3 ㎜로 2015년은 파종 전후로 가뭄이 심하였다. 한편 시험대상 품종의 경장은 30품종 모두 2015년에 비해 2014년에 길었는데, 이는 6월~8월의 일조시간이 2014년(504.3 시간)에 비해 2015년(616.8 시간)이 훨씬 길었음에도 2015년도에 같은 기간의 강우량이 2014년의 절반 정도에 불과하여 영양생장 기간 동안의 수분 부족 영향이 큰 것으로 보인다.

Corresponding author: Tel. 031-695-4048, E-mail: mjseo77@korea.kr

PA-26

저 질소 환경에 적합한 옥수수 교잡종 선발

류시환*, 서영호, 박종열, 최재근, 박기진, 용우식, 이정훈, 이장용, 김경희

강원도 홍천군 두촌면 장남길 26 강원도농업기술원 옥수수연구소

옥수수의 생산량 증대에 질소는 매우 중요한 역할을 하고 있으며, 단위 면적당 생산량 증대를 위해 일정 수준까지 질소 시비량을 증가시키고 있다. 그러나 척박한 토양 환경 또는 경제적 여건으로 인해 충분한 질소를 투입하지 못하는 경우 옥수수 생산량은 급격히 저하될 수 있다. 현재 개발된 옥수수 품종은 적합한 시비 조건하에서 육성되었으므로 저 비료 환경에서의 생산성은 검증되지 못하는 실정이다. 본 연구는 질소 시비량이 낮은 환경에서 옥수수 수량성이 높은 교잡종을 선발하고자 2014년 홍천에서 수행하였다. 질소 시비 수준은 표준시비(17kg/10a)와 저비(6kg/10a) 조건에서 각각 215교잡종을 이용하여 수량성을 평가하였다. 또한 각 질소 수준에서 생산된 시험 교잡종 종실의 주요 성분 함량을 NIR을 이용하여 분석하였다. 215 교잡종 옥수수의 평균 수량성은 표준시비구에서 909kg/10a, 저비구에서 629kg/10a로 저비구의 수량성은 표준시비구의 69% 수준이었다. 저 비료 시험 교잡종 중에서 14CA006등 5교잡종은 수량성이 850kg/10a 이상이고 표준시비구 대비 수량성이 85%이상으로 저 비료 환경에서 적응성이 우수한 유전형으로 평가되었다. NIR을 이용한 옥수수 종실 성분 분석 결과, 표준시비구와 저비구의 단백질 함량은 각각 9.0%와 6.2%, 지방함량은 3.3%와 3.4% 전분 함량은 64.2%와 66.7%로 종실 성분 중에서 질소 수준에 따른 변이는 단백질이 가장 크게 나타났다. 14CA175등 6교잡종은 단백질 함량이 7.3% 이상이고 표준시비구 대비 함량이 80%이상으로 저비료 환경에서도 단백질 함량이 높게 유지될 수 있는 유전형으로 평가되었다. 본 연구의 결과로 선발된 교잡종은 저 비료 환경 적응형 옥수수 품종육성 및 품종육성을 위한 유용자원으로 활용가치가 높을 것으로 판단된다.

Corresponding author: Tel. 033-248-6913, E-mail: shr8921@korea.kr

PA-27

Variation of Soybean Sprout Characteristics in Two Breeding Populations

Mirwais Ghani, Akbota Makulbekova, Sovetgul Asekova, Minsu Kim, Chul-Woo Park, Jae-Eun Jeong, Dong-Ho Lee, Jong Tae Song, Jeong-Dong Lee*

School of Applied Biosciences, Kyungpook National University, Daegu 41566, Korea

Soybean sprouts found to be rich in health-promoting phytochemicals. Soybean sprouts are known to contain vitamins, sterols, tocopherols, minerals, lipids, sugars and phenolic compounds. The objective of the present study was to evaluate inbred lines, from two different crosses, for several desirable sprout characteristics that included sprout length, sprout hypocotyls length, thickness, and sprout yield. A total of 172 F8 lines from Bosuk x KLG11183 cross and 186 F5 lines from KLG11525 x KLG11183 cross, were planted in 2015 at Gyeongsangbuk-do Agricultural Research Service farm, Daegu, Republic of Korea. The mature plants were harvested and dry seeds were used for sprout experiments. Sprouts were grown at 20 ℃ and relative humidity of 80 % and darkness growth chamber for five days. Significant variation for sprout whole length, hypocotyls length, hypocotyls thickness and sprout yield among the inbred lines was observed. Inbred lines from Bosuk x KLG11183 cross showed, total sprout length from 7.8 to 19.2 cm with an average of 13cm, sprout weight from 90 to 500 % with an average of 267%, hypocotyls length from 4.65 to 12.9 cm and thickness from 1.38 to 2.8mm. Similarly, lines from KLG11525 x KLG11183 cross showed total sprout length from 9.1 to 19.9 cm with an average of 14.2 cm, sprout weight from 116 to 555% with an average of 329%, hypocotyls length from 5.55 to 13.05cm and thickness from 1.41 to 2.45mm. The phenotype variation observed for sprout related traits including sprout yield among the soybean inbred lines indicated that some of the inbred lines may have potential to be used in developing varieties suited for sprout usage.

Corresponding author: Tel. 053-950-5709, E-mail: jdlee@knu.ac.kr

PA-28

친환경 안전 조사료 생산이 가능한 다수성 사료용 벼 품종 '영우'

안억근[1*], 이상복[1], 원용재[1], 이점호[3], 장재기[1], 정응기[1], 최임수[1], 정국현[1], 김명기[4], 이정희[1], 조영찬[2], 최용환[1], 양창인[4], 하운구[1], 정종민[2], 서정필[3], 김정주[5], 정오영[2], 전용희[1], 홍하철[2], 이규성[1], 김보경[2], 김병주[1]

[1]경기도 수원시 권선구 수인로 126 농촌진흥청 국립식량과학원 중부작물부
[2]전라북도 완주군 이서면 혁신로 181 농촌진흥청 국립식량과학원
[3]전라북도 전주시 완산구 농생명로 300 농촌진흥청
[4]강원도 철원군 동송읍 태봉로 2346 농촌진흥청 국립식량과학원 철원출장소
[5]경상북도 상주시 화서면 중화로 2161 농촌진흥청 국립식량과학원 상주출장소

2015년 국내 쌀 생산량은 433만톤, 연간 일인당 쌀 소비량이 62.9㎏로 생산량은 감소하지 않으면서 소비는 지속적으로 줄어들고 있어 구조적으로 공급 과잉 현상이 심화되고 있는 실정이다. 사료용 벼는 논의 형상과 기능을 유지하면서 이러한 수급불균형을 해결할 수 있는 좋은 수단임에도 불구하고 밥쌀용과 비교하여 소득이 낮아 정부보조금 없이는 농가 현장에서 재배를 기피하는 경향이 있어 수량성 향상 등을 통한 경제적 가치를 올릴 필요가 있다. 이번에 육성한 사료용 벼 '영우'는 도열병, 흰잎마름병(균계 K1, K2, K3, K3a), 줄무늬잎마름병, 벼멸구 및 애멸구에 저항성이 있어 병충해 방제에 들이는 노력 및 비용을 절감할 수 있어 친환경 안전 조사료 생산이 가능할 뿐만 아니라 농업경영비도 절감 할 수 있다. 또한 출수기가 8월 15일로 8월 말에서 9월 상순에 수확이 가능하여 동계사료작물과 이모작 작부체계 적용에 유리한 점이 많아 연중 양질 조사료 생산을 가능하게 한다. '영우'의 지상부 건물수량은 중부평야, 영남평야 및 호남평야지 4개소에서 3년간 시험한 결과 평균 20톤/ha으로 '녹양' 대비 높은 수량을 나타내 경제적 가치도 높일 수 있을 것으로 기대된다. 더구나 가축이 소화 흡수할 수 있는 사료의 영양가 지표인 가소화양분총량(TDN)도 일반 사료작물과 비교하여 떨어지지 않아 사료적 가치가 높다고 판단된다. 이처럼 복합내병충성, 숙기단축을 통한 이모작 작부체계 적용 가능, 높은 지상부 건물수량 및 가소화양분을 보유한 '영우'는 밥쌀용과 비교해 거의 동등한 수준까지 경제적 가치를 올릴 수 있을 것으로 기대되어 재배 확대 시 쌀 생산조정을 통한 수급조절에 일익을 담당할 것으로 생각된다.

Corresponding author: Tel. 031-695-4027, E-mail: okahn@korea.kr

PA-29

A New Boxthorn(*Lycium chinense* Miller) Variety with Tetradiploid and Self-compatibility 'Whasu'

Jung-Il Ju*, Tug-Sang Yun, Bo-Hee Lee, Young-Chun Park, Su-Dong Kim, Min-Sik In, Hyun-Ho Kim

Boxthorn Experiment Station of Chungnam-Do ARES, Cheongyang 33319, Korea

The new boxthorn line, CBP06419-243 was selected from the hybrids(F1) between CBP03310-250(IT232705) and CBP05399-1 to breed the cultivar with self-compatibility and high quality. These lines used for crossing was tetradilpoid induced by the colchicine treatment on bud. Its preliminary yield test was performed from 2009 to 2011 and the selected line was named 'Cheongyang 18'. Its regional yield trials were carried out in Cheongyang, Yesan and Jindo from 2012, 2014, 2015 and Cheongyang 18 was registered as the new variety, Whasu, in 2015. The specific characteristics were summarized as follows;

Tree shape is semi-open type and the leaf is lanceolate. The flowers are distinctly larger than a variety of diploid. The fruit type is medium size, long oblong and yellowish red. Branching by pruning its sprout was generated less than the check variety, Cheongmeong. The infection rates on leaves to *Eriophys macrodonis* Keifer was as strong as 7.7 percent. Anthracnose on fruits in open field was slightly severe compared to the check variety, but the infection rates in rain shelter greenhouses was similar. The content of betaine and free sugar in dried-fruits were higher than that of the check. The dried-fruit yield was decreased about 13 percent in open field, but increased 18 percent in rain shelter greenhouses. This variety was suitable for cultivation in plastic film greenhouses because of self-compatibility and high-yielding. It is not necessary the companion variety.

Corresponding author: Tel. 041-635-6384, E-mail: cnswhtbar@korea.kr

PA-30

자포니카벼 팔공 유래 도열병 내구저항성 QTL탐색

백만기[1*], 박현수[1], 신운철[1], 정종민[1], 남정권[1], 권순욱[2], 김보경[1], 조영찬[1]

[1]전라북도 완주군 이서면 혁신로 181 농촌진흥청 국립식량과학원
[2]경상남도 밀양시 삼랑진읍 삼랑진로 1268-50 부산대학교 생명자원과학대학

도열병은 전 세계 벼 재배에서 가장 큰 피해를 주는 병해이며, 저항성품종을 육성하여 이용하는 것이 가장 효과적인 방법이다. 도열병 저항성 관련 유전연구는 광범위하게 이루어져 왔으나 병의 발병시기가 길고 유전현상이 복잡하며 도열병균의 레이스 변이가 심하여 저항성 품종이 쉽게 break down 되었고 내구저항성이 강화된 도열병 저항성품종의 육성이 계속 요구되어 왔다. 우리나라에서 1987년 육성된 팔공벼는 지속적인 안정된 저항성을 유지하는 내구저항성 (durable resistance)으로 알려져 있다. 일품벼/2*팔공벼 BC_1F_{7-8} BIL 집단에 대한 japonica 유전적 배경의 SNP chip을 활용하여 genotyping으로 팔공벼의 내구저항성 관련유전자 QTL을 분석하였다. 94 BIL 계통은 2013년 철원과 익산, 12014년 익산과 운봉에서 도열병밭못자리검정을 실시하였다. 그 결과 팔공은 1-2의 저항성 반응, 일품은 7-9의 이병성 반응을 보였고 BIL 계통은 0-3의 저항성 쪽으로 편의 된 0-9 반응의 분포를 보였다. 이들 결과에 대한 저항성 관련 QTL은 염색체 2번, 4번, 7번, 11번, 12번에서 16개의 QTL이 탐색되었고 bn2.1(30.2 cM), bn2.3(80.5 cM), bn4.1(16.7 cM), bn4.2(109.9 cM), bn7.2(71.6 cM), bn11.1(54.3 cM), bn11.2(99.2 cM) 등의 QTL은 표현형 변이의 15.7-56.7%를 설명하였다. 이후 이들 좌위의 병저항성 관련 ORF의 존재에 대한 검색 및 이들 정보를 활용한 분자표지 개발을 추진하고 있다.

Corresponding author: Tel. 063-238-5214, E-mail: baekmg@korea.kr

PA-31

바이오에너지 작물 억새의 우량 억새 육종을 위한 바이오매스 수량 결정 핵심 형질 탐색

임수현, 육민정, 김도순*

서울특별시 관악구 대학동 서울대학교 농업생명과학대학 식물생산과학부

억새는 다년생 C4 화본과 식물로서 높은 바이오매스 수량과 다양한 기후대에서 분포하는 높은 환경 적응성을 가지고 있어 바이오에너지 작물로 활발히 연구되고 있다. 하지만 억새의 안정적인 수량 확보를 위해서는 최소한 3년의 재배기간이 필요하기 때문에 바이오에너지용 억새 품종을 육종하기 위한 육종연한 및 기본 연구기간이 길게 소요되는 한계가 있다. 위와 같은 한계를 극복하기 위해 이른 재배시기에도 억새의 바이오매스 수량을 예측할 수 있는 핵심 형질(기후학적 형질 및 농업적 형질)을 탐색하고자 연구를 수행하였다.
한국과 동북아시아 지방에서 수집한 184개의 참억새 생태형과 93개의 물억새 생태형을 재식하여 4년에 걸쳐 억새 유전자원의 출아 및 개화시기와 관련된 기후학적 형질과 수량과 관련 있는 잎과 줄기와 관련된 생육 형질을 조사하였다. 조사된 형질들을 연차별 바이오매스 수량과 상호연관분석을 시행한 결과, 출수기, 엽면적과 줄기생육형질(초장, 줄기개수, 줄기두께, 건물중)이 바이오매스 수량과 연관성이 높은 것으로 확인되었다. 또한 억새 초기 재배시기의 형질들과 안정적 수량을 보이는 4년차 바이오매스 수량과의 상호연관성 평가 결과, 2년차 조사 형질 중 엽면적, 초장, 줄기두께, 줄기 건물중이 4년차 바이오매스 수량과 높은 상호연관성을 보이는 것을 확인할 수 있었다. 따라서 본 연구결과를 바탕으로 우량 억새 유전자원의 초기 선발 및 새로운 품종의 초기 평가를 통한 바이오매스 수량 예측이 가능할 것으로 판단되며 이는 억새 육종연한을 줄여 바이오매스용 억새 품종 개발에 크게 기여할 것으로 평가된다.

Acknowledgements: 본 연구는 농촌진흥청 LMO 환경위해성 평가기관 사업(과제번호: PJ01126901)의 지원에 의해 수행되었다.

Corresponding author: Tel. 02-880-4542, E-mail: dosoonkim@snu.ac.kr

PA-32

내재해성 및 튀김율이 높은 팝콘용 옥수수 신품종 '지팝콘'

최재근[1*], 박종열[1], 장은하[2], 류시환[1], 서영호[1], 박기진[1], 용우식[1], 이정훈[1], 김경희[1]

[1]강원도 홍천군 두촌면 장남길 26 강원도농업기술원 옥수수연구소
[2]강원도 춘천시 충열로 83 강원도농업기술원 원예연구과

튀김옥수수를 이용한 국내 팝콘시장은 연간 5천억 규모로 형성되어 있으며, 대부분 수입산 알곡을 이용하고 있다. 수입산이 대부분인 팝콘 알곡을 국내산 품종으로 대체하기 위하여 2012년에 강원도옥수수연구소에 "오륜"품종을 개발하여 전국에 40ha의 재배단지를 형성하여 국내시장에 보급되고 있다. 본 연구는 오륜품종보다 내재성이 강하고 튀김율이 높은 품종을 개발하고자 수행하였다. "지팝콘"은 튀김용 모집단에서 분리된 GP3를 모본, GP4를 부본으로 하여 개발하였으며, 수량성은 "오륜" 대비 6%증수한 464kg/10a로 수량이 높으며, 도복지수는 1.5로 "오륜"의 3.5보다 낮아 내재해성도 강하며, 100립중은 15.5g으로 "오륜" 16.0g보다 소립인 특성을 갖고 있다. 튀김율은 알곡 수분이 11.0~12.0%일 때 "지팝콘"이 28.3배로 "오륜"의 25.9배 보다 높아 가공용으로도 적합한 특성을 가지고 있어 앞으로 농가에 보급하여 재배단지를 확대하면 수입산을 대체할 품종으로 기대한다.

Corresponding author: Tel. 033-248-6921, E-mail: jaekeun@korea.kr

PA-33

조숙 내도복 다수성 조사료용 겉귀리 '다조'

김양길[1*], 박형호[1], 오영진[1], 박종호[1], 강천식[1], 박종철[1], 김경호[1], 최규환[2], 홍기흥[3], 박태일[1], 정영근[1], 김보경[1], 이광원[1]

[1]전라북도 완주군 이서면 혁신로 181 농촌진흥청 국립식량과학원
[2]전라북도 익산시 서동로 413 전라북도농업기술원
[3]충청남도 예산군 신암면 추사로 167 충청남도농업기술원

귀리는 생육기간이 타 맥류보다 긴편이나 신장속도가 빠르고 보리, 밀보다 건물수량이 많으며 사료가치 및 가축의 기호도가 높아 국내 축산 농가의 사료비절감에 크게 기여하고 있다. 또한 다양한 작부체계(추파, 춘파, 하파)로 재배가 가능하여 2모작, 3모작 등의 틈새 작물로 이용되고 있다. 따라서 이에 적합한 품종을 육성하기 위해 2004년에 하파적응성이 좋은 조숙, 다수성 품종인 "Swan(IT021338)을 모본으로, 내한 내도복 등의 특성을 가진 "식용귀리(IT128172)/7A202-210(IT128825)//CI7763(IT133501)" 계통을 부본으로 인공교배하여. 조숙 내도복 다수성인 총체담근먹이용 '다조'를 개발하였다. '다조"는 줄기 굵기가 삼한귀리보다 가늘며 이삭형은 산수형이고 종실색은 갈색, 종실 길이는 중정도이다. 출수기는 삼한귀리에 비해 전작(제주, 예산, 익산)에서 5월 1일로 6일, 답리작(전주, 익산)에서 5월 3일로 5일 빨랐다. 초장은 106㎝로 삼한보다 3㎝ 정도 길고, 경수(1,116개/㎡)는 많으며, 엽신비율은 적은반면 이삭비율은 높다. 내한성과 도복정도는 삼한귀리와 비슷하다. '다조'의 건물수량성은 전작에서 13.17톤/ha으로 7% 증수, 답리작 12.16톤/ha으로 4% 증수하였다. 조단백질 함량은 6.7%정도이나 TDN 수량은 7.44톤/ha으로 삼한귀리보다 2% 높으며, 사일리지 등급은 2로 삼한귀리와 비슷하였다. '다조'는 1월 최저평균기온이-4℃ 이상인 지역에 보급 될 것으로 기대 된다.

Corresponding author: Tel. 063-238-5225, E-mail: kim5yk@korea.kr

PA-34

구기자나무의 비가림하우스 재배시 용도별 적합 품종선발

주정일*, 윤덕상, 박영춘, 이보희, 인민식, 김현호

충남 청양군 운곡면 충남농업기술원 인삼약초연구소 청양구기자시험장

구기자나무는 고추, 토마토, 감자 등과 같은 가지과(*Solanceae*)에 속하고, 이용부위는 열매를 건조한 구기자, 뿌리의 껍질을 벗겨 말린 지골피, 이른 봄에 채취하는 구기순과 구기엽 등 다양하다. 구기자는 빗물에 의하여 크게 전파되는 탄저병 등 병 발생을 억제하기 위하여 비가림 비닐하우스에서 재배하는 것이 좋다. 이에 비가림하우스에서 구기자 8품종에 대하여 생과 ·건과 이용 적합성, 수량, 색택 및 주요 성분을 비교하였다.
생과 유통 중 품질을 저하시키는 무름과 발생이 적으면서 과피가 두껍고 씨앗이 적은 품종은 '청명'과 '화수'이었다. 적색도/황색도로 생과의 붉은 정도를 비교한 결과 색택이 양호한 품종은 '청운'과 '화수'이었다. 따라서 구기자 '화수' 품종이 열매가 크고 과즙이 많으며 유통 중 무름과 발생이 적어 생과를 생산하기 위한 품종으로 적합할 것으로 판단되었다. 열매크기는 신품종이 27.1~40.1g/100과 로서 청양재래 15.0g에 비하여 뚜렷하게 증대되어 열매가 크고 수확이 편리하였다. 비가림하우스에서 건구기자의 수량이 많은 품종은 '청명', '호광', '청당' 등 이었다. 따라서 비가림하우스에서 건구기자 생산에 적합한 품종은 '청명'이 적합할 것으로 판단되었다. 기능성분으로 Zeaxanthin 함량은 열매 평균 0.065mg/g, 잎 평균 0.139mg/g로서 잎에서 높았고, 품종별로는 '호광'이 다른 품종에 비하여 높았다. 뿐만 아니라 '호광' 품종은 다른 품종에 비하여 당도도 높아 건강기능성을 위한 품종으로 소비자에게 추천할 수 있을 것으로 판단되었다. 구기자의 지표성분인 Betaine은 품종에 0.82~1.29mg/g로 <대한약전>의 규정 0.5mg/g보다 높았고, 품종별로는 '청명'이 생약재 생산을 위한 품종으로 적합할 것으로 판단되었다.

Corresponding author: Tel. 041-635-6384, E-mail: cnswhtbar@korea.kr

PA-35

중부지역 적응 복합내병성 벼 신품종 '삼광1호'의 농업적 특성

이정희[1*], 원용재[1], 조영찬[1], 최임수[1], 이점호[2], 양창인[1], 김명기[1], 안억근[1], 서정필[2], 이상복[1], 전용희[1], 성열규[1], 정응기[1], 하운구[1], 장재기[1], 정국현[1], 윤미라[1], 강경호[1], 박향미[1], 황기호[1], 노재환[1], 김보경[1]

[1]경기도 수원시 권선구 수인로 126 농촌진흥청 국립식량과학원
[2]전주시 완산구 농생명로 300 농촌진흥청

중부지역 재배에 적합한 중생 벼 품종은 '화성'과 '하이아미' 등이 있지만 아직 다양성이 부족하다. 또한 지구온난화에 의한 병해충 발생에 대비하여 안정적 식량생산을 하기 위해 재배안정성을 갖추면서 밥맛이 우수한 품종 육성이 더욱 필요하다. '삼광1호'의 출수기는 8월7일로 화성보다 1일 빠른 중생종이고 벼키는 77㎝로 '화성'보다 6㎝ 작다. 화성과 비교하여 이삭당 벼알수는 많으며 등숙비율이 비슷하고 현미천립중은 21.7g으로 가벼운 편이다. '삼광1호'는 벼의 3대 주요 병해인 도열병, 흰잎마름병 및 줄무늬잎마름병에 강하고, 쌀알은 심복백이 거의 없어 맑고 깨끗하며, 밥맛이 화성과 추청보다 우수한 품종이다. 도정특성에서 백미완전립율과 완전미도정수율이 '화성'보다 높다. 수량성은 지역적응시험 보통기 보비재배(11개소)에서 5.62 MT/ha로 화성대비 8% 증수된 수량성은 보였으며 중부평야지, 중서부해안지 및 남부중산간지가 적응지역이다. '삼광1호'는 복합내병성이면서 밥맛과 도정특성이 우수하여 생산자, 도정 및 유통업자, 소비자들이 모두 만족할 수 있는 품종으로 중부지역에 적응하는 중생 품종을 다양화하고 우리 쌀 경쟁력 강호와 쌀 소비확대에 기여할 것으로 생각된다.

Corresponding author: Tel. 031-695-4032, E-mail: lejehe@korea.kr

PA-36

국내 자포니카 유전자원 이용 GWAS 분석에 의한 도열병 저항성 유전자 탐색

조영찬[1*], 백만기[1], 권순욱[2], 박현수[1], 정종민[1], 남정권[1], 김보경[1]

[1]전라북도 완주군 이서면 혁신로 181 농촌진흥청 국립식량과학원
[2]경남 밀양시 삼랑진읍 삼랑진로 1268-50 부산대학교 생명자원과학대학

우리나라 자포니카 벼 유전자원을 이용한 고양식미 및 저항성 벼품종 개발에 대한 관심이 높아지고 있으며, 재래벼 및 잡초성 벼로 부터 도열병 등 재배 안정성 확충을 위한 저항성 유전자 탐색이 이루어져 왔다. 최근 자포니카 유전적 배경의 SNP chip이 개발되어 (Nagasaki et al. 2010), 자포니카 유전자원 집단에 대한 genotyping 및 유전자/QTL 탐색이 가능하게 되었다. 국내육성 자포니카 24품종, 재래벼 26품종, 잡초벼 22 계통, 자포니카 고세대 육성계통 19개, 일본 주요 품종 5개 등 96개 유전자원 집단에 대해 도열병 밭못자리 검정을 하였다. 전장 유전체 분석(GWAS)을 위한 genotyping은 768개 SNP로 구성된 chip을 Illumina array 분석을 하였다(Illumina Inc., San Diego, CA, USA). SNP calling은 Genome Studio software (Illumina Inc.)의 genotyping module v2011.1로 수행하여 false data 마커 68개와 monomorphic 마커 20개, 5% 이하의 minor allele frequency 마커 58개를 제외한 622개 SNP 마커에 대해 calling하였다. GWAS 분석은 Weighted Mixed Liner Model (PCA+K, MLM)을 이용하여 수행하다. SNP 마커와 형질간 연관성 분석을 위한 Q-Q plot은 각 형질에 대해 이론적 LOD 값과 관측 LOD 값간 관계로부터 얻어졌고, Manhattan plot과 Q-Q plot graphic들은 *R* package qqman으로 작성하였다(Turner 2014). LOD 값 2.5 이상의 마커들은 potential candidate로 고려하였다. 도열병 저항성 관련 QTL 분석 결과, 1번, 2번, 3번, 4번, 6번, 7번, 8번, 9번 및 12번 염색체상에서 22개 putative QTLs가 확인되었고, 이들 QTL들은 표현형 변이를 6.8-14.9%를 설명하였다. gbn1.3 (*Pi35*), gbn2.1(*Pi14*), gbn4.1(*pi21*, *qLB4.1*), gbn4.2(*Pi39*), gbn6.1(*Piz*, *Pizt*, *Piz5*, *Pi9*, *Pi2-2*, *Pi26*, *Pi40*), gbn8.1(*Pi33*), gbn12.1(*Pi62*), gbn12.2(*Pita*, *Pita2*, *Pi20*, *Pi25*) 및 gbn12.3(*Pi-GD3*, *Pi21*) 등의 QTL 좌위에서는 기존에 다수의 저항성 유전자가 보고되었다.

Corresponding author: Tel. 063-238-5211, E-mail: yccho@korea.kr

PA-37

Protein Dynamics of Rice Seedling Leaves in Response to High Temperature Stress

Sang-Woo Kim[1], Swapan Kumar Roy[1], Soo-Jeong Kwon[1], Hyeong-Jun Park[1], Je-Hyeok Yu[1], Ki-Hyun Kim[2], Yong-Gu Cho[1], Chul-Won Lee[1], Sun-Hee Woo[1*]

[1]Department of Crop Science, Chungbuk National University, Cheong-ju 28644, Korea
[2]Chungbuk Agricultural Research and Extension Services, Ochang 28130, Korea

The present study was conducted to explore molecular mechanisms of high temperature at seedling stage using high temperature tolerant and sensitive rice cultivars as Dongan and Ilpum respectively. Rice seedlings grown at 28/20°C (day/night) were subjected to 7-day exposure to 38/28°C for high-temperature stress, followed by 2-D based proteomic analysis on biological triplicates of each treatment. The growth characteristics exhibited that Dongan showed tolerance than Ilpum towards high temperature stress. High temperature has an adverse effect in the seedling stage both in high temperature sensitive and tolerant cultivar. Two dimensional gels stained with silver staining, a total of 722 differential expressed protein spots (≥ 1.5-fold) were identified using Progenesis SameSpot software. However, 38 differentially expressed protein spots were analyzed using LTQ-FT-ICR mass spectrometry. Of these, 9 proteins were significantly induced while 10 reduced in response to high temperature treatment. Major changes were associated with the proteins involved in the carbohydrate metabolism, photosynthesis, and stress responses. Proteome results revealed that high temperature stress had an inhibitory effect on carbon fixation, ATP production and photosynthetic machineries pathway. The expression level of mRNA is significanlty correlated with the results obtained in the proteome investigation. Taken together, the obtained results may be helpful to identify the proteomic changes and the associated genes and to gain a better understanding on the molecular mechanisms involved in tolerance of rice at seedling stage.

Corresponding author: Tel. +82-43-261-2515, Email: shwoo@chungbuk.ac.kr

PA-38

Complementary Screening Method for Phytophthora Blight Resistance and Varietal Difference in Sesame(*Sesamum indicum* L.)

Eun-Young Oh[1*], Sung-Up Kim[1], Young-Nam Yoon[2], Myung-Hee Lee[1], Suk-Bok Bae[1], Myung-Sik Kim[1], Un-Sang Yeo[1], Chan-Sik Jung[3], In-Seok Oh[1]

[1]Upland Crop Breeding Research Div, Department of Southern Area, NICS, RDA
[2]Crop Production Technology Research Div, Department of Southern Area, NICS, RDA
[3]Herbal Crop Research Div, Department of Herbal Crop Research, NIHHS, RDA

Phytophthora blight disease of sesame, caused by *Phytophthora nicotianae* is one of the serious disease which gives a huge loss of yield in Korea. This study was conducted to verify the screening method of phytophthora blight resistance by artificial inoculating in seedling stage. To apply the method to sesame resistance breeding, inoculation time, scoring of disease symptom and optimal density of inoculum were modified from former research(Park et al., 2004). The inoculum, *Phytophthora nicotianae*(KX160000) which isolated from sesame field at Gyeongju was used on study in the form of zoospore suspension. The optimal time of inoculation was the second true leaves emerging stages, of which almost equivalent to 14-days after seeding. At the density of 10^5 per ml of zoospores, discoloration of basal stem appeared three days after inoculation. After seven days, seedlings withered in susceptible group. Sixty eight sesame varieties were screened and symptom severity were graded in 1-9 scale. Thirty five varieties including 'Miheuk' showed highly susceptible, 'Suji' and other fifteen varieties evaluated as susceptible. Whereas seventeen varieties including 'Goenbaek' showed barely no symptom after inoculation. In the screening, resistant and susceptible varieties were highly diverged in all KX160000 inoculated groups. This modified method could be an useful selection tool in disease resistant sesame breeding.

Corresponding author: Tel. 031-296-6898, E-mail: koreabreed@hotmail.com

PA-39

베타글루칸 함량이 높고 흰가루병 저항성인 찰성 쌀보리 '베타원'

박종철*, 이미자, 김양길, 강천식, 박종호, 오영진, 박태일, 김경호, 이광원, 정영근

전북 완주군 이서면 혁신로 181, 국립식량과학원 작물육종과

국내 쌀보리는 80년대 이후 찰성 인자를 도입하면서 주로 취반용으로 이용되어져 왔다. 취반용 보리는 단백질, 찰성 뿐 아니라 건강 기능성분인 베타글루칸도 중요한 품질 요인 중의 하나이다. '베타원'은 기존 품종들에 비해 베타그루칸 함량이 약 2배 높은 고 기능성 쌀보리 신품종으로 2015년도 육성되었다. '베타원'은 보리호위축병과 흰가루병에 저항성인 특성을 가지고 있다. 종실은 약한 노란색을 띄면서 취반 후 색도의 기호성이 좋고 보릿가루가 고운 품질 특성을 보인다. '베타원'은 아밀로스 함량이 높은 Glacier AC38과 베타글루칸 함량이 높은 Shikoku Hadaka 97을 2007년도에 인공교배하였다. F3 이후 계통을 전개하면서 병해 저항성이며 출수기, 성숙기, 도복 등 농업적 형질 특성이 우수한 우량 계통을 선발하여 특성을 고정화 하였다. 이후 생산력 검정 시험을 통해 수량성을 검정하여 익산 121호로 명명하여 2013년부터 3 개년간 지역적응 시험을 수행하였다. 익산 121호는 파성이 III으로서 대비품종의 IV에 비해 춘파 적응성이 좋은 특성을 가지고 있으며, 특히 3 개년간 병해 저항성 검정 결과에서 흰가루병과 보리호위축병에 저항성이었다. 익산 121호는 답리작에서 318kg/10a의 수량성으로 새찰쌀보리와 비슷한 다수성을 보였다.
품질특성 분석 결과에서도 보리의 기능성분인 베타글루칸 함량이 11.4%로 새찰쌀보리의 6.5%에 비해 약 2배 정도 높았으며 현재까지 육성된 품종들 중 가장 높은 특성을 보였다. 새찰쌀보리에 비해 보릿가루의 입도가 작아 가공 제품용으로도 적합한 특성을 보였다. 이에 따라 2015년 직무육성 신품종선정심의회 심의를 거쳐 베타글루칸 함량이 높은 우수한 찰성 쌀보리 신품종 "베타원"을 육성하였다.

Corresponding author: Tel. 063-238-5226, E-mail: pacc43@korea.kr

PA-40

항산화 성분과 품질이 우수한 흑색 종실 맥주용 보리 신품종 '흑호'

박종철*, 김양길, 강천식, 박종호, 오영진, 박태일, 김경호, 이광원, 정영근

전북 완주군 이서면 혁신로 181, 국립식량과학원 작물육종과

맥주용 원료로 이용되는 2조 겉보리 신품종 '흑호'를 개발하였다. '흑호'는 국내 처음 육성된 흑색 종실의 맥주용 보리이다. 유색 종실의 특성으로 총 페놀, DPPH 등 항산화 성분 함량이 높은 특성을 가지고 있다.
'흑호'는 2005년도 흑색 종실의 유전자원 Black barley와 다수성이며 맥주용 품질이 우수한 호품보리를 인공 교배하여 육성하였다. F3 이후 계통을 전개하면서 출수가 빠르고 초형이 우수한 우량 라인을 선발하여 특성을 고정화 하였다. 이후 생산력 검정 시험을 통해 수량성이 우수한 계통을 선발하여 익산 170호로 명명하여 2012년부터 3 개년간 지역적응 시험을 수행하였다. 지역적응 시험은 맥주보리 주 재배 지역인 전남, 경남, 제주와 전북 지역에서 수량성과 지역별 적응성을 검정하였다.
2014년도 수량성이 우수하고 항산화 성분 특성을 가진 흑색 종실 맥주용 보리로 신품종으로 선정되어 '흑호'로 명명되었다. '흑호'는 배유 부분까지도 유색을 보이는 2조 겉보리이다. 출수기, 도복, 병해 저항성 정도는 호품과 비슷한 특성을 가지고 있다. 수량성은 유색이면서도 다수성으로 개발된 '호품'과도 비슷한 수량을 나타내었다. 맥주용 원맥 품질에서 천립중이 48g으로 호품의 44gg에 비해 대립인 특성이다. 1등급 종실 비율도 92%로 호품의 89%에 비해 우수하였다. 맥아 품질에서도 맥아 수율은 85% 등 호품과 비슷한 우수한 맥주용 특성을 보였다. '흑호'의 항산화 성분 함량은 원맥과 맥아에서 호품에 비해 높게 조사되었다. '흑호'는 호품에 비해 총 페놀 함량은 12%, 안토시아닌 함량은 24% 높았다. '흑호'는 기능성 맥주용의 원료로 활용하거나 종실의 유색을 이용한 보릿가루 등 다양한 용도로의 이용이 가능한 품종이다.

Corresponding author: Tel. 063-238-5226, E-mail: pacc43@korea.kr

PA-41

도복에 강한 소립 나물용 콩 '소연'

강범규[1*], 김현태[1], 최만수[1], 고종민[1], 서민정[2], 신상욱[1], 서정현[1], 구성철[1], 윤홍태[1], 백인열[3], 오인석[1]

[1]경남 밀양시 점필재로20 국립식량과학원 밭작물개발과
[2]경기도 수원시 수인로126 국립식량과학원 중부작물과
[3]전북 완주군 이서면 혁신로181 국립식량과학원 기획조정과

'소연'은 나물용 콩 표준품종인 '풍산나물콩'과 같이 발아특성이 우수하고 콩나물 재배 시 배축 생장 속도와 길이 등이 생산에 적합하면서도, 도복에 강해 재배가 용이하여 가공업체 및 생산자에게 유리할 것으로 기대된다. '소연'은 2003년 '소강'을 모본, '녹채'를 부본으로 인공교배하여 '04~'05년도에 F_1, F_2 세대를 양성하고 '06년~'10년 F_3~F_7 계통을 전개 및 선발하여 생산력검정시험과 4개 지역 지역적응시험을 거쳐 육성하였다. '소연'은 화색이 백색, 엽형이 피침형, 종실은 구형, 담갈색 제색의 황색 종피의 고유특성을 지니고 있으며 개화기는 7월 30일, 성숙기는 10월 5일로 '풍산나물콩'보다 빠르며 100립중은 10.1g으로 '풍산나물콩'보다 작다. 내재해성 검정에서 내도복성 검정 결과 '소연'은 시험포장(소연: 1, 풍산: 5)과 2배 밀식 포장(소연: 1, 풍산: 7)에서 '풍산나물콩' 대비 내도복성이 매우 우수했고, 40℃에서 48시간 처리하여 조사한 협개열성 또한 2.2%로 매우 낮았다. '소연'의 수량은 지역적응시험을 실시한 4개 지역 평균 353kg/10a였으며 콩나물 재배 특성검정에서는 발아세 97.0%, 발아율 98.0%, 경실률 1.0%, 배축길이 8.3cm, 수율 615%로 풍산나물콩과 대등하였다.

Corresponding author: Tel. 053-663-1120, E-mail: hellobk01@korea.kr

PA-42

탈립 개선 생육기간 100일 단기성 콩 '중모3013'

강범규[1*], 김현태[1], 고종민[1], 최만수[1], 이병원[2], 신상욱[1], 서정현[1], 오은영[1], 백인열[3], 윤홍태[1], 오인석[1]

[1]경남 밀양시 점필재로20 국립식량과학원 밭작물개발과
[2]경기 수원시 수인로126 국립식량과학원 수확후이용과
[3]전북 완주군 이서면 혁신로181 국립식량과학원 기획조정과

생육기간이 100일 내외로 짧은 단기성 콩은 맥류나 양파·마늘 등 동작물과 안정된 작부체계를 구성하여 토지 이용도를 높이고 수익을 향상할 수 있다. 그러나 일반적인 단기성 콩은 짧은 생육기간으로 인해 수량이 낮고 탈립성이 높아 적기에 수확하지 못할 경우 손실량이 많은 특징을 가지고 있어 이를 개량할 필요가 있다. '중모3013'은 표준품종인 새올콩보다 수량성이 높고 탈립성이 개선된 품종으로 '큰올콩'을 모본으로 'KS4694'를 부본으로 2005년 인공교배하여 조합번호 YS1703을 부여하였으며 계통육종법으로 '06년~'07년 F_1, F_2 세대를 양성·선발하고 '08년~'10년 F_3 이후 계통을 전개 후 YS1703-2B-2-1-1-1-1 계통을 선발하여, '11년~'12년도에 생산력검정시험을 실시하고 '밀양259호'의 계통명을 부여한 후 '13~'15년 3개년간 4개 지역에서 지역적응시험을 실시하였다. '중모3013'은 엽형이 난형이고 화색은 백색, 모용색은 회색의 유한형이며, 일반적 하대두형 생육특성을 지니고 있고 종실은 100립중 26.5g의 제색이 황색인 편구형이다. 지역적응시험에서 생육일수는 94일~103일이고 성숙기는 9월 하순이었다. '중모3013'의 자반, 갈반, 미이라 등 종실 이병립율은 4.6%로 '새올콩'보다 높고 바이러스 유묘검정 결과 상위엽 모자이크 반응을 나타내는 등 단점이 있으나 탈립 정도를 조사한 결과 포장에서는 '새올콩'이 9(약), '중모3013'이 5(중)로, 실내검정에서는 40℃, 48시간 처리한 후 꼬투리 개열 정도가 '새올콩'이 99.4%, '중모3013'이 38.2%로 개선된 것으로 조사되었다. 수량 또한 '새올콩'이 218kg/10a, '중모3013'이 268kg/10a로 23% 증수되었다.

Corresponding author: Tel. 053-663-1120, E-mail: hellobk01@korea.kr

PA-43

토마토 풋마름병 저항성 검정방법 개선

안영은[1], 김상규[1], 고호철[1], Binod P. Luitel[1], 성정숙[1], 이주희[1], 윤문섭[1], 백형진[1], 류경열[1], 이준대[2], 허온숙[1*]

[1]전북 전주시 완산구 농생명로 370 농촌진흥청 농업유전자원센터
[2]전북 전주시 전북대학교 원예학과

토마토 풋마름병은 *Ralstonia solanacearum*에 의해 발생하며, 토양에서 뿌리를 통해 침입한 병원균은 기주의 물관에서 증식하여 물관을 폐쇄하여 시들음 증상을 일으키다. 병원균과 기주의 유전적인 요인이 저항성 또는 감수성의 결정에 중요한 역할을 하지만 온도에 의해 영향을 받는다고 알려져 있고, 병원균의 생육적온은 28℃~30℃로 높은 편이다. 농업유전자원센터에서는 보유중인 토마토 유전자원을 대상으로 *Ralstonia solanacearum*의 인공접종을 통한 유묘검정법으로 저항성을 평가하고 있다. 하지만 온도제어가 어려운 유리온실에서의 저항성 평가는 접종 당시의 외기에 많은 영향을 받아 균일한 평가가 가능한 시기가 매우 제한적이다. 기존 방법을 개선하기 위하여 유리 온실과 growth chamber를 이용하여 비교 실험을 실시하였다. 토마토 풋마름병 병원균 *Ralstonia solanacearum*은 국립원예특작과학원 채소과에서 분양받았고, 식물재료로는 저항성 체크품종 4품종(스페셜, B.blocking, FBR, 써포트), 이병성 체크품종 1품종(슈퍼도태랑)을 사용하여 4월 11일에 종자를 50공 연결포트에 파종하였다. 5월 11일에 유묘의 뿌리를 칼로 상처를 내고, 각 식물체의 토양에 10^7 CFU/ml 농도의 세균현탁액 10ml을 주입하여 접종 후 온실 및 growth chamber에 넣어 발병을 조사하였다. 접종 후 온실의 야간 온도는 20℃, growth chamber는 주·야간 온도 28℃, 주간14시간 동안 광을 조사하였다. 접종 후 2주후에 처리별 발병정도를 조사한 결과, 감수성 품종인 “슈퍼도태랑”은 온실에서 발병이 더딘 반면 growth chamber에서는 모든 개체가 100% 발병률을 보였다. 저항성 품종 4품종도 온실에서는 전혀 발병하지 않았으나 growth chamber 에서는 평균 발병지수 2.0를 나타냈다. 위 결과에 따라 토마토 풋마름병의 발병은 온도와 밀접하게 관련되어 있음을 알 수 있었고 정밀검정을 위해서는 온도조절이 가능한 growth chamber를 이용하는 것이 지속적이고 효율적인 개선법이라 여겨진다.

Corresponding author: Tel. 063-238-4942, E-mail: oshur09@korea.kr

PA-44

잎이 얇고 작은 구를 형성하는 배추 계통 '원교20042호' 육성

박수형, 장하영, 장석우, 채원병, 박민영

국립원예특작과학원 채소과

배추(Kimchi cabbage)는 한국의 주요 10대 채소 중 하나로, 전통 발표식품인 김치의 주재료로 활용되며 최근엔 샤브샤브와 쌈용으로 이용이 증가하고 있다. 그런데 최근 제주도에 이어 울릉도까지 모든 배추 재배 작형에서 뿌리혹병이 발병하고 있으며, 발병시 피해도 커서 제한 요인이 되고 있다. 따라서 국립원예특작과학원에서는 뿌리혹병에 저항성인 배추 품종을 육성코자 지속적인 노력을 하고 있다.

'원교20042호'는 농촌진흥청 국립원예특작과학원에서 2007년에 국내 시판품종인 '노랑관동'의 뿌리혹병 저항성 선발개체를 뇌수분으로 세대진전하여 육성된 계통이다. 최종선발을 위해 종묘회사와 공동으로 포장 품평회를 실시하여('11) '0750-8-1-1'을 선발하였다. 선발 계통은 직무육성신품종 심의를 거쳐 2014년에 '원교20042호'로 품종보호출원 하였다.

'원교20042호'는 반포합형으로 결구를 형성하며 속잎색이 노랗고 겉잎색은 진한 초록색이다. 구중은 1,899.2g으로 구의 폭과 높이는 각각 17.5cm, 27.9cm로 다소 좁은 구를 형성한다. 겉잎과 속잎의 수는 각각 14.3개, 66.5개 이며, 숙기는 중간으로 3년 평균 채종량이 723개 이다.

'원교20042호'는 뿌리혹병 race4에 저항성을 보이면서도 속잎색이 노랗고 잎이 얇고 고소하여 쌈용 등으로 소비를 확대할 수 있을 것으로 기대된다. 해당 품종은 2015년 전용실시를 통하여 농가와 계약 재배(약 1만평)를 하고 있으며, 올해는 그 수요가 확대되어 재배 면적을 10만평 수준으로 확대할 계획으로 종자를 생산하고 있다.

Corresponding author: Tel. 063-238-6622, Fax. 063-238-6605, E-mail: psh@korea.kr

PA-45

멜론 흰가루병 race동정 및 국·내외 시판품종의 저항성검정

홍예지, 김회택, 박종인, 노일섭*

국립순천대학교 생명산업과학대학 원예학과

멜론 흰가루병균은 전 세계에서 28개의 race가 존재한다고 보고되었으며, 국내에서는 본 연구팀에 의해 2014년도에 멜론 재배농가들에서 수집한 흰가루병 균주로부터 race 1, race N2, race A를 동정하였으며, 국내에서 발생하고 있는 흰가루병균은 *Podosphaera xanthii* 사상균임을 보고하였다(Kim et al. 2016). 본 연구는 2015년도에 국내 멜론 산지 4곳(순천, 하동, 창녕, 안성)으로부터 수집한 흰가루병균(PMS1154, 대연S-1, 대연S-2, 섬머얼스, 151, U2, 동부478)에 대하여 기내에서 7번의 계대배양을 통하여 단일 포자를 분리하였다. 이렇게 분리된 7개의 균주 및 8개의 판별계통(SCNU1154, PMR45, WMR29, PMR5, MR-1, PI124112, Edisto47, PI414723)을 이용하여 leaf disc법에 의해 race 동정을 수행하였다. 그 결과, 2개의 균주(섬머얼스, 대연S-2)는 SCNU 1154 판별계통에서 이병성을 나타내었으며 나머지 7개의 판별계통에서는 저항성을 나타내어 race 1으로 판명되었다. 그러나 5개의 균주(PMS1154, 151, 대연S-1, U2, 동부487)는 SCNU 1154와 PI414723 두 판별계통에서 이병성, 6개의 판별계통에서는 저항성을 나타내어 아직 국내에서 보고되어지지 않은 race N1으로 판명되었다. 이렇게 동정된 멜론 흰가루병 race 1과 race N1을 이용하여 국내·외 멜론 시판 17품종의 저항성 검정을 실시한 결과, 국외 3품종 'Honey dew green flash'(이탈리아), 'Honey dew green flash'(미국), 'ME-47593'(중국)은 race 1과 race N1에 대하여 저항성을 나타내었으나, 국내육성 품종을 포함한 나머지 14 품종은 이병성을 나타내었다. 따라서 국내 멜론 육종에 있어서 race 1 및 N1에 대한 품종육성이 요구되어진다. 이에 본 연구팀은 국내에서 동정된 4개의 흰가루병균 race (race 1, N1, N2, A)에 대한 저항성 유전자 해석 및 저항성 유전자 마커개발을 수행 중이며, 이것은 흰가루병 저항성 멜론 계통 및 품종 육성에 유용하게 이용 될 것으로 기대된다.

Acknowledgements: 본 연구는 농림축산식품부, 해양수산부, 농촌진흥청, 산림청 Golden Seed 프로젝트 사업(원예종자사업단, 과제번호: 213003-04-4-SB110) 및 수출전략기술개발사업(312065-05-4-HD030)에 의해 이루어진 것임.

Corresponding author: Tel. 061-750-3249, E-mail: nis@sunchon.ac.kr

PA-46

식용 고구마 신품종 ‘호감미’

이형운[1*], 이준설[1], 정미남[2], 양정욱[1], 남상식[1], 한선경[1], 김재명[1], 안승현[2], 송연상[1], 황엄지[1], 이경보[1]

[1]전남 무안군 무안로 199 국립식량과학원 바이오에너지작물연구소
[2]전북 완주군 이서면 혁신로 181 국립식량과학원 기획조정과

고구마는 식이섬유, 미네랄, 비타민뿐만 아니라 안토시아닌, 베타카로틴과 같은 항산화 성분을 다량 함유하고 있어 건강기능성 식품으로 인식되고 있으며 10a당 소득도 1,693천원(’14)으로 높다. 고구마의 단위면적당 생산량은 2000년 21.4톤/ha에서 2014년 15.7톤/ha으로 26% 이상 감소하였는데 이는 식미는 우수하나 병해충에 약한 품종의 재배면적이 확대된 것이 주원인이다. 특히 덩굴쪼김병은 단위면적당 수량 감소의 주요 원인으로서 품종의 덩굴쪼김병 저항성은 고구마 재배 농가의 품종 선택에 많은 영향을 미친다. 고구마 신품종 ‘호감미’는 농촌진흥청 국립식량과학원 바이오에너지작물연구소에서 식미가 우수하고 덩굴쪼김병에 저항성인 고구마 우량계통을 육성하기 위하여 괴근 육색의 주요색이 농황색이고 괴근 모양과 수량성이 양호하며 내병성인 ‘AB95007-2(IT258225)'를 모본으로 하고 덩굴쪼김병에는 감수성이나 식미가 우수한 ‘안노이모’를 부본으로 하여 2008년도에 교배하였다. 2009년에 실생개체선발시험에서 1,021개체를 시험하여 괴근의 육색 및 모양, 비대가 양호한 27계통을 선발하였다. 2010년부터 2011년까지 계통선발시험과 2012년부터 2013년까지 생산력검정시험을 실시하여 괴근 수량성, 상품성, 식미가 우수한 'MI2008-12-04' 계통을 ‘목포91호’로 계통명을 부여하였다. 2014년부터 2015년까지 6개지역에서 2년간 지역적응시험을 수행한 결과 지역적응성이 양호하였으며 2015년 12월 농촌진흥청 농작물직무육성신품종선정심의회에서 신품종으로 선정되어 ‘호감미(Hogammi)’라 명명하였다. ‘호감미’의 껍질색은 홍색, 육색은 담주황색이며, 찐고구마 육질은 점질, 괴근 모양은 장방추형이다. 생고구마 총유리당 함량과 찐고구마 당도가 10.6g/100g dw, 29.7Brix°로 표준품종인 ‘율미’ 대비 각각 28%, 11% 높고 생고구마의 베타카로틴 함량이 9.8mg/100g dw이다. ‘호감미’의 덩굴쪼김병 저항성은 중강, 고구마뿌리혹선충 저항성은 중정도이다. ‘호감미’의 보통기재배 상품괴근수량은 24.1MT/ha으로 율미 대비 4% 증수하였으며, 주당상품괴근수는 3.5개, 상품괴근평균중은 124g/개이다. 신품종 고구마 ‘호감미’는 식미와 상품성이 우수하고 덩굴쪼김병에도 강하여 소비자와 농가 선호도 모두 충족시킬 수 있을 것으로 기대된다.

Corresponding author: Tel. 061-450-0141, E-mail: leehu79@korea.kr

PA-47

Regional Variation of BaYMV Based on Nucleotide Sequences

Sang-Min Kim*, Bong Choon Lee, Ji-Eun Ra

Crop Foundation Research Div., National Institute of Crop Science, Wanju-Gun, Jeollabuk-Do, 55365, Korea

Phylogenetic analysis were conducted to show the regional variation of nucleotide sequences among 9 regional isolates. In Korea, 4 regional strains based on the site of BaYMV-resistance bioassay of Barley yellow mosaic virus are reported. Barley showing yellow mosaic symptoms from Jeonnam and Jeonbuk area were collected and virus detection were conducted by RT-PCR, 2014. BaYMVs were partially cloned, sequenced and analysed. 9 regional BaYMV isolates showed identical amino acid sequences of coat protein. The amino acid at 132 position of VPg region are known to have correlation with the infectivity of BaYMV, overcoming the *rym*4. In BaYMVs from bioassay site in Iksan and Naju, the amino acid at 132 position of VPg showed the same type identical to European strain II, overcoming the *rym*4 and other isolates also showed majority to European strain II. Full length sequencing of BaYMVs from 3 bioassay sites is on going for the comparison of bioassay results and nucleotide sequences.

Corresponding author: Tel. 063-238-5344, E-mail: kimsangmin@korea.kr

PA-48

중북부 고랭지 적응 내병성 조생 벼 진부62호

현웅조[1*], 정종민[2], 이상복[3], 이정희[3], 원용재[3], 안억근[3], 성열규[1], 김병주[3]

[1]강원도 춘천시 충열로 251 국립식량과학원 춘천출장소
[2]전북 완주군 이서면 혁신로 181 국립식량과학원 작물육종과
[3]경기도 수원시 수인로 125 국립식량과학원 중부작물부 중부작물과

우리나라는 최근 몇 년 동안 연속된 풍년과 소비감소로 인해 쌀 재고가 사회문제로 대두되고 있다. 그러나 불과 몇 년 전인 1971년, 1980년, 그리고 1993년 발생한 냉해로 인해 식량 위기를 경험했으며, 특히 180년에 발생한 냉해는 우리나라 벼 재배면적의 약 64%에 피해를 주어 34%에 달하는 벼 수확량 감소를 초래하였다. 또한 세계적으로는 식량부족에 대한 우려와 함께 지구온난화, 엘리뇨 등으로 홍수, 가뭄, 폭설, 여름철 이상저온과 같은 기상이변이 지구촌 곳곳에서 속출하고 있다. 최근 우리나라에서도 봄철 가뭄, 동해안 지역의 잦은 폭설, 주기적으로 찾아오는 여름철 이상저온 등 크고 작은 기상이변이 해마다 발생하고 있어 쌀의 안정적 공급을 강화하기 위한 대비가 필요한 실정이다. 벼 냉해를 막는 가장 좋은 방법은 내냉성이 우수한 벼 품종의 개발이다. '진부62호'는 내냉성과 더불어 내병성이 향상된 중북부 고랭지에 적응하는 조생품종 육성을 목적으로 단교배 된 SR30247(진부/운광)과 SR30248(진부/그루)를 각각 모부본으로 하여 2006년에 복교배 되었다. 계통육종법에 의해 세대를 진전시킨 후 고정세대 계통들 중에서 품질이 우수하고 도열병 및 흰잎마름병 저항성을 보인 SR31017-IR46-1-1-1-2를 선발하여 진부62호의 계통명을 부여하였다. 향후 지역적응성 검정 후 품종출원 하여 내냉성 품종 다양화 및 재배 안전성 강화에 부응할 것으로 기대된다.

PA-49

Enhancement of Rice Resistance to Bacterial Blight by Overexpressing BrCP3 Gene of *Brassica rapa*

Marjohn Nino[1], Hye-Jung Lee[1,2], Jae-Young Song[1], Seon-Kyeong Song[1], Kwon-Kyoo Kang[3], Illsup Nou[4], Yong-Gu Cho[1*]

[1]Department of Crop Science, Chungbuk National University, Cheongju 28644, Korea
[2]Current Address, Korea Seed & Variety Service, Kimchon 39660, Korea
[3]Department of Horticulture, Hankyong National University, Ansung 17579, Korea
[4]Department of Horticulture, Sunchon National University, Sunchon 57922, Korea

Brassica rapa cysteine protease 3 is an endopeptidase member of C1A family (papain-like) and CA clan of cysteine protease. Members of papain-like CP have emerged to be key enzymes involved in cell death in response to biotic and environmental stresses. Recent progress of CP research features its diverse and overlapping role in basal and effector-triggered immunity. This study was carried out to characterize *BrCP3* gene in Chinese cabbage and explore its function in rice – *Xanthomonas oryzae* pv. *oryzae* pathosystem. Phylogenetic analysis and BLASTP search of its amino acid sequence to the Arabidopsis Protein TAIR 10 database identified *BrCP3* as the closest ortholog of Arabidopsis *RD21a*. The full-length cDNA of *BrCP3* was cloned and transformed into the genome of japonica rice cv. Gopum. Constitutive overexpression of the transgene is driven by Ubi-1 promoter in *pFLCIII* vector. Regenerated single copy overexpression rice lines were inoculated with three *Xoo* Korean isolates. Regulation of rice resistance through cysteine protease activity is evident in the overexpression lines which showed enhanced immunity to three isolates as depicted by reduced lesion length compared with the wild type. Our initial results implicate an interesting biological function of *BrCP3* in rice system that has never been reported before.

Acknowledgements: This research was supported by a grant from the National Research Foundation (NRF) programs (2014R1A2A1A11052547) funded by the Korean Ministry of Science, ICT and Future Planning, Republic of Korea.

Corresponding author: E-mail: ygcho@cbnu.ac.kr

PA-50

Comparative Transcription Profiles of Compatible and Incompatible Interactions of Rice with *Xanthomonas oryzae* pv. *oryzae*

Marjohn Nino[1], Joonki Kim[1], Franz M. Nogoy[1], Jae-Young Song[1], Shadi Rahimi[1], Kwon-Kyoo Kang[2], Ho-Jin Ryu[3], Yong-Gu Cho[1*]

[1]Department of Crop Science, Chungbuk National University, Cheongju 28644, Korea
[2]Department of Horticulture, Hankyong National University, Ansung 17579, Korea
[3]Department of Biology, Chungbuk National University, Cheongju 28644, Korea

Bacterial blight, caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*), is an emerging disease of rice in Korea causing damage to rice quality and yield. To identify genes crucial to resistance to *Xoo*, a whole-genome oligonucleotide microarray of two popular *japonica* rice cultivars, Dongjin and Jinbaek, with opposing reactions to *Xoo* Korean strain K2, were used to infer transcripts of inducible genes between compatible and incompatible interactions at 48 hour post inoculation. A total of 1,721 differentially expressed genes, designated as K2-induced differentially expressed genes (K2-DEGs), were identified. A large number of inducible genes are more evident in the resistant cultivar, Jinbaek, which is threefold higher than in susceptible cultivar, Dongjin. Based on their functional annotations, the K2-DEGs were assigned to 12 categories, including transcriptional regulator, which is most abundant, followed by protein modification and degradation, and defense response. The up-regulation of most transcriptional regulator genes in resistant cultivar implies that gene regulatory network leading to incompatible interaction is orchestrated by transcription factors. Interestingly, the defense-related genes belong to diverse class of resistance proteins including NBS-LRR, pathogenesis-related, and receptor kinases. Most of these DEGs were assigned in cytoplasm and nucleus, corroborating the idea that involved R genes may be targeted to the nucleus to trigger full immunity response to pathogen.

Acknowledgements: This research was supported by a grant from the National Research Foundation (NRF) programs (2014R1A2A1A11052547) funded by the Korean Ministry of Science, ICT and Future Planning, Republic of Korea.

Corresponding author: E-mail: ygcho@cbnu.ac.kr

PA-51

수경재배(분무경)에서 특이적으로 발견되는 검은뿌리병의 원인균 규명

윤수영[1*], 김보슬, 옥선[2]

[1]울산광역시 울주군 삼동면 작동리 ㈜애그로닉스 스마트팜팩토리사업부
[2]경상남도 김해시 주촌면 농소리 ㈜애그로닉스 천연물소재사업부

본 연구에서는 인삼의 수경재배시 자주 발생하는 검은뿌리썩음병의 주요원인균이 *Thielaviopsis basicola*라는 것을 밝혀냈다. 최근 농업분야에서 노동시간과 노동강도를 줄이고 수익성을 향상하기 위해서 수경재배가 많이 보급되고 있다. 수경재배를 이용한 작물은 기존 배지(상토)재배와는 재배환경이 달라 일반적인 재배작물의 병원이 되는 균이 아닌 다른 균이 원인이 되어 해를 입는 경우가 많다. 또한 수경재배의 주요목적 중 하나인 청정재배의 규정으로 인해 농약을 사용하지 않아 병의 피해가 큰 경향이 있다. 그러므로 수경재배시 병해에 대한 대응책은 노지재배와 달라야 하며, 이를 위해서 수경재배시 발생되는 여러 병해에 대한 원인을 정확하게 밝혀내는 것이 무엇보다 중요하다.
본 연구팀은 수경재배에서 발생하는 검은뿌리썩음병의 원인을 밝히고자 감염된 인삼과 인삼뿌리에서 분리한 균을 PDA 배지에서 배양하여 각각 경상대 김진우 교수팀과 한국 미생물보존센터(KCCM)에 의뢰하여, 양측으로부터 그 원인균이 *Thielaviopsis basicola*이라는 것을 밝혀냈다. 인삼의 수경재배시 *Thielaviopsis basicola*에 의해서 발생하는 검은뿌리썩음병은 주근에서는 발견되지 않으며 미세근에서 나타나는 특징이 있다. 주된 병변은 최초 일부 미세근에서만 관측되던 검은색 포자가 시간경과 후 전체 미세근을 뒤덮게 된다. 이로 인해 감염이 심한 미세근은 탈락되며, 그 결과로 인해 인삼의 생장이 느려지게 된다.
본 연구의 기여는 수경인삼에서 자주 발생하는 검은뿌리썩음병의 원인균이 *Thielaviopsis basicola*라는 것을 규명함으로서, 향후 이를 예방하고 방제하기 위한 초석을 마련했다는데 그 의의가 있다. 현재 본 연구팀은 *Thielaviopsis basicola*에 의한 피해를 막기 위한 예방법과 치료법을 계속해서 연구 중이다.

Corresponding author: Tel. 052-710-3063, E-mail: yunsu@agronics.co.kr

PA-52

토마토 풋마름병 저항성 검정방법 개선

안영은[1], 김상규[1], 고호철[1], Binod P. Luitel[1], 성정숙[1], 이주희[1], 윤문섭[1], 백형진[1], 류경열[1], 이준대[2], 허온숙[1*]

[1]전북 전주시 완산구 농생명로 370 농촌진흥청 농업유전자원센터
[2]전북 전주시 덕진구 백제대로 567 전북대학교 원예학과

토마토 풋마름병은 *Ralstonia solanacearum*에 의해 발생하며, 토양에서 뿌리를 통해 침입한 병원균은 기주의 물관에서 증식하며 시들음병 증상을 일으킨다. 병원균에 대한 저항성 반응은 기주의 유전적 특성과 환경에 의해 영향을 받고 온도가 발병여부에 중요한 역할을 한다. 최근 토마토 풋마름병 저항성 검정은 유묘검정법을 이용하여 유리온실에서 실시하고 있으나 유리온실에서는 발병환경, 즉 최적의 온도조건을(26～29℃) 유지하기가 곤란하여 평가시기가 매우 제한적인 측면이 있었다. 유용한 풋마름병 저항성 자원을 선발하기 위하여 유리 온실과 생육상(growth chamber)을 이용하여 비교 실험을 실시하였다. 풋마름병 저항성 평가를 위하여 저항성 대비품종 4개(스페셜, B.blocking, FBR, 써포트)와 이병성 대비품종 1개(슈퍼도태랑)를 4월 11일에 파종하였다. 파종 후 30일이 경과한 토마토 유묘 뿌리에 상처를 내고 10^7 CFU·mL^{-1} 농도의 *R. solanacearum* 현탁액을 유묘 당 10 mL 주입하여 접종하였다. 온실 환경은 야간온도 20℃±2℃, 주간온도 28℃±2℃로 조절하였고, 생육상은 주·야간 온도 28℃±1℃, 광도 15 Klux, 광주기는 명조건 14시간, 암조건 10시간으로 조절하였다. 접종 2주 후에 발병정도를 조사한 결과 감수성 품종인 '슈퍼도태랑'은 온실에서 발병이 적었으나 생육상에서 모든 개체가 100% 발병률을 보였다. 저항성 4품종도 온실에서는 전혀 발병하지 않았으나 생육상에서는 평균 발병지수 2.0을 나타냈다. 따라서 토마토 풋마름병 발병은 온도와 밀접하게 관련되어 있었고, 유용한 자원선발을 위해서는 온도조절이 가능한 생육상을 이용하는 것이 효과적인 것으로 평가되었다.

Corresponding author: Tel. 063-238-4942, E-mail: oshur09@korea.kr

PB-01

Glu-B1al 대립유전자를 지닌 국내 재래종 밀 특성

윤영미[1,2], 김지은[1], 강천식[2], 이종열[3], 박철수[1*]

[1]전북대학교 농업생명과학대학 작물생명과학과
[2]국립식량과학원
[3]국립농업과학원

글루텐의 점탄성이 강력한(Extra-Strong) 빵용 캐나다 적립 경질 소맥(CWRS)에서 주로 발견되는 *Glu-B1al*은 Glu-B1x7이 과다 발현 하는 것으로 알려져 있다. 이러한 *Glu-B1al*은 *Glu-B1b*, *f*, *i*에 비해서 글루텐의 점탄성이 강력하기 때문에 *Glu-D1d* 대립유전자를 포함해서 제빵 품질 개선을 위해 최근 많은 연구가 이루어지고 있다. 본 연구에서는 국내 재래종 100계통과 국내 25 품종에 대한 *Glu-B1al* 존재 여부를 SDS-PAGE, PCR과 RP-HPLC를 이용하여 탐색하였다. SDS-PAGE는 *Glu-B1al*을 지닌 CWRS인 Glenlea을 표준품종으로 하여 비교 평가하였고, PCR은 $Bx7^{OE}$ 표지인자(TaBAC1215C06-F517/TaBAC1215C06-R964)를 이용하여 Glenlea와 같은 844bp를 지닌 계통을 선발하였다. SDS-PAGE와 PCR을 통하여 *Glu-B1al*을 지닌 국내 재래종 밀 1 계통을 선발하였다. RP-UPLC를 이용하여 총 고분자 글루테닌 서브유닛(HMW_T)에대한 Bx7의 비율을 분석한 결과, *Glu-B1b*를 지닌 계통은 0.27~0.33의 값을 보였으며, *Gllu-B1c*를 지닌 계통은 0.27이었으며, *Glu-B1al*을 지닌 Glenlea와 재래종은 각각 0.52와 0.43으로 나타났다. 같은 *Glu-B1al*이지만 Glenlea는 *Glu-B1al*이면서 동시에 8*밴드를 지니는 *Glu-B1u*를 지니기 때문이다. 또한 빵용인 Glenlea는 *Glu-D1d*를 지니지만 재래종은 *Glu-D1a*을 지니는 것으로 나타났다. *Glu-B1al*은 주로 미국과 캐나다 빵용 밀에서 만 발견되었는데 국내 재래종에서 발견 된 것은 향후 국내 밀 품종 육성 프로그램에서 국산밀의 글루텐 점탄성 향상과 제빵 적성 개선에 유용하게 활용이 가능할 것으로 생각한다.

Corresponding author: Tel. 063-270-2533, E-mail: pc89@jbnu.ac.kr

PB-02

국내 밀 품종의 글리아딘 및 *Spa* 유전자 평가

김지은[1], 윤영미[1,2], 강천식[2], 이종열[3], 박철수[1*]

[1]전북대학교 농업생명과학대학 작물생명과학과
[2]국립식량과학원
[3]국립농업과학원

본 연구에서는 국내 밀 품종의 가공적성 향상을 위하여 A-PAGE와 PCR을 이용한 γ -와 ω -글리아딘과 밀 저장 단백질 발현에 관련 있는 Spa 유전자를 평가하였다. 국내 40개 밀 품종은 A-PAGE를 이용하여 분석한 결과, Gli-1 조성에 따라 13개 패턴으로 구분되었으며, Gli-A1, Gli-B1과 Gli-D1에서는 각각 7개, 5개와 6개 대립유전자가 나타났다. A-PAGE 분석 결과와 γ -글리아딘에 특이적인 프라이머로 검정한 결과를 비교 분석한 결과, A-PAGE 분석에서 *Gli-A1f*, *Gli-A1h*와 *Gli-A1l*을 지닌 품종은 GliA1.2에서만 밴드를 나타내었고, Gli-B1h과 Gli-B1f 지닌 품종은 GliB1.2에서 밴드를 나타내었으며, *Gli-D1f*, *Gli-D1m*과 *Gli-D1o*를 지닌 품종은 모두 GliD1.1에서만 밴드를 나타내었다. 나머지는 GliD1.1과 GliD1.2에서 밴드를 나타내었다. γ -45와 γ -42은 올밀과 중모2003을 제외하고 A-PAGE의 γ -글리아딘 패턴이 일치하였다. 그러나 국내 밀 품종의 ω 5-글리아딘을 분석한 결과 품종간에 차이가 없는 것으로 나타났다. Spa 유전자를 분석한 결과, 국내 밀 품종은 *Spa-A1*에서만 변이가 나타났고, *Spa-B1*과 *Spa-D1*에서는 차이가 없는 것으로 나타났다.

Corresponding author: Tel. 063-270-2533, E-mail: pc89@jbnu.ac.kr

PB-03

고경도 분자표지 개발 위한 고정계통을 이용한 딸기 F_2 집단 구축 및 경도 측정법 비교

김진희*, 이선이, 안율균, 이은수, 김정호

국립원예특작과학원 채소과

우리나라는 딸기에 대한 생명공학 기반이 부족한 상황이며 다양한 형질별 분자표지를 개발하고 육종소재 대한 유전체 분석을 병행하면 품종개발 수준을 선진국과 경쟁이 가능한 단계까지 향상시킬 수 있다. 특히 국내 신선딸기의 수출 증대를 위하여 수출에 유리한 고품질의 고경도 품종 육성이 절실히 요구되고 있다. 하지만 딸기는 영양번식을 주로 하는 8배체 식물이기에 다른 작물에 비해 분리 집단을 구축하여 유전 분석 하에 한계가 많다. 본 연구에서는 경도 연관 분자표지 개발을 위해 국내외 재배품종을 자식하여 육성한 딸기 고정계통을 이용하여 계통별 특성조사와 연계하여 분리집단을 구축하였다. 우선 국내외 재배품종 13종으로부터 2004년부터 7~9세대 자식으로 100여개의 자식 계통을 육성하였으며, 딸기의 고경도와 저경도의 기준을 정하기 위해서 개체별 특성조사 평균이 25~30 (g/mm^2)이면 고경도, 13~20 (g/mm^2)이면 저경도로 판단하였다. 총 8개의 유래계통이 고경도로 지정되었으며 총 9개의 유래계통이 저경도로 지정되었다. 그 중 세대 진전 중에 분리가 일어나지 않았고 일정하게 15이하의 수치를 보인 사치노까/챈들러 유래계통이 저경도 계통으로 선발되었으며 베니홋베, 도요노카 유래 계통이 고경도 계통으로 선발되어 교배가 이루어졌다. 이러한 과정으로 확보한 F_1 식물체를 이용하여 F_2 딸기 집단을 구축하였다. 마커 개발을 위한 경도 측정 방법에 대해서도 고정 경도계와 간이 경도계의 결과를 비교, 부석한 결과, 고정 경도계를 활용할 경우 값의 차이를 보이지 않는 5mm 탐침에 비해 8mm의 경우 뚜렷한 경도 차이를 나타내어 향후 집단 분석 등에 용이할 것으로 판단하였다. 구축된 F_2 집단은 향후 경도 형질 관련 유전분석 및 마커 개발에 활용될 것이며 다른 형질을 목적으로 한 집단 구축도 가능하다.

Corresponding author: Tel. 063-238-6672, Fax. 063-238-6605, E-mail: sayzinni@korea.kr

PB-04

화색이 선명한 황색 대륜화 절화용 거베라 '레모나이트' 육성

정용모[1*], 황주천[1], 진영돈[1], 이병정[1], 이상대[2], 권오창[3]

[1]경남 창원시 경남농업기술원 화훼연구소
[2]경남 진주시 경남농업기술원 연구개발국
[3]부산시 사하구 하단동 동아대학교 생명자원과학대학

경상남도농업기술원 화훼연구소에서, 거베라 재배농가에서 선명한 화색의 품종선택 기회를 더욱 많이 제공하고 외국품종의 로열티부담 경감을 위하여 2015년 화색이 선명한 황색 절화용 거베라 '레모나이트'를 육성하였다. 2010년 4월 핑크색 대륜계의 '프랜드'(281141)를 모본, 황색 대륜계의 '오존'(281149)을 부본으로 인공교배를 실시하여 5월 하순, 교배조합으로부터 492개의 종자를 획득하였다. 교배 후 결실이 된 종자는 6월 중순 경, 채종 즉시 파종하였으며, 그 중 361개의 종자가 발아(발아율 73.4%)하였다. 파종 1개월 후, 발아된 유묘는 본엽이 4～5매 전개되었을 때 화훼연구소 유리온실내의 선발 포장에 정식하였다. 정식 후 교잡 1세대를 육묘하여 2010년 11월 하순 경, 화색이 선명하고 수량이 많은 우수개체(1027-009)를 1차로 선발하였다. 그 후 특성이 우수한 1027-009(경남교G-55호)개체를 2011년 7월, 생장점배양에 의해 개체증식 후 2011년 10월경 조직배양묘의 순화를 거쳐서, 2012년 3월 중순, 화훼연구소 유리온실내의 특성검정 포장에 정식하여 2015년 9월까지 3회에 걸쳐 생육 및 수량특성 검정을 실시하였다. 특성검정을 실시한 결과 화색, 화형, 수확량 등 품질과 수량이 우수하다고 판단되어 2015년 농작물 직무육성 신품종심의회의 심의를 거쳐 '레모나이트'(Lemonight)로 명명하였다. '레모나이트' 품종의 생육 및 개화특성 조사를 위하여 대조품종으로 '포커스(CFG0072)'를 사용하였다. '레모나이트' 품종은 화색이 선명한 황색(6A) 반겹꽃으로, 화폭이 12.4cm 정도인 절화용 대륜화이다. 또한 포기당 연간 평균절화수량은 47.5송이 정도이며, 절화수명은 약 13.5일 정도이다. 개화소요일수는 92.4일로 대비품종 '포커스'의 94.2일에 비하여 약 2일 정도 빠르며 이때 개화엽수는 약 9.3매 정도이다. '레모나이트' 품종의 설상화의 길이와 폭은 각각 5.2m와 1.2cm 로 대조품종 '포커스'의 5.3cm, 1.3cm와 비슷하다. 화경 직경은 상부와 하부 각각 0.6cm, 0.8cm 정도로 대조품종 '포커스'의 상부 0.6cm, 하부 0.7cm와 비슷한 편이다. 재배상의 유의사항은 지온의 관리 및 양·수분의 흡수가 쉽도록 가능한 이랑을 높게 만들고, 여름철 고온기의 생리장해 및 고온에 의한 꽃봉오리의 유실 방지를 위하여 차광재배하여 온도상승을 막아주고 환기에 주의하는 것이 좋다.

Corresponding author: Tel. 055-254-1614, E-mail: ymchung@korea.kr

PB-05

Genetic Analysis of Canadian Maize (*Zea mays* L.) Inbred Lines Using SSR Markers Under Cold Stress

Muhammad Qudrat Ullah Farooqi, Rahul Vasudeo Ramekar, Shi Jun Ma, Kyu Jin Sa, Ju Kyong Lee*

Department of Applied Plant Sciences, College of Agriculture and Life Sciences, Kangwon National University, Chuncheon, 200-701, Korea

In this study, using 100 cold tolerant linked simple sequence repeat (SSR) markers with the analysis of genetic diversity, relationship and association; eight high and low cold temperature tolerant inbred lines were investigated. The total of 319 alleles were identified among them 128 were high tolerant specific alleles and 61 were low tolerant specific alleles; while reaming were shared alleles. From the identification of high and low specific alleles; a total 80 SSR markers were identified under high specific cold tolerant alleles and 52 SSR's were detected under low specific alleles. The alleles located on loci's were ranged between 2 to 5 alleles per locus with average of 3.86. The major allele frequency varied from 0.39 to 0.53 with average of 0.47 using power marker version 3.25. The average gene diversity and polymorphic information content from all lines were 0.63 and 0.58 respectively. From UPGMA analysis, the dendrogram represented two main cluster groups as the eight high and low cold tolerant maize inbred lines were closely associated with each other. The identification and characterization of high and low cold tolerant maize lines with useful in maize breeding studies and the results from this study could serve as useful molecular markers.

Corresponding author: Tel. 033-250-6415, E-mail: jukyonglee@kangwon.ac.kr

PB-06

Cold Stress Evaluation Among Maize (*Zea Mays* L.) Inbred Lines in Different Temperature Conditions

Muhammad Qudrat Ullah Farooqi, Ju Kyong Lee*

Department of Applied Plant Sciences, College of Agriculture and Life Sciences, Kangwon National University, Chuncheon, 200-701, Korea

Maize (*Zea mays* L.) is a tropical region crop that resists to grow under sensitive temperature. The study was conducted to evaluate the performance of Canadian maize inbred lines under controlled cold stress conditions (5℃, 10℃, and 23℃) during 2014-2015. Data were recorded by measuring following parameters; i.e. germination rate, index, root length, and seed vigour index. Five higher and three lower tolerant inbred lines were screen out. Using Analysis of Variance (ANOVA) data was analyzed, while means values were compared using Tukey's Honest Significant Difference (HSD) Test at α = 0.05 and at α = 0.01. Correlation was done using Genstat software. A strong correlation ($P < 0.05$) was found between germination rate and germination index under all stress conditions. There is also strong correlation with germination rate to root length and vigour index under 5℃ stress condition compared to 10℃ and 23℃. It is observed from our findings that 22 maize inbred lines performed better under 5℃ cold temperature and thus in Korean environment; it had potential to develop maize hybrids to increase grain yield under environmentally stressful conditions.

Corresponding author: Tel. 033-250-6415, E-mail: jukyonglee@kangwon.ac.kr

PB-07

Genetic Diversity and Association Analysis for Agronomic Traits in RDA-Genebank Maize Lines

O Gyeom Kim, Kyu Jin Sa, Ju Kyong Lee*

Department of Applied Plant Sciences, College of Agriculture and Life Sciences, Kangwon National University, Chuncheon, 200-701, Korea

We assessed the genetic and phenotypic variation of 105 maize lines of RDA-Genebank (Zea mays L.) and made association analyses with respect to 11 agronomical traits, using 100 simple sequence repeats (SSR). In genetic diversity analysis, the 100 SSR loci are confirmed a total of 1,104 alleles in total 105 maize lines. The average number of alleles per locus was 11.0. The average GD and PIC value was 0.73 and 0.70, respectively. The average MAF was 0.41. From population structure analysis, the whole maize lines were divided into two major groups and one admixed group based on the membership probability thresholds of 0.80. Between these two major groups, first group and second group were contained the 35 and 46 maize lines, respectively. In addition, association analysis was performed with a mixed linear model and a general linear model. The five marker-trait associations involving five SSR markers were observed using the mixed linear model, with a significance level of $P<0.01$. The 72 marker-trait associations involving 42 SSR markers were observed with the general linear model. And also we confirmed five significant marker-trait associations (SMTAs) in mixed linear model and general linear model. In the SMTAs, two loci were associated with stem diameter, one locus was associated with ear row number, leaf width, leaf length. These results should prove useful to breeders in the making the new inbred lines and selection of parental lines using molecular marker.

Corresponding author: Tel. 033-250-6415, E-mail: jukyonglee@kangwon.ac.kr

PB-08

교배를 통해 발생 된 미숙 종자로부터 감귤 3배체의 탐색

박석만*, 박재호, 윤수현

농촌진흥청 국립원예특작과학원 감귤연구소

감귤 품종 육성에 있어 종자의 유무는 소비자들 기호에 많은 영향을 줌으로 중요한 형질 중의 하나이다. 대부분의 감귤 교잡종의 경우 종자를 갖으며 이러한 교잡종의 무핵화를 위한 다양한 연구가 수행 중에 있다.
그중 한 방법으로 3배체 육성 방법이 있다. 이 방법은 3배체 개체의 생식세포 형성 교란에 의하여 임성이 떨어지는 특성을 이용하는 것으로 외국의 경우 4배체에 교배를 통해 3배체를 획득한다. 그러나 이 경우 효율성은 높으나 우수한 4배체를 확보한 후에야 교배가 가능한 한계가 있다. 또 다른 방법으로는 교배를 통해 생성된 미숙종자로부터 3배체를 확보하는 방법이다. 이는 교배 조합에 따라 차이는 있지만 교배를 통해 생성된 미숙종자의 경우 3배체 발생 확률이 3%~7%라고 알려져 있다.
본 연구에서는 2015년 교배를 통해 생성된 25개 교배조합 2387개의 미숙 종자를 기내 파종하여 3배체의 획득율을 조사하였다. 25개의 교배 조합 중 18개 조합에서 종자의 발아가 이루어 졌으며 발아율은 최저 1.5%에서 최고 92.9% 이었다. 발아된 18개 조합 중 3배체는 10개 조합 34개체를 확보하였으며 확보된 3배체와 발아율과의 상관관계는 확인되지 않았다. 가장 높은 3배체 획득율을 보인 교배 조합은 KG03 × 미하야 조합으로 28%(7개체)의 획득율을 보였으며 다음으로는 W.MURCOTT × 미하야 조합으로 10.6%(5개체)의 획득율을 보였다. 3배체를 획득한 교배조합들의 평균 3배체 획득율은 1.4%로 기존에 보고된 수치 보다는 낮게 나타났으며 이는 모본과 부본의 친화성에 따른 차이인 것으로 생각된다.

Corresponding author: Tel. 064-730-4142, E-mail: babau2000@korea.kr

PB-09

유용 유전자 도입을 위한 벼 캘러스의 고효율 형질전환 시스템 구축

박지선[1,2*], 문기범[1], 하장호[1], 장지영[1], 김미진[1], 박상언[2]. 전재흥[1], 김현순[1]

[1]대전광역시 유성구 과학로 125 한국생명공학연구원 식물분자의약연구센터
[2]대전광역시 유성구 대학로 99 충남대학교 농학과

식물 분자농업은 식물을 일종의 공장개념으로 확대 적용하여 산업적으로 가치가 높은 유용물질들을 대량생산하는 분야로 최근 많은 각광을 받고 있다. 그 중에서 벼의 캘러스 배양은 대량 배양이 가능하고 유용 단백질의 획득이 높아 산업현장에서 기대가 높은 기술이다. 본 연구는 이러한 캘러스의 활용도를 높이기 위한 벼의 효율적인 형질전환 시스템을 구축하기 위해 수행되었다. 동진 벼 종자에서 유도된 캘러스에 pCAMBIA1301 벡터가 도입된 *Agrobacterium tumefaciens* LBA4404를 이용하여 gus유전자를 도입하였다. 공동배양 후 hygromycin 항생제 배지에서 1차로 선발하였고, 선발된 캘러스는 gus염색을 통해 2차 선발하였다. 가장 효율적인 선발 기간 확립을 위해 배양 기간을 달리하여 효율을 비교하였다. 선발 배지에서 3주, 6주(1차 계대배양), 9주(2차 계대배양) 동안 배양된 캘러스를 각각 gus염색 한 결과 평균 0%, 93.5%, 92.3%로 확인되었다. 선발된 캘러스를 3주간 더 배양한 뒤 다시 gus염색을 하여 3차선발을 한 결과 6주, 9주 동안 배양된 캘러스는 각각 평균 99.6%, 99.5%였고, 이를 다시 3주간 더 배양한 뒤 gus염색을 한 결과 각각 99.6%, 99.3%로 3차 선발 결과와 유사하였다. 이를 통해 2차 선발된 캘러스의 약 99%가 *Agrobacterium*에 의해 gus유전자가 안정적으로 도입되었음을 알 수 있었다. 즉, 유전자 도입이 이루어진 형질전환 캘러스의 선발 기간은 6주가 가장 효율적이다. 선발된 캘러스는 재분화 배지에서 식물체의 재분화를 유도하였고, 재분화된 식물체는 PCR 및 gus염색을 통해 유전자가 안정적으로 발현되고 있음을 확인하였다. 또한 T1세대 개체에서도 유전자가 안정적으로 발현하였다. 따라서 본 실험에서 구축한 형질전환 시스템을 기반으로 하여 유용 단백질의 생산, 활용이 기대된다.

Corresponding author: Tel. 042-860-4494, E-mail: pjs12315@kribb.re.kr

PB-10

베이지색계 투톤 화색의 스프레이형 카네이션, ‘Marble Magic’ 신품종

김미선, 유봉식*, 정재아, 박종택, 신학기, 김도국

농촌진흥청 국립원예특작과학원

지중해연안에 자생하던 Dianthus속 식물인 카네이션은 여러해살이 화초로서 화색이 선명하고 다양하다. 1840년 프랑스에서 4계통이 육성된 이후 영국, 미국 등에서 개량되어 화색, 꽃의 크기, 꽃잎수 등이 개량되어 원예종으로서 온실절화용 계통으로 발달되었다. 우리나라에서 재배하고 있는 대부분의 카네이션 품종은 이탈리아, 스페인 등에서 육성한 수입품종이며 과거에는 특정시기(어버이날, 스승의날)에만 소비되는 경향이었으나 요즘에는 웨딩용, 일반 장식용 꽃으로 많이 사용되고 있다. 특히 화색이 다양하고 향기도 강하며 무엇보다 절화수명이 길며 생육온도가 10℃ 내외로 낮아 겨울철 난방비도 저렴한 장점이 있어 우리나라에서 재배환경에 적합한 품목이다. 카네이션은 2014년 기준 기준 재배면적 72ha, 생산액 130억원으로 절화생산액 4위품목이나, 해외종묘의도가 매우 높고 종묘비가 주당 500~700원으로 비싸 농가 경영부담이 크다. 특히 최근에는 중국산 절화 카네이션의 수입량 증가에 따른 국내재배면적도 감소추세에 있어 종묘의 국산화율 제고를 통한 재배농가의 경쟁력 강화가 절실하다. 이를 해결하기 위해 국립원예특작과학원에서는 우수한 국산품종 육성을 위한 연구를 수행하고 있으며, 2015년 투톤화색의 스프레이 품종 ‘Marble Magic’을 육성하였다. 카네이션 ‘Marble Magic’은 2011년도에 수집자원 ‘0932-1’ x ‘0909-1’를 교배하여 선발 및 특성검정 후 2015년 농촌진흥청 직무육성품종심의회를 거쳐 최종적으로 품종화하였다. 카네이션‘Marble Magic’은 절화용 스프레이형으로 베이지색 바탕색에 진적색의 줄무늬 및 테두리가 있는 투톤의 화색으로 시장성 매우 높은 우수한 화색이며 꽃이 균형미가 있고 볼륨감이 우수하다. 특히, 고온적응성이 높아 여름철 고온기에 고사율이 적고 생육이 강건한 재배적 특성이 있고 시범재배시 농가, 경매자의 기호성이 매우 높아(4.1/5점만점) 본격적인 생산준비중이다. 고온기 하우스내 온도가 30℃이상 7일이상 재배시 품질이 떨어질 우려가 있으며 겨울철 화아발달기에는 야간온도를 8℃이상 높여주고 주간온도를 25℃가 넘지 않도록 관리한다.

Corresponding author: Tel. 063-238-6810, Fax. 063-238-6805, E-mail: kimms290@korea.go.kr

PB-11

A New Hardy Kiwi Cultivar, 'SH-1' with Large Fruit and High Yield

Youngki Park*, Jae-Hee Kim, Sea-Hyun Kim

Div. of Special Purpose Tree, National Institute of Forest Science, Suwon 441-350, Korea

A new hardy kiwi (*Actinidia arguta*) cultivar, 'SH1' (Boeun 4-1) was developed at the National Institute of Forest Research (NIFoS) in 2015. This new cultivar of hardy kiwifruit was developed through selection from Korea. The goals of this research were to evaluate the yielding of fruit and their fruit characteristics of hardy kiwi selected from different regions in Korean Wild. Different varieties of *A. arguta* grown in Korea, were investigated in what concerns fruit weights, fruit length and their yielding. *A. arguta,* which is called hardy kiwifruit, has an edible smooth skin. It contains high amounts of sugar, ascorbic acid, and vitamin C. It is native to northern China, Korea, and Japan. From the flower of *A. arguta*, liac alcohol epoxide was isolated and identified. *A. deliciosa* is known as kiwifruit and originated from southwestern China. The fruit of *A. deliciosa* is appreciated for its sweet, slightly acidic flesh and high nutritional value, especially because of its high concentration of vitamin C like *A. arguta*. The average weight, length and diameter of new cultivar, SH1 were 18.8g, 37.3mm and 33.1mm, respectively. Soluble solids of the this cltivar was 20.5 °Brix, which was 1.5 times higher than other clones.

Corresponding author: Tel. 031-290-1196, E-mail: woodpark@korea.kr

PB-12

밝은 분홍색 홑꽃 절화용 스프레이국화 ‘허니핑크’ 육성

황주천[1*] 진영돈[1], 정용모[1], 안동춘[1], 이병정[1], 이상대[2], 정병룡[3]

[1]경남 창원시 의창구 대산면 경남농업기술원 화훼연구소
[2]경남 진주시 경남농업기술원 연구개발국
[3]경남 진주시 가좌동 경상대학교 농업생명과학대학 원예학과

경남농업기술원 화훼연구소에서 2011년 10월에 화색이 우수한 분홍색 홑꽃인 ‘King Fsisher’를 모본, 조기개화성의 백색 홑꽃 ‘Eye Ball'(CFC0065)을 부본으로 인공교배하여 교배조합으로부터 427개의 종자를 획득하였다. 2012년 2월 상순 실생개체를 파종, 육묘, 정식하여 특성 검정하였으며, 초세가 강하고 화형·화색이 우수한 KE12-1037, 1129, 1241, 1274, 1326, 1401 등 우수 6개체를 1차로 선발하였다. 선발된 우수개체를 다시 8월 상순에 정식하여 자연재배 특성검정 결과 성장세가 좋고 초세가 항하며, 착화성이 우수한 ‘KE12-1274’ 개체를 2차 선발하였다. 선발된 우수개체를 삽목에 의해 개체증식한 후 화훼연구소 특성검정온실 내에 정식하였으며, 2013년부터 2014년까지 2년간에 걸쳐 1～2차 생육특성검정을 통해 안정성, 균일성과 흰녹병 저항성 등을 조사하였다. 2015년에는 계통번호 ‘경남교CS-49호’를 부여하여 3차 특성검정을 수행해 안정성과 균일성에 대한 연차별 재현성 그리고 주년생산성(자연, 촉성, 억제재배) 및 품평회와 시장출하 등을 통해 생산자와 소비자의 기호도 평가를 받았다. 그 결과 기호도 평가에서 4.52점/5.0(n=60)로 대조품종인 ‘킹피셔’의 3.85에 비해 화색·화형 등 품질이 월등히 우수하다는 평가를 받고 시장출하에서도 소비자 반응이 좋다고 판단되어 2015년 농작물 직무육성신품종심의회 심의를 거쳐 ‘허니핑크(honey Pink)’로 명명하고 국립종자원에 품종보호출원 하였다. ‘허니핑크’ 품종의 자연개화기는 10월 중하순이며, 분홍색(RHS color chart RP74D)의 홑꽃 화형인 스프레이 국화로서 착화성이 우수하고 줄기직경이 5.7mm 로 강하여 절화 중 부러짐으로 인한 결손이 적고 작업성이 우수히다. 또한 촉성, 억제재배시 단일처리 후 개화소요기간은 7.0주 이내로 빠르고 초장 114.5cm, 꽃 직경 6.1cm로 대조품종인 ‘킹피셔(King Fisher)'에 비해 초장이 13cm 정도 크며 성장세가 우수하다. 꽃자루 길이는 11cm 정도로 약간 길며, 착화수는 본당 17.2화 정도로 대조보다 4개 정도 많이 달리고 생장유형은 단일줄기형으로 직립한다. 절화수명은 약 21.8일 정도로 대조품종보다 4일 정도 길고 휴면이 약하며, 비닐하우스 내에서 연중재배가 가능하다. 재배상 유의사항은 초기 생육증진을 위해 비배관리에 힘쓰고 하계 고온기에는 화색발현을 위해 한 낮엔 차광율 30% 정도의 한랭사로 차광을 해 주고 환기도 충분히 해 주는 것이 좋다.

Corresponding author: Tel. 055-254-1622, E-mail: gypso@korea.kr

PB-13

양성자빔 처리량에 따른 고추 종자의 발아율과 생존율 분석

이예린, 정규미, 김해인, 이준대*

전라북도 전주시 전북대학교 원예학과

고추는 우리나라에서 경제적으로 큰 비중을 차지하고 있는 대표적인 원예작물로서 매년 병 발생에 의한 피해가 급증하고 있다. 최근에는 많은 복합내병성 품종이 개발되고 있지만 육종에 사용할 수 있는 새로운 병 저항성 유전자원은 점점 줄어들고 있다. 본 연구는 양성자빔을 이용해 돌연변이를 창성하여 육종에 활용할 수 있는 새로운 병 저항성 유전자원을 찾고자 하였다. 그에 앞서 본 실험에서는 고추 탄저병 저항성 품종인 'AR레전드' 종자를 사용하고 57 MeV 양성자빔으로 조사하여 돌연변이 개체를 유기할 수 있는 조건을 확립하고자 하였다. 조사선량은 65, 100, 170, 220, 300, 330, 360, 460, 530 및 560 Gy를 처리하였으며, 발아율과 생존율을 조사하였다. 그 결과 파종 5일 후에는 높은 선량에 따라 발아율 차이를 보였으나, 파종 15일 후에는 많이 회복되어 530과 560 Gy를 제외한 나머지 선량군에서는 대체로 비슷한 발아율을 보였다. 그러나 파종 21일 후 생존율을 조사한 결과 높은 선량에 따라 생존하는 개체가 낮은 것을 확인하였으며, 이는 발아 후 유전적·환경적인 원인에 의해 고사한 것으로 보인다. 따라서 57 MeV 양성자빔을 이용하여 고추 돌연변이를 유기하기 위해서는 530 Gy 이상의 양성자빔을 처리해야 할 것으로 판단된다.

Corresponding author: Tel. 063-270-2560, E-mail: ajfall@jbnu.ac.kr

PB-14

소득작물 후작지 적응 단기성 벼 '단평' 육성

손영보[1*], 조준현[1], 이지윤[1], 이종희[2], 오성환[1], 박동수[1], 송유천[1], 권영업[1]

[1]경상남도 밀양시 농촌진흥청 국립식량과학원 남부작물부 논이용작물과
[2]전라북도 전주시 농촌진흥청 연구정책국 연구운영과

우리나라의 경지면적은 2014년 현재 1,691천ha로 이중 논 면적은 934천ha로 2013년 보다 30천ha 감소하였다(통계청, 2014년 농업면적통계). 또한 농가인구 1인당 경지면적('10)은 미국 32.08ha, 프랑스 14.08, 일본 1.59보다 작은 0.73ha로 주요국에 비해 크게 작은 수준이다(농림수산식품통계연보 2010). 농지전용 증가로 논 면적이 감소고 있고, 쌀 가격의 하락으로 논을 기반으로 하는 농가의 소득이 감소되고 있다. 이러한 상황에서 논에서 벼와 접목하여 재배할 수 있는 다양한 소득작물을 재배하는 작부체계 개발이 활발히 진행 되고 있다. 이에 다양한 작부체계에 적응이 가능한 단기성 벼 품종이 필요하다.
'단평'은 소득작물 후작지에 적응 할 수 있는 복합내병성을 가진 단기성 벼를 육성하고자 2006/2007년 동계에 남평벼를 모본으로 사용하고 조생종이면서 도열병 저항성 유전자(Pizt)를 가진 Sasanishiki BL4를 부본으로 인공교배하여 남평벼를 반복친으로 3회 여교배하여 육성하였다. 2007년 하계에 F_1개체를 양성하여 고정시킨 계통들 중에서 출수기가 빠르고 미질이 양호한 YR27761-B-B-B-5-1을 선발하여 밀양285호의 계통명을 부여하였다. 2013~2015년 3년간 지역적응시험을 거쳐 '단평'을 육성하였다. 출수기는 만기재배에서 8월26일로 표준품종인 금오벼보다 1일 빠른 단기성 품종이다, 수당립수는 71개이며, 현미천립중은 22.7g, 등숙비율은 89.6%, 백미 완전미율은 94.6% 이다. 쌀수량은 만기재배에서 평균 5.05MT/ha이다. '단평'은 영남 평야지 소득작물 후작지에 적응성이 높은 단기성 벼 품종이다.

Corresponding author: Tel. 055-350-1157, E-mail: pongpong1124@korea.kr

PB-15

Adaptation of Autumn-Sown Faba Bean Lines in South Korea

Soon-Jae Kwon*, Jai Hyunk Ryu, Sang Wook Jeong, Min Kyu Lee, Jin-Baek Kim, Si-Yong Kang

Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongup, Jeonbuk 580-185, Korea

Faba bean (*Vicia faba* L.) is one of important versatile and cool-season pulse crop. It is grown for food, feed, vegetable, or cover crop purposes in many countries. The most informative feature of faba bean is grown as a winter annual. The objective of this study was to evaluate winter hardness faba beans of 256 individual lines. In middle Oct, 2015, fifty seeds of each line were sown in PE film mulching (22 seeds) and non-mulching field (28 seeds), at Advanced Radiation Technology Institute in Jeongeup. In mulching field, 193 of 256 lines survived more than one plants of 22 plants, four lines showed winter hardness higher than 80 percentage survival (17 plants). In non-mulching field, 178 lines survived more than one plants of 28 plants, and 10 lines were survived more than 80%. In contrast, survival plants in mulching field had higher plant height than non-mulching field in middle of April, 2016, averagely 20 cm. Ultimately, two lines (230-5 and 310-6) had higher than 80% survival rate in both field. These results will be very useful for autumn-sown of functional pulse crops at southern South Korea, and faba bean will provide great opportunity for mutation breeding.

Corresponding author: Tel. 063-570-3312, E-mail: soonjaekwon@kaeri.re.kr

PB-16

중북부평야지 조생종 등숙기간 고온 경과시 쌀 품질 변화

조윤상[1*], 정정수[2], 이지우[1], 함진관[1], 김상수[1]

[1]강원도 춘천시 충열로 83 강원도농업기술원 작물연구과
[2]강원도 철원군 김화로 93 강원도농업기술원 인삼약초연구소

최근 기후변화에 기인한 온도 상승으로 벼 생육단계별 재배 환경도 서서히 변화되고 있다. 고품질 쌀을 생산하기 위한 등숙기 적산온도는 1,100℃, 일평균 등숙적온 20 ~ 22℃라고 이미 설정되어 있다. 중북부평야지에서 조생종 벼의 등숙기간중 고온이 쌀 품질 및 수량에 미치는 영향을 보고자 본 연구를 수행하였다. 일반 노지 재배 포장에서 등숙기간중 고온을 인위적 경과를 유도하기 위하여 4월 27일 조기 이앙하였다. 조기 이앙에 따른 품종별 출수기는 진부올벼는 7월 2일, 백일미, 한설벼는 7월 9일, 조운 7월 10일, 진옥벼 7월13일, 오대벼 7월 15일로 적기 이앙에 비해 10일 정도 단축되었다. 쌀 품질 변화는 출수 후 수확시기를 달리하여 백미완전미율 등 품질 비교 검토하였다. 그 결과 모든 품종에서 고품질 쌀 생산 적정 기준이 되는 출수 후 40일 평균기온은 25.8 ~ 26.3℃로 매우 높은 온도를 경과하였다. 또한 적산온도는 1,030 ~ 1,050℃이었다. 수확일수에 따른 쌀 수량은 통계적 유의성이 관찰되지는 않았다. 백미완전미율은 품종간 차이는 있었으나 대부분 적기 이앙에 비해 떨어지는 경향을 보여 주고 있다. 이밖에 제현율, 현백율, 도정율 등은 수확일수 차이에 의한 통계적 유의성은 관찰되지 않았다. 이는 등숙 초기 고온은 배와 배유의 세포분열 및 탄수화물 축적에 유리하나 등숙 후기엔 조직의 노화를 촉진하여 분상질 증가와 완전미 감소에 영향을 미치는 것을 확인할 수 있었다.

Corresponding author: Tel. 033-248-6053, E-mail: choyouns@korea.kr

PB-17

The Selection of Sweet Sorghum (*Sorghum bicolor* L. Moench) Germplasms Suitable for the Korea

Jaihyunk Ryu, Soon-Jae Kwon, Sang-Wook Jeong, Min Kyu Lee, Hong-Il Choi, Jin-Baek Kim, Si-Yong Kang*

Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongup, Jeonbuk 580-185, Korea

Sweet sorghum (*Sorghum bicolor* L. Moench) accumulates fermentable sugars in the stem and is increasingly being studied as a potential source of feedstock for bioethanol production. The objective of this study was to evaluate biomass, sugar content and grain yield in 250 sweet sorghum germplasms from RDA and ICRISAT. These lines were cultivated at the breeding farm and 152 cultivars were verified whether seed production was possible in south Korea and seed yield more than 500 $kg \cdot ha^{-1}$ in 101 germplasms. The heading date of 152 cultivars spanning from 57 to 95 day after seeding. The plant height had a mean of 264.5 cm and ranged from 70 cm to 430 cm. The highest plant height was recorded to Bhiwapur wani from India. The sugar content of all the cultivars ranged from 9 to 21.6 brix. The highest sugar content was recorded to SOG132 from Korea. Thirty-five cultivars were not extractable juice. The highest juice yield was recorded to Dansusu2ho cultivar. Except for eight cultivars (Dansusu2ho, Dansusu4ho, JM4621, HDW325, HDW518, DRM36, Pi246716, PI196058), the cultivars tested are potential sources of both sugar and grain yields. These results could be used to select sorghum cultivars for mutation breeding programs

Corresponding author: Tel. 063-570-3310, E-mail: sykang@kaeri.re.kr

PB-18

고추의 나출 소포자 배양 시 배양 방법 및 하층 고체배지의 charcoal 농도가 소포자배 발생에 미치는 영향

박은준, 양은영*, 이인성, 채수영, 노미영, 김옥례, 박태성, 문지혜, 조명철

국립원예특작과학원 채소과

종자 수출시장 확대 및 수출액 증대를 위해서는 각 목표 시장별 우수한 형질을 가진 자원의 보유여부가 매우 중요하다고 할 수 있다. 우리나라 고추 육종에 활용되어 온 유전자원의 변이는 폭이 제한적이므로, 빠른 기간 내에 계통 육성이 가능한 반수체 육종법 활용이 필요하다. 고추 약배양의 경우 각 연구기관 및 종묘회사 자체적으로 배양법을 확립하여 현재 약배양을 이용한 상업용 품종 보급이 이루어지고 있으나 체세포 유래 2배체 형성이 많다는 것이 가장 큰 문제라고 할 수 있다. 소포자 배양은 이러한 약배양의 단점을 보완하고 배형성률을 높일 수 있는 방법으로 이미 배추과 채소 육종에는 실용적으로 사용되고 있으나 고추에서는 아직 본격적으로 실용화되지 못한 상황이다. 본 연구는 실용적인 고추 소포자 배양기술 확립을 위해 나출 소포자 배양 시스템을 확립할 목적으로 배양 방법 및 charcoal 농도가 소포자 배발생에 미치는 영향을 조사하였다. LV2319 및 서울대 위탁 교배조합(SNU, 선충저항성/역병저항성)의 F_2 집단을 식물재료로 사용하였으며, 후기 1핵성 소포자에서 초기 2핵성 화분을 배양하기 위해서 2/4~3/4이 보라색으로 착색된 약이 들어있는 꽃봉오리를 채취하였다. 소포자 나출 후 체세포 조직과 소포자의 분리, 소포자 수확과 수세 과정을 거쳐 31℃에서 3일 동안 고온처리 후 25℃에서 3주 동안 배양하였다. 배양 방법에 따른 배발생 효율 조사를 위해 액체배양, 이층배양 그리고 액체배양 후 이층배양을 실시하였다. Charcoal 농도에 따른 소포자배 발생 효율을 조사하기 위해서는 고체배지에 charcoal을 0, 0.1, 0.5 및 1%를 첨가하여 3주 동안 배양한 후 발생한 소포자배의 수를 계수하였다. 발생한 소포자배는 재분화 배지에 옮겨 7주간 배양 후 흙으로 옮겨 순화시켰다. 배양 3주후 관찰결과 LV2319 품종의 경우에는 구형, 어뢰형, 심장형 및 자엽배가 발생한 반면, SNU 품종의 경우에는 배발달 초기인 구형배만이 관찰되었다. 본 실험결과는 고추에서 다수의 소포자배를 생산할 수 있는 배양시스템을 확립하는데 중요한 기초자료가 될 것으로 판단된다.

Corresponding author: Tel. 063-238-6613, Fax. 063-238-6605, E-mail: yangyang2@korea.kr

PB-19

Effects of Gamma-ray Irradiation on Radio Sensitivity in Lentil bean (*Lens culinari* L.).

Min-kyu Lee, Jaihyunk Ryu, Sang Wook Jeong, Jin-Back Kim, Si-Yong Kang, Soon-Jae Kwon*

Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, 29, Geumgu-gil, Jeongeup-si, Jeollabuk-do, 56212, Korea

This study examined radiation damage and the optimal gamma-ray dose for mutation breeding in lentil (*Lens culinari* L.) crop. Four individual lines (L-C, L-2, L-8 and L-9), had remarkable growth character in south korea, irradiated by 50, 70, 100, 200, 300, 400, 500 Gy. The germination rate of seed decreased as the dose increased over 50 Gy in all lines. The median lethal dose (LD_{50}) was approximately 127 (L-C), 74 (L-2), 95 (L-8) and 144 (L-9) Gy. The median reduction dose (RD_{50}) for plant height, number of leaves, root length, and flash weight was 156, 176, 150, 180 for L-C, 253, 198, 127, 142 for L-2, 188, 175, 200, 190 for L-8 and 162, 210, 224, 184 for L-9. The growth characteristics of the M_1 generation decreased as the dose increased over 70 Gy. There were some difference in LD_{50} and RD_{50} among lines. The optimal dose of gamma irradiation for lentil mutation appears to be in 70 Gy (L-2, L-8) and 100 Gy (L-C, L-9). We performed the comet assay to observe nuclear DNA damage induced by gamma-ray irradiation. In comet assay, a clear difference was identified over 100 Gy treatments. With increasing doses of gamma-ray in the range of 50 to 500 Gy, the rate of head DNA was decreased significantly from 97.5% to 81.6%. Tail length was consecutively increased from 1.9㎛ to 17.4 ㎛. This result will be useful for construct mutant pool of lentils

Corresponding author: Tel.: +82-63-570-3312, E-mail: soonjaekwon@kaeri.re.kr

PB-20

소나무 종자생산능력에 따른 개량효과 추정을 통한 최적 선발강도

김진중, 나성준, 심동환, 우관수, 한상억*

경기도 수원시 오목천동 국립산림과학원 임목육종과

본 연구는 소나무 채종원(N 36° 27 E 126° 22)을 대상으로, 구과분석을 통한 선발방법 및 강도에 따른 개량효과를 추정하여 종자생산 효율성을 높이는 채종원 관리기술을 마련하기 위해 수행하였다. 본 연구결과는 종자생산능력을 바탕으로 선발방법(개체선발, 가계선발)과 강도(10~90%)에 따라 개량효과, 잔존 가계수 변화, 상대유효집단크기를 추정하여 최적의 선발방법 및 강도를 구명하였다. 구과 분석은 85개 클론을 대상으로 클론 당 3～5개의 구과를 분석하였으며, 2009년부터 2년에 걸쳐 조사하였다. 2009년 구과무게와 종자생산능력은 각각 16.6g과 116.8개로 나타났으며, 2010년에는 각각 17.1g과 97.8개로 나타나, 구과무게와 종자생산능력 간에는 유의한 상관이 없는 것으로 나타났다.
선발방법 및 강도별 개량효과를 추정한 결과, 모든 선발강도에서 개체선발이 가계선발보다 높은 개량효과가 추정되었으며, 가계선발의 경우 높은 선발강도에도 불구하고 개량효과가 저조한 것으로 나타났다. 선발강도에 따른 가계수는 개체선발이 가계선발 보다 모든 선발강도에서 높게 유지되었으며, 상대유효집단크기는 가계선발의 경우 모든 선발강도에서 일정하게 유지되는 반면, 개체선발은 선발강도가 강할수록 감소하는 경향을 나타내었다. 본 소나무 채종원의 개량효과를 극대화하기 위해서는 개체선발이 유리하였지만, 유전다양성 측면에서는 가계선발이 유리한 것으로 나타났다. 따라서 본 채종원 관리자는 목적하는 개량효과의 달성과 유전다양성을 유지하기 위해 선발방법 및 강도를 적절히 선택하여야 한다.

Acknowledgements: 본 연구는 2016년도 국립산림과학원 석·박사연구원의 지원에 의해 이루어진 것임.

Corresponding author: Tel. 031-291-1124, E-mail: sanguhan@korea.kr

PB-21

Determination of Sulfur-containing Amino Acid Contents in a Core Collection of Wild Soybean (*Glycine soja*)

Woon Ji Kim[1], Juhyun Im[1], Yu Ri Kim[1], Soo-Kwon Park[2], Sungtaeg Kang[3], Soon-Chun Jeong[4], Jung-Kyung Moon[5], Bo-Keun Ha[1*]

[1]Division of Plant Biotechnology, Chonnam National University, Gwangju, 61186, Korea
[2]National Institute of Crop Science, Rural Development Administration, Wanju, 55365, Korea
[3]Department of Crop Science & Biotechnology, Dankook University, Cheonan, 31116, Korea
[4]Bio-Evaluation Center, Korea Research Institute of Bioscience and Biotechnology, Cheongju, 28116, Korea
[5]National Institute of Agricultural Sciences, Rural Development Administration, Wanju, 55365, Korea

Wild soybean (*Glycine soja*) is the wild ancestor of cultivated soybean (*Glycine max*) and retains valuable gene pool for improving agronomic traits in soybean. Recently, Rural Development Administration (RDA) of the Republic of Korea developed a core collection (ver. 1) of wild soybean consisting of 206 accessions. In this study, we determined the sulfur-containing amino acid contents in the core collection. The 206 accessions were planted in the experimental field of Chonnam National University, 2015. The harvested seeds were used for analyzing amino acids with an amino acid auto-analyzer (S433-H, SYKAM). Out of 206 accessions, the 99 accessions were completely analyzed. The total amino acid contents of 99 accessions ranged from 32896.35 to 55670.42 (mg/100g) with the mean of 46703.94 (mg/100g). The cystine contents ranged from 222.79 to 774.46 (mg/100g) with the mean of 497.52 (mg/100g). The methionine contents ranged from 339.12 to 696.76 (mg/100g) with the mean of 503.45 (mg/100g). Also, all amino acids represents a positive correlation with each other. Especially, two wild soybean accessions showed high content of cystine (682.23mg/100g, 774.46mg/100g) and methionine (696.76mg/100g, 635.70mg/100g), respectively. These accessions will be introgressed into cultivated soybean cultivars for genetic researches and breeding programs.

Corresponding author: Tel. 062-530-2055, E-mail: bkha@jnu.ac.kr

PB-22

Agronomic Trait Evaluation on European Common Wheat Germplasms

Jin Seok Yoon, Yong Weon Seo*

Department of Biosystems and Biotechnology, Korea University, Seoul 136-713, Korea

Wheat is one of the major staple human food sources in the world. In the present, the crop productivity is dramatically reduced by severe climatic change such as drought, heat and cold. To cope with such adverse environment, employment of various wheat genetic resources in breeding program is necessary. Furthermore, evaluation of wheat germplasms that are consisted of diverse genetic backgrounds is prerequisite for cross breeding. Here, total 240 European wheat lines consisting landraces and cultivars that were provided from the National Plant Germplasm System (NPGS, ARS) were evaluated for major agronomic parameters. Either quantitative and qualitative characteristic is scored at the Korea university research farm during '14-'15 planting year. The average heading date of most of European wheat lines showed very late than Korean common wheats. The distribution of phenotypic traits as well as yield parameters such as plant height, spike length and awn length, liter weight were evaluated. There is a germplasm that showed dwarf type can be a promising source for lodging resistance breeding. The germplasm also showed diverse splike, stem and seed color (white yellow, yellow, brown, purple and red). Also, the germplasm showed various phenotype traits such as plant type and spike type. These evaluated data could be useful information for wheat breeder cope with the unfavorite climatic change.

Acknowledgements: This work was supported by a grant from Reginoal Subgenebank Support Program (No. PJ0121382016), Rural Development Administration, Republic of Korea.

Corresponding author: Tel. +82-2-3290-3005, E-mail: seoag@korea.ac.kr

PB-23

한국 콩 품종의 isoflavone 함량의 변이와 다변량 분석에 의한 품종군 분류

김현명[1], 왕정은[1], 박병덕[1], 윤건식[2], 한정아[3], 김홍식[1*]

[1]충청북도 청주시 서원구 충대로1 충북대학교 농업생명환경대학 식물자원학과
[2]충청북도 청주시 청원구 오창읍 가곡길 46 농업기술원
[3]경기도 연천군 신서면 도신로 3번길 경기도 농업기술원

1913년부터 2013년까지 국내에서 육성된 172품종에 대한 종실의 isoflavone 성분함량의 변이를 구명하고 다변량분석에 의한 품종군을 분류하고자 본 연구를 수행하였다.
Isoflavone의 총 함량 평균은 837.2μ g/g이었고, 206.3~2666.2μ g/g의 범위였다. 각 그룹 성분별 변이는 aglycone group의 평균함량이 10.0μ g/g이었고, 2.2~33.1μ g/g의 범위였으며, glucoside group의 평균함량은 202.4μ g/g이었으며 36.9~801.8 μ g/g의 범위였다. Malonylglucoside group의 평균함량은 599.1μ g/g이었고 143.6~1796.4μ g/g의 범위에 있었고, acetylglucoside group의 평균함량은 27.5μ g/g이었으며 3.7~103.9μ g/g의 범위에 있었다. Isoflavone 성분에 대한 주성분분석을 실시한 결과 제 1-3주성분까지의 누적기여도는 89.14%였다. 군집분류에서 평균거리를 0.8로 하였을 때 7개의 군집으로 분류되었고, Ⅰ군집은 전체 품종의 57.6%가 속하는 큰 군집이었고, 그 다음으로 Ⅲ군집이 35.5%를 이루는 큰 군집이었으며 나머지 군집은 5개 이하의 품종이 속하는 소군집이었다.

Corresponding author: Tel. 031-261-2513, E-mail: hongsigk@chungbuk.ac.kr

PB-24

Biological Responses of Soybean (*Glycine max* L.) Exposed to Proton-beam

Juhyun Im, Woon Ji Kim, Sin Ji Kim, Eun Ji Jeong, Yuri Kim, Bo-Keun Ha*

Division of Plant Biotechnology, Chonnam National University, Gwangju, 61186, Korea

Soybean is an important crop in the world, providing protein and oil. It also contains abundantly secondary metabolite. In general, gamma-ray is an important mutagen to induce mutations for a new agronomic trait and have been mainly used in crop mutation breeding programs during 80 years. But spectrum of plant somatic variation induced by gamma-ray is not varied, so breeders need a new Linear Energy Transfer (LET), such as proton-beam. In this study, we investigated the effects of soybean exposed to proton-beam. Seeds of three Korean elite soybean cultivars (‘Kwangan’, ‘Daepung’, and ‘Pungsannamul’) were irradiated with 57 MeV proton-beams in the range of 50-400 Gy. The biological responses including germination rate, survival rate, plant height, fresh weight (shoot/root), dry weight (shoot/root), and SPAD value were investigated from the leaves of 4-week-old plants. The germination rates of all varieties did not show any significant differences. However, survival rate, plant height, and fresh weight of shoot were significantly decreased above 100 Gy. Also, there were significant differences in SPAD values among treatments except for Deapung.

Corresponding author: Tel. 062-530-2055, E-mail: bkha@jnu.ac.kr

PB-25

Molecular Mapping of Quantitative Trait Loci for Forage Quality Traits in a Cross Between PI483463 and Hutcheson in Soybean

Sovetgul Asekova, Krishnanand P. Kulkarni, Minsu Kim, Jeong-Hwa Kim, Jong Tae Song, Jeong-Dong Lee

School of Applied Biosciences, Kyungpook National University, Daegu 41566, Korea

Soybean [*Glycine max* (L.) Merr.] is one of the important forage legume crops in the world. Understanding the genetic basis of forage quality traits in soybean could help improve the nutritive quality of forage soybean. This study was aimed at mapping quantitative trait loci (QTLs) for crude protein (CP), crude fat (CF), neutral detergent fiber (NDF) and acid detergent fiber (ADF) in soybean. A total of 188 RILs from a cross of PI483463 and Hutcheson were grown for three consecutive years. Plants were harvested at the R6 stage and utilized for measuring each quality trait using Near-Infrared Reflectance Spectroscopy. The variance components of genotype, environment and genotype x environment interactions found to be significant for the measured quality traits. Significant positive as well as negative correlations were observed among forage quality traits. Composite Interval Mapping identified six QTLs for CP, two QTLs for CF, six QTLs for NDF and two QTLs for ADF. Individual QTLs explained phenotypic variation in the range of 7.04 - 26.46 for CP, 6.62 - 29.33 for CF, 5.79 - 28.19 for NDF, and 7.66 - 41.72 for ADF respectively. Favorable alleles for the majority of the QTLs identified for CF, ADF and NDF were contributed by the wild parent PI483463. Coincident QTLs for all the forage quality traits were detected on chromosome19. QTLs identified in the present study could find valuable in crop improvement programs for developing improved forage quality cultivars.

Corresponding author: Tel. 053-950-5709, E-mail: jdlee@knu.ac.kr

PB-26

Selection and Characterization of Gamma Ray-induced Soybean Mutant Lines Based on Seed Coat Color

Young Eun Jang, Jung Eun Hwang, In Jung Jung, Soon-Jae Kwon, Joon-Woo Ahn, Jin-Baek Kim, Si-Yong Kang, Hong-Il Choi*

Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongeup, 56212, Korea

Mutation breeding is a efficient method to develop new varieties in modern breeding area. Gamma rays have been utilized to induce mutation, which is already applied to develop several soybean cultivars. Seed coat color is an important soybean trait that soybeans with black or brown coat color have been generally accepted as high quality dietary source for health because of their antioxidant activity. Two elite soybean cultivars, Danbaek and Daepung were irradiated with 250 Gy gamma rays. The seeds of 73 M_8 plants derived from Danbaek (D) and 152 from Daepung (DP) were harvested and screened for selection of dark seed coat color in 2015. Nine plants from the D population had black or brown seed coat color. The seed number per plant was varied from 93 to 412, and 193 on the average. Among the DP population, 32 plants had black or brown seed coat color that had the seed number per plant from 86 to 402 with an average of 181. Their 100 seed weights of D and DP populations took averages of 19.6 g and 19.7 g, respectively. These results suggest that gamma ray-induced mutation can be used for development of soybean lines with altered seed coat color.

Corresponding author: Tel. 063-570-3298, E-mail: hichoi@kaeri.re.kr

PB-27

Selection of Soybean Germplasm for Breeding Program Applications in Central Asia

Akbota Makulbekova, Sovetgul Asekova, Minsu Kim, Cheol-Woo Park, Jae-Eun Jeong, Dong-Ho Lee, Mirwais Ghani, Jong Tae Song, Jeong-Dong Lee*

School of Applied Biosciences, Kyungpook National University, Daegu 41566, Korea

Kazakhstan is landlocked state in Central Asia with vast territory. Soybean is being produced in southern part of state, but domestic demand for oilseeds are not fully satisfied. Therefore, nowadays a high attention is being given to soybean production recent days, especially to spread it to the northern parts of country. Additionally, development of livestock production requires an introduction of new and more nutritious fodder crop. Soybean is found to be attractive crop with its rich seed composition of protein, oil contents and carbohydrates. Objective of this research was to evaluate early maturing soybean lines from germlasm collection for desired phenotypes and seed yield, in order to use them in future breeding programs. A total of 138 soybean accessions including 103 germplasm lines from Korea, 2 from America, 7 from Korea and 21 from Kazakhstan cultivars were evaluated for days to flower, flowering to maturity, days to maturity, protein and oil contents. The experimental lines and varieties were tested under two planting dates – May 25 and June 29 at the affiliated experiment and practice fields of Kyungpook National University, Gunwi, Korea. The results revealed significant variation for evaluated agronomic traits. Based on maturity, lodging, plant shape, and seed yield we have selected 30 promising lines. Those lines are under yield testing with normal yield testing plot in 2016. The promising lines that will be selected by this year end, can be good germplasm to contribute soybean production in Central Asia.

Corresponding author: Tel. 053-950-5709, E-mail: jdlee@knu.ac.kr

PB-28

고 Oleic Acid 콩 청국장의 특성

이동호[1], 김병오[2], 이정동[1*]

[1]대구광역시 북구 대학로 80 경북대학교 농업생명과학대학 응용생명과학부
[2]대구광역시 북구 대학로 80 경북대학교 농업생명과학대학 식품공학부

2015년 질병관리본부 보고에 따르면 심장질환과 뇌혈관질환 그리고 고혈압성질환은 우리나라 10대 사망원인 중 각각 2위, 3위, 10위를 차지하고 있을 만큼 심혈관계질환은 현대인의 건강을 위협하고 있다. 지방산 중 oleic acid가 심혈관계질환 예방에 효과가 있다고 보고되고 있다. 일반적인 콩에는 oleic acid가 약 23% 있는데 최근 oleic acid가 약 80% 포함되어있는 콩이 육성되어 이를 이용한 기능성 콩 식품 개발에 대한 연구가 필요하다. 본 연구에서는 oleic acid 함량이 높은 콩으로 대표적인 발효식품인 청국장제조가 가능한지를 평가하였다. 고 oleic acid 콩 품종인 호심과 대조 품종인 대풍으로 청국장을 만들고, 발효시간(0, 24시간, 48시간, 72시간)에 따라 두 품종간의 청국장관련 형질을 비교하였다. 조사 항목은 수분함량, pH, 생균수, protease activity 그리고 amino type nitrogen이었다. 수분함량은 호심 청국장에서 60.1±2.4%, 대풍 청국장에서 59.3±1.9%로 나타났다. pH는 두 가지 청국장 모두 발효 72시간에서 pH 7.5로 가장 높게 나타났다. 생균수는 두 가지 청국장 모두 발효 24시간에서 9.3CFU/g로 가장 높은 생균수를 나타났다. Protease activity는 발효 72시간에서 호심 청국장과 대풍 청국장이 각각 552U/g와 522U/g로 가장 높게 나타났다. Amino type nitrogen은 발효 후 72시간에서 호심 청국장과 대풍 청국장이 각각 582mg%/g과 590mg%/g로 가장 높게 나타났다. 본 실험을 통해 두 품종으로 만든 청국장에서 조사한 모든 청국장 특성 관련 형질이 발효 시간별로 비슷한 수준으로 확인 되었다. 따라서, 고 oleic acid인 호심으로 정상적인 청국장을 만들 수 있는 것으로 확인 되었고 청국장의 기능성과 고 oleic acid 기능을 동시에 가지는 고 기능성 청국장으로 국민건강에 기여할 수 있을 것으로 기대가 된다.

Corresponding author: Tel. 053-950-5709, E-mail: jdlee@knu.ac.kr

PB-29

Genome-wide Detection of Variations Among Three Sprouting Soybean Varieties by Resequencing

Hong-Il Choi, Young Eun Jang, Jung Eun Hwang, Injung Jung, Sung Min Han, Yeong Deuk Jo, Sang Hoon Kim, Soon-Jae Kwon, Joon-Woo Ahn, Jin-Baek Kim, Si-Yong Kang*

Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongeup, 56212, Korea

Soybean sprouts are one of the most popular ingredients in East Asian cuisine. We resequenced the whole genomes of three soybean varieties for sprouts, Bangsakong, a gamma-irradiated mutant line B25 derived from Bangsakong, and Pungsannamulkong derived from Bangsakong x KLS87092 with high coverage. 101-bp paired-end sequencing using Illumina HiSeq platform yielded a mean of 39 Gb per sample, corresponding to 35x coverage of the soybean genome. After quality checking and trimming, averagely 33.4 Gb of the clean reads were aligned to the soybean reference genome (Glyma2.0). Around 91% of the reads from each sample were mapped, covering >96% of the reference genome. More than 2.4 million SNP loci and 367 thousand InDel loci were found with differential distribution that 56% of the SNPs and 72% of InDels were located in non-repetitive regions on the genome. One to one comparison of the polymorphic loci revealed around a million SNPs and 70 thousand InDels between samples, respectively. The heterozygosity of the SNPs detected between each sample was ~2%, while that of the InDels ranged from 25 to 91%. This result implies inaccuracy of the preliminary InDel prediction, or may be derived from unstable inheritance of InDels induced by gamma rays. Detailed characterization of the variation are needed based on the genetic background and traits of the varieties.

Corresponding author: Tel. 063-570-3310, E-mail: sykang@kaeri.re.kr

PB-30

약배양 이용 조생 거대배아 찰벼 계통 육성

박현수, 신운철, 정종민, 백만기, 남정권, 이건미, 조영찬, 김보경

전라북도 완주군 이서면 혁신로 181 농촌진흥청 국립식량과학원

본 연구는 약배양을 이용하여 조생 거대배아 찰벼 계통을 조기에 개발하고자 수행되었다. 내병성이면서 도복에 강한 특성을 갖고 있는 자포니카 초다수 중만생 품종인 '드래찬'을 모본으로 하고 조생 거대배아 찰벼 유전자원인 '청향나 *ge*'를 부본으로 하여 F_1을 육성하였다. 단교잡하여 육성된 F_2 종자의 메벼와 찰벼의 분리비는 3:1로 찰성은 하나의 열성유전자에 의해 작용하는 것으로 나타났고, 일반배아와 거대배아는 기존에 알려진 3:1의 분리비보다 거대배아형이 적게 나왔다. F_2 종자에서 거대배아 찰벼 종자를 선별하여 F_2 식물체를 육성하였고 출수기가 조생인 개체의 이삭을 채취하여 약배양을 수행하였다. 육성된 43개 약배양 계통들은 조생 거대배아 찰벼로, 이중 벼흰잎마름병 및 줄무늬잎마름병 저항성 유전자 *Xa3*와 *Stvb-i*에 대한 분자표지 선발을 통해 17계통을 선발하였다. 선발된 계통은 현미 무게에 대한 배아 무게비율이 5.4-10.8%로 드래찬(2.9%)보다 높은 거대배아형을 나타냈다. 17계통 중 농업형질이 양호한 6계통을 거대배아 품종인 큰눈, 눈큰흑찰과 함께 생산력검정시험을 수행하여 농업형질 특성을 조사하였다. 선발계통은 출수기가 7월23일에서 8월2일인 조생종으로 거대배아 찰벼 특성을 나타내며 간장이 작고 도복에 안정적인 특성을 나타냈다. 수량성은 420-430 kg/10a로 중만생 메벼인 드래찬(519 kg/10a), 큰눈(460)에 비해서는 적었으나 조생 찰벼인 청향나 *ge*(342)와 눈큰흑찰(387)보다는 높았다. 이들 계통들은 벼흰잎마름병 K1, K2, K3와 줄무늬잎마름병에 대한 저항성을 확보하였으나 수발아가 높은 단점을 나타냈다.

Corresponding author: Tel. 063-238-5216, E-mail: mayoe@korea.kr

PB-31

Genotype by Environment Interaction(GGE) Biplot Analysis of Sesame Under Multi-Environmental Conditions

Kang-Bo Shim*, Sung-Gook Kim, Seong-Hyu Shin, Kun-Ho Jung, Chung-Guk Kim, Sung-Gi Heu

Crop Cultivation & Environment Research Division, NICS, Suwon 4411-707, Korea

This experiment was conducted at the different seven sites using total seven sesame varieties during the year of 2013～2015. Environment PC1 score had both negative and positive values indicating different response of yield performance among sesame varieties across environments due to the effects of G × E interactions. Environment PC2 scores also had both positive and negative scores. This gave rise to crossover, leading to inconsistent genotype yield performance across environments. Miryang and Suwon were most discriminating (informative). Otherwise, Cheongwon, Andong and Naju showed much less discriminating. Test environments that are consistently non discriminating (non-informative) provide little information on the genotypes. A test environment that has a smaller angle with the AEA(Average Environment Axis) is more representative of other test environments. Thus, Cheongwon, Naju and Miyang are most representative whereas Suwon and Iksan were least representative. Genotypes Miryang52, Koppoom and Miryang53 are unstable. Whereas, Kyeongbuk20, jinki and Kanghuk which showed shorter projections were relatively stable over the environments. The genotypes that combined good performance with stability include Kyeongbuk20 because it is closeness to the mean yield and short projection of the genotype marker lines.

Corresponding author: Tel. 031-695-0650, E-mail: shimkb@korea.kr

PB-32

FASCICULATE Regulates Plant Architecture Including Cluster Flowers and Plant Height in Pepper (*Capsicum annuum*)

Min-Young Kang, Koeun Han, Byoung-Cheorl Kang*

Department of Plant Science, Plant Genomics and Breeding Institute, and Vegetable Breeding Research Center, College of Agriculture and Life Sciences, Seoul National University, Seoul 151-921, Korea

The overall plant shape is determined by genetic program. Regulation of plant architecture is an important agronomic trait for agricultural plants. *Capsicum annuum* 'MicroPep' shows cluster flowers and short height. By contrast, *C. annuum* 'Jeju' shows typical pepper architecture. In this study, we crossed *C. annuum* 'MicroPep' and *C. annuum* 'Jeju' to identify the genetic loci controlling plant architecture. A total of 117 F_2 plants were genotyped using genotyping-by-sequencing (GBS) method and 2,612 single nucleotide polymorphisms (SNPs) were detected. Linked SNPs with same genotype were called as bin, and 1,731 cM bin map with 983 bins were constructed. Using bin map and the phenotype of F_2 population, one locus determining MicroPep and Jeju plant shape was mapped on chromosome 6. This locus was also identified to control the plant height from quantitative trait locus (QTL) analysis, while there were 5 additional QTLs on chromosome 1 and 11 for plant height. At this locus of chromosome 6, *FASCICUATE* (*FA*) was colocalized indicating that this gene is a strong candidate for the gene controlling the cluster flower phenotype and plant height. This locus can explain 24% of total phenotypic variations. The successfully identification and characterization of *FA* gene can provide a chance for study of architecture in pepper.

Corresponding author: Tel. 82-2-880-4563, E-mail: bk54@snu.ac.kr

PB-33

Agronomic Traits of Soybean Line with Kunitz Trypsin Inhibitor and Lectin Protein-Free

Jin-A Kim, Sung-Jin Han, Sang-Woo Choi, Dong-Hui Kang, Su-Jin Lee, Jong-Il Chung*

Division of Applied Life Science, Graduate School, Gyeongsang National University, Chinju 52828, Korea

Soybean is an economically important leguminous seed crop for feed and food products that are rich in seed protein, oil and saccharides. Also, black soybean has been known as medicinal food. However, Kunitz trypsin inhibitor (KTI) and lectin proteins are a main antinutritional factor in mature black soybean seed. The genetic removal of the KTI and lectin proteins will improve the nutritional value of black soybean seed. The objective of this research was to develop a new black soybean lines with double recessive allele for both KTI and lectin protein. A total of 179 F_2seeds were obtained from the cross of"Gaechuck#1" (*Le/Le, ti/ti* genotype) and "LE-16" (*le/le, Ti/Ti* genotype) parents. The segregation ratios for the presence or absence of KTI and lectin proteins in the F_2 seed generation were well fitted to an expected 3:1 ratio.The segregation ratios of 9 : 3 : 3 : 1 (113 *Ti_Le_*: 28 *Ti_lele*: 30 *titiLe_*: 8 *titilele*) between *Ti* gene and *Le* gene in F_2 seed generation were observed (χ^2=3.71, P=0.5 − 0.1). From eight F_2 seeds with double recessive allele (*ti/ti*, *le/le* genotype), one new strain (*titilele,* both KTI and lectin protein free) was developed. New strain has black seed coat, black hilum and green cotyledon in mature seed and 100-seed weight was 19.5g. This strain will be helpful in breeding program for selecting black soybean line with lacking both KTI and lectin protein.

Corresponding author: Tel. 055-772-1872, E-mail: jongil@gnu.ac.kr

PB-34

Marker-Assited Selection for Soybean Line with Low Content of Raffinose and Stachyose Using *rs2* Gene

Su-Jin Lee, Sung-Jin Han, Sang-Woo Choi, Dong-Hui Kang, Jin-A Kim, Jong-Il Chung*

Division of Applied Life Science, Graduate School, Gyeongsang National University, Chinju 52828, Korea

Soybean [*Glycine max* (L.) Merr.] seed is one of the major food sources for protein, oil, carbohydrates, isoflavones, and many other nutrients to humans and animals. Raffinose and stachyose are main antinutritional factors in soybean seed. The objective of this research was to select genotypes with low content of raffinose and rtachyose using *rs2* gene marker. Breeding populations were developed using the parent with low content of raffinose and stachyose. F1 seeds obtained were planted and F2 seeds were harvested. Individual F2 seeds were planted in the field. Young leaves will be collected from the individual F_2 plants. The F2 plants with recessive allele (*rs2rs2* genotype) will be selected using *rs2* gene marker, Content of raffinose and stachyose will be detected by HPLC.

Corresponding author: Tel. 055-772-1872, E-mail: jongil@gnu.ac.kr

PB-35

Identification and Quantification of Flavonoids from the Seed of Rice Mutant (*Oryza sativa* L.)

Backki Kim[1], Su Jang[1], Sunmin Woo[2], Hee-Jong Koh[1*]

[1]Department of Plant Science, Research Institute for Agriculture and Life Sciences, and Plant Genomics and Breeding Institute, Seoul National University, Seoul 151-921, Korea
[2]Lab. of Pharmacognosy, College of Pharmacy, Seoul National University 1 Gwanak-ro, Gwank-gu, Seoul 151-742, Korea

Flavonoids are widely distributed group of plant phenolic compounds which are potential source of active natural health-promoting compounds. While anthocyanin extensively studied in colored rice, C-glycosylflavones are less reported. This study was carried out to determine the major C-glycosylflavones and profile flavonoids in high flavonoid rice mutant seed using UPLC-QTOF-MS. UPLC-QTOF-MS analyses showed that a total of 19 C-glycosylflavones were identified and the isoorientin, isoorientin-2”-O-hexoside, chrysoeriol-2”-O-hexosyl-C-hexoside, chrysoeriol-6, 8-diC-hexoside, apigenin-2”-O-hexosyl-8-C-hexoside, isovitexin and isoscoparin were the major flavonoid compounds among 19 C-glycosylflavones in high flavonoid rice seed. Quantitative analysis was conducted using the seven major C-glycosylflavones with extracts of embryo and endosperm of high flavonoid rice. These results revealed that isoorientin was highly accumulated in both embryo and endosperm compared to wild type. In addition, extremely high level of isoorientin accumulation was observed in mutant embryo and endosperm than those of wild type. Significant differences ($p<0.05$) in antioxidant activities which determined by DPPH, FRAP, and TAEC assay, respectively were found in embryo and endosperm of mutant rice. These results indicated that these C-glycosylflavones may be useful for understanding flavonoids biosynthesis in rice and contribute to improving the functional quality of rice grain.

Corresponding author: E-mail: heejkoh@snu.ac.kr

PB-36

Genetic Mapping Study of New Sugary Endosperm Mutant, *SUGARY-2* in Rice

Yunjoo Lee*, Mi-Ok Woo, Gileung Lee, Eunbyeol Koh, Hee-jong Koh

Department of Plant Science and Research Institute for Agriculture and Life Sciences, and Plant Genomics and Breeding Institute, Seoul National University, Seoul 151-921, Korea

Starch biosynthesis is one of the most important pathways that determine both grain quality and production in rice. Sugary endosperm, the mutant trait for starch biosynthesis, has been reported that it had full of carbohydrates instead of starch even after maturity. We newly obtained a sugary type mutant by chemical mutagenesis from a Korean *japonica* cultivar, Hwacheong. Here, we report the mapping of another sugary gene, named *sugary-2* (*sug-2*), which is controlling rice grain thickness especially in the presence of *sugary-1* (*sug-1*). The *sug-2* mutant exhibited wrinkled, translucent, and amber-colored endosperm with high soluble sugar content as known as the phenotype of *sug-1*. However the phenotype of *sug-2* differs slightly from the *sug-1*. The grain of *sug-2* is easily polished making it more commercially feasible with less wrinkled feature. To identify the sugary genes, map-based cloning strategy was applied. Genetic analysis revealed that the phenotype of *sug-2* was controlled by epistatic interaction of two recessive genes, one of which was the same gene as *OsISA1* on chromosome 8. The other candidate gene was found to be located on chromosome 4. Fine mapping is in progress to identify *sug-2*. These results will be helpful in elucidating the starch biosynthesis of rice endosperm variation and breeding sugary endosperm rice varieties for digestible food.

Corresponding author: Tel. 02-880-4541, E-mail: heejkoh@snu.ac.kr

PB-37

벼 재조합집단을 이용한 고양식미 집단의 식미관련 특성 분석

정종민*, 신운철, 백만기, 박현수, 남정권, 조영찬, 김보경

전북 완주군 이서면 혁신로 181, 농촌진흥청 국립식량과학원

우리 쌀의 경쟁력 확보 및 쌀 소비 확대를 위해 외국의 양질미 품종과 유전적으로 차별화되고 소비자들의 기호에 맞는 우리 고유의 식미를 갖는 고품질 신품종 개발이 필요하다. 본 연구는 식미가 우수한 쌀 품종 개발을 위한 식미관련 QTL/유전자 탐색을 위하여 수행되었다. 식미치가 낮은 '팔공벼'와 고품질 '하아아미'를 교배하여 재조합 자식성 집단(F_6, 190계통)을 육성하여 식미와 연관된 아밀로스함량, 밥의 윤기치, Rapid Viscosity Analyzer (RVA)에 관련된 특성 등을 분석하였다. 모본과 부본에 대한 식미특성 검정 결과 밥의 윤기치는 '하이아미'가 77.3, '팔공벼'가 67, 단백질 함량은 '하이아미'가 6.3%, '팔공벼'가 7.3% 이었고 아밀로스 함량은 '하이아미'와 '팔공벼'가 각각 17%로 차이가 없었다. RVA 특성은 하이아미가 팔공벼에 비해 강하점도가 높고 치반점도는 낮게 나타나 식미치가 양호할 것으로 생각되었다. RIL 집단의 아밀로스 및 단백질 함량은 정규분포 양상을 나타내었으나 RVA 관련 특성 중 치반점도와 최종점도는 각각 모본과 부본쪽으로 다소 치우친 분포를 보였고 양친의 범위를 넘어서는 초월 분리현상을 보이는 개체들이 다수 존재하였다. RIL 집단에 대한 쌀의 이화학적 성분취반 물성 및 식미치 간의 상관관계를 분석한 결과, 밥의 윤기치는 아밀로스 함량, 치반점도와는 정의상관 관계를, 단백질 함량, 최고점도, 최저점도 및 강하점도와는 부의 상관관계를 보였다. 단백질 함량이 낮으며 최고점도 및 강화점도가 높을수록 밥의 윤기치가 높아지는 특성을 보였다. 이들 결과를 활용하여 식미관련 유전자/QTL을 분석하고 유전체 정보를 활용하여 고유 식미관련 분자표지 개발 수행 중에 있다.

Corresponding author: Tel. 063-223-5217, E-mail: jjm0820@korea.kr

PB-38

안토시아닌 고함유 알곡용 옥수수 색소2호 품종 개발

박기진*, 박종열, 류시환, 서영호, 최재근, 용우식, 이정훈, 김경희

강원도 홍천군 두촌면 장남길 26 강원도농업기술원 옥수수연구소

국내 재배 옥수수는 풋옥수수 용도인 찰옥수수가 대부분을 점유하고 있지만 직접 또는 단순가공 형태로 소비되고 있어 부가가치가 낮은 실정으로 새롭고 보다 높은 부가가치를 창출할 신품종 개발이 시급하다. 안토시아닌을 대량 함유한 옥수수는 이런 면에서 옥수수의 부가가치를 극대화 할수 있는 새로운 작물로 정착이 가능하다고 판단된다. 옥수수연구소는 '00년부터 관상용옥수수에서 안토시아닌 우량 계통을 선발하고 육종모집단을 구성 새롭게 개량함으로서 '10년 색소1호(안토시아닌 포엽이용), '13년 청춘찰(안토시아닌 찰옥수수), '14년 색소2호(안토시아닌 알곡이용) 품종을 개발하는 성과를 거두었다. 색소2호는 '08년 중국과 캐나다에서 수집한 자색인 알곡 옥수수 자원을 활용하여 지속적으로 분리 육종하였다. 특히 동계세대촉진 육종과정을 적극 활용하여 분리 및 교잡종을 생산하여 3개년 강원도 지역적응시험('11～'12, '14년)을 거쳐 '14년 강원도 자체 직무육성신품종선정심의회에서 품종 결정되었다. 색소2호는 자체 알곡수량은 455㎏/10a 수량을 보여 낮은 수량이지만 알곡의 안토시아닌 함량은 685㎎/100g정도로 검정색찰옥수수인 미흑찰 알곡의 안토시아닌 함량 53㎎/100g보다 13배 많은 함량을 보였다. 알곡의 안토시아닌은 직접적인 식용이 가능하여 앞으로 식가공 재료로 직접 활용할 수 있는 제품이나 상품개발이 이루어지게 되면 옥수수의 부가가치를 높일 수 있다.

Corresponding author: Tel. 033-248-6911, E-mail: kjp@korea.kr

PB-39

도입 감 유전자원 '흑시' 2 품종의 주요 생육특성

김은경*, 박두상, 김성철, 최성태, 안광환, 김은석

경남 김해시 진영읍 하계로138, 경상남도농업기술원 단감연구소

감은 과실의 성숙이 진행됨에 따라, 카로티노이드 색소의 생합성에 의해 과피색이 대부분 황색 또는 오렌지색 계열의 색을 띠게 된다. 그런데, 일본과 중국에서 도입한 감 유전자원 중 하나인 '흑시'는 과피가 검은색으로 착색되는 특이한 품종으로서 일본의 흑시단감과 중국의 흑시떫은감 두 가지 형태가 있으며, 현재 감 산업에서 재배자들의 많은 관심이 집중되고 있다. 그러나 도입 유전자원인 '흑시'의 국내 환경에서의 생육특성 조사 분석은 미흡하므로, 특성조사와 함께 대조 품종과의 비교를 통해 육종의 소재 및 타 용도로의 활용 가능성을 검토하였다. 흑시단감과 흑시떫은감에 대해 각각 서촌조생과 산청단성시를 대조 품종으로 하여 2014년부터 2년간 경남 김해에 위치한 단감연구소 시험포장에서 조사한 결과, 흑시단감의 개화기는 5월 18일로 대조 품종인 서촌조생보다 3일이 늦었고, 성숙기는 10월 28일로 대조 품종보다 36일이 늦은 만생종이었다. 신초길이는 20.5cm로 서촌조생보다 길었으며, 수세는 비슷하였고, 과형은 단원추형으로 동일하였다. 과중은 158g으로 서촌조생에 비해 20g정도 적었고, 당도는 1.7°Brix 낮았으며, 경도는 4.6N 낮았다. 육질은 치밀하나 식미는 미흡하였다. 흑시떫은감의 개화기는 5월 17일로 산청단성시보다 3일이 늦었고, 성숙기는 10월 23일로 산청단성시와 비슷하였다. 수세는 산청단성시보다 조금 약했고, 과중은 14g 적었으며, 당도는 1.0°Brix 낮았고, 경도는 8.7N 높았다. 과육의 수분이 부족하고 질감이 텁텁하여 식용으로는 미흡하였다. 이와 같은 결과를 토대로 흑시단감과 흑시떫은감은 식용보다는 관상용으로 활용하는 것이 적합하고, 향후 과피색 발현에 관련된 생리적 기작에 대한 연구가 필요할 것으로 판단되었다.

Corresponding author: Tel. 055-254-1553, E-mail: kim2471@korea.kr

PB-40

유용 농업형질 탐색을 위한 EMS 처리에 의한 옥수수 돌연변이체 유도

김경화, 박수권, 옥현충, 홍하철, 김선림, 손범영 김둘이*

농촌진흥청 국립식량과학원

유용 농업형질을 가진 식량작물 개발을 위하여 방사선 및 EMS(Ethyl Methane Sulfonate)를 이용한 돌연변이 육종은 물리적, 화학적 자극을 통해 자연 상태에서 낮은 빈도로 발생하는 돌연변이의 발생 빈도를 높여주는 기술로 안전성이 입증되었으며, 전 세계적으로 식량작물, 화훼류 및 과수류 신품종 개발에 활발하게 이용되고 있다.
EMS 처리에 의하여 제초제 저항성 및 내염성 돌연변이 옥수수를 선발하기 위하여 0.3, 0.5, 0.7, 0.9% 농도에 각각 8, 12, 16 시간 처리 조건으로 돌연변이체를 얻기 위하여 광평옥 Inbred 라인 KS 124와 KS85가 사용되었다. 또한 EMS 농도 0.5%에 8, 12, 16 시간 처리 조건으로 강다옥 Inbred 라인 KS140과 KS141을 이용하여 돌연변이를 유도하였다.
광평옥 Inbred 두 라인에 대해 농도별 0.3, 0.5, 0.7, 0.9% 처리 조건하에서 돌연변이된 옥수수에 대해 개화기까지의 표현형을 분석한 결과 세 조건의 처리 시간 모두에서 0.7% 처리구에서부터 심한 생육 장애를 일으키며 수술과 암술이 발생되지 않아 종자를 얻을 수 없었다. 반면, 0.3과 0.5%에 각각 8 시간 처리한 처리구에서는 무처리구에 비해 생육은 약간 나쁘지만 암술과 수술에 이상이 없었고, 정상적인 개화가 이루어져 종자를 얻을 수 있었다. 또한 강다옥의 두 Inbred 라인에 대해 가장 적정한 EMS 처리 조건은 0.5% 농도에 8시간 처리구에서 광평옥과 마찬가지로 무처리구보다 생육은 다소 불량하지만 암술과 수술에 이상이 없었고, 정상적인 개화가 이루어져 종자 생산이 가능하였다. 따라서 유용 농업형질을 가진 옥수수 돌연변이체 확보를 위해서는 EMS 농도와 처리 시간이 중요할 것으로 생각되어진다.

Corresponding author: E-mail: dykim22@korea.kr

PB-41

고양식미 저아밀로스 향미 벼 신품종 “골든퀸3호”

이원도[1], 조유현[1*], 강시용[2], 박용진[3], 권순욱[4]

[1]경기도 수원시 권선구 매실로 85
[2]전라북도 정읍시 금구길 29 한국원자력연구원 첨단방사선연구소
[3]충청남도 예산군 예산읍 대학로 54 공주대학교 산업과학대학
[4]경상남도 밀양시 삼랑진읍 삼랑진로 1268-50 부산대학교 식물생명과학과

‘골든퀸3호’는 고기능성 양질미 품종개발을 목적으로 농업회사법인 주식회사 시드피아에서 육성되었으며, 2004년 하계에 저아밀로스 특성을 가지는 유메츠쿠시와 밀키퀸 교배후대 계통 JCH33M- 15-1-9-1을 부본으로 하고 야생재래향미 자원에서 유래한 HJ-11계통을 모본으로 교배하여 2004년부터 2012년까지 매년 포장에서 계통재배하면서 저향 및 저아밀로스 특성을 갖고, 재배안전성, 수량성 및 밥맛이 우수한 계통을 선발, 고정하였다. 선발된 계통을 SP005호로 계통명을 부여하고, 2013년 ~ 2014년에 난괴법 3반복으로 생산력검정을 수행하여 품종의 균일성과 안정성을 확인하여 ‘골든퀸 3호’라고 명명하였다. ‘골든퀸3호’는 중부지역 보통기 재배에서 8월 13일경에 출수하는 중생종으로 간장이 75cm로 단간이며 주당수수 14.7개 정도이다. 현미천립중은 21.5g, 장폭비 1.62로 단원형의 중소립종이다. 아밀로스함량이 12.5% 정도인 저아밀로스 벼로서 불투명 배유를 보이고, 단백질 함량은 6.0% 정도이며, 백미 수량은 5.47MT/ha로 추청벼 대비 110% 수준이다. ‘골든퀸3호’는 쌀에서 은은한 누룽지 향이 나는 향미 품종으로 밥맛이 우수하여 농가소득 증대에 기여할 것으로 판단된다.

Corresponding author: Tel. 070-4125-7959, E-mail: seedpia.001@gmail.com

PB-42

Performance of Mexican Wheat Gemplasms in Korean Environment for Selection Breeding

Jin Seok Yoon, Yong Weon Seo*

Department of Biosystems and Biotechnology, Korea University, Seoul 136-713, Korea

Wheat is the most important crop species considering both cultivation area and consumption in the world. Wheat is consumed by many population as cookies, bread and noddle, etc. However, the dramatic climatic change occurred throughout the world unable to keep stable yield production. Furthermore, introduction of genetic resources in the wheat breeding is highly limited nowadays. These difficulties let us finding new genetic resources from the diversities. Wheat germplasms have diverse properties such as abiotic/biotic stress resistance, lodging resistance, high yield, good end-use quality and early flowering, which should be needed in Korean wheat breeding program. In this study, we evaluated agronomic traits of Mexican wheat lines. Total 355 wheat lines consisting 5 Korean wheat cultivars and 350 Mexican lines (consisted by cultivars, landraces, breeding lines) were evaluated for their quantitative and qualitative agronomic characteristics in the Korea university research farm. Although Maxican lines showed wide distribution of heading date, the average heading date is similar to Koran wheat cultivars. The phenotypic parameters and some of yield components were evaluated and lines with favorite scores will be selected. The lines with typical phenotypes such as dwarf stature, various seed and spike colors also selected for further study. We also find presence of rust (leaf/stem) resistance and lodging resistant in the Mexican lines. These comparative analysis between Korean cultivars and Mexican germplasms should provide useful information for development of Korean wheat lines.

Acknowledgements: This work was supported by a grant from Reginoal Subgenebank Support Program (No. PJ0121382016), Rural Development Administration, Republic of Korea.

Corresponding author: Tel. +82-2-3290-3005, E-mail: seoag@korea.ac.kr

PB-43

Grain Color Segregation of a F_3 from Yellow Seed Coat x Deep Purple Seed Coat in Wheat (*Triticum aestivum* L.)

Paulina Calderón Flores[1], Jong Yeol Lee[2], Yong Weon Seo[1*]

[1]Division of Biotechnology, Korea University, Seongbuk-Gu, Seoul 136-713, Korea
[2]National Academy of Agricultural Science, RDA, Jeonju, 560-500, Korea

Grain color is an important trait since it has been shown that is affects two relevant characteristics of wheat, grain dormancy and resistance to preharvest sprouting. We study the segregation ratio of an F_3 generation. For the F_1 generation, lines of wheat (*Triticum aestivum* L.) with a distinct phenotype in their seed color, Yellow (Ye) and Deep Purple (DP) were crossed. Since grain color is determined by the maternal genotype, the phenotype of F_3 grains from F_2 plants is controlled by the F_2 genotype, meaning we had to wait until the F_3 to analyze the color segregation. We used the Chi-square (X^2) test to evaluate the goodness of fit for the number of genes related to the color segregation in our population. We bulked our plants in groups based on their seed color, rating them from 0 to 9, were 0 was light yellow and 9 deep purple. The best fit was for the ration 12 yellow: 3 brown: 1 deep purple, which means there is a dominant epistasis, with a X^2 of 2.075 and with a p value of 0.90-0.10; this kind of segregation is related to a dominant allele at one locus that masks the expression at another locus. Furthermore, we analyzed some phenotypic data using the segregation ratio (12:3:1) to study if there is correlation of the seed color and the phenotypic data (chlorophyll content, main shoot length, width of the tallest leaf, etc.) during the plant development.

Acknowledgement: This work was carried out with the support of "Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ01102102)" Rural Development Administration. Republic of Korea.

Corresponding author: Tel. 02-3290-3005, E-mail: seoag@korea.ac.kr

PB-44

LOX3 유전자 결핍 계통의 저장조건에 따른 이화학적 특성 변화

신운철[1*], 김정주[2], 박현수[1], 정종민[1], 백만기[1], 남정권[1], 조영찬[1], 김보경[1]

[1]전라북도 완주군 이서면 혁신로 181, 국립식량과학원 작물육종과
[2]경상북도 상주시 화서면 중화로 2161, 국립식량과학원 상주출장소

벼는 수확 후 즉시 소비하는 경우도 있으나 대부분 저장하면서 소비하게 되는데, 그동안 노화가 발생하게 되고 품질이 저하된다. 쌀의 노화는 쌀의 물리, 화학적 특성 변화에 의한 자연적인 현상으로서, 이에 따라 취반, 가공특성, 식미, 영양가 및 상품성 등의 품질 관련 요인이 변하게 된다. 저장 중 쌀 성분의 변화는 지방의 변화가 가장 먼저 일어나고, 다음 전분의 변화와 함께 단백질의 변화가 진행된다. 저장된 쌀의 고미취는 소량으로 존재하는 지질의 주도적 역할에 의해서 발생되며 지질의 가수분해 및 산화반응에서 시작하여 지질산화물과 단백질과의 반응, 지방과 전분과의 반응 등에 의하여 발생한다. 고미취의 주성분은 휘발성 carbonyl 화합물인 hexanal 및 pentanal 등의 aldehyde이다. Dawdam의 유리지방산은 일반품종과 비슷하나 LOX3 유전자 결핍으로 저장기간이 늘어남에 따라 고미취 증가 폭이 낮고, 고온저장(35℃)시 일반벼에 비해 고미취 성분변화가 없는 것으로 밝혀졌다. 본과제는 LOX3 유전자가 결핍된 Dawdam을 이용하여 육성된 우량계통의 저장조건에 따른 품질 변화가 적어 고미취 발생이 적은 품종을 육성하고자 수행하였다. LOX3 유전자가 결핍된 15계통에 대하여 고온(35℃)과 저온(15℃)에서 4개월간 저장한 후에 취반미의 물성, 종자 발아율 및 lipoxygenase 효소활성 변화를 분석하였다. 저장온도가 높을수록 취반미의 경도와 점착성은 커지는 경향을 보였으며, 응집성, 부착성, 탄성, 씹힘성은 저장기간과 저장온도에 따라 뚜렷한 차이가 없었다. 그 중 HR29062-B-98-2-1-B은 저온 및 고온에서 4개월 저장 후에 발아율이 각각 99.3 94.0%으로 높았으며, lipoxygenase 효소활성은 저온 및 고온에서 4개월 저장 후에 각각 3,304, 1,601unit/㎎ protein으로 낮아 추후 저장성이 향상된 품종 개발에 활용될 수 있을 것으로 생각된다.

Corresponding author: Tel. 063-238-5215, E-mail: biocheman@korea.kr

PB-45

쓰러짐에 강하고 앙금 가공적성이 우수한 팥 신품종 '홍진'

송석보[1*], 고지연[1], 우관식[1], 정태욱[2], 최명은[1], 여운상[1], 고종철[1], 김정인[1], 문중경[3], 최유미[3], 곽도연[1], 오인석[1]

[1]농촌진흥청 국립식량과학원
[2]농촌진흥청 연구정책국
[3]농촌진흥청 국립농업과학원

'홍진'은 중생 다수성이며 앙금 가공적성이 우수한 품종육성을 목적으로 1999년 하계에 국립식량과학원에서 단간이며 다수성인 SA9206-2B-6-1-2-3-3-2를 모본으로 하고 앙금적성이 우수한 수원38호를 부본으로 인공교배하여 F_3이후부터는 계통육종법에 의하여 육성 선발하였다.
2011~2012년 생산력검정시험에서 쓰러짐에 강하고 수량성이 우수하여 "밀양23호"로 계통명을 부여하고 2013~2015년 지역적응시험을 실시한 결과, 앙금 가공적성이 우수하고 내재해성 품종으로 우수성이 인정되었다.
'홍진'의 개화일수는 55일로 충주팥 보다 5일 정도 늦지만 생육일수가 92일로 4일 빠른 중생종 이다. 경장은 54㎝로 단간이며 협당립수는 6.9개로 충주팥보다 많고 쓰럼짐에 강하다. 100립중은 15.4g으로 중대립이며 ha당 평균수량은 199MT/ha으로 충주팥 대비 8% 증수되는 품종이다.
홍진의 재배적응지역은 우리나라 전지역에서 재배가 가능하며, 종피두께와 종피비율은 적고 앙금수율이 높아 팥을 이용한 가공식품에서 수입산 보다 품질에서 유리할 것으로 기대된다.

Corresponding author: Tel. 055-350-1243, e-mail: songsb1254@korea.kr

PB-46

녹색자엽 검정콩자원의 주요형질과 SNP Marker를 이용한 Core Collection 작성

이은자[1*], 최홍집[1], 배정숙[1], 김세종[1], 이정동[2]

[1]대구광역시 북구 동호동 189 경상북도농업기술원 작물육종과
[2]대구광역시 북구 산격동 경북대학교 농업생명과학대학 응용생명과학부

국내에는 다양한 검정콩 자원들이 존재하기 때문에, 녹색자엽을 가진 검정콩 품종을 육성하기 위해 원하는 유전자원을 찾는데 많은 시간적, 자본적 제약이 따른다. 이러한 문제점을 해결할 수 있도록 녹색자엽 검정콩 유전자원의 다양성을 유지하면서, 핵심집단을 작성하기 위해 본 시험을 수행하였다. 핵심집단 작성에 사용된 실험재료는 국립농업유전자원센터로부터 검정콩 유전자원 1,500점을 분양 받아 이 중 녹색자엽인 검정콩 452점과 경북지역 수집유전자원 15점을 실험에 사용하였다. 본 시험은 경상북도농업기술원 시험포장에서 2013년부터 2015년까지 3년간 주요형질과 품질관련 성분을 조사하였고, 분자유전학적 기법을 이용한 분석을 수행하였다.
주요형질은 화색, 성숙기, 경장, 백립중, 병저항성, 도복, 엽형, 립장, 립폭, 립두께 등을 조사하였고, 품질관련 성분은 조지방, 조단백, 안토시아닌 함량을 분석하였다. 분자유전학적 기법을 이용한 유연관계 분석 및 핵심집단 작성에는 6k SNP array로 분석을 실시하였으며, Phylogenetic tree는 MEGA6 프로그램을 이용하여 분석하였다.
주요형질의 경우 화색은 10점이 흰색이었고, 나머지는 모두 자색이었다. 경장은 90cm 이상이 44%, 60cm 이하가 15% 정도였다. 백립중은 소립종 9%, 중립종 5%, 대립종 18%, 극대립종은 68%이었다. 엽형은 75% 이상 난형을 보였으며, 25%는 4가지의 다양한 형태를 보였다. 안토시아닌의 평균함량은 72.0mg/g이었고, 최소 3.5mg/g에서 최대 167.6mg/g의 함량을 보였다. 조지방의 평균함량은 18.9%였으며, 최저 14.1%에서 최대 23.5%의 함량을 보였다. 녹색자엽 검정콩의 다형성 분석을 위해 NJ/UPGMA tree를 작성한 결과 5개의 major 그룹과 80여개의 minor 그룹으로 나누어지는 것이 확인되었다. 또한 PowerCore(v.1.0, 국립농업유전자원센터) 프로그램을 이용하여 89점으로 구성된 핵심집단을 구축하였다. 추후 조사된 주요형질 및 품질특성 자료를 이용하여 Core collection 구축에 활용할 예정이다.

Corresponding author: Tel. 053-320-0283, E-mail: dock0409@korea.kr

PB-47

흑미와 적미의 기능성 성분이 집적된 유색미 “흑진미”

이종희[1*], 조준현[2], 서우덕[3], 이지윤[2], 손영보[2], 오성환[2], 신동진[2], 송유천[2], 허연재[2], 박동수[2], 권영업[2]

[1]전라북도 전주시 완산구 농생명로 300 농촌진흥청 연구운영과
[2]경상남도 밀양시 점필재로 국립식량과학원 논이용작물과

‘흑진미’는 흑미의 안토시아닌 합성에 관여하는 유전자 Ra와 적미의 프로안토시아닌 생합성에 관여하는 유전자 Rc를 집적하여 기능성 성분이 강화된 신형질 유색미 품종을 개발하고자 육성된 품종이다. 2008/2009년 동계 1차에 흑미 품종인 보석흑찰을 모본으로 사용하고, 적미 품종인 홍진주를 부본으로 사용하여 인공교배를 실시하였다. F_4세대에 출수 전에 계통당 일련번호를 부여하여 MAS를 위한 DNA샘플을 채취하였다. 적미의 종피색에 관여하는 프로안토시아닌 생합성 Rc유전자를 가진 계통은 DNA 마커를 이용하여 선발하였다. 포장에서 생육과 초형이 양호한 계통을 선발하여 2012년 하계 생산력 검정을 통해 YR28620-B-11-B-B-B-1을 밀양290호로 계통명을 부여하였으며, 지역적응시험을 수행한 후 ‘흑진미’로 명명되었다.
흑진미의 농업적 특성은 중만생종이면서 간장이 73cm로 작은 반직립형 초형을 가지고 있다. 수당립수가 적고 등숙율은 77.5%이며, 수량은 470kg/10a로 흑남벼 대비 89%수준이다. 흑진미의 안토시아닌함량이 60.2mg/100g으로 보석흑찰 58.7mg/100g과 비슷하지만, 폴리페놀함량은 13.3mg/100g으로 보석흑찰 7.68mg/100보다 73% 높았으며, 플라보노이드 3.18mg/100g, 보석흑찰 1.71mg/100g 85% 증가되었다. 또한 고성능액체크레마토그라피를 이용하여 흑진미의 기능성 성분을 분석한 결과 보석흑찰과 홍진주 고유의 크레마토그램을 모두 가진 것을 확인하였다. DPPH법으로 활성산소 라디칼 제거하는 능력(IC50)을 분석한 결과 흑진미는 27.9㎍/㎖로 보석흑찰 62.5㎍/㎖와 홍진주85.6㎍/㎖보다 추출용매가 소량 요구되어 항산화활성도가 높은 것으로 나타났다.

Corresponding author: Tel. 063-238-0751, E-mail: ccriljh@korea.kr

PB-48

자생 억새의 유전적 다양성 및 유연관계

육민정, 임수현, 박해림, 김도순*

서울특별시 관악구 대학동 서울대학교 농업생명과학대학 식물생산과학부

한국을 포함한 동아시아는 억새의 자생지로서 다양한 억새 유전자원이 분포할 것으로 기대되며, 자생 억새의 유전적 변이는 유용작물 육성에 필수적인 자원이다. 따라서 본 연구에서는 한국 및 주변국에서 수집된 억새 283종의 유전적 다양성 및 유연관계를 알아보고자 배수성 검정 및 SSR 마커 분석이 수행되었다. 배수성 검정 및 SSR 마커 분석 결과, 283종의 억새 수집종은 크게 두 개의 그룹으로 분류되었으며 이는 기존의 분류학적 그룹- *Triarrhena* 아속, *Miscanthus* 아속-과 일치한다. PcoA 분석에 따르면, 첫 번째 그룹은 *Triarrhena* 아속에 속하는 물억새(*M. sacchariflorus*) 및 *M. lutarioriparius* 수집종으로 구성되었으며 물억새의 경우 2배체에서 4배체까지 다양한 배수성이 나타났다. 두 번째 그룹은 *Miscanthus* 아속에 속하는 참억새 및 *M. floridulus* 수집종으로 구성되었는데 대부분의 수집종은 2배체였고 3배체 수집종이 일부 포함되었다(참억새 3종 및 물억새 2종). 집단구조분석에 따르면, 집단의 수가 2일 때(K=2) PCoA 분석과 유사한 결과를 나타냈다. ΔK 값을 이용하여 추정한 실제 집단의 수는 5개였는데, *Triarrhena* 아속은 하나의 population을 유지한 반면 *Miscanthus* 아속은 집단의 수가 증가함에 따라 4개의 subpopulation으로 나뉘어져 보다 다양한 유전형이 존재하는 것이 확인되었다. 한편, *M.* x *giganteus*는 두 아속의 유전형이 혼입된 형태를 보였으며 *Triarrhena* 그룹과 유전적으로 보다 밀접한 것으로 나타났다. 본 연구를 통해 한국 및 주변국에 자생하는 억새 집단 내에 다양한 유전적 변이가 존재함을 밝혔으며, SSR 마커 및 배수성 분석이 억새 종 분류에 효과적임을 알 수 있다.

Acknowledgements: 본 연구는 농촌진흥청 LMO 환경위해성 평가기관 사업(과제번호: PJ01126901)의 지원에 의해 수행되었다.

Corresponding author: Tel. 02-880-4542, E-mail: dosoonkim@snu.ac.kr

PB-49

흰잎마름병에 강한 조기출하용 조생찰벼 '운백찰'

남정권[1], 신운철[1*], 김우재[1], 박현수[1], 백만기[1], 정종민[1], 조영찬[1], 김정주[2], 고재권[1], 김보경[1]

[1]전라북도 완주군 이서면 혁신로 181, 국립식량과학원 작물육종과
[2]경상북도 상주시 화서면 중화로 2161, 국립식량과학원 상주출장소

우리나라에서 쌀을 이용한 다양한 가공품 개발을 위해 찰벼수요가 증가하고 있다. 찰벼가격은 재배면적에 따라 가격 변동이 심하므로 조기 출하할 수 있는 조생종 찰벼품종의 개발이 필요하다. 국립식량과학원은 2005년 하계에 조생종인 운봉36호와 진부찰이 교배된 F1을 모본으로 하고, 흰잎마름병에 강하면서 다수성인 운광을 부본으로 인공교배를 하여 F1을 양성하였고, F3 이후 계통은 계통육종법에 따라 우량 계통을 선발하였다. 선발된 우량계통을 '운봉54호'로 계통명을 부여하여 2013～2015년까지 3년간 지역적응시험을 실시한 결과, 그 우수성이 인정되어 '운백찰'로 품종명을 부여하였다. '운백찰'의 출수기는 7월 27일로 '오대'보다 1일 빠른 조생종이며, 간장은 65cm로 단간이며 내도복성이다. '운백찰'은 벼 흰잎마름병(K1～K3)과 도열병에 강하지만 기타 병해충에는 약한 품종이다. '운일찰'의 쌀 수량은 2013～2015년 실시한 지역적응시험 보통기 보비재배에서 5.44MT/ha로 메벼인 오대보다 1% 높은 다수성 품종이다. '운백찰'의 적응지역은 중북부평야, 중산간지 및 남부고랭지이다. '운백찰'은 찹쌀의 백도가 높아 상품성이 우수하며, 수량성이 높아 추석전 조기출하용으로 확대보급 할 가치가 있는 조생찰벼로 생각된다.

Corresponding author: Tel. 063-238-5202, E-mail: namjk725@korea.kr

PB-50

슈퍼홍미의 유전적 특성 연구

함태호[1*], 권순욱[2], 류수노[1]

[1]서울 종로구 대학로 86 한국방송통신대학교 농학과
[2]경남 밀양 삼량진읍 부산대학교 생명자원과학대학 식물생명과학과

연평균 1인당 쌀 소비량은 2014년 65.1kg 이며, 하루 소비량으로 환산했을 때 하루에 밥 두 공기(한 공기는 쌀 100g)도 소비되지 못하는 양이다. 급격한 쌀 소비 감소에 대응하여 쌀의 부가가치를 높이기 위해 다양한 가공특성 및 기능성 품종연구가 활발히 진행되고 있다. 슈퍼홍미는 흑진주벼와 수원 425호 교잡 후대 계통에서 선발된 C3GHi 계통과 종실이 큰 대립벼1호를 인공교배한 후대에서 계통육종으로 육성한 품종이다. 출수기는 9월 5일로 슈퍼자미보다 10일 늦은 만생종이며, 간장은 94.7 cm 로 슈퍼자미보다 13 cm 큰 장간이다. 포기당 이삭수는 5.4개로 적지만 이삭당 벼알수는 154.0개로 슈퍼자미 보다 28% 많다. 현미의 천립중은 26.8g 으로 슈퍼자미와 비슷하다. 슈퍼홍미의 정조 길이는 9.05 cm이고 폭은 3.79 cm로 슈퍼자미보다 큰 대립이며 정현비율은 81.7% 이다. 기존의 갈색 유색미 품종인 건강홍미, 적진주, 홍진주와 교배 모본인 흑진주, 수원425호, C3GHi 품종, 그리고 같은 교배모본으로 육성된 슈퍼자미, 슈퍼자미2호 품종에 유색미 발현 관련 유전자 마커와 SSR 마커를 이용하여 유전자 특성을 조사하였다. 유전자 마커 분석결과 슈퍼홍미는 기존에 알려진 갈색 유색미 관련 유전자인 *Rc, Rd* 유전자가 아닌 다른 유전자에 의해 적갈색이 발현되고 있으며, 흑자색 유색미 관련 유전자인 *Prpb* 유전자를 가지고 있는 것으로 조사되었다.

Corresponding author: Tel. 02-3668-4630, E-mail: lion78@daum.net

PB-51

국내외 쌀귀리 유전자원의 품질 분석

김경훈[1*], 김경민[1], 박형호[2], 이상학[1], 이나리[1], 현종내[1], 권영업[1]

[1]경남 밀양시 점필재로 20, 농촌진흥청 국립식량과학원 남부작물부 논이용작물과
[2]전북 완주군 이서면 혁신로 181, 농촌진흥청 국립식량과학원 기술지원과

귀리는 베타글루칸, 단백질, 지방, 비타민 B군이 풍부하여 최근 슈퍼푸드로 선정되면서 건강 기능성 식품으로 인식되어 소비가 증가하고 있다(2002, 타임지). 이에 국내외에서 재배되고 있는 식용 쌀귀리를 수집하여 품질을 확인하고자 한다. 유전자원센터와 USDA에서 수집한 쌀귀리 유전자원 58점과 국내 세관을 통해 수입되어 들어온 귀리 11점을 포함한 총 69점을 수집하여 단백질, 베타글루칸, 조지방 함량 및 지방산 조성에 대해서 분석하였다. 그 결과, 단백질 함량은 11.0～20.6%의 분포를 나타내었고 15.0%이상인 쌀귀리가 20점이었으며, 그 중 'Branwen' 유전자원이 가장 높았다. 조지방 함량은 5.6～11.2%의 분포를 나타내었고 10.0% 이상인 쌀귀리가 4점이었으며, 그 중 'X345-1-B4-20-1(PI605531)' 유전자원이 가장 높았다. 반대로, 조지방 함량이 7.0% 이하인 쌀귀리가 12점이었고, 그 중 'Branwen'과 'NO.6884' 유전자원이 5.6%로 가장 낮았다. 베타글루칸 함량은 3.5～6.5%의 분포를 나타내었고, 그 중에서 'krykansky', 'Yenmesh' 유전자원이 6.5%로 가장 높았다. 지방산 조성 분석 결과, 주된 지방산은 linoleic acid, oleic acid 및 palmitic acid이었고, 그 중에서 linoleic acid와 oleic acid가 전체 지방산의 76.8～83.5%를 차지하였다. 향후 이 수집한 쌀귀리 유전자원을 활용하여 국내 고품질 쌀귀리를 육성해나가는데 교배모본으로 활용할 예정이다.

Corresponding author: Tel. 055-350-1173, E-mail: k2h0331@korea.kr

PB-52

흑색 내도복 다수성 겉보리 신품종 '흑다향'

김양길[1*], 박종철[1], 김경호[1], 이미자[1], 강천식[1], 오영진[1], 한옥규[1], 윤건식[2], 배정숙[3], 조수현[4], 박종호[1], 정영근[1], 김보경[1], 이광원[1], 박태일[1]

[1]전북 완주군 이서면 혁신로 181 농촌진흥청 국립식량과학원
[2]충청북도 청주시 청원구 오창읍 가곡길 46 충청북도농업기술원
[3]대구광역시 북구 칠곡중앙대로 136길 47 경상북도농업기술원
[4]강원도 춘천시 충열로 83 강원도농업기술원

최근 웰빙시대에 부응한 다양한 기능성 칼라 식품이 개발되어 소비자들의 관심이 높아짐에 따라 채소는 물론 곡류에 있어서도 유색 미, 유색 콩 등과 같은 유색 기능성이 가미된 곡류의 소비가 증가하고 있다. 따라서 이에 적합한 품종을 육성하기 위해 2005년에 조숙, 대립, 다수성 품종인 "큰알보리1호(IT213217)를 모본으로, 흑색 찰성 특성을 가진 "마산과맥(IT268885)/ Mortoni(IT111490)" 계통을 부본으로 인공교배하여. 흑색 메성이고 내도복성이면서 다수성인 보리차용 '흑다향'을 개발하였다. '흑다향"은 6조이며 파성이 Ⅲ인 병성 겉보리로 이삭의 형태는 밀수형이고, 종실색은 흑색으로 까락이 길며 탈망성이 좋다. 출수기는 올보리에 비해 전작(수원, 춘천, 청원)에서 4월 30일로 3일, 답리작(대구, 익산, 전주)에서 4월 25일로 2일 늦다. 간장은 76㎝로 올보리보다 7㎝ 정도 짧은 중간형으로 내도복성이며, 수장(5.1㎝)은 길고 1수립수(57개)가 많다. 천립중(35.9g)은 올보리보다 1.3g 무거웠다. 병해저항성 중 보리호위축병은 올보리와 비슷하였으며, 내한성은 올보리보다 다소 약하였다. '흑다향'은 단백질 함량(11.3%)이 비슷하나 폴리페놀 함량(0.162%)이 높고, DPPH(41.3%)이 활성이 높다. 보리차 특성으로서 볶음 처리에 의한 동일한 조건에서의 보리차 색도(L)가 진하고, 적색(a) 및 황색(b) 높다. 수량성은 전작에서 4.52톤/ha으로 6% 증수, 답리작 3.67톤/ha으로 5% 증수하였다. '흑다향'은 1월 평균기온이-6℃ 이상인 지역에 보급 될 것으로 기대 된다.

Corresponding author: Tel. 063-238-5225, E-mail: kim5yk@korea.kr

PB-53

Whole Genome Re-sequencing for Detecting Specific DNA Polymorphisms in *Brachypodium distachyon* Mutant Induced by Gamma Radiation

Man Bo Lee, Yong Weon Seo*

Dept. of Biotechnology, Korea University, Seoul 136-713, Korea

Brachypodium distachyon (*B. distachyon*) is a member of Poaceae such as rice, wheat, and barley. *B. distachyon* has been used as a model system for agricultural important cereal crops and biofuel feedstocks. Gamma radiation is widely adopted to generate genetic variations in crops. *B. distachyon* was subjected to chronic gamma radiation. M_5 mutants were developed by self-pollination of individual M_2 mutants. Phenotypes were investigated using M_2 to M_5 mutant lines. A total of 3 mutant lines which showed dwarf, late maturity, and/or seed color change were selected. The 3 mutant lines and wild type were used for whole genome re-sequencing. Genomic DNAs were sequenced using the Illumina HiSeq 2500 platform. More than 100 million reads were produced by whole genome re-sequencing in each plants and a minium of mean depth of coverage was 32.95x. DNA polymorphisms, including single nucleotide polymorphisms, inserts, and deletions, were detected using GATK. DNA polymorphisms were filtered to removing flase-positive detection. DNA polymorphisms which were identified in both WT and mutant line were excluded. Mutant line specific DNA polymorphisms were isolated by comparison with other mutant lines. In addition, so-called large-effect DNA polymorphisms such as missense, nonsense, splicing site, and frameshift mutation were collected. The DNA polymorphisms information in mutant lines can be utilized for functional genomics in *B. distachyon* and other cereal crops.

Acknowledgement: This study was supported by the Cooperative Research Program for Agriculture Science & Technology Development (Project Nos. PJ01102102, PJ01103501), Rural Development Administration, Republic of Korea.

Corresponding author: Tel. 02-3290-3005, E-mail: seoag@korea.ac.kr

PB-54

벼 저아밀로스 품종 육성에 대한 연구동향 분석

이종희[1*], 정태욱[1], 조준현[2], 이지윤[2], 손영보[2], 오성환[2], 신동진[2], 송유천[2], 허연재[2], 박동수[2]

[1]전라북도 전주시 완산구 농생명로 300 농촌진흥청 연구운영과
[2]경상남도 밀양시 점필재로 국립식량과학원 논이용작물과

식량안보와 쌀 자급률을 안정적으로 유지하기 위해서는 쌀 품질의 고급화와 그의 용도를 다양화하여 소비를 촉진하고 새로운 부가가치를 창출 할 필요가 있다. 쌀의 새로운 부가가치 창출을 위해 기존의 밥쌀용 품종과 차별화된 배유특성을 가진 품종 개발이 지속적으로 추진되어 왔다. 저아밀로스 품종은 배유의 외관특성이 반투명(translucent) 또는 흐릿한 흰색(hazy white)으로 나타나고, 아밀로스 함량은 7.1～14% 정도로 메벼와 찰벼의 중간 정도이다. 또한 메벼보다 전분의 점성이 강하고 팽화성이 높은 이화학적 특성을 가지고 있다. 국내에서 개발된 저아밀로스 품종은 일품벼 MNU(N-methyl-N-nitrosourea)처리로 육성된 백진주가 최초 개발되었으며, 도입유전자원을 이용해서 만미벼, 건양2호, 월백 등이 개발되었다. 저아밀로스 형질에 대한 유전연구를 통해서 찰성(Wx) 유전자와 대립관계에 있는 Wx-mq와 Wx1-1이 보고되어 있으며, 찰성 유전자(wx)와 비대립관계에 있으면서 단순열성유전자를 가진 변이체가 탐색되었는데 자포니카 품종 'Kinmaze'에 MNU를 처리하여 유기된 돌연변이체에서 du-1, du-2, du-3, du-4 및 du-5의 유전자가 밝혀졌다(Satou & Omura 1981, Yano et al. 1988). 국내에서는 화청벼 유래의 du6A, du6B 와 Du7 유전자가 보고된 바 있다. 저아밀로스 유전자에 대한 분자유전학적 연구를 살펴보면, 찰성 유전자와 대립관계에 있는 유전자는 GBSSI의 염기서열 결실이 원인이라고 보고되었다. 비대립 유전자인 du1, du2, du3 du12(t)에 대해서는 벼 염색체 2번, 3번, 6번, 10번에 위치하는 것으로 밝혀져 있으며, du-1과 du-2는 waxy pre-mRNA 유전자의 변이에 의해서 저아밀로스 형질이 발현된다고 보고되었다.

Corresponding author: Tel. 063-238-0751, E-mail: ccriljh@korea.kr

PB-55

더덕의 계통별 생육특성 검정 및 유효성분 분석

엄유리[1*], 이이[2], 김호방[3], 허목[1], 정진태[1], 김연복[1], 차선우, 정찬식[1], 김성철[1]

[1]농촌진흥청 국립원예특작과학원 인삼특작부 약용작물과
[2]충북대학교 농업생명환경대학 특용식물학과
[3]㈜바이오메딕 생명과학연구소

더덕의 주요성분인 lancemaside는 triterpenoid 사포닌계 물질로 항암, 기억력증진 및 염증개선 등 다양한 약리효과가 보고되고 있다. 본 연구에서는 2종의 더덕의 주요성분을 정량 분석하여 더덕 계통별 함유량을 비교 분석하고 차후 품종화 할 수 있는 후보 유전자원을 선발하고자 한다. 공시재료는 국립원예특작과학원 인삼특작부에서 재배되고 있는 26종의 더덕 유전자원으로 하였다. 농업형질관련 생육조사는 농림축산식품부 국립종자원의 특성조사요령에 따라 지하부 생육특성을 조사하였다. 사포닌 분석을 위한 더덕의 뿌리시료는 동결건조하여 분쇄 후 정량하였고 90% MeOH에서 추출한 후 사용하였다. Lancemaside A 와 lancemaside B의 분석은 UPLC Q-TOF/MS로 수행하였다. 분석된 데이터 값은 평균±표준오차(means±SE) 값으로 나타내었으며 실험값의 통계처리 및 유의성 검정은 SAS프로그램을 사용하여 분산분석과 DMRT로 유의성을 검증하여 통계처리 하였다. 그 결과 lancemaside A는 21번 계통이 9.29ppm/g 로 가장 높은 함량을 보였고 17번 계통 8.53ppm/g, 37번 계통 8.51ppm/g, 35번 계통이 8.39ppm/g 로 나타났다. Lancemaside B는 31번 계통 3.41ppm/g, 17번 계통 2.52ppm/g, 21번 계통 2.47ppm/g, 37번 계통 1.99ppm/g으로 정량분석 하였다. 본 연구에서는 품종육성을 위해 수집된 26종의 더덕 유전자원간 주요 약용 성분인 lancemaside A 와 lancemaside B 함량을 정량분석 하였으며 분석결과를 활용하여 차후 더덕 계통선발에 활용할 수 있을 것이라고 사료된다.

Corresponding author: Tel. 043-871-5665, E-mail: urspower@korea.kr

PB-56

초당옥수수(SweetCorn) 정역교배 후대 계통의 발아특성

최홍집[1*], 오태영[1], 배정숙[1], 이은자[1], 김세종[1], 소윤섭[2], 이주경[3]

[1]대구광역시 북구 칠곡중앙대로 136길 47 경상북도농업기술원 작물육종과
[2]충청북도 청주시 서원구 충대로 1 충북대학교 농업생명환경대학 식물자원학과
[3]강원도 춘천시 강원대학길 1 강원대학교 농업생명과학대학 생명자원과학부

초당옥수수(super sweet corn) 신품종 육성에 있어서 가장 중요한 형질중의 하나는 교잡종의 발아특성과 유묘 활력이다. 발아율 향상을 위해서는 발아능력이 우수한 양친 계통을 육성하는 것이 선행되어야 하므로, 본 시험은 발아능력과 유묘 활력이 우수한 계통을 육성하기위하여 수행하였다.
시험재료는 외국에서 시판되고 있는 초당옥수수 10품종을 사용하여 2013년부터 2016년 3월까지 경상북도농업기술원 시험포장과 동계비닐온실에서 이들 품종 간 정역교잡을 통해 복교잡종을 만들고 세대별로 자가수분 시켜 5세대까지 진전시켜 후대에 분리되는 계통들의 발아력과 유묘생육 정도를 조사하여 발아율이 우수한 계통을 선발하는 시험을 수행하였다.
본시험에 사용한 복교잡종의 발아율은 정역교배에 따른 차이가 있었으나 기존 품종과는 비슷한 경향이었다. F_3세대에서 각 교배조합별 후대 계통들에 대한 발아율을 조사한 결과 조합간의 평균 발아율의 차이가 크게 나타났으며, 조합내의 계통 간 차이도 큰 차이를 보였다. F_3세대에서 발아율이 우수한 계통을 선발하여 자가수분 시켜 F_4 세대를 얻은 다음 발아율 검정 결과 선발된 계통 대부분이 우수한 발아능력을 가지고 있었다. 또한 신규 계통양성을 위해 품종간 교배 후대 분석에서 발아율은 정역교배 결과 큰 차이가 있는 것으로 조사되었다. 또한 F_4 세대 403계통에 대하여 토양에서 발아율을 조사한 결과 평균 발아율은 24.3%이었고, 발아율이 75% 이상인 고발아 계통수는 22계통으로 5.4% 정도였다. 선발한 22계통은 F_5 세대에서도 발아율이 높았다. 이러한 결과로 초당옥수수의 발아율이 후대에 안정적으로 유지됨을 알 수 있었고 향후 지속적으로 발아관련 형질을 조사 분석하여 발아율이 우수한 계통육성과 초당옥수수 품종개발을 위한 자료로 활용할 계획이다.

Corresponding author: Tel. 053-320-0226, E-mail: chj1217@korea.kr

PB-57

Protein Profiling from Disomic Addition Lines of Wheat Carrying *Leymus racemosus* Chromosomes

Won-Ju Lee[1], Seong-Woo Cho[2], Hisashi Tsujimoto[3], Sun-Hee Woo[1*]

[1]Department of Crop Science, Chungbuk National University, Cheong-ju 28644, Korea
[2]Crop Breeding Division, National Institute of Crop Science, RDA, Wanju-gun 55365, Korea
[3]Arid Land Research Center, Tottori University, Hamasaka, Tottori 680-0001, Japan

Wheat (*Triticum aestivum* L.) is widely cultivated worldwide due to its value as a staple food and protein source. In the present study, proteomics analysis was performed to profile protein expression and identify the function of protein using wheat disomic addition lines carrying each pair of *L. racemosus* chromosomes for using the wheat improvement programs. The purpose of this study is to identify protein expression in each disomic addition line compared to CS. We performed two dimensional electrophoresis. Two dimensional gels stained with coomassie brilliant blue (CBB), a total of 1566 differentially expressed proteins were identified by Progenesis Same Spots software from the cultivars. However, a total of 90 protein spots were identified to be either present or absent or showing significantly differential expression when the difference threshold was set to more than 1.5 fold. However, out of the 90 differentially protein spots, a total of 74 spots were sorted for mass spectrometry analysis. MALDI-TOF/MS identified 40 protein spots from CS, 8 in Lr.[A], 5 in Lr.[E], 5 in Lr.[F], 2 in Lr.[H], 4 in Lr.[I], 7 in Lr.[J], 1 in Lr.[K], 1 in L r.[L], and 3 in Lr.[N], respectively. All proteins were classified into 11 groups based on their function. The function in metabolic processes was further grouped into metabolism, biological process and phosphorus metabolic process of which proteins in metabolism was the most abundant type as 33%.

Corresponding author: Tel. +82-43-261-2515, Email: shwoo@chungbuk.ac.kr

PB-58

The Antibacterial Effect of NOA in Watermelon Seeds.

Dahyun Moon, Wook Kim*

Department of Biosystems and Biotechnology, Korea University, Seoul, 136-713, Korea

Acidovorax avenae (BFB) is a serious bacterial disease in watermelon.
The purpose of this research was to investigate the effect of gas form NOA as an antibacterial agents in plant disease. This novel oxidant agent (NOA) is a commercial bleaching and disinfection agent as gas or liquid form. Watermelon seeds surface were inoculated with *Acidovorax avenae.* The antibacterial effect of NOA was evaluated accordance with gas treatments in watermelon seeds. NOA treatment at various condition of treatment time, the colony forming unit (CFU) of *Acidovorax avenae* and the germination percentage of seed were determined.
Colonies of *Acidovorax avenae* inoculated onto the watermelon seeds were inactivated using NOA. The inactivation of *Acidovorax avenae* colonies was found to be significantly increased by NOA treatment. The effect of treatment depends on the treatment time with concentration of NOA. The antibacterial effect was enhanced by treatment with gas form of NOA.

Corresponding author: Tel. 02-3290-3046, E-mail: kwook@korea.ac.kr

PB-59

쌀의 생산년도에 따른 인지질 함량의 변이

홍지화[1*], 안종성[2], 김용경[2], 최경후[1], 이민휘[1], 이진호[3], 박영준[1], 김현태[1]

[1]경상북도 김천시 율곡동 국립농산물품질관리원 시험연구소 품질조사과
[2]경상북도 김천시 율곡동 국립농산물품질관리원 시험연구소 안전성분석과
[3]경상북도 김천시 율곡동 국립농산물품질관리원 품질검사과

양곡관리법(제20조의 4, 양곡의 혼합금지)에 따라 생산년도가 다른 양곡의 혼합이 금지되어 있으나 생산년도가 다른 쌀을 혼합하여 유통 판매하면서 연산 및 혼합비율을 거짓으로 표시하는 사례가 증가하고 있다. 쌀의 생산년도(연산)를 육안으로 판별하는 것은 매우 어려운 실정이며 G·O·P 시약과 구아야콜 처리를 이용하여 쌀의 신선도를 감정하고 있으나 연산을 판별하기 위한 연구는 국내외적으로 미흡하기에 이에 대한 연구가 필요한 실정이다. 따라서 과학적인 연산 판별법 개발을 위하여 고분해능 질량분석기(TOF, Time of flight)를 이용하여 연산 간에 차이 나는 대사체 성분을 탐색한 결과, 인지질(Phospholipid)을 신곡 및 구곡 판별을 위한 지표물질로 선정하였다. 본 연구에서는 생산년도가 확실한 벼 2012년산 10점, 2013년산 10점, 2014년산 40점, 2015년산 40점을 수집하여 벼를 쌀로 가공한 후 분석시료로 활용하였다. 쌀의 인지질 종류 중 Phosphatidyl choline(PC)의 함량은 액체크로마토그래피-질량분석기(LC-MS/MS)를 이용하여 인지질 성분별 질량 값의 피크면적을 산출하였다. 인지질 분석결과 2015년산(햅쌀, 신곡)과 2012년산, 2013년산, 2014년산(묵은쌀, 구곡)간에 6개의 인지질 성분과 인지질 산화물에서 인지질 함량의 차이가 나타났다. 총 12개의 PC 성분을 변수로 활용하여 통계 분석한 결과 신곡과 구곡간의 거리는 4.16으로 나타났고 분류 적중률은 97%로 나타났다. 본 연구에서 수집된 벼의 생산년도에 따라 쌀의 인지질 성분 함량에서 차이가 나타나므로 향후 다양한 환경에서 보관된 벼를 수집하여 인지질 분석을 통한 쌀의 신곡·구곡 판별 정확도를 분석할 예정이다.

Corresponding author: Tel. 054-429-7722, E-mail: hongjh19@korea.kr

PB-60

산화훈증제를 이용한 양배추종자 감염 병원균 살균효과 검증

권혁[1], 박세준[2], 김욱[1*]

[1]서울특별시 성북구 안암동5가 고려대학교 바이오시스템공학과
[2]서울특별시 성북구 안암동5가 고려대학교 생명자원연구소

채소종자의 종자소독은 이미 다양하게 밝혀져 있다. 대표적인 종자 소독법으로는 온탕침지, 약제침지, 건열처리가 있다. 본 연구에서는 새로운 건열처리에 산화훈증처리를 추가하여 그 효과를 검정하고자 하였다. 특히, 종자감염병 중 십자화과 작물에서 검은 썩음병을 내는 *Xanthomonas campestris* 균을 이용하여 산화훈증제와 열처리를 복합처리하여 살균효과를 알아보고자 본 연구를 수행하였다. *Xanthomonas campestris*균을 인위 감염한 시킨 채소 종자를 산화훈증제 처리와 열처리의 복합처리를 비교해 본 결과 산화훈증제 처리와 열처리와의 순차적 처리에 의해 감소한 것을 확인할 수 있다.

Corresponding author: Tel. 02-3290-3046, E-mail: kwook@korea.ac.kr

PB-61

Composition and Content Analysis of Ginsenosides from Adventitious Roots (AR) and Callus-derived Roots (CR) Proliferated from Korean Wild Ginseng and Comparative Characteristics in Morphology

Hong-yu Li[1], Hyeon-Jin Sun[2], Hong-Gyu Kang[2], Hyo-Yeon Lee[1,2]

[1]Faculty of Biotechnology, Jeju National University, Jeju, 690-756, Korea
[2]Subtropical Horticulture Research Institute, Jeju National University, Jeju, 690-756, Korea

Korean wild ginseng (Panax ginseng C.A. Meyer) belongs to Araliaceae family, which is one of the most widely used medical plants for human health since ancient times, and has been developed into various kinds of dietary supplement with increasing market demand. The beneficial effects of ginseng are attributed to ginsenosides—glycosylated dammarene-type tetracyclic triterpene compounds and have been reported concentrate mostly in adventitious roots. Phamaceutical values of ginsenosides like enhancing immunity, anti-tumor, anti-aging have been investigated over recent times. However, wild ginseng is very limited and has been overexploited and field cultivation of ginseng is long-lasting and labor-intensive, therefore tissue and organ culture have been exploited as a biotechnological alternative for more efficient and controllable production of ginseng and its active metabolites. The adventitious roots (AR) were proliferated from Korean wild ginseng maintained on MS (Murashige and Skoog,1962)with Naphthalene acetic acid (NAA) and Indole-3-acetic acid (IAA). Calluses were induced from adventitious roots by callus induction medium, callus-derived roots (CR) were induced from somatic embryos by roots induction medium. In our study, CR showed higher growth radio than AR, and also performed a more positive phenotype in secondary roots formation either in solid medium culture or liquid medium culture. Composition and content analysis of ginsenosides is supposed by performing High Performance Liquid Chromatography.

Acknowledgements: This has been published with the support of CK-I (university for Creative Korea) project under the Ministry of Education.

Corresponding author: E-mail: hyoyeon@jejunu.ac.kr

PB-62

고추 핵심집단의 원예적 특성평가 및 DB구축

양현천[1], 김상규[1], 고호철[1], Binod P. Luitel[1], 성정숙[1], 이주희[1], 윤문섭[1], 백형진[1], 류경열[1], 이준구[2], 허온숙[1*]

[1]전북 전주시 완산구 농생명로 370 농촌진흥청 농업유전자원센터
[2]전북 전주시 전북대학교 원예학과

농업유전자원센터에서 보유중인 3,700여 고추 자원 중에서 유전적 다형성을 보인 253자원을 핵심집단으로 선발하여 원예적 특성 평가를 실시하고 그 결과를 데이터베이스화 하였다. 253자원의 종 분포를 살펴보면,*C. annuum, C. baccatum, C. chinense, C. frutescens, C. chacoense, C. eximium* 이 각각 178점, 20점, 28점, 24점, 1점, 2점이 포함되어 있다. 2015년도에 IT103410 등 253자원을 농업유전자원센터 비닐하우스에 공시하여 개화소요일수, 화색, 과중, 과색 등 30여 항목을 고추 유전자원 특성조사 및 관리요령에 따라 조사하였고 화기, 식물체, 과실의 이미지 정보를 구축하였다. 자원에 따라 개화소요일수가 51-65일, 66-80일, 81-95일 96-110일인 것이 각각 45자원, 115자원, 101자원, 37자원 이었으며 126일인 것도 1자원 있었다. 화색은 백색, 연녹색, 백색에 황색밴드, 백색에 자색, 자색으로 구분하여 조사하였으나, 자색의 경우 자색 농도의 정도가 다양하였으며, 백색에 자색인 꽃의 경우 테두리만 자색인 경우와 꽃 내부 또는 외부가 자색인 경우 등 여러 형태가 존재하여 화색 코드를 더욱 다양하게 설정할 필요가 있음을 알게 되었다. 과중(g) 분포를 살펴본 결과 *C. annuum* 종을 제외한 재배종과 야생종, 야생근연종, 재래종들은 과실크기가 작아 과중이 10g 미만인 자원이 약 50%를 차지하며, 과중이 많이 나가는 자원은 파프리카와 유사한 형태의 자원이었다. 미숙과는 녹색이 가장 많이 관찰되었으며, *C. annuum*의 경우 녹색, 연녹, 백색의 순의 분포를 보이며 *C. baccatum* 도 같은 경향이었다. 숙과색은 적색이 가장 많이 관찰되었으며, *C. chinense*에서 다양한 숙과색을 보이고 특이적으로 갈색, 자색의 숙과가 관찰되었다. 평가된 자원들의 특성은 농업유전자원정보 통합관리시스템에 데이터베이스화 하여 언제든지 활용할 수 있게 하였다.

Corresponding author: Tel. 063-238-4942, E-mail: oshur09@korea.kr

PB-63

‘중모1024’의 고온등숙 내성 지배유전자위 표지를 위한 유전연관분석

조성우, 정지웅*, 전재범, 김우재, 강경호, 고재권, 김현순, 김보경

전라북도 완주군 이서면 혁신로 181 국립식량과학원 작물육종과

지구온난화로 인한 기후 변화는 전 세계적인 문제로 인식되고 있는데, IPCC는 최근 100년간 세계의 평균기온이 0.74℃ 상승하였다고 보고하였다. 우리나라를 비롯하여 쌀을 주곡으로 삼는 동아시아에서는 기후변화에 의한 벼 재배기간의 고온여건이 종실중 감소와 종실전분의 원활한 합성을 저해하여 수량과 외관품위를 저하하는 주된 요인으로 지목되고 있다. 이에 따라 벼 등숙기의 고온조건에서도 안정적인 수량성과 양호한 쌀 외관품위를 견지할 수 있는 벼 품종개발의 필요성이 부각되고 있다. 본 연구는 국내육성 조생 벼 품종인 ‘남일’에 아지드화나트륨을 돌연변이원으로 처리한 돌연변이 후대 계통 중 고온등숙성이 양호한 ‘중모1024’의 획득형질발현에 관여하는 유전자위를 탐색하여 정밀분자표지를 개발함으로써 ‘중모1024’의 고온등숙 내성유전인자를 국내육성 타 고품질 벼 품종에 원활히 이전하는데 그 목적을 두고 있다. ‘중모1024’의 고온등숙 내성을 지배하는 목표유전자위를 표지하기 위한 유전분석집단으로 원품종인 ‘남일’과 ‘중모1024’ 간 교잡후대 F_2 집단을 육성하였다. 설정된 온도조건 하에서 유전분석집단의 표현형분산을 평가하기 위해 이삭 패는 시기와 간장, 분얼수 등 작물학적 외관특성이 유사한 F_2 개체들을 선별하였다. 두 가지 온도조건 즉, 고온(평균 30℃; 최고 34℃, 최저: 26℃) 및 적온(평균 26℃; 최고 30℃, 최저 22℃)이 설정된 생육상에 140개 F_2 개체씩을 배치한 후 완숙기까지 처리하였다. 각 온도조건별로 처리된 F_2 개체들의 간장, 수장, 수수, 천립중 등 주요 작물학적 특성을 조사하였으며, 등숙기 고온조건에 의한 쌀 외관품위 저하정도를 가름하기 위해 쌀 품위분석기(FOSS Cervitec 1625 Grain Inspector)를 이용하여 F_2 개체들의 현미완전립율을 평가하였다. 원품종(남일)과 그 돌연변이후대계통(중모1024)간의 교잡으로 작성된 유전분석집단를 이용한 연관지도 작성을 위해 각 F_2 개체에서 DNA를 추출하였으며, ‘남일’과 ‘중모1024’ 전장유전체분석(Re-sequencing)자료를 비교분석하여 양친 간 SNP를 분자표지로 활용하여 집단 내 개체들의 유전자형을 판정, 연관지도 초안을 작성하고 있다.

Corresponding author: Tel. 063-238-5236, E-mail: jrnj@korea.kr

PB-64

The Complete Chloroplast Genome of *Pennisetum glaucum* L. Using Illumina Sequencing

Sebastin Raveendar*, Jung-Ro Lee, Kyung Jun Lee, Myoung-Jae Shin, Yang-Hee Cho, Kyung-Ho Ma, Gi-An Lee

National Agrobiodiversity Center, NAS, RDA, Jeonju 54874, Korea

The complete chloroplast genome sequence of Pearl millet (*Pennisetum glaucum* [L.] R. Br.), an important grain and forage crop in the family Poaceae, is first reported in this study. The complete cp genome sequence of *P. glaucum* is 138,172 bp in length with 38.6% overall GC content and exhibits a typical quadripartite structure comprising one pair of inverted repeats (22, 275 bp) separated by a small single-copy region (12,409 bp) and a large single-copy region (81,213). The *P. glaucum* 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. Nine genes contain one or two introns. Pair-wise alignments of cp genome were performed for genome-wide comparison. This newly determined cp genome sequence of *P. glaucum* will provide valuable information for the future breeding programs of valuable cereal crops in the family Poaceae.

Corresponding author: Tel. 063-23-4863, E-mail: ravibteri@rediffmail.com

PB-65

Genetic Diversity and Population Structure of Asian Tomato Accessions Based on SSR Marker

Sebastin Raveendar*, Gi-An Lee, Kyung Jun Lee, Myoung-Jae Shin, Yang-Hee Cho, Kyung-Ho Ma, Jung-Ro Lee

National Agrobiodiversity Center, NAS, RDA, Jeonju 54874, Korea

Tomato (*Solanum lycopersicum* L.) is economically one of the most important and widely grown plants in the family Solanaceae. Understanding the genetic diversity of conserved accessions is vital for additional collection of tomato germplasm. The present study was performed to determine the genetic diversity and population structure of 375 tomato including cherry tomato accessions from Asia using 25 SSR markers. 199 alleles were detected at an average of seven alleles per SSR locus. The average major allele frequency and polymorphic information content (PIC) were 0.78 and 0.27, respectively. Model-based structure analysis revealed the presence of two suppopulations (Pop-1; 195 accessions, Pop-2; 98 accessions) including admixtures (82 accessions), which was consistent with clustering based on the genetic distance. The results of this study provide effective information for future germplasm conservation and improvement programs in tomato.

Corresponding author: Tel. 063-23-4863, E-mail: ravibteri@rediffmail.com

PB-66

Flavonol and Glycoalkaoid Contents in Tomato Leaves and Their Antioxidant Activites

Kyung Jun Lee*, Gi-An Lee, Jong-Ro Lee, Sebastin Raveendar, Myoung-Jae Shin, Yang-Hee Cho, Kyung-Ho Ma*

National Agrobiodiversity Center, NAS, RDA, Jeonju 54874, Korea

Recently, the leaves of tomato plant that contained several active compounds including alkaloids, steroids and flavonols have been studied for the treatment of variety of diseases and as anti-cancer, antioxidant and anti-gout. In this study, in order to evaluate the usability of tomato leaves, the content of flavonols and glycoalkaloids and antioxidant activities were investigated in 50 tomato leaves. Among flavonols and glycoalkaloids of tomato leaves, naringenin and tomatine were the highest concentrations (429.7 ± 410.3 mg/100g; 925.6 ± 483.1 mg/100g, respectively). DPPH, ABTS, TPC, and NO assay were ranged from 10.3 to 39.5 (%), 21.3 to 59.7 (%), 16.8 to 59.9 mgGAE/g, and 24.8 to 71.5 (IC50), respectively. Using relative antioxidant capacity index (RACI), IT189949 exhibited the highest antioxidant activity. These results will expand the chemical constitution database and provide information on tomato leaves and could be valuable for the development of functional foods or feed-additives.

Corresponding author: Tel. 063-23-4861, E-mail: lkj5214@korea.kr

PB-67

A Comparative Study on Antioxidant Activities of Leaves Extracts Between Adzuki Bean and Soybean

Kyung Jun Lee*, Gi-An Lee, Jong-Ro Lee, Myoung-Jae Shin, Sebastin Raveendar, Yang-Hee Cho, Kyung-Ho Ma

National Agrobiodiversity Center, NAS, RDA, Jeonju 54874, Korea

Leaves of adzuki bean (AL) and soybean (SL) have used as a source of traditional foods in some Korean locations. In this study, in order to evaluate the usability of their leaves, antioxidant activities were investigated using DPPH, ABTS, ferric-reducing antioxidant power (FRAP), Reducing Power (RP), and total phenolic content (TPC). TPC in AL and SL showed wide variations, ranging from 38.1 to 134.4 and 10.9 to 109.6 mgGAE/g, respectively. DPPH, ABTS, FRAP, and RP in AL were ranged from 13.2 to 86.5 (IC50), 18.7 to 24.7 mgASC/g, 35.6 to 134.4 mgASC/g, and 12.2 to 30.5 mgASC/g, respectively, whereas DPPH, ABTS, FRAP, and RP in SL showed 12.0 to 25.0 (IC50), 8.7 to 26.5 mgASC/g, 126.5 to 544.0 mgASC/g and 48.9 to 167.8 mgASC/g, respectively. Among five antioxidant assay, DPPH (AL, 25.6 ± 17.1 IC50; SL, 13.8 ± 2.2 IC50), FRAP (AL, 88.0 ± 28.4 mgASC/g; SL, 285.1 ± 97.3 mgASC/g), TPC (AL, 101.4 ± 31.0 mgGAE/g; SL 60.1 ± 30.0 mgGAE/g), and RP (AL, 18.4 ± 3.2 mgASC/g; SL, 102.6 ± 26.5 mgASC/g) showed significant difference between the AL and SL. These results will expand the database for antioxidant activity and provide information on leaves of adzuki bean and soybean which are valuable for development of functional foods and feed-additives resources.

Corresponding author: Tel. 063-238-4861, E-mail: lkj5214@kroea.kr

PB-68

중만생 복합저항성 양식미 신품종 '효원 6호'

임다은[1], 왕헝[1], 이아림[1], 장성규[1], 박소연[1], 송수향[1], 권순욱[1,2*]

[1]경상남도 밀양시 삼랑진읍 삼랑진로 1268-50 부산대학교 식물생명과학과
[2]경상남도 밀양시 삼랑진읍 삼랑진로 1268-50 부산대학교 생명산업융합연구원

최근 쌀 품종은 수량성 증대는 물론이고 밥맛이 좋은 고품질 벼 품종 개발이 소비자로부터 요구되고 있으며, 각종 병해충에 강한 복합저항성 품종의 개발이 요구되고 있다. 본 연구는 이러한 요구를 충족하는 품종 육성을 위해 수행되었으며, 2004년 복합저항성을 보이는 '화영벼'와 밥맛이 우수한 'Koshihikari'를 인공교배하여 2005년 F_2 개체를 확보하였고, 2006년부터 2012년까지 매년 포장에서 계통재배하면서 종자 및 쌀의 외관 특성이 우수하고, 재배안전성이 우수한 계통(JS14- 12-36-8-5-3-1-1-1)을 선발, 고정하였다. 선발된 계통을 HY103호로 계통명을 부여하고, 2013년, 2014년에 난괴법 3반복으로 생산력검정을 수행한 결과, 품종의 균일성과 재배안정성을 확인하여 '효원 6호'로 명명하였다. '효원 6호'는 수원지역에서 8월 22일경에 출수하는 중만생종으로 간장이 85.7cm, 주당 이삭수가 14.5개 수준이었다. 현미 천립중 21.4g 정도의 중소립종이며, 장폭비는 1.69의 단원형이다. 현미의 단백질함량과 아밀로스 함량은 각각 6.7%, 17.7% 수준이며, 목도열병, 흰잎마름병 및 줄무늬잎마름병에 중정도의 저항성을 보였으며, 멸구에 대한 저항성은 없었다. 10a 당 쌀 수량은 538kg으로 화영벼의 104% 수준이다.

Corresponding author: Tel. 055-350-5506, E-mail: swkwon@pusan.ac.kr

PB-69

일경일화 향기나는 한국 춘란 신품종 '아리향'

김동용[1*], 박소연[2], 김용철[2], 권순욱[2]

[1]전라북도 군산시 대야면 회미로 1044 새만금생명공학센터
[2]경상남도 밀양시 삼랑진읍 삼랑진로 1268-50 부산대학교 식물생명과학과

형태적으로 소형 심비디움에 속하는 춘란(Cymbidium goeringii)은 잎이 작고 내한성이 강하여 심비디움류 중에서 가장 북쪽까지 분포되어 있는 종으로서 국내에서도 강원, 전북, 충남, 경남 등 비교적 넓은 지역에 분포하고 있다. 한국 춘란은 일경일화성의 개화습성을 가지고 있으며, 3~4월에 황록색을 꽃을 피우고, 반음지성 식물로서 향기는 거의 없는 것으로 알려져 있다. 최근 중국 등 주요 난 소비자들은 덩치가 큰 양란 심비디움 및 대형종 동양란을 기피하고, 향기가 있는 중소형 춘란을 선호하고 있으나, 이에 부합하는 육종 연구가 미흡하며 여전히 자연돌연변이 개체들이 재배되고 있는 실정이다. 새만금생명공학센터에서는 수입되는 동양란을 대체하고, 경쟁력 있는 한국 춘란 품종을 육성하고자 본 연구를 수행하였다. 2001년 중국 춘란 '대부귀'와 원판화이며 무늬가 없는 한국 춘란 수집종(Acc. No. SC-005)을 인공교배 하여 기내 배양하였으며, 2009년 재배시험을 통해 형질 고정을 확인하고, 2009년 라이좀 증식을 통해 이듬해 포장 재배를 통해 형질변형이 없음을 확인하였다. 한국 춘란 신품종 '아리향'은 잎에 무늬와 광택이 없고, 약간 비틀림이 있으며, 길이가 약 19cm의 소형종이다. 꽃은 봉심에 투구가 있는 원판 투구화로서, 일경일화이며, 약한 옥색으로 청향을 갖는다.

Corresponding author: Tel. 0502-504-5724, E-mail: kdy5724@naver.com

PB-70

식용 자색고구마 신품종 '단자미'

이형운[1*], 이준설[1], 정미남[2], 양정욱[1], 남상식[1], 한선경[1], 김재명[1], 안승현[2], 송연상[1], 황엄지[1], 이경보[1]

[1]전남 무안군 무안로 199 국립식량과학원 바이오에너지작물연구소
[2]전북 완주군 이서면 혁신로 181 국립식량과학원 기획조정과

자색고구마는 안토시아닌 색소를 다량 함유하고 있어 항산화 및 항암 작용이 뛰어나고, 심혈관계 질환 등 예방에 효과가 있는 건강기능성 식품이다. 또한 자색고구마는 식품 제조용 분말, 음료, 와인, 제과, 잼, 칩 등 식품 가공산업에 널리 이용되고 있어 6차 산업화 식품소재로의 이용가치가 매우 높다. 기존 자색고구마 품종은 식미가 떨어져 주로 가공용으로 이용되고 있어 용도 다양화를 위해 당도가 높고 식미가 우수한 자색고구마 품종 개발이 필요하다. 고구마 신품종 '단자미'는 농촌진흥청 국립식량과학원 바이오에너지작물연구소에서 식미가 우수한 자색고구마 계통을 육성하기 위하여 2007년도에 괴근 육색이 담자색이고 식미가 양호한 '연자미(IT258826)' 품종을 모본으로 하고 괴근 육색이 농황색이며 식미가 우수한 '연황미(IT258821)' 품종을 부본으로 하여 교배하였다. 2008년에 실생개체선발시험에서 825개체를 시험하여 괴근의 모양, 육색 및 비대가 양호한 43계통을 선발하였다. 2009~2010년의 계통선발시험, 2011~2012년의 생산력검정시험, 2013~2015년의 지역적응시험을 수행하여 식미가 우수하고 수량성과 지역적응성이 양호한 'MI2007-34-03' 계통을 최종 선발하여 '단자미(Danjami)'로 명명하였다. '단자미'의 괴근 껍질색은 자색, 육색은 담자색이며, 괴근 모양은 방추형이다. '단자미'의 안토시아닌 색소 함량은 대비품종인 '신자미'의 41% 수준이며, 총폴리페놀 함량과 항산화활성(DPPH 라디컬 소거능)은 각각 2.49 CAE g/100g dw와 76%로 대비품종보다 약간 높았으나 통계적인 유의차는 없었다. '단자미'의 생고구마 총유리당 함량과 찐고구마 당도는 각각 9.4g/100g dw와 31.3Brix°로 대비품종 대비 5.6%, 21% 높다. '단자미'의 덩굴쪼김병 저항성은 중정도이며, 고구마뿌리혹선충 저항성은 강이다. '단자미'의 보통기재배 상품괴근수량은 21.5MT/ha으로 대비품종의 79% 수준이며, 주당상품괴근수는 2.8개, 상품괴근평균중은 136g/개이다. '단자미'는 당도가 높고 식미가 우수하여 자색고구마의 용도 다양화 및 고당도 자색고구마를 이용한 건강기능성 가공제품 개발 활성화에 기여할 것으로 기대된다.

Corresponding author: Tel. 061-450-0141, E-mail: leehu79@korea.kr

PB-71

Digital Phenotyping of *crepiastrumdenticulum* Revealed Phenotypic Variation Among Natural Populations

Sungyul Chang, Unseok Lee, HyoungSeok Kim*

Natural Products Research Center, Korea Institute of Science and Technology (KIST), 679 Saimdang-ro, Gangneung, Gangwon-do 210-340, Korea

A medicinal plant, *Crepidiastrumdenticulum*, has inhabitant ranges including Korea, China, and Japan and many other East Asia countries. In Korea, *C. denticulum* utilized as herbal medicine because it is known for health promoting effects such as protecting oxidative stress in a liver. Chemical compounds were extracted and analyzed for the human health but genetic research on this species were lacking. For that reasons, there were a little researches were undertaken to understand pathways of chemicals for benefit to human. Digital phenotyping were emerging as new tools to study general physiology of a plant or traits of researchers interests. Therefore, We proposed utilizing digital phenotyping as other dimension for the plant research where other omics tools were lacking. Populations of *Crepidiastrumdenticulum* were planted and acquired digital images period around 50 days and 7 times in a day. It revealed general growth habit within in a population. Furthermore, it hinted the possibilities to separated phenotypes among populations by chemical composition within populations. It could apply the other research areas if other omics approached were hard to access or lacking.

Corresponding author: Tel. 033-650-3660, E-mail: hkim58@kist.re.kr

PB-72

Improving The Grain Quality of High Tryptophan Rice

Franz Marielle Nogoy[1], Hye-Jung Lee[1,2], Marjohn Nino[1], Me-Sun Kim[1], Sothea Ouk[1], Yu-Jin Jung[3], Kwon-Kyoo Kang[3], Illsup Nou[4], Yong-Gu Cho[1*]

[1]Department of Crop Science, Chungbuk National University, Cheongju 28644, Korea
[2]Current Address, Korea Seed & Variety Service, Kimchon 39660, Korea
[3]Department of Horticulture, Hankyong National University, Ansung 17579, Korea
[4]Department of Horticulture, Sunchon National University, Sunchon 57922, Korea

Fortification with vitamins in rice is a feasible solution to directly reach consumers who suffer nutritional problems. In order to improve the nutritional quality of rice, identification and characterization of suitable mutants associated with the metabolism or catabolism of essential amino acids is needed. In this study, we explore on tryptophan, a limiting amino acid in almost all protein sources and is very important because it is converted in our brains as a neurotransmitter serotonin. To consume high amount of tryptophan, it must be taken with good source of carbohydrates like rice. In our study, we have high tryptophan rice lines containing base mutation in one of the precursor enzymes of tryptophan biosynthesis, anthranilate synthase α -2 (ASA2) resulting to 20~25 fold higher tryptophan level in mature seeds than its wild type, Donganbyeo. However, the grain quality of these high tryptophan rice lines is very low. We try to improve their eating quality by crossing them to popular Korean varieties, Hopumbyeo and Samgwangbyeo. Insensitive lines for tryptophan feedback inhibition are screened by growing in medium containing amino acid analogues, 5-methyl tryptophan (5MT). *In vitro* screening of each progenies enables us to select in each generation the rice lines with tolerance to 5MT. After a series of *in vitro* screening and phenotypic selection in the field, the F4 progeny containing the same mutation in ASA2 gene from its parent showed an improvement in their grain quality.

Acknowledgements: This research was supported by iPET, Ministry for Food, Agriculture, Forestry and Fisheries, Republic of Korea.

Corresponding author: E-mail: ygcho@cbnu.ac.kr

PB-73

Classification of Korean Rice Varieties for Varietal Characteristics Using Morphological Description

Me-Sun Kim[1], Hye-Jung Lee[1,2], Dal-A Yu[1], Joonki Kim[1], Marjohn Nino[1], Franz Nogoy[1], Sothea Ouk[1], Eun-Ju Jeong[1], Jae-Young Song[1], Kwon-Kyoo Kang[3], Yong-Gu Cho[1*]

[1]Department of Crop Science, Chungbuk National University, Cheongju 28644, Korea
[2]Current Address, Korea Seed & Variety Service, Kimchon 39660, Korea
[3]Department of Horticulture, Hankyong National University, Ansung 17579, Korea

The International Union for the Protection of New Varieties of Plants (UPOV) promotes an effective system of plant variety protection and encourages the development of new varieties of plants. International convention was initiated to standardized the system efforts and strengthen the policy. The establishment of cultivar discrimination system is very important to distinguish varieties between domestic and foreign agricultural products. It is necessary for the protection of breeders' rights. In addition, it will help for more efficient and quality management of plant breeding. This study was conducted to establish a database for rice identification using morphological characters which include number of tillers and panicle per plant, spikelets per panicle, yield, plant maturity, height, leaf pigments, flag leaf angles, and rice bran. The whole rice population was grouped into three based on leaf angles, majority members of which retained the flag leaf angle-character until maturity stage. Most rice accessions did not exhibit anthocyanin pigments on the leaves particularly on the first leaf, leaf blade, leaf sheath and auricle, except for varieties classified as black rice. In the case of grain, many accessions produced secondary branching, and showed no awn. For agronomic traits, productive tiller and panicle per plant were higher in early flowering varieties, while spikelets per panicle and ripened grain were higher in late flowering varieties, and yield was higher in medium flowering varieties. All data were then pooled for cluster analysis which revealed three major independent clusters and four minor clusters.

Acknowledgements: This research was supported by iPET, Ministry for Food, Agriculture, Forestry and Fisheries, Republic of Korea.

Corresponding author: E-mail: ygcho@cbnu.ac.kr

PB-74

Modification of Starch Composition by Regulation of SSS1 Gene Using RNAi and Antisense Technology in Rice

Moo-Geun Jee[1], Hye-Jung Lee[1,2], Dal-A Yu[1], Me-Sun Kim[1], Marjohn Niño[1], Franz Nogoy[1], Kwon-Kyoo Kang[3], Illsup Nou[4], Yong-Gu Cho[1*]

[1]Department of Crop Science, Chungbuk National University, Cheongju 28644, Korea
[2]Current Address, Korea Seed & Variety Service, Kimchon 39660, Korea
[3]Department of Horticulture, Hankyong National University, Ansung 17579, Korea
[4]Department of Horticulture, Sunchon National University, Sunchon 57922, Korea

An increasing preference for good eating quality of rice among consumers has become one of the important considerations in rice breeding. Amylose content is a leading factor affecting eating quality of rice. Amylose composition is determined by the relative activity of soluble starch synthase (SSS) and granule-bound starch synthase (GBSS). This study focused on modifying the expression of SSSI gene which is responsible for amylopectin and amylose synthesis in rice by using RNA interference (RNAi) and antisense technology. The transgenic rice plants showed various amylose content in rice grains. Favorable rice lines were selected according to genomic PCR, transgene expression and amylose contents analysis. A semi-quantitative RT-PCR was carried out to determine the expression level of SSSI gene after flowering of transgenic rice and wild type. Down-regulation of SSSI gene in transgenic plants was evident in the decreasing expression in rice grains. Accordingly, scanning electron microscopy (SEM) analysis revealed uniform size with smooth curves starch granules in down-regulation rice lines, in contrast with the non-uniform granules in wild type. Results indicated that RNAi-SSSI and antisense-SSSI transgenic lines produced low amylose contents from 10 to 16% that fell between glutinous and non-glutinous rice. This study showed that down-regulation of endogenous SSSI may improve the eating quality in rice.

Acknowledgements: This work was supported by a grant from the Next-Generation BioGreen 21 Program, RDA and iPET, Ministry for Food, Agriculture, Forestry and Fisheries, Republic of Korea.

Corresponding author: E-mail: ygcho@cbnu.ac.kr

PB-75

Development and Characterization of Endophyte Free Tall Fescue New Variety

Ki-Won Lee*, Md. Atikur Rahman, Sang-Hoon Lee, Ki-Yong Kim, Hee Chung Ji, Tae Young Hwang, Gi Jun Choi

Grassland and Forages Division, National Institute of Animal Science, RDA, Cheonan, Korea

Korea's grassland area was 417,000 ha in the 1970s, and intensive grassland area formation was initiated, but it stands at 35,763 ha as of 2014, and the area is decreasing gradually. A new tall fescue variety (*Festuca arundinacea* Schreb.), named Greenmaster3ho, was developed by the National Institute of Animal Science, Rural Development Administration in Korea from 2010 to 2014. For synthetic seed production of this new variety, five superior clones, 09XFa02, 09XFa03, 09XFa11, 09XFa13, and 09XFa14 were selected and polycrossed. The agronomic growth characteristics and forage production capability of the seeds were studied at Cheonan from 2010, and regional trials were conducted in Cheonan, Hoengseong, Jeju, and Jinju from 2012 to 2014. Greenmaster3ho showed enhanced disease resistance, persistence, and regrowth ability as compared to Fawn. The dry matter yield of Greenmaster 2 was 29% higher (15,119 kg/ha) than that of Fawn. However, the nutritive value of both varieties was similar. This study developed a new tall fescue variety with excellent environmental adaptability, aiming to make a contribution to the vitalization of the Korean grassland industry

Corresponding author: Tel. 041-580-6757, E-mail: kiwon@korea.kr

PB-76

고추 핵심집단의 원예적 특성평가 및 DB구축

양현천[1], 김상규[1], 고호철[1], Binod P. Luitel[1], 성정숙[1], 이주희[1], 윤문섭[1], 백형진[1], 류경열[1], 이준구[2], 허온숙[1*]

[1]전북 전주시 완산구 농생명로 370 농촌진흥청 농업유전자원센터
[2]전북 전주시 덕진구 백제대로 567 전북대학교 원예학과

농업유전자원센터에서 보유중인 3,700여 고추 자원 중에서 유전적 다형성을 보인 253자원을 핵심집단으로 선발하여 원예적 특성 평가를 실시하고 그 결과를 데이터베이스화 하였다. 253자원의 종 분포를 살펴보면, *C. annuum, C. baccatum, C. chinense, C. frutescens, C. chacoense, C. eximium* 이 각각 178점, 20점, 28점, 24점, 1점, 2점이 포함되어 있다. 2015년도에 IT103410 등 253자원을 농업유전자원센터 비닐하우스에 공시하여 개화소요일수, 화색, 과중, 과색 등 30여 항목을 고추 유전자원 특성조사 및 관리요령에 따라 조사하였고 화기, 식물체, 과실의 이미지 정보를 구축하였다. 개화소요일수는 자원에 따라 51-65일, 66-80일, 81-95일 96-110일인 것이 각각 45자원, 115자원, 101자원, 37자원 이었으며 126일인 것도 1자원 확인되었다. 화색은 백색, 연녹색, 백색에 황색밴드, 백색에 자색, 자색의 5종으로 구분하여 조사하였으나, 자색의 경우 색의 강도가 다양하였으며, 백색에 자색인 꽃의 경우 테두리만 자색인 경우와 꽃 내부 또는 외부가 자색인 경우 등 여러 형태가 존재하여 화색 코드를 더욱 다양하게 설정할 필요가 있음이 확인되었다. 과중(g) 분포를 살펴본 결과 *C. annuum* 종을 제외한 다른 종들의 과실무게는 10g 미만인 자원이 약 50%를 차지하며, 과중이 많이 나가는 자원은 파프리카와 유사한 형태의 자원이었다. 미숙과는 녹색이 가장 많이 관찰되었으며, *C. annuum*의 경우 녹색, 연녹, 백색의 순의 분포를 보이며 *C. baccatum*도 같은 경향이었다. 숙과색은 적색이 가장 많이 관찰된 반면, *C. chinense*에서는 갈색, 자색 등 다양한 색을 나타내었다. 평가된 자원들의 특성은 농업유전자원정보 통합관리시스템에 DB로서 구축하여 활용할 수 있게 하였다.

Corresponding author: Tel. 063-238-4942, E-mail: oshur09@korea.kr

PC-01

Development of Antigen-antibody Fusion Protein Expression System Using Chinese Cabbage

Jinhee Kim*, Eun Su Lee, Hye-Eun Lee, Yul-Kyun Ahn, Jeong Ho Kim, Jongpil Hong

Vegetable Research Division, National Institute of Horticultural and Herbal Science, RDA, 100, Nongsaengmyeong-ro, Iseo-myeon, Wanju-gun, Jeollabuk-do, Korea

The edible vaccine derived from crop is easy to achieve safety, and its price is cheap because of the mass production by agriculture system. To acquire edible vaccine fusion protein for colorectal cancer which is a serious disease in worldwide, we used various form of immunoglobulin Fc (IgM, IgG and IgA) and J chain. The J chain is expected to induce a fusion protein complex when co-expressed with other immunoglobulins. Chinese cabbage was selected to develop edible vaccine due to the high protein expression rate. The agrobacterium transformation method was used to express each proteins in the Chinese cabbage. The T_0 transformants were acquired successfully. The four transgene (J-chain, EpCAM-IgM, EpCAM-IgG and EpCAM-IgA) and hygromycin selection marker was confirmed by PCR using gene specific primers. EpCAM-IgM, EpCAM-IgG, EpCAM-IgA and J chain were confirmed. The transformation efficiency was approximately 3 %. The crude proteins from T_0 plants were extracted and the over-expressed proteins were detected by immunoblot assay. The over-expression of EpCAM-IgM was confirmed. We are expecting to acquire vaccine fusion protein complex by crossing T_1 plants expressing J-chain and immunoglobulin protein each. The plants generated by this procedure will provide an efficient edible vaccine to prevent cancer disease in the near future.

Corresponding author: Tel. 063-238-6672, Fax. 063-238-6605, E-mail: sayzinni@korea.kr

PC-02

Comparative Analysis of Complete Chloroplast Genome Sequence of *Cynanchum wilfordii* and *Cynanchum auriculatum*

Inkyu Park, Wook-Jin Kim, Sang-Min Yeo, Yong-Min Kang, Byeong-Cheol Moon*

K-herb Research Center, Korea Institute of Oriental Medicine, Daejeon 305-811, Korea

The root of *Cynanchum wilfordii,* Cynanchi Wilfordii Radix (named'Baekshuo'in Korean), is one of the most important herbaceous medicinal ingredient and has great economic value in Korea. However, the root of *C. auriculatum* has been distributed as an adulterant of *C. wilfordii* on the Korean market due to morphological similarities. In this study, we determined complete chloroplast genome (cpDNA) sequences of two *Cynanchum* species based on the Illumina sequencing platform. The cpDNA sequences of *C. wilfordii* and *C. auriculatum* was 161,184 and 160,840 bp in length, respectively. Both cpDNA was composed 114 unique functional genes, 80 protein coding gene, 4 rRNA gene, and 30 tRNA genes. We obtained SSRs of 448, 497 and tandem repeats of 24, 25 in *C. wilfordii* and *C. auriculatum,* respectively. Among these, we identified five highly variable regions enough to distinguish two species, four IGS (*trnH-GUG* -*psbA*, *trnQ-UUG* - *psbK*, *rps2* - *rpoC2*, *trnN-GUU* - *ycf1*) and one genic region (*accD*). These results suggest that the sequence variabilities of cpDNA could provide the useful genetic information for the development of molecular discrimination marker to identify Cynanchi Wilfordii Radix from the root of *C. auriculatum*.

Corresponding author: Tel. 042-868-9530, E-mail: bcmoon@kiom.re.kr

PC-03

Development of Transposon Based Molecular Markers Useful for Construction of Linkage Map and Identification QTL Related to Agronomic Traits in Maize

Rahul Vasudeo Ramekar[1], Kyong-Cheul Park[2], Kyu Jin Sa[1], Nam-il Park[3], Ju Kyong Lee[1*]

[1]Department of Applied Plant Sciences, College of Agriculture and Life Sciences, Kangwon National University, Chuncheon, 200-701, Korea
[2]Department of Agricultural Life Science, Kangwon National University, Chuncheon 200-701, Korea
[3]Department of Plant Science, Gangneung-Wonju National University, Gangneung-si 210-702, Korea

Transposable elements (TEs) are DNA sequences that move around in the genome, generating variations in plants and animals. Transposons are categorized into two classes according to the mechanism underlying their transposition; RNA intermediate class 1 and DNA intermediate class 2. Transposable elements contribute ~ 85% of the maize genome. Majority of maize genes are located within 1 kb of an annotated transposon. Particularly, class 2 DNA elements were found more often in genic regions than class 1. Mutator element belongs to class 2 transposon. It has transposition frequency of 10-3 to 10-5 per gene per generation. They are able to jump in promoter, exon, intron, 5' leader region and 3' untranslated region affecting target gene expression patterns. Also they are capable of reshuffling the host genome by capturing gene fragments, making it a perfect candidate for utilizing it as a genetic marker. In maize, typical characteristics of Mutator family includes a conserved 50-200bp terminal inverted repeat (TIR) which is associated with Transposition activity of the elements. This research was carried out in order to develop Mutator based transposon markers, designed on conserved TIR region of Mutator element. We used Transposon insertion display technique (modified version of AFLP) allowing detection of Mutator elements in maize lines. The common basis of this method is an adaptor-mediated multiplex PCR amplification of genomic restriction fragments that, contains a transposon markers sequence with the variable length of DNA sequences flanking the insertion sites. Further this newly developed transposon markers were used for constructing a linkage map and to identify QTLs related to agronomic traits in maize.

Corresponding author: Tel. 033-250-6415, E-mail: jukyonglee@kangwon.ac.kr

PC-04

The Draft Complete Mitochondria Genome Sequence of Wild Potato Relatives, *Solanum commersonii*

Kwang-Soo Cho*, Ji-Hong Cho, Ju-Seong Im, Hong-Sik Won, Yong-Ik Jin, Su-Young Hong, Hong-Seob Yoo

Highland Agriculture Research Institute, National Institute of Crop Science, Rural Development Administration, Pyeongchang 5481, Korea

Solanum commersonii Dunal is a well-known wild potato belonging to Solanaceae family and commonly used as materials for somatic hybridization due to various biotic and abiotic stress resistance. The complete miochondria genome of *S. commersonii* was performed by *de novo* assembly using a small amount of whole genome sequencing data by NGS. The mitochondria genome of *S. commersonii* was 464,535 bp in length. The mean coverage of sequencing was 401x. A total of 113 genes were annotated including 79 protein-coding genes, 30 tRNA genes and 4 rRNA genes. We also sequenced on mitochondria genome of cultivated potato, *S. tuberosum*, cv, Superior, and conducted comparative analysis. Sequence alignment revealed 3 InDel region between *S. commersonii* and *S. tuberosum* in their mitochondria genomes, allowing InDel markers to be developed. The markers could distinguish the two species and we could use these InDel markers to mitochondria genotyping in somatic hybrids and their progenies. The results obtained in this study can be applied to select proper mitochondiral genotypes in potato breeding program, especially somatic hybrids with wild relative species, *S. commersonii*.

Acknowledgements: This work was supported by Korea Institute of Planning and Evaluation for Technology inFood, Agriculture, Forestry and Fisheries(IPET) through Golden Seed Project funded by Ministry of Agriculture, Food and Rural Affairs (MAFRA) (No.213001-04-4-SB530), Republic of Korea.

Corresponding author: Tel. 033-330-1650, E-mail: kscholove@korea.kr

PC-05

AtSIZ1 Positively Controls DNA Methyltransferase CMT3 Activity by its Sumoylation in *Arabidopsis*

Sung-Il Kim[1], Jun Soo Kwak[1], Joo Yong Kim[1], Hak Soo Seo[1,2*]

[1]Department of Plant Science, Research Institute for Agriculture and Life Sciences, and Plant Genomics and Breeding Institute, Seoul National University, Seoul 151-921, Korea
[2]Bio-MAX Institute, Seoul National University, Seoul 151-818, Korea

The activities and stability of mammalian DNA and histone methyltransferases are regulated by post-translational modifications such as phosphorylation, ubiquitination and sumoylation; however, it is unclear how the activities of these enzymes are regulated at the post-translational level in plants. Here, we show that the DNA methylation activity of *Arabidopsis* CHROMOMETHYLASE 3 (CMT3) is positively regulated by the E3 SUMO ligase AtSIZ1. The methylation level of the *Arabidopsis* genome, including transposons, was significantly decreased in the *siz1-2* mutant than in wild-type plants. E3 ligase activity of AtSIZ1 directly binds CMT3 to sumoylate and the DNA methyltransferase activity of CMT3 was increased by this modification. In addition, the methylation levels of many genes, including the nitrate reductase gene *NIA2*, were decreased in *siz1-2* and *cmt3* plants than in wild-type plants. Furthermore, the CHG methylation activity of CMT3 was detected specifically for *NIA2* and not *NIA1* (the other nitrate reductase gene in *Arabidopsis*), indicating that CMT3 selectively controls the CHG methylation levels of target genes. Taken together, our results indicate that the sumoylation of CMT3 is important for its role in the regulation of gene expression and that AtSIZ1 positively regulates the epigenetic repression of CMT3-mediated gene expression.

Acknowledgements: This research was supported by Basic Science Research Program through the National Research Foundation of Korea (NRF) funded by the Ministry of Education (2015057573).

Corresponding author: E-mail: seohs@snu.ac.kr

PC-06

Gibberellin Controls Plant Growth by Stimulating SLY1 Sumoylation and Activity

Sung-Il Kim[1], Jun Soo Kwak[1], Hak Soo Seo[1,2*]

[1]Department of Plant Science, Research Institute for Agriculture and Life Sciences, and Plant Genomics and Breeding Institute, Seoul National University, Seoul 151-921, Korea
[2]Bio-MAX Institute, Seoul National University, Seoul 151-818, Korea

Gibberellins affect the various processes of plant development including germination, cell division and flowering. Extensive studies have been carried out to address the mechanisms on gibberellin effects on plant growth. However, such studies have been focused to DELLA protein; the regulatory mechanisms controlling SLEEPY1 (SLY1), a protein interacting with DELLA proteins as components of the SCF^{SLY1} complex, at the post-translational level have not been studied. Here, we show that the E3 SUMO ligase AtSIZ1 regulates GA signaling by sumoylating SLY1. SLY1 was less abundant in *siz1-2* than in wild-type, but the DELLA protein RGA was more abundant in *siz1-2* than wild-type. SLY1 also accumulated to a high level in the SUMO protease mutant *esd4*. Transgenic *sly1-13* mutants over-expressing SLY1 were phenotypically similar to wild-type plants; however, *sly1-13* plants over-expressing a mutated mSLY1 protein (K122R, a mutation at the sumoylation site) retained the mutant dwarfing phenotype. Over-expression of SLY1 in *sly1-13* mutants resulted in a return of RGA levels to wild-type levels, but RGA accumulated to high levels in mutants over-expressing mSLY1. RGA was clearly detected in *Arabidopsis* co-expressing AtSIZ1 and mSLY1, but not in plants co-expressing AtSIZ1 and SLY1. In addition, sumoylated SLY1 interacted with RGA and SLY1 sumoylation was significantly increased by GA. Taken together, our results indicate that AtSIZ1 positively controls GA signaling through SLY1 sumoylation

Acknowledgements: This work was supported by a grant from the Next-Generation BioGreen 21 Program (Plant Molecular Breeding Center no. PJ01108701), Rural Development Administration, Republic of Korea.

Corresponding author: E-mail: seohs@snu.ac.kr

PC-07

AtSIZ1 Positively Controls Gibbrellin-mediated Seed Dormancy Break and Germination

Sung-Il Kim[1], Joo Yong Kim[1], Hak Soo Seo[1,2*]

[1]Department of Plant Science, Research Institute for Agriculture and Life Sciences, and Plant Genomics and Breeding Institute, Seoul National University, Seoul 151-921, Korea
[2]Bio-MAX Institute, Seoul National University, Seoul 151-818, Korea

Seed germination is the first development stage in the lifecycle of a plant, which influences subsequent vegetative growth and reproduction. Here, we show that the E3 SUMO ligase AtSIZ1 affect germination. Less than half of the *siz1* mutant seeds were germinated, even after a short period of ripening. However, their germination rates increased to wild-type germination rates after a short period of imbibition at low temperatures or long periods of ripening. In addition, exogenous gibberellin (GA) treatment increases the germination rates of the *siz1* mutants to the wild-type level. In transgenic plants, suppression of *AtSIZ1* gave rise to post-translational degradation of SLEEPY1 (SLY1), a positive regulator of GA signaling, during germination, and inducible *AtSIZ1* overexpression caused increased SLY1 levels. In addition, overexpressing wild-type SLY1 in *sly1* mutants increased their germination rates to wild-type levels, on the other hand, the germination rates of mSLY1 overexpressing *sly1* mutants was similar to that of *sly1*. The *siz1* mutant seeds in immature developing siliques were much lower germination rates than those of the wild type. Moreover, in the *siz1* mutants, *SLY1* and *DELAY OF GERMINATION 1* (*DOG1*) transcript levels were lower than those of the wild type, while the *DELLA* and *ABSCISIC ACID INSENSITIVE 3* (*ABI3*) transcript levels were higher than those of the wild type. Overall, these results indicate that the reduced germination rates of the *siz1* mutants is caused by impaired GA signaling owing to low SLY1 levels and activity, as well as lower dormancy attributable to high expression levels of dormancy-related genes including *DOG1*

Acknowledgements: This work was supported by a grant from the Next-Generation BioGreen 21 Program (Plant Molecular Breeding Center) (Grant number PJ01108701), Rural Development Administration, Republic of Korea.

Corresponding author: E-mail: seohs@snu.ac.kr

PC-08

Identification of Two Novel Mutant *ANS* Alleles Responsible for Inactivation of Anthocyanidin Synthase and Failure of Anthocyanin Production in Onion (*Allium cepa* L.)

Eun-Young Kim[1], Cheol-Woo Kim[2], Min-Seon Choi[2], Sunggil Kim[1*]

[1]Department of Plant Biotechnology, Biotechnology Research Institute, Chonnam National University, Gwangju 500-757, Korea
[2]National Institute of Horticultural & Herbal Science, RDA, Muan, 534-833, Korea

Two genes (*DFR-A* and *ANS*) encoding dihydroflavonol 4-reducatase (DFR) and anthocyanidin synthase (ANS) enzymes in the anthocyanin biosynthesis pathway, respectively, are complementarily involved in anthocyanin production in onion (*Allium cepa* L.). Eleven inactive *DFR-A* alleles have been reported, with only a single inactive *ANS* allele previously identified. Two additional inactive *ANS* alleles are reported in this study. A mutant *ANS* allele containing a 4-bp insertion at the end of exon1 was identified from yellow bulbs of the F_2 population in which the *DFR-A* genotype was homozygous for an active allele. The 4-bp insertion caused a frame-shift mutation and resulted in creation of a premature stop codon at the start of exon2. This mutant *ANS* allele was designated ANS^{PS} allele. RT-PCR results showed that transcripts of the ANS^{PS} allele were almost undetectable in yellow F_2 bulbs, implying the involvement of nonsense-mediated mRNA decay. A cleaved amplified polymorphic sequence (CAPS) marker was developed for detection of the ANS^{PS} allele. Another inactive *ANS* allele was identified from the light-red F_1 populations showing complementation between *DFR-A* and *ANS* genes. A critical amino acid change of the strictly conserved serine residue into leucine was found in this mutant allele designated ANS^{S188L}. In addition, seven variants of active *ANS* alleles were identified from diverse onion germplasm. A stepwise process consisting of PCR amplification and sequencing of PCR products was devised to identify three inactive (ANS^{PS}, ANS^{S188L}, and ANS^{G229R}), one leaky (ANS^{P}), and two active *ANS* alleles (ANS^{L} and ANS^{h1}).

Corresponding author: Tel. 062-530-2061, E-mail: dronion@jnu.ac.kr

PC-09

Characterization of rDNAs and Telomeric Repeats Distribution in a Tetraploid *Chrysanthemum zawadskii*

Abigail Rubiato Cuyacot[1], Franklin Hinosa Mancia[1], Yoon-Ha Ju[1], Ki-Byung Lim[2], Yoon-Jung Hwang[1,3*]

[1]Department of Convergence Science, Sahmyook University, Seoul 139-742, Korea
[2]Department of Horticultural Science, Kyungpook National University, Daegu 702-701, Korea
[3]Department of Life Science, Sahmyook University, Seoul 139-742, Korea

Karyotypic and cytogenetic characteristics of *Chrysanthemum zawadskii* Herbich ssp. *lucidum* (NAK.) Y. Lee, a *Chrysanthemum* species located from Ulleung Island, South Korea was studied to have an insight of its basic genetic and genomic characteristics and to contribute in the karyo-systematic study of the genus *Chrysanthemum* that belongs to the tribe Anthemideae. In this study, fluorescence *in situ* hybridization (FISH) analysis was employed to characterize the ploidy level, chromosome constitution, and distribution of 5S and 45S ribosomal DNAs (rDNA) as well as the *Arabidopsis*-type telomere repeats $(TTTAGGG)_n$ in *C. zawadskii* Herbich ssp. *lucidum* (NAK.) Y. Lee chromosomes. The somatic metaphase chromosome numbers of *C. zawadskii* Herbich ssp. *lucidum* (NAK.) Y. Lee were observed to be tetraploid (2n=4x=36). Four (4) loci of 5S rDNA signals were observed in the middle of the long arms and eight (8) loci of 45S rDNA signals were located at the termini of the short arms of the chromosomes. The localization pattern of rDNAs in this study was observed on separate chromosomes. However, the *Arabidopsis*-type telomeric repeats were found to co-localize with 45S rDNA sites, which detected at the ends of both chromosome arms. The co-localization of telomeric sequences and 45S rDNA were also observed in other *Chrysanthemum* species with various ploidy, thus implying the co-localization as its general feature. This study will help towards unravelling the karyotypic trends and role of polyploidy in evolution the genus *Chrysanthemum* and of the tribe Anthemideae.

Acknowledgements: This work was carried out with the support of "Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ01095307)" Rural Development Administration, Republic of Korea.

Corresponding author: Tel. 02-3399-1718, E-mail: hyj@syu.ac.kr

PC-10

Analysis of Differentially Expressed Genes During Root Development of Maize with RNA Sequencing

Jun-Cheol Moon[1*], Sun-Goo Hwang[1], Byung-Moo Lee[2]

[1]Agriculture and Life Sciences Research Institute, Kangwon National University, Chuncheon 24341, Korea
[2]Department of Life Science, Dongguk University-Seoul, Seoul 04620, Korea

For identification of gene regulations during root emergence and formation, we have conducted the RNA-Sequencing analysis with two independent replicated experiments of each sample, which collected from the emergence stage (VE) and two leaf stage (V2) of maize. The raw RNA-seq. data were filtered the redundant reads of row quality and then the filtered data were mapped short reads to a reference genome sequence (*Zea mays* cv. B73). We have harbored numberous surviving reads generated with average mapping rate of 93.7%. To determine specific genes controlling root development, we have compared the mRNA levels of genes in shoot and root tissues on different stage (VE and V2). A total of 1,286 genes, which are composed of 675 up-regulated genes and 611 down-regulated genes, were differentially expressed in each tissue between VE and V2. Also, 52 genes were commonly exhibited the altered gene expression levels, including the 29 up-regulations and 23 down-regulations, in both tissue among different development stages. This result suggests the functional differences of genes involved in plant developmental mechanism of shoot and root.

Acknowledgements: This research was supported by Basic Science Research Program through the National Research Foundation of Korea (NRF) funded by the Ministry of Education (grant no. NRF-2015R1D1A4A01015702), as well as a grant from the Golden Seed Project, Ministry of Agriculture, Food and Rural Affairs (MAFRA), Ministry of Oceans and Fisheries (MOF), Rural Development of Korea (RDA), and the Korea Forest Service (KFS) (project no. 213001-04-4-SB920)

Corresponding author: Tel. 033-250-7214, E-mail: jcmoon73@kangwon.ac.kr

PC-11

The *Inquieta* Gene of Tomato is Involved in Trichome Development

In-Taek Hwang, Na-Rae Jeong, Jin-Ho Kang*

Graduate School of International Agricultural Technology and Crop Biotechnology Institute/GreenBio Science and Technology, Seoul National University, Pyeongchang 25354, Korea

Trichomes are hair-like structures on the aerial surface of many plant species. Trichomes are well characterized for their role as physical and chemical barriers for defense against herbivore attack. Here, we describe the characterization of a monogenic recessive mutant of tomato (*Solanum lycoperisicum*) called *inquieta* (*ini*). All trichome types produced on *ini* plants show distinct morphological defects, including swelling and bending development. Genetic mapping experiments positioned the *Ini* locus within a 1.5 cM interval on chromosome 11. Previous studies with *Arabidopsis thaliana* showed that mutations in genes involved in the formation of the actin cytoskeleton cause swelling and aberrant development of trichomes. So we used the tomato genome sequence and the Arabidopsis genes related to actin cytoskeleton to identify *Ini* candidate genes in the mapping region. One gene was of particular interest because it encodes a protein involved in the actin cytoskeleton formation. Use of this gene as a molecular marker in mapping experiments showed that this gene strictly co-segregates with the target locus in a mapping population of 135 F_2plants.Inaddition,thetrichomemorphologyof*ini* mutant is very similar to that of tomato *hairless* mutant which is susceptible to herbivorous insect attack, suggesting that *Ini* is also involved in insect resistance. The identification of *Ini* can be used to develop solanaceous plants resistant to arthropod herbivores.

Corresponding author: Tel. 033-339-5841, E-mail: kangjinho@sun.ac.kr

PC-12

Application of SNP Markers for Disease Resistance and Capsaicinoid Content in Pepper and Paprika Cultivars Using Fluidigm EP1™ System

Haein Kim, Ye Rin Lee, Kyumi Jeong, Jundae Lee*

Department of Horticulture, Chonbuk National University, Jeonju 54896, Korea

Pepper is one of the most important crops in Korean agricultural industries. However, it has been caused by several pepper diseases, which damage the quality and reduce the production, including *Phytophthora* root rot (*P. capsici*), anthracnose (*Colletotrichum acutatum and C. capsici*), powdery mildew (*Leveillula taurica*), *Tobacco mosaic virus* (TMV), *Tomato spotted wilt virus* (TSWV), *Cucumber mosaic virus* (CMV), and some *Potyvirus*. Therefore, it is getting important to develop pepper varieties which are resistant to these diseases and have high capsaicinoid content. For this reason, it is necessary to develop a high-throughput genotyping system which can analyze a number of samples with multiple SNP markers. In this study, we aimed to genotype 191 pepper samples with 24 SNP markers using Fluidigm 192.24 Dynamic Array, which yields 4,608 data points at one time. We re-designed 24 SNP markers from STS or HRM markers for *Phytophthora* root rot (M3-2, M3-3), anthracnose (CcR9, CA09g12180, CA09g19170), powdery mildew (Ltr4.1-40344, Ltr4.2-585119), CMV (Cmr1-2), TSWV (Tsw1-1, Tsw1-2), TMV (L4), Potyvirus (pvr1, pvr2), and capsaicinoid content (qdhc2.1-1335057, qdhc2.2-43829, qcap3.1-40134, qcap6.1-299931, qcap6.1-299931). Plant materials were a total of 191 samples consisting of 33 pepper cultivars, 23 paprika cultivars, 39 pepper accessions, and one negative control. As the result, 18 SNP markers were successfully analyzed. This approach can be helpful to multiplex many SNP markers for foreground selection in pepper breeding programs.

Corresponding author: Tel. 063-270-2560, E-mail: ajfall@jbnu.ac.kr

PC-13

Analysis of The Genetic and Epigenetic Diversity Among Different Corn Varieties

Neha Roy*, Min-Ji Lim, Sung-Il Lee, Nam Soo Kim

Department of Molecular Bioscience, Kangwon National University, Chuncheon 200-701, Korea

Maize is an important crop species that has been subjected to intensive breeding programs. Understanding the genetic diversity in maize is thus vital for crop improvement and breeding studies. Current study performed four different multi-allele detecting marker systems, amplified fragment length polymorphism (AFLP), sequence specific amplified polymorphism (SSAP), methylation sensitive amplified polymorphism (MSAP) and transposon element methylation display (TD-MSAP) to analyze genetic and epigenetic variation and diversity among dent, waxy, and sweet corns. The (epi) genetic diversity, (epi) genetic distance, gene flow, genetic frequency, cluster analysis, PCoA and AMOVA analysis were calculated. Cultivar differentiation is well established in maize and the results suggest that not only genetic but also epigenetic variations are responsible for the differentiations obtained in maize. Estimates of genetic relationship were significantly correlated between AFLP, SSAP and MSAP datasets. The current study is the first report on the systematic comparison of TD-MSAP with other marker systems. The genetic variation detected by TD-MSAP revealed higher than those of AFLP, SSAP, and MSAP but were in discordance with the genetic relationships. These dissimilarities between TD-MSAP and other marker systems can be informative for understanding the genetic relationships between the species
Neha Roy

Corresponding author: Tel. 82-10-3665-2201, E-mail: nehadear2201@gmail.com

PC-14

포도 유전체 육종 근접지원용 웹 데이터베이스 구축

이봉우[1], 이정희[1], 김상미[1], 김지은[1], 조강희[2], 조성환[1*]

[1]대전광역시 유성구 테크노1로 11-3, ㈜씨더스
[2]전라북도 완주군 이서면 농생명로 100, 농촌진흥청 국립원예특작과학원

최근 육성 품종에 대한 보호권 강화에 따라 국내 포도 품종 육성 및 고유의 육종 기술 개발의 필요성이 대두되고 있으며, 유전체 분석 기술을 통하여 분자마커 및 유전체 정보를 이용한 유전체 육종의 중요성이 증가하고 있다. 이러한 흐름에 맞추어 국내에서도 국립원예특작과학원을 중심으로 전 세계 약 900여점의 포도 유전자원과 200여종의 GBS 데이터, 40여종의 Resequencing 데이터 등을 확보하여 보유하고 있다. 그러나 이러한 유전체 데이터를 실질적인 육종으로 활용하기 위한 소통과 공유의 장, 즉 육종가가 이용 가능한 형태로 유전체 정보를 재가공하여 제공하는 접근 통로가 없어 육종소재로서의 활용이 부족한 실정이다. 따라서 보유하고 있는 자원들에서 유용 형질들을 발굴하고, 형질과 연관된 유전자 및 분자마커를 개발하여 제공하는 시스템 개발이 필요한 시점이다. 이에 따라 포도 유전체 육종의 근접지원을 목표로 최적화된 웹 데이터베이스를 구축하고자 한다. 웹 데이터베이스는 크게 핵심 데이터와 분자육종 지원 툴(tool)로 설계하였다. 포도 유전자 정보 및 DNA 마커 정보, 유전지도 및 유전자 발현 분석 결과 등 핵심 데이터를 가공하여 유용 정보 데이터베이스를 구축하여 제공할 것이다. 유전체 육종으로의 활용을 돕기 위한 툴(tool)로는 포도 genome browser, CAPS marker design tool 및 교배실생의 효율적 선발을 위한 MAB graphic viewer 등을 개발하여 핵심 데이터를 육종에 효과적으로 이용할 수 있도록 제공할 예정이다. 흩어져 있는 유전체 정보를 육종으로의 활용 가능한 형태로 가공하여 제공함으로써 형질연관 마커 개발 등 육종 효율을 증대시키기 위한 지원을 통해 포도 육종을 가속화할 수 있다. 또한 포도 중심의 웹 데이터베이스에서 제공하는 유전체 분석 결과물은 향후 이형접합성(heterozygsity)이 높은 과수작물에 확장 적용 가능한 분자육종 기술의 토대가 될 것이다.

Corresponding author: Tel. 042-710-4035, E-mail: shjo@seeders.co.kr

PC-15

Identification of SNP and InDel Sites in Strawberry Using a Next-generation Resequencing Approach

Ye Rin Lee, Haein Kim, Kyumi Jeong, Jundae Lee*

Department of Horticulture, Chonbuk National University, Jeonju 54896, Korea

Strawberry is one of the most popular berry fruits in the world, and the cultivated strawberry (*Fragaria* x *ananassa*) is octoploid (2n=8x=56). There have been many diseases occurring in strawberry. Among them, *Phytophthora cactorum* damaged the fruit quality and reduced the production of fruits. In order to analyze the resistance to *Phytophthora cactorum*, two strawberry cultivars, 'Sulhyang' (a susceptible parent) and 'Senga-Sengana' (a resistant parent), were used as parents. The parental genomes were sequenced by a next-generation sequencing (NGS) method. The reference genome size of *F.* x *ananassa* is about 720 Mb. The sequences were available from the strawberry GARDEN database (http://strawberry-garden. kazusa.or.jb/). A total of 30.6 Gbp and 25.2 Gbp of raw sequence data were obtained in ‘Senga-sengana’ and ‘Sulhyang’, respectively. Through the trimming process, the lengths of the sequences were shortened to 21.8 Gbp for 'Senga-sengana' and 19.0 Gbp for 'Sulhyang', which were still 30- and 26-times longer than the reference genome. Then, the mapping process was conducted by aligning with reference genome using a BWA (0.6.1-r104) program. As the result, 'Senga-sengana' and ‘Sulhyang’ covered 530 Mbp (75.97%) and 533 Mbp (76.52%) of the reference genome, respectively. By comparing the sequences between ‘Senga-sengana’ and ‘Sulhyang’, a total of 12,720 SNP and 2,208 InDel sites were identified. Finally, we have designed the primer-sets to analyze 3,144 SNPs and 416 InDels.

Corresponding author: Tel. 063-270-2560, E-mail: ajfall@jbnu.ac.kr

PC-16

Development of EST-SSR Markers Through *de novo* RNA Sequencing for Genetic Diversity and Association Study in Kenaf (*Hibiscus cannabinus* L.)

Sang Wook Jeong[1], Soon-Jae Kwon[1*], Jaihyunk Ryu[1], Minkyu Lee[1], Joon-Woo Ahn[1], Jin-Baek Kim[1], Sang Hoon Kim[1], Hee-Bong Lee[2], Si-Yong Kang[1]

[1]Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongup, Jeonbuk 580-185, Korea
[2]Chungnam National University Dept. of Applied Botany

Kenaf (*Hibiscus cannabinus* L.) is a multipurpose crop, but a lack of genetic information hinders genetic and molecular research on this crop. In this study, we aimed to develop EST-SSR markers from mutant and wild-type cultivars, and to assess the genetic diversity of the kenaf resources. A total of 33 Gb of nucleotide sequence data comprising 130,480 unigenes was assembled by *de novo* RNA-sequencing of six kenaf cultivars, and 5,619 SSRs were identified from these unigenes. Tri-nucleotide motifs occurred most frequently (82.67%) followed by di- (10.93%), tetra- (4.34%), and penta-nucleotide (2.06%) motifs. In total, 515 polymorphic EST-SSRs were derived by pairwise comparisons of the cultivars based on *in silico* analyses. Of these, 70 markers were successfully validated and revealed genetic differentiation among six *de novo* RNA-sequenced cultivars. We used the six cultivars, together with 39 kenaf accessions from worldwide collections to assess genetic diversity and to characterize the newly developed EST-SSR markers. The number of alleles per locus ranged from 2 to 8, with an average of 2.89. Polymorphism information content (PIC) and genetic diversity values ranged from 0.08 to 0.79 and 0.08 to 0.82, with average values of 0.37 and 0.43, respectively. The phylogenetic tree and population structure showed that the 45 accessions could be clearly divided into three major groups based on different days to flowering (DTF) traits. Genetic differentiation among the DTF groups showed a proportionally high level of variance (F_{st}=0.296). Association analysis between the DTF and the markers revealed three significant marker-trait associations at $P < 0.001$ using two representative methods (Q GLM and Q+K MLM). Furthermore, using a multiplex PCR with three markers, DTF could be perfectly discriminated. These markers will be useful in marker-assisted selection after further validation with segregating populations of kenaf.

Corresponding author: Tel. 063-570-3312, E-mail: soonjaekwon@kaeri.re.kr

PC-17

A Bioinformatic Platform for Designing Cross-Species Intron-Spanning Genic Markers in Legumes

Jin-Hyun Kim[1], Chaeyoung Lee[1], Joo-Seok Park[2], Yoram Choi[2,] Hong-Kyu Choi[3*]

[1]Department of Medical Bioscience, Dong-A University, Busan, Korea
[2]Department of Applied Bioscience, Dong-A University, Busan, Korea
[3]Department of Genetic Engineering, Dong-A University, Busan, Korea

Genetic markers are tools that can facilitate molecular breeding, even in species lacking genomic resources. An important class of genetic markers is those based on orthologous genes, because they can guide hypotheses about conserved gene function, a situation that is well documented for a number of agronomic traits. For under-studied species a key bottleneck in gene-based marker development is the need to develop molecular tools (e.g., oligonucleotide primers) that reliably access genes with orthology to the genomes of well-characterized reference species. Here we report an efficient platform for the design of cross-species gene-derived markers in legumes. The automated platform, named CSGM Designer (URL: http://tgil.donga.ac.kr/CSGMdesigner), facilitates rapid and systematic design of cross-species genic markers. The underlying database is composed of genome data from five legume species whose genomes are substantially characterized. Use of CSGM is enhanced by graphical displays of query results, which we describe as “circular viewer” and “search-within-results” functions. CSGM provides a virtual PCR representation (eHT-PCR) that predicts the specificity of each primer pair simultaneously in multiple genomes. CSGM Designer output was experimentally validated for the amplification of orthologous genes using 16 genotypes representing 12 crop and model legume species, distributed among the galegoid and phaseoloid clades. Successful cross-species amplification was obtained for 85.3% of PCR primer combinations. CSGM Designer spans the divide between well-characterized crop and model legume species and their less well-characterized relatives. The outcome is PCR primers that target highly conserved genes for polymorphism discovery, enabling functional inferences and ultimately facilitating trait-associated molecular breeding.

† Equal contributors

Corresponding author: E-mail: hkchoi@dau.ac.kr

PC-18

GM 콩의 도입유전자 이동에 미치는 화분 매개충의 영향

이범규[1*], 손수인[1], 권순종[2], 박기웅[3], 정영수[4], 이시명[1]

[1]전라북도 전주시 국립농업과학원 생물안전성과
[2]경기도 수원시 국립식량과학원 중부작물과
[3]대전광역시 충남대학교 식물자원학과
[4]부산광역시 동아대학교 유전공학과

전 세계적으로 GM(genetically modified, 유전자변형) 작물의 재배면적은 지속적으로 증가하고 있이며, 이에 따른 GM 작물의 잠재적 위해성에 대한 우려도 증가되고 있는 실정이다. GM 작물의 환경에 대해 가장 큰 우려 중 하나는 GM 작물의 도입유전자가 근연종 및 이종간으로 교잡되어 이동하는 것이다. 콩은 GM 작물 중 가장 많이 재배되는 작물로 국내에도 많은 양이 수입되고 있으며, 특히 우리나라 콩의 야생종인 *G. soja*의 원산지로 GM 콩으로부터의 유전자이동성 조사는 국내 콩 다양성 보존과 LMO 안전관리를 위해 매우 중요하다. 본 연구에서는 콩의 화분 매개충으로 보고된 꿀벌과 총채벌레를 대상으로 이들 방화곤충이 GM 콩의 도입유전자 이동에 관여하는지를 알아보고자 하였다. 유전자이동에 의한 교잡종은 총채벌레 처리구에서 GM 콩 화분원으로부터 비교적 근거리인 15, 75, 105cm에서 3개체가 발견되었다. 꿀벌 처리구와 아무 매개충이 처리되지 않은 무 처리구에서는 모두 근거리에서 교잡종이 발견되지 않아 총채벌레가 GM 콩으로부터 화분을 매개했을 가능성이 제시되었다. 꿀벌 처리구에서는 GM 화분원에서 가장 거리가 먼 300cm에서 1개의 교잡종 개체가 발견되어 꿀벌의 특성 상 먼 거리까지의 화분 이동 가능성이 제시되었다.

Corresponding author: Tel. 063-238-4716, E-mail: leebk3@korea.kr

PC-19

Gene Transferability from Genetically Modified *Brassica napus* to *B. rapa* and Trait Analysis of F_1 Hybrids

Soo-In Sohn[1*], Young-Ju Oh[2], Kyeong-Ryeol Lee[1], Ho-Cheol Ko[3], Ancheol Chang[1], Bumkyu Lee[1], Doh-Won Yun[1], Gang-Seob Lee[1], Sung-Dug Oh[1], Hyun-Suk Cho[1], Yeon-Hee Lee[1]

[1]Department of Agricultural Biotechnology, National Institute of Agricultural Sciences, Jeonju, Korea
[2]Institute for Future Environmental Ecology Co., Ltd, Jeonju, Korea
[3]National Agrobiodiversity Center, National Institute of Agricultural Sciences, Jeonju, Korea

A number of studies have been conducted on hybridization between transgenic *Brassica napus* and *B. rapa* or backcross of F_1 hybrid to their parents. However, trait changes must be analyzed to evaluate hybrid sustainability in nature. In the present study, *B. rapa* and transgenic (*BrAGL20*) *B. napus* were hybridized to verify the early flowering phenomenon of F_1 hybrids, and F_1 hybrid traits were analyzed to predict their impact on sustainability. F_1 hybrids bloomed later than transgenic *B. napus*, but without vernalization, owing to the expression of the *BrAGL20* transgene. The size of F_1 hybrid seeds was intermediate between those of *B. rapa* and transgenic *B. napus*, and ~40% of F_1 pollen exhibited abnormal size and morphology. The form of the F_1 stomata was also intermediate between that of *B. rapa* and transgenic *B. napus*, and the number of stomata was close to the parental mean. Among various fatty acids, the content of erucic acid exhibited the greatest change, owing to the polymorphism of parental *FATTY ACID ELONGASE 1* alleles. Furthermore, F_2 hybrids could not be obtained. However, BC_1 progeny were obtained by hand pollination of *B. rapa* with F_1 hybrid pollen, with an outcrossing rate of 50%.

Corresponding author: Tel. 063-238-4712, E-mail: sisohn@korea.kr

PC-20

Genetic Diversity Analysis of Boysenberry Using SSR Markers

Woon Ji Kim[1], Juhyun Im[1], Sanghun Kim[1], Ee Yup Kim[2], Han Jig Jo[2], Si-Yong Kang[3], Bo-Keun Ha[1*]

[1]Division of Plant Biotechnology, Chonnam National University, Gwangju, 61186, Korea
[2]Bioplus Co., Wanju, 55310, Korea
[3]Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongeup, 56212, Korea

Boysenberry, a *Rubus* hybrid between a trailing blackberry and Loganberry, possess distinctive polyphenol compounds, which demonstrated positive biological effects on human health. Recently, several new boysenberry genotypes were developed from mutation breeding technology. In this study, we evaluated genetic diversity in 10 boysenberry genotypes by using SSR markers. A total of 87 SSR markers developed from expressed sequence tag (EST) and genomic libraries in blackberry, red raspberry, and strawberry were used in PCR amplifications. All primer pairs produced successfully amplification products, ranging from 1 to 5 alleles per locus. Average polymorphism information content (PIC) was 0.22, ranging from 0 to 0.58. According to a cluster analysis, all the mutant boysenberry genotypes can be classified into one category. Although the level of genetic diversity revealed by SSR markers in 10 boysenberry genotypes was low, these SSR markers will be useful for future genetic diversity, QTL mapping, and gene cloning studies in boysenberry.

Corresponding author: Tel. 062-530-2055, E-mail: bkha@jnu.ac.kr

PC-21

Comparison of Anthocyanins and Antioxidant Capacity in Colored-wheat Mutant Lines

Min Jeong Hong[1], Bo Mi Nam[1], Sang Hoon Kim[1], Joon-Woo Ahn[1], Si-Yong Kang[1], Dea Yeon Kim[2], Yong Weon Seo[2], Jin-Beak Kim[1*]

[1]Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, 29 Geumgu, Jeongeup 580-185, Korea
[2]Division of Biotechnology, Korea University, Seongbuk-Gu, Seoul 136-713, Korea

Wheat grain is recognized as a good source of nutrient crop which can be a rich source of various antioxidants, vitamins, minerals, and fibers. In the recent years, wheat breeding has been aimed on increasing the content of bioactive compounds to improve disease prevention and health promotion. We selected five genetically fixed mutant lines with altered grain color, which was induced gamma irradiation. Selected wheat mutants were evaluated for their total anthocyanin by UV-VIS spectrophotometer. To clarify the relationship between the expression of anthocyanin biosynthesis genes and anthocyanin accumulation, their correlations were analyzed according to grain color. In addition, we examined the expression of anthocyanin biosynthesis-related genes (*CHS*, *CHI*, *F3H*, *DFR*, *ANS*, *UFGT)* with whole grain. Each anthocyanin components (cyanidin-3-glucose, peonidin-3-glucose, and cyanidin-3-rutinoside) were investigated by HPLC. Antioxidant activities of the wheat seed extracts by the methanol were analyzed by measuring DPPH radical scavenging activities. To elucidate the molecular mechanisms for antioxidant activity in wheat seeds, the transcripts of antioxidant related gene (*APX*, *CAT*, *GPX*, *GR*, *DHAR*, *MDAR*, *CuZnSOD*, *MnSOD*) were examined. Some antioxidant gene expression and total anthocyanin contents were positively correlated with the antioxidant capacity. We identified wheat mutant lines with colored-grain which had varying characteristics, such as anthocyanins and antioxidant capacities.

Corresponding author: Tel. 063-570-3313, E-mail: jbkim74@kaeri.re.kr

PC-22

벼 형질전환 Callus에서 돼지콜레라 항원 유전자의 발현

이주영, 김용호*

충남 아산시 신창면 순천향대학교 의료생명공학과

돼지콜레라를 예방하기 위한 곡물 백신 개발의 일환으로 연구가 수행되었다. 점막면역보조제인 Cholera toxin subunit B (CTB)와 항원 FasG 유전자를 융합한 CTB::FasG를 vector에 삽입한 후 agrobacterium을 매개로 벼에 형질전환시켰다. Southern blotting으로 확인한 형질전환체 T1의 잎을 explant로 하여 MS 배지에서 callus를 유도한 후 12개월까지 callus를 계대배양하며 삽입유전자의 안정성을 확인하였다. TaqMan RT-PCR법으로 확인한 explant의 삽입유전자 copy 수는 1~8이었으며, callus는 계대배양 11개월까지 삽입유전자가 안정적으로 발현됨을 확인할 수 있었다. 따라서 이는 추후 식물경구백신 개발의 가능성을 높이는 수단으로 이용될 수 있으리라 판단된다.

Corresponding author: Tel. 041-530-1281; E-mail: yohokim@sch.ac.kr

PC-23

Physiological Analysis of Wheat Cultivars Under Heat Stress Condition

Chan Seop Ko[1], Dae Yeon Kim[1], Young Up Kweon[2], Jong Nae Hyun[2], Kyung Hun Kim[2], Yong Weon Seo[1*]

[1]Department of Biosystems and Biotechnology, Korea university, Anam-ro 145, Seong-Buk, Seoul, Korea
[2]Dept. of Southern Area Crop Science, NICS, Miryang, Korea

The global climate has been changing in the last decades. These changes include elevated CO2 concentration, warming temperatures, and changes in rainfall patterns. To adapt wheat cultivars to the future climate, we need to understand the mechanism of response to elevated temperature and how tolerance to heat can be improved. To achieve maximum yield, optimum temperature in wheat is generally considered to be between 15℃ and 20℃ during grain development stage. High temperature that exceeds 30℃ during grain filling stage in Korea climate leads to reduction in grain numbers and grain mass by reduction of photosynthesis rate. At the grain filling period, two wheat cultivars, 'Keumgang' and 'Jokyung', were grown under heat stress condition for 10 days (day/30℃-35℃, night /20℃-25℃). After heat treatment, two wheat cultivars were recovered under optimized condition and harvested for further study. Physiological trait, such as chlorophyll content, seed weight, seed number, spikelet number, activities of antioxidant enzymes from two different wheat cultivar were measured to validate effect of heat stress on physiological changes and distinctions between 'Keumgang' and 'Jokyung'. Chlorophyll content, seed weight, seed number, and spikelet number were decreased in heat stress condition, and the results indicated that damaged chlorophyll by heat stress reduced photosynthesis rate and inhibited normal growth. In addition, the phenotype date reveals that 'Jokyung' showed more sensitive to heat stress than 'Kuemgang'.

Acknowledgements: This work was carried out with the support of " R&D agenda Agriculture & Technology development program (Project No. PJ0122732016) " Rural Development Administration, Republic of Korea.

Corresponding author: Tel. 02-3290-3005, E-mail: seoag@korea.ac.kr

PC-24

Development of a HRM Marker Tightly Linked to Genic Male-sterile Gene (*ms*$_1$) in Paprika

Kyumi Jeong, Ye Rin Lee, Haein Kim, Jundae Lee*

Department of Horticulture, Chonbuk National University, Jeonju 54896, Korea

Paprika (*Capsicum annuum* L.), a colored sweet pepper, is one of the most important vegetable crops in Korea. The cultivation area, exports, and production amount of paprika have been annually increasing. Genic male sterility (GMS) caused by *ms*$_1$ gene in paprika is widely used for commercial F_1 hybrid seed production because it can save labor and costs. It has previously developed the GMSP-CAPS marker linked to paprika *ms*$_1$ gene, and the marker was located at about 1 to 2 cM distant from the *ms*$_1$ locus on chromosome 5. In this study, we developed the HRM marker tightly linked to the *ms*$_1$ gene, which was identified by comparing between phenotypes and genotypes of 398 individuals from two F_2 segregating populations through a screening of GMSP-CAPS-linked primer sets. Male-fertile (*Ms*$_1$*Ms*$_1$ or *Ms*$_1$*ms*$_1$) and male-sterile (*ms*$_1$*ms*$_1$) plants were segregated into 288 and 93, respectively, fitting the expected ratio of 3:1. For applicability test, the HRM marker was subjected to paprika breeding lines and cultivars. As a result, the marker genotypes were almost matched with the phenotypes of 398 individuals. In addition, 23 F_1 commercial varieties were tested by the HRM marker in order to determine whether the *ms*$_1$ gene was used or not. Consequently, a heterozygous markertype (*Ms*$_1$*ms*$_1$) and a homozygous male-fertile markertype (*Ms*$_1$*Ms*$_1$) appeared in 8 and 15 F_1 varieties, respectively. Also 5 of 8 and 15 of 23 F_1 varieties were confirmed by the F_2 segregation analysis, resulting in cosegregation of markertypes and phenotypes. This HRM marker can be helpful to develop GMS maternal lines of paprika.

Corresponding author: Tel. 063-270-2560, E-mail: ajfall@jbnu.ac.kr

PC-25

A Molecular Marker Linked to Saline Tolerance in Durum Wheat from Semi-desert

Sang Heon Kim[1], Inès Yacoubi[2], Yong Weon Seo[1*]

[1]Department of Biosystems and Biotechnology, Korea University, Seoul 136-713, Korea
[2]Centre de biotechnologie de Sfax (CBS), Sfax, Tunisia

Durum wheat (*Triticum turgidum* ssp. *durum*) is an economically important crop which is consumed worldwide. In desert and semi-desert regions, salinity stress diminishes durum wheat yield. Durum wheat accessions from semi-desert lands in Tunisia were implemented to evaluate their saline tolerance. Plants at the 3rd leaf stage were exposed to saline treatment by repeatedly drowning pots in NaCl solution. Based on diverse growth criterions, the salt tolerance trait index (STTI) and salt tolerance index (STI) were calculated and used as yardstick to determine the saline tolerance of plants. To verify the genetic distance among the durum wheat accessions, their genetic relationships were analyzed using microsatellites. Based on STI and the genetic relationship analysis, 6 durum wheat accessions, which are showing contrast saltine tolerance but closely akin, were selected to develop sequence characterized amplified region (SCAR) markers determined by the sequences of PCR products derived from microsatellites. A SCAR marker generated a PCR band which was existing in saline tolerant lines but missing in saline sensitive lines. The results indicate that the developed SCAR marker would be beneficial to prospective breeding program for saline tolerant durum wheat.

Acknowledgement: This work was carried out with the support of "Next-Generation BioGreen21 Program for Agriculture & Technology Development (Project No. PJ01103501)" Rural Development Administration. Republic of Korea.

***Corrresponding author:** Tel. 02-3290-3005, E-mail: seoag@korea.ac.kr

PC-26

Transcriptome Analysis of Pre-harvest Sprouting Korean Wheat using RNAseq

Jae Yoon Kim, Dae Yeon Kim, Yong Weon Seo*

Department of Biotechnology, Korea University, Seoul 136-713, Korea

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 In this study, we performed transcriptome analysis between Keumkang (susceptible) and Woori (tolerance). The DAF (Day After Fertilization) 35 of keumkang and Woori spikes were harvested to perform transcriptome analysis using RNA-sequencing. Each transcriptome was compared with PHS treated at DAF 35 Keumkang and Woori spikes. Six cDNA library from the DAF 35 of Keumkang and Woori wheat grain, PHS treated DAF 35 of Keumkang and Woori, and ABA treated DAF 35 of Keumkang and Woori were constructed and sequenced. A total of 53.37 Gb of high-quality reads were obtained using HiSeq 2500. The average mapping rate of assembled transcripts were 88.98%. A total of 86 DEG (51 annotated) were upregulated in PHS treated DAF 35 Woori library in comparison with PHS treated DAF 35 Keumkang library. We selected 8 DEG which were up-regulated and 9 DEG down-regulated in both PHS treated and ABA treated DAF 35 Woori library in comparison with PHS and treated DAF 35 Keumkang library and perforemd qRT-PCR to validate expression profiles for selected DEG. Cytochrome P450 was predominantly expressed in the PHS treated Woori wheat. Whereas F-box/RNI-like superfamily protein was drastically upregulated in the 6 day after PHS treated Woori wheat. These findings have important implications in the molecular mechanisms underlying regulation of PHS and seed dormancy in cereals.

Acknowledgements: This work was carried out with the support of the Next-Generation BioGreen21 Program for Agriculture & Technology Development (Project No. PJ01103501), Rural Development Administration, Republic of Korea. This work was also supported by the National Research Foundation of Korea (NRF) grant funded by the Korea government (MSIP) (NRF-2014R1A1A1003621)

Corresponding author: Tel. 02-3290-3464, E-mail: seoag@korea.ac.kr

PC-27

Transcriptomic Dynamics of Wheat Peduncle at Different Developmental Stages

Cheol-Won Lee, Yong-Weon Seo*

Department of Biosystems and Biotechnology, Korea University, Seoul 136-701, Korea

In general, the mechanism of flowering in wheat has been explained with three interactive pathways such as light signaling, flowering integrators and winter temperatures (vernalization). Of these, light signaling specially works on flowering through the regulation of the incoming oscillations of many circadian clock genes, receiving light using the photoreceptor like red/far-red light receptors (phytochromes) or blue/ultraviolet A light receptors (cryptochromes) and responding to day length related to photoperiod genes. The regulatory or out-put factors of flowering already explained were usually studied using flag leaf or floral meristem. However, we propose that the peduncle, which is a shoot part between bottom of the spike and leaf sheath of flag leaf, could be an important tissue that is responsible for flowering considering the role of photoreceptor. RNA-Seq was performed to test for transcriptomic dynamics in the wheat peduncle which was either covered or uncovered by leaf sheath of flag leaf at different development stages. With this, we also analyzed GO terms and kegg pathway which genes specially function in the peduncle when wheat face floral transition. The obtained results will provide valuable information to understand mechanisms of flowing regulation in wheat breeding program aiming early maturity.

Acknowledgement: This work was carried out with the support of “Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ01103501)” Rural Development Administration. Republic of Korea.

Corresponding author: Tel. 02-3290-3005, E-mail: seoag@korea.ac.kr

PC-28

Identification of *CBF*s in rye and Their Expressions Under Various Abiotic Stresses

Woo Joo Jung, Yong Weon Seo*

Department of Biosystems and Biotechnology, Korea University, Seoul 136-701, Korea

Rye (*Secale cereale*) is one of the most freezing stress-tolerant species in the Triticeae. Freezing tolerance, which is acquired after a certain period of cold acclimation, is mainly regulated by CBF (C-repeat binding factor) genes. CBF genes are known to possess AP2 DNA-binding domain, and work as a transcription factor regulating COR (cold-responsive) genes. CBF genes in *Secale cereale* were isolated by PCR-based cloning in the past study, but their sequence information is insufficient to study each of their functions. In this study, we identified CBF gene families in rye via bioinformatic approaches. Rye 454-cDNA reads from root, crown, stem and spike were downloaded and used as a BLASTdb. Wheat CBF families, consisting of the largest group in the Triticeae, were used as queries and rye sequences with high identity were identified. The putative *ScCBF* sequences were assembled using CAP3 program and accuracy of the assembly was validated by matching with the 454-cDNA reads. AP2 DNA-binding domain of each contig was identified using SMART program. Also, the coding region of CBF families in rye, wheat, barley and *Brachypodium* was aligned to develop a phylogenetic tree using MEGA7. Finally, *ScCBF*s gene expression was analyzed under various stress conditions as well as exogenous phytohormone application. The sequence information resulting from this study will be helpful for characterization of each gene in further studies.

Acknowledgement: This work was carried out with the support of "Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ01103501)" Rural Development Administration. Republic of Korea.

Corresponding author: Tel. 02-3290-3005, E-mail: seoag@korea.ac.kr

PC-29

Comparison of Physiological Changes in 1BL.1RS Translocation and its NIL Under Cold Stress

Woo Joo Jung, Yong Weon Seo*

Department of Biosystems and Biotechnology, Korea University, Seoul 136-701, Korea

Cold stress is one of the most severe damages in plant growth even leading to death. Plants adapt to cold through the process of cold acclimation, in which complex molecular and physiological interactions are involved. Signaling molecules such as diverse sugar compound and ROS (reactive oxygen species) are thought to play an important role in cold acclimation. In the Triticeae crops, rye (*Secale cereale*) shows the most cold stress-tolerant phenotype with high survival rate after freezing stress. 1BL.1RS translocation lines possess the short arm of rye chromosome 1 (1RS) instead of the short arm of 1B chromosome of wheat. Thanks to its tolerance to various biotic and abiotic stress resistance in 1RS, 1BL.1RS has been widely utilized in wheat breeding. However, its performance under cold stress has not been fully investigated yet. In this study, physiological changes of a 1BL.1RS translocation line and its NIL (near-isogenic line) without 1RS under freezing stress were observed. The plants were grown in a growth chamber (12/12 h, 16/12℃) until the fourth leaf emerged, and acclimated at 8, 6 and 4℃ each for 5 days. The freezing stress was treated at -5℃ for 24 h, followed by recovery at 4℃ and regeneration in the normal condition. After 5 days of the regeneration, survival rate of each germplasm was scored. At every stage of the acclimation, freezing treatment, and recovery, total shoots were sampled for the measurement of proline content, sugar content, and antioxidant enzyme activity. The result of this study could be utilized for studying cold stress tolerance in 1BL.1RS translocation.

Acknowledgement: This work was carried out with the support of “Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ01103501)” Rural Development Administration. Republic of Korea.

Corresponding author: Tel. 02-3290-3005, E-mail: seoag@korea.ac.kr

PC-30

한국 보급 및 특수품종의 SSR마커에 의한 유전적 유연관계와 품종판별

이가영[1], 곽상철[1], 김믿음[1], 장은규[2], 황세구[3], 김홍식[1*]

[1]충청북도 청주시 서원구 충대로1 충북대학교 농업생명환경대학 식물자원학과
[2]경기도 연천군 신서면 도신로 3번길 경기도 농업기술원
[3]충청북도 청주시 청원구 오창읍 가곡길 46 농업기술원

국내의 콩 보급 및 특수품종 30품종을 SSR 마커를 이용하여 유전적다양성과 유연관계를 분석하고, 품종판별체계를 확립하여 육종의 기초자료로 활용코자 하였다. 국내에서 과거에 재배되었거나 현재에 재배되고 있는 보급 및 특수품종 콩을 20개의 SSR 마커로 분석한 결과, 대립인자는 총 273개가 확인 되었고, 각 유전자좌별로 Satt339가 최소 7개이었고, Sat_374, Sat_076, Sat_245가 최대 18개가 확인되었으며, 평균 대립인자는 13.65개이었다. 대립인자의 범위는 361~107 bp 이었고, AW132402가 163~143 bp로 범위가 가장 작았으며, Satt185가 252~121 bp의 범위로 가장 컸다. 유전적 다양성(PIC value)는 0.7828~0.9293의 범위였고, Satt164가 0.7828로 가장 낮았으며, Sat_245가 0.9293으로 가장 높았고, 평균 0.8672로 유전적 다양성이 다소 높았다. 다형성이 높은 1개의 SSR마커와 2개 마커를 이용한 4개 조합 1) Sat_245 + Sat_342, 2) Sat_245 + Satt 197, 3) Sat_245 +Sat_076, 4) Sat_245 + Sat_022의 어느 조합을 사용하여도 한국 콩 보급 및 특수품종 30품종이 모두 판별되었다.

Corresponding author: Tel. 043-261-2531, E-mail: hongsigk@chungbuk.ac.kr

PC-31

The Development of Drought Resistance Bottle Gourd (*Lageneraria siceraria* Standl.) Using *Agrobacterium*-mediated Transformation.

Shin-Hwan Cho, Yul-Kyun Ahn*, Jin-Hee Kim, Jong-Pil Hong, Eun-Su Lee, Jeong Ho Kim, Do-Sun Kim

Vegetable Research Division, National Institute of Horticultural and Herbal Science, RDA, 100, Nongsaengmyeong-ro, Iseo-myeon, Wanju-gun, Jeollabuk-do, Korea

식물은 생장함에 있어서 기후나 외부환경의 영향을 받는다. 특히 물이나 온도조건은 식물의 생장에 가장 큰 영향을 미치며 작물의 생산량에도 영향을 미친다. C-repeat binding factor (CBF)는 식물의 cold-response pathway에서 transcription factor로 작용하여, 저온에 의해 유도된 후 cold response 유전자의 발현을 조절한다. 이 연구에서는 대목으로 사용되는 bottle gouard (*Lageneraria siceraria* Standl.)에 *agrobacterium*을 이용하여 CBF 유전자를 형질전환하여 가뭄상태에서 저항성이 있는지 확인하였다. 형질전환체와 비형질전환체를 각각 가뭄을 처리하여 식물체의 키와 잎의 너비와 길이, 개수 등 원예적 특성을 조사하였다. 그 결과 CBF3 유전자가 도입된 형질전환체가 비형질전환체보다 가뭄상태에서 더 잘 자라는 것을 확인할 수 있었다. 식물의 키는 약 2배 정도 잘 자랐으며, 잎의 너비나 길이도 형질전환체가 더 잘 자랐다. 또한 잎의 개수도 2~3장 더 많이 관찰되어, 종합해보면 형질전환체가 건조에 강한 특성이 있음을 확인할 수 있었다. 따라서 CBF3가 도입된 형질전환체는 건조에 강한 특성이 있어 가뭄시 작물의 생장이나 생산량 증대에 많은 효과를 줄 수 있다.

Corresponding author: E-mail: sky-zeus@hanmail.net

PC-32

Genome-wide Discovery of Simple Sequence Repeat Marker Based on Complete Genome Sequencing of *Capsicum baccatum* and *Capsicum annuum*

Sandeep Karna[1], Yul-Kyun Ahn[1*], Jin-Hee Kim[1], Eun-Su Lee[1], Sena Choi[1], Eun-Young Yang[1], Jeong-Ho Kim[1], Tae-Hwan Jun[2]

[1]Vegetable Research Division, National Institute of Horticultural & Herbal Science, Rural Development Administration, Jeonju-55365, Korea
[2]Department of Plant Bioscience, Pusan National University, Busan-46241, Korea

Rapid advancement in genome sequencing platforms provides ample opportunity for the development of DNA-based molecular markers. Two pepper varieties, *Capsicum baccatum* (PRH1) and *Capsicum annuum* (Saengryeg), were resequenced to develop simple sequence repeat (SSR) markers based on a comparison with the reference genome *Capsicum annuum cv.* CM334. A total number of 907,839 and 2,282,442 SSRs were discovered for PRH1 and Saengryeg respectively. Further, we have analyzed chromosome wise distribution of SSR. Chromosome 1 contains maximum number of SSRs (99,584 and 231,465) where as chromosome 8 contain least number (48,326 and 120,763), respectively. This study describes the discovery of numerous SNP and SSR markers that might be useful for molecular breeding and QTL mapping in pepper.

Corresponding author: Tel. 063-238-6674; Fax. 063-238-6605, E-mail: aykyun@korea.kr

PC-33

Pedigree Integration of Soybean [Glycine max L. Merrill] Cultivars in Korea

Chaeyoung Lee[1], Jin-Hyun Kim[1], Joo-Seok Park[2], Yoram Choi[2], Hong-Kyu Choi[3*]

[1]Department of Medical Bioscience, Dong-A University, Busan, Korea
[2]Department of Applied Bioscience, Dong-A University, Busan, Korea
[3]Department of Genetic Engineering, Dong-A University, Busan, Korea

Soybean [Glycine max (L.) Merrill] is one of the most important crops in the world and in Korea as well. Since the official start of soybean breeding program in Korea at which a landrace 'Jangdanbaekmok' was first released to promote cultivation in1913, approximately one century has elapsed. Currently, a total of 178 soybean varieties are registered at two representative Korean national institutes, the RDA-Genebank Information Center (http://www.genebank.go.kr) and the Korea Seed & Variety Service (http://www.seed.go.kr). Of these, 155 varieties (87.1%) have been developed through hybridization-based breeding technologies, of which most cultivars (133 varieties, 85.8%) have been released in the last twenty five years. In this review, we attempted to integrate all the information for individual cultivars and to rebuild a breeding pedigree including the entirety of registered Korean soybean varieties. The analysis has resulted in a total of four pedigrees involving 168 cultivars (94.4% out of 178 cultivars), which form the broadest network of pedigrees. Each of pedigrees highlights different key varieties within the context of progenitor networks derived from crossing of various elite parental lines as follows; pedigree I-'Kwangkyo', 'Hwangkeumkong', 'Paldalkong' and 'Sinpaldalkong2', pedigree II-'Baegunkong', 'Jangyeobkong' and 'Keunolkong', pedigree III-'Danyeob', 'Pangsa' and 'Eunhakong'. These pedigrees also reveal purpose (i.e., desirable traits)-driven development of characteristic soybean varieties during the past century of breeding history in Korea. We expect that the pedigree reconstructed in this study will provide breeders with information useful to design breeding schema and guidance towards the genomics-assisted soybean improvement in the future.

Corresponding author: E-mail: hkchoi@dau.ac.kr

PC-34

Biosafety Assessment for Drought-tolerant Transgenic Rice (CaMsrB2-23) : Progeny Stability Study for Three Generations

Sung-dug Oh, Youngshin Kwak, Daesu Park, Doh-won Yun, Soo-in Sohn, Bumkyu Lee, Ancheol Chang*

Department of Agricultural Biotechnology, National Institute of Agricultural Sciences (NIAS), Rural Development Administration (RDA), Jeonju, Korea

Genetically modified (GM) crops have been developed worldwide through the recombinant DNA technology and commercialized by various agricultural biotechnological companies. Commercialization of genetically modified (GM) crops will be required the assessment of risk associated with the release of GM crops. The purpose of this research is a molecular characterization of introduced T-DNA in transgenic rice T4 ~ T6 generation lines harboring a pepper *MsrB2* gene under the control of stress inducible *Rab21* promoter, as a part of biosafety evaluation for drought-tolerant transgenic rice (CaMsrB2-23). We identified the structure and sequence of transformation vector of T-DNA and analyzed insertion sites, flanking sequences, and generational stability of inserted T-DNA in transgenic rice lines. The transformation vector was consisted of right border, a selectable marker herbicide resistance unit (*CaMV 35S* promoter*:bar:Nos* terminator), a drought-tolerant *CaMsrB2* gene unit (*Rab21* promoter*:CaMsrB2:PinII* terminator), and left border in sequential order. Based on the adaptor-ligation PCR and whole genome sequence database, we confirmed that T-DNA was introduced two copies (head to head type) at the position of 2,471,957 ~ 2,472,049 bp of chromosome No. 8. From the generational stability study, T-DNAs were stably inherited through the T4 to T6 generations, and also stable expression of *bar* gene from T-DNA was confirmed. It was also confirmed that the backbone DNA of transformation vector containing antibacterial gene (*aadA*) was not present in CaMsrB2-23 rice genome. These results will be filed to biosafety assessment document of CaMsrB2-23 rice.

Corresponding author: E-mail: abychan@korea.kr

PC-35

Identification of Tuber-Endophytic Bacteria in *Gastrodia elata* with Novelty of Soil *Proteobacteria*

Eung Jun Park*, Muho Han, Hyo-Ryeon Lee, Mi Na Choi, Dae Bong Kang

Department of Forest Genetic Resources, Korea Forest Research Institute, Suwon 16631, Korea

Soft rot disease can cause 60% loss in the actual yield of *Gastrodia elata (G. elata)* compared to non-contaminated. Next-generation sequencing based metagenomics approach has many potential advantages in microbial genomics researches. Bacterial genomic DNA (gDNA) were isolated from *G. elata* tuber and soft rot tissue with tuber surface or cultivating soil, respectively. The isolated gDNA were identified by using PCR-based amplicon sequencing approach. A total of 889 taxa were detacted by 16S rDNA sequence and ITS analysis. We identified the based on amplicon sequencing of rDNA and ITS identity values, a total of 16 different phylum were found at the contaminated spawn; Acidobacteria (6%), Actinobacteria (14%), Armatimonadetes (1.5%), Bacteroidetes (6.8%), Chlorobi (0.9%), Chloroflexi (7.5%), Cyanobacteria (2.3%), Elusimicrobia (0.8%), Firmicutes (12%), Gemmatimonadetes (1.6%), Nitrospirae (1%), Planctomycetes (4%), Proteobacteria (31%), Spirochaetes (0.3%), Tenericutes (0.6%), Verrucomicrobia (3%) and others (6.7%). These results suggested that the isolated Proteobacteria are one of the candidate of tuber soft rot-associated pathogens.

Corresponding author: Tel. +82-31-290-1167, E-mail: pahkej@korea.kr

PC-36

Overexpression of a Novel Gene, E3 ubiquitin Ligase, Induce Coiled Branches (*cbr*) in Arabidopsis mutants

Gyu Tae Park[1], Jagadeesh Sundaramoorthy[1], Seokhyung Lee[1], Jeong-Dong Lee[1], Jeong Hoe Kim[2], Hak Soo Seo[3], Jong Tae Song[1*]

[1]School of Applied Biosciences, Kyungpook National University, Daegu, Korea
[2]Department of Biology, Kyungpook National University, Daegu, Korea
[3]Department of Plant Bioscience, Seoul National University, Seoul, Korea

The wild relatives of soybean [*Glycine soja* Sieb. and Zucc.] have curly/wavy nature whereas cultivated varieties are upright. To investigate the molecular mechanism of development contributing to coiled morphology, screening was carried out from Arabidopsis activation tagging lines obtained by activation T-DNA treatment that have curly/wavy morphology. The mutant named *cbr*, was found to have a wavy and curly morphology with *c*oiling *br*anches. 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. Ubiquitylation has been linked virtually to every cellular process including plant development. E3 ubiquitin ligase has been reported to recognize target proteins that are to be ubiquinated for further degradation by the proteasome complex. Therefore, we are performing 2-DE and Y2H experiments to find specific substrate(s) of the novel E3 ubiquitin ligase gene.

Acknowledgements: This work was carried out with the support of "Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ01108702)" Rural Development Administration, Republic of Korea.

Corresponding author: Tel. +82-53-950-7753, E-mail: jtsong68@knu.ac.kr

PC-37

Uncovering the Role of DDMP Saponins in Soybean Through Molecular Characterization of DDMP Saponin-deficient Mutants

Jagadeesh Sundaramoorthy[1], Gyu Tae Park[1], Seokhyung Lee[1], Jeong-Dong Lee[1], Hak Soo Seo[2], Jong Tae Song[1*]

[1]School of Applied Biosciences, Kyungpook National University, Daegu, Korea
[2]Department of Plant Bioscience, Seoul National University, Seoul, Korea

Saponins are a group of secondary metabolites available in soybean [*Glycine max* (L.) Merr.]. Soybean saponins are classified as group A and DDMP saponins. Group A saponins are undesirable component of food products due to bitterness and astringency. In contrast, DDMP saponins and their derivatives are not possessing bitterness and astringency but beneficial to human health when consumed as regular diet. The objective of the present study was to identify and characterize the gene which is encoding a protein responsible for biosynthesis of DDMP saponins, and then finally to reveal a role of saponins in soybean plants. We isolated two EMS mutant lines (PE2248 and PE2371) with DDMP-deficient saponins. The breeding cross has been made with these two mutants with two cultivars, Pungsannamul and Wooram to study the segregation and genetic linkage analysis, respectively. The segregation analysis showed that the mutant phenotype is controlled by single recessive gene. The position of locus (*Sg-7*) involved in the biosynthesis of DDMP deficient saponins was mapped using bulk segregation and dCAPS analysis on chromosome 16 (130 kb) between two SNP markers. The genomic sequencing of *Sg-7* gene showed a single nucleotide polymorphism in PE2248 (G626A) and PE2371 (C137T) mutant lines and new alleles were named *sg-7-a* and *sg-7-b*, respectively. Complementation between two mutations by crossing of PE2248 and PE2371 exhibited that the mutation sites lie on the same gene. The gene *Sg-7* will be further characterized by cloning and overexpression studies.

Acknowledgements: This work was carried out with the support of "Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ01108702)" Rural Development Administration, Republic of Korea.

Corresponding author: Tel. +82-53-950-7753, E-mail: jtsong68@knu.ac.kr

PC-38

The AT-hook Motif-containing Proteins AHL27 and AHL29 Regulate Hypocotyl Elongation by Enhancing Auxin Biosynthesis in *Arabidopsis*

Kyounghee Lee[1], Pil Joon Seo[1,2*]

[1]Department of Bioactive Material Sciences and Research Center of Bioactive Materials, Chonbuk National University, Jeonju 561-756, Korea
[2]Department of Chemistry and Research Institute of Physics and Chemistry, Chonbuk National University, Jeonju 561-756, Korea

Hypocotyl elongation is extensively controlled by hormone signaling networks. In particular, auxin metabolism and signaling play key roles in light-dependent hypocotyl growth. Nuclear matrix facilitates to organize exquisitely the DNA within the nucleus, and their dynamic interactions are related to gene regulation. The conserved scaffold/matrix attachment regions (S/MARs) are anchored to the nuclear matrix by the AT-HOOK MOTIF CONTAINING NUCLEAR LOCALIZED (AHL) proteins in *Arabidopsis*. Here, we found that the AHL27 and AHL29 redundantly regulate auxin biosynthesis in the control of hypocotyl elongation. The light-regulated AHL proteins bound directly to MAR regions of the *YUCCA 9* (*YUC9*) promoter and suppressed its expression to inhibit hypocotyl growth in light-grown seedlings. In addition, they also promoted deposition of repressive epigenetic marks, including H3K9me3 and H3K27me3, at the *YUC9* locus to further elaborately control auxin biosynthesis. In support of this, the long hypocotyl phenotype of dominant-negative *sob3-6* mutant in light was suppressed by auxin bionsynthesis inbitior, yuccasin and auxin transport inhibitor, 1-naphthylphthalamic acid. These results suggest that coordination of matrix attachment and chromatin modification underlies auxin biosynthesis in light-dependent hypocotyl growth.

Corresponding author: Tel. 82-63-270-3423; Fax. 82-63-270-3408, E-mail: pjseo1@jbnu.ac.kr

PC-39

Expression of Antimicrobial Peptides Thanatin(S) in Transgenic Rice Enhanced Resistance to Phytopathogenic Fungi and Bacteria

Yeo Jin Jung[1], Jong Hee Kim[1], Yu Jin Jung[1], Yong Gu Cho[2], Ill Sup Nou[3], Kwon Kyoo Kang[1*]

[1]Dept. of Horticultural life science, Hankyong National University, Ansung 456-749, Korea
[2]Dept. of Crop Science, Chungbuk National University, Cheongju 361-763, Korea
[3]Dept. of Horticulture, Sunchon National University, Sunchon 540-742, Korea

Thanatin(S) is an analog of thanatin, an insect antimicrobial peptide possessing strong and broad spectrum of antimicrobial activity. In order to investigate if the thanatin could be used in engineering transgenic plants for increased resistance against phytopathogens, the synthetic thanatin(S) was introduced into rice plants. To increase the expression level of thanatin(S) in plants, the coding sequence was optimized by plant-preference codon. To avoid cellular protease degradation, signal peptide of rice PR1 was fused to N terminal of thanatin(S) for secreting the expressed thanatin(S) into intercellular spaces. To evaluate the application value of thanatin(S) in plant disease control, the synthesized coding sequence of PR1 signal peptide (PR1SP)-thanatin(S) was ligated to plant binary vectors pPin-Bar (with FLAG tag). Meanwhile, in order to observe the subcellular localization of PR1SP-thanatin(S)-GFP and thanatin(S)-GFP, the sequences of PR1SP-thanatin(S) and thanatin(S) were respectively linked to pGWB5 (with GFP tag). The constructs were transformed into rice via Agrobacterium-mediated transformation. The transformants with PR1SP-thanatin (S)-FLAG fusion gene were analyzed by genomic PCR, real-time PCR, and western blots and the transgenic rice plants introduced respectively PR1SP-thanatin(S)-GFP and thanatin(S)-GFP were observed by confocal microscopy. Transgenic plants expressing PR1SP-thanatin(S)-FLAG fusion protein showed antifungal activity against, rice blast, as well as antibacterial activity against leaf blight. And the results from confocal observation showed that the GFP signal from PR1SP-thanatin(S)-GFP transgenic rice plants occurred mainly in intercellular space, while that from thanatin(S)-GFP transgenic plants was mainly detected in the cytoplasm and that from empty vector transgenic plants was distributed uniformly throughout the cell, demonstrating that PR1 signal peptide functioned. In addition, thanatin(S) and thanatin(S)-FLAG chemically synthesized have both in vitro antimicrobial activities against blast and leaf blight. So, thanatin(S) is an ideal candidate AMPs for the construction of transgenic crops endowed with a broad-spectrum resistance to phytopathogens and the strategy is feasible to link a signal peptide to the target gene.

Acknowledgements: This work was supported by a grant from the Next-Generation BioGreen 21 Program (The National Center for GM Crops, No. PJ011245) of the Rural Development Administration, Republic of Korea.

Corresponding author: Tel. 031-670-5107, E-mail: kykang@hknu.ac.kr

PC-40

Recurrent Parent Genome Recovery Analysis in a Marker Assisted Backcrossing (MAB) System of Tomato (*Solanum lycopersicum* L.)

Yu Jin Jung[1], Jong Hee Kim[1], Heo Ju Lee[1], Myoung Kwon Kim[2], Ill Sup Nou[3], Kwon Kyoo Kang[1*]

[1]Department of Horticulture, Hankyong National University, Ansung City, Gyeonggi-do, Korea
[2]Tomato Life Science and Research , Cheongju 28171, Korea
[3]Department of Horticulture, Sunchon National University, Jungangno, Suncheon, Jeonnam, Korea

Backcross breeding is the most commonly used method for incorporating a resistance gene into a rice cultivar. Linkage between the resistance gene and undesirable units can persist for many generations of backcrossing. Marker-assisted backcrossing (MABC) along with marker-assisted selection (MAS) contributes immensely to overcome the main limitation of the conventional breeding and accelerates recurrent parent genome (RPG) recovery. The MABC approach was employed to incorporate (a) TYLCV resistance gene(s) from the donor parent HAN 1, the TYLCV-resistant inbred line, into the genetic background of Red fruit, a popular high-yielding line that is TYLCV susceptible, to develop a TYLCV-resistant line improved variety. In this perspective, the recurrent parent genome recovery was analyzed in early generations of backcrossing using SNP markers. Out of 375 SNP markers, 70 markers were found polymorphic between the parents, and these markers were used to evaluate the plants in subsequent generations. Background analysis revealed that the extent of RPG recovery ranged from 65.50% to 90.3% and from 82.40% to 96.70% in BC1F1 and BC2F1 generations, respectively. In this study, the recurrent parent genome content in the selected BC2F2 lines ranged from 92.7% to 97.7%. The average proportion of the recurrent parent in the selected improved line was 95.98%. MAS allowed identification of the plants that are more similar to the recurrent parent for the loci evaluated in backcross generations. The application of MAS with the MABC breeding program accelerated the recovery of the RP genome, reducing the number of generations and the time for incorporating resistance against tomato pathogen.

Acknowledgements: This research was supported by the Golden Seed Project (Center for Horticultural Seed Development, No. 213003-04-1-SBC10), the Ministry of Agriculture, Food, and Rural Affairs (MAFRA), the Ministry of Oceans and Fisheries (MOF), the Rural Development Administration (RDA), and the Korea Forest Service (KFS).

Corresponding author: Tel. 031-670-5107, E-mail: kykang@hknu.ac.kr

PC-41

Identification of an SNP Variation of Elite Tomato (*Solanum lycopersicum* L.) Lines using Genome Resequencing Analysis

Yu Jin Jung[1,2], Hyo Ju Lee[1], Ill Sup Nou[3], Yong Gu Cho[4], Myong Kwon Kim[5], Hoy-Taek Kim[3], Kwon Kyoo Kang[1,2*]

[1]Department of Horticulture, Hankyong National University, Ansung 17579, Korea
[2]Institute of Genetic Engineering, Hankyong National University, Ansung 17579, Korea
[3]Department of Horticulture, Sunchon National University, Suncheon 57922, Korea
[4]Department of Crop Science, Chungbuk National University, Cheongju 28644, Korea
[5]Tomato Life Science and Research, Cheongju 28171, Korea

The completion of the tomato genome sequence and recent advances in DNA sequencing technology allow in-depth characterization of genetic variation present in the tomato genome. Cultivated tomato lines show low molecular but high phenotypic diversity. We resequenced the genomes of four elite tomato lines with an Illumina HiSeq 2000 sequencer. We generated, on average, 84 million 100-bp paired-end reads per line. Mapped reads covered 89.0-93.4% of the mapped *S. lycopersicum* reference genome (782 Mb). On average, 0.42 single nucleotide polymorphisms (SNPs)/kb and 0.05 short insertions and deletions (InDels)/kb were found in the four elite lines. The highest number of SNPs was 558,526 found in tomato line 13-1084. We identified many SNPs and InDels, derived from 1012 genes, in region 7-62 Mb of chromosome 5 in the four elite lines. The same pattern of multiple SNPs was detected on chromosome 5 in lines 13-1151 and 10-3321, deriving from genes in region 0-2 Mb, and many homozygous SNPs and InDels were detected on chromosome 1 of these two lines. The same pattern of multiple SNPs and InDels derived from genes located between regions 53-60 Mb of chromosomes 4 and 11 was found in the four elite lines. The SNPs and InDels identified in this resequencing study will serve as useful genetic tools and candidate polymorphisms in the search for DNA variations associated with valuable phenotypic diversity.

Acknowledgements: This research was supported by the Golden Seed Project (Center for Horticultural Seed Development, No. 213003-04-1-SBC10), the Ministry of Agriculture, Food, and Rural Affairs (MAFRA), the Ministry of Oceans and Fisheries (MOF), the Rural Development Administration (RDA), and the Korea Forest Service (KFS).

Corresponding author: Tel. 031-670-5107, E-mail: kykang@hknu.ac.kr

PC-42

The *Arabidopsis* RING Finger E3 Ligase MIEL1 Negatively Regulates Abscisic Acid Signaling by Promoting Protein Turnover of MYB96

Hong Gil Lee[1*], Pil Joon Seo[1,2]

[1]Department of Bioactive Material Sciences and Research Center of Bioactive Materials, Chonbuk National University, Jeonju 561-756, Korea
[2]Department of Chemistry and Research Institute of Physics and Chemistry, Chonbuk National University, Jeonju 561-756, Korea

Abscisic acid (ABA) is an essential phytohormone that regulates plant responses to various environmental challenges. Controlled protein turnover is an important molecular scheme in ABA signal transduction. Here, we report that the Really Interesting New Gene (RING)-type E3 ligase MYB30-Interacting E3 Ligase 1 (MIEL1), which is involved in the hypersensitive defense response, also regulates ABA sensitivity by promoting MYB96 turnover in *Arabidopsis*. Germination of *MIEL1*-deficient seeds was hypersensitive to ABA, whereas *MIEL1*-overexpressing transgenic seeds (35S:*MIEL1*) showed the reduced sensitivity during germination. MIEL1 interacts with MYB96, an unequivocal regulator of ABA signaling, and stimulates its ubiquitination for protein turnover. Genetic analysis further confirmed that *MIEL1* and *MYB96* act on a same genetic pathway in the control of ABA sensitivity. Together, these results suggest that the MIEL1 E3 ligase is an important regulator of ABA signaling and also acts as a pivotal crosstalk between abiotic and biotic stress signaling.

Corresponding author: E-mail: pjseo1@jbnu.ac.kr

PC-43

Reducing the Expression of *SSIVa* via ZFN Results in Dwarf Phenotype in Rice and Increased Level of Starch Content

Yu-Jin Jung[1], Franz Marielle Nogoy[2], Ill-Sup Nou[3], Jong-Seong Jeon[4], Yong-Gu Cho[2], Kwon-Kyoo Kang[1*]

[1]Department of Horticulture, Hankyong National University, Ansung 17579, Korea
[2]Department of Crop Science, Chungbuk National University, Cheongju 28644, Korea
[3]Department of Horticulture, Sunchon National University, Sunchon 57922, Korea
[4]Department of Genetic Engineering, Kyunghee University, Yongin 17104, Korea

Many successful studies on genome editing in plants have been published. One of the popular genome editing technology used in plants is Zinc Finger Nuclease (ZFN), which are chimeric proteins composed of synthetic zinc finger-based DNA binding domain and a DNA cleavage domain. The goal of this research is to utilize ZFNs to induce a double-stranded break in SSIVa, a soluble starch synthase involved in starch biosynthesis pathway, leading to the regulation of the SSIVa expression. The isoform SSIVa is not well studied, by modifying endogenous loci in SSIVa, we can explore on the specific roles of this gene in starch biosynthesis and other possible functions it might play. In this study, we produced transgenic plants with targeted mutagenesis in SSIVa displaying deletion and substitution events with respect to the original sequence of SSIVa. The transgenic plants exhibited low starch contents, dwarf phenotype and no grain filling. The mRNA expression of SSIVa in transgenic plants is lower than the wild type as expected while the expression of other starch synthesis related genes showed various levels of mRNA expression. Once again, we showed through this report that ZFNs can efficiently cleave and stimulate mutations at an endogenous target gene in rice and regulation of SSIVa can lead to reduced plant height, no grain filling and lower starch content.

Acknowledgements: This work was carried out with the support of “Cooperative Research Program for Agriculture Science & Technology Development (Project title: Breeding and Utilization of gene targeted mutagenesis in rice seed color, Project No. PJ01119202)”Rural Development Administration, Republic of Korea.

Corresponding author: Tel. 031-670-5104, E-mail: kykang@hknu.ac.kr

PC-44

Expression Analysis of Abiotic Stress Responsive Novel Genes in *Brachypodium distachyon* L.

Jin Seok Yoon[1], Jae Yoon Kim[2], Yong Weon Seo[1*]

[1]Department of Biosystems and Biotechnology, Korea University, Seoul 136-701, Korea
[2]Division of Biotechnology, Korea University, Seoul 136-701, Korea

Plants have been provoked by various harsh environmental stressed such as drought, salinity, cold and freezing. These stresses have a potential damage to the plant growth, development and crop productivity. One of novel gene which have been reported as charperone-like activity plays a role in transcriptional regulator by ABA and sugar signaling as well as resistance respond to abiotic stresses. The charperone-like activity genes were identified in various crops such as tomato, maize and rice but absence in *Arabidopsis*. Charperone-like activity genes from *Brachypodium distachyon* were reported 5 small family but the functions were still unclear. In this study, we identified 5 charperone-like activity genes in Bd21 line using database collection with BLASTP in *Brachypodium* database v3.1 (Phytozome 11). The sequence alignment and phylogenic analysis were performed to compare the orthologs from other crops. In order to identification of gene expression profiles, the qRT-PCR was carried out using gene specific primers in vegetative and reproductive tissues with ABA, PEG, NaCl and H_2O_2 treatment. ABA, PEG and H_2O_2 were up-regulated transcript accumulation in the leave at vegetative stage. Subcellular localization reveal that all charperone-like activity proteins targeted to plasma membrane. These results will be helpful for functional characterization to understand abiotic stress response mechanism in the monocot plants.

Acknowledgements: This work was carried out with the support of "Next-Generation BioGreen21 Program for Agriculture & Technology Development (Project No. PJ0110352016)" Rural Development Administration. Republic of Korea.

Corresponding author: Tel. +82-2-3290-3005, E-mail: seoag@korea.ac.kr

PC-45

Expression Analysis of Five *Arabidopsis* PDLP5 Homologous Genes in Watermelon During Biotic and Abiotic Stresses

Jong-Pil Hong, Hye-Young Suh, Jeong-Ho Kim, Yul-Kyun Ahn, Jinhee Kim, Eun Su Lee, Hye-Eun Lee*

Vegetable Research Division, National Institute of Horticultural and Herbal Science, RDA, 100, Nongsaengmyeong-ro, Iseo-myeon, Wanju-gun, Jeollabuk-do, Korea

Watermelon (*Citrullus lanatus* var. lanatus) is one of the important crops of South Korea. Although efforts have been made to generate disease-resistant varieties, defense signal pathway in watermelon is still unknown. *Arabidopsis* Plasmodesmata-located protein 5 (PDLP5) is known to control cell-to-cell communication and defense signaling. Five *Arabidopsis* PDLP5 (AtPDLP5) homologous genes were identified in watermelon, using the genome database. The five putative watermelon PDLPs had two GNK2 domains and showed high sequence identities to AtPDLP5. Their mRNAs were expressed in three watermelon varieties, PI189225, Au-Producer, and 920533. Each mRNA was differently expressed after infection of *Colletotrichum orbiculare*, *Didymella bryoniae*, and *Pseudomonas syringae*. In addition to pathogen infection, their expression patterns were different under abiotic stresses (drought, salt, and cold) and on salicylic acid treatment. The Cla006974 mRNA had an addition band in the 920533 variety treated with *D. bryoniae* or exposed to salt stress. Based on these findings, it is proposed that five putative watermelon PDLPs are involved in defense against fungal pathogen and abiotic stresses. Also, Cla006974 could be useful as a marker for the selection of resistant varieties in the molecular screening of the Gummy stem blight.

Corresponding author: E-mail: hongjp92@korea.kr

PC-46

Expression Analysis of Pepper Esterase (PepEST) Homologous Genes in Watermelon During Biotic and Abiotic Stresses

Jong-Pil Hong, Jeong-Ho Kim, Jinhee Kim, Yul-Kyun Ahn, Eun Su Lee, Hye-Eun Lee*

Vegetable Research Division, National Institute of Horticultural and Herbal Science, RDA, 100, Nongsaengmyeong-ro, Iseo-myeon, Wanju-gun, Jeollabuk-do, Korea

Watermelon (*Citrullus lanatus* var. lanatus) is one of the important crops of South Korea. Although efforts have been made to generate disease-resistant varieties, defense signal pathway in watermelon is still unknown. A pepper esterase (PepEST) is known to resistant against anthracnose fungus and control the expression of pathogenesis-related (PR) genes. Seven PepEST homologous genes were identified in watermelon, using the genome database and analysis of protein domain. The seven putative watermelon ESTs had abhydrolase domains and the consensus motif -GXSXG-. Among seven genes, five were expressed in three watermelon varieties, PI189225, Au-Producer, and 920533. Each mRNA was differently expressed after infection of *Colletotrichum orbiculare* and *Didymella bryoniae*. In addition to pathogen infection, their expression patterns were different under abiotic stresses (drought, salt, and cold) and on salicylic acid treatment. Based on these findings, it is proposed that five putative watermelon ESTs are involved in defense against fungal pathogen and abiotic stresses.

PC-47

Genome-wide Identification and Analysis of Rice Genes Preferentially Expressed in Pollen at an Early Developmental Stage

Tien Dung Nguyen[1], Sunok Moon[2], Van Ngoc Tuyet Nguyen[1], Yunsil Gho[2], Moon-Soo Soh[3], Jong Tae Song[1], Gynheung An[2], Sung Aeong Oh[1], Soon Ki Park[1], Ki-Hong Jung[2]

[1]School of Applied Biosciences, Kyungpook National University, Daegu 702-701, Korea
[2]Graduate School of Biotechnology and Crop Biotech Institute, Kyung Hee University,Yongin 446-701, Korea
[3]Department of Molecular Biology, Sejong University, Seoul 143-747, Korea

Microspore production using endogenous developmental programs has not been well studied. The main limitation is the difficulty in identifying genes preferentially expressed in pollen grains at early stages. To overcome this limitation, we collected transcriptome data from anthers and microspore/pollen and performed meta-expression analysis. Subsequently, we identified 411 genes showing preferential expression patterns in early developing pollen samples of both japonica and indica cultivars. The expression patterns of these genes are distinguishable from genes showing tapetum-preferred expression patterns in the inner most layer of the anther wall. Gene Ontology enrichment and MapMan analyses indicated that microspores in rice are closely linked with protein degradation, nucleotide metabolism, and DNA biosynthesis and regulation, while the tapetum is strongly associated with cell wall metabolism, lipid metabolism, secondary metabolism, and RNA biosynthesis and regulation. We also generated transgenic lines under the control of the promoters of eight microspore-preferred genes and confirmed the preferred expression patterns in plants using the GUS reporting system. Furthermore, *Cis*-regulatory element analysis revealed that pollen specific elements such as GTGANTG10, POLLEN1LELAT52, SITEIIATCYTC, and 5659BOXLELAT5659 were commonly identified in the promoter regions of eight rice genes. Our study will provide new sights on early pollen development in rice, a model crop plant.

Corresponding author: Tel. 053-950-7751, E-mail: psk@knu.ac.kr

PC-48

Application of Rice Microspore-preferred Promoters to Manipulate Early Pollen Development Through a Heterologous System

Tien Dung Nguyen[1], Sunok Moon[2], Moe Moe Oo[1], Rupesh Tayade[1], Moon-Soo Soh[3], Jong Tae Song[1], Sung Aeong Oh[1], Ki Hong Jung[2], Soon Ki Park[1*]

[1]School of Applied Biosciences, Kyungpook National University, Daegu 702-701, Korea
[2]Graduate School of Biotechnology and Crop Biotech Institute, Kyung Hee University, Yongin 446-701, Korea
[3]Department of Molecular Biology, Sejong University, Seoul 143-747, Korea

Based on microarray data analyzed with developing anthers and pollen grains, we identified nice *rice microspore preferred* (*RMP*) genes, designated as *RMP1* to *RMP9*. In this study, promoter activity of *RMP* originated from monocotyledonous rice was investigated in a heterologous system of dicotyledonous *Arabidopsis* for the extending of biotechnological applicability. The significant GUS expression during developmental stages from microspore to mature pollen was observed in transgenic plants driven by *RMP1, RMP3, RMP4, RMP5* and *RMP9* promoters. Interestingly, while the *RMP2* and *RMP6* directed GUS expression in pollen at early stage, uni-cellular and bi-cellular stages, *RMP7* and *RMP8* seems to be expressed at late stage, tri-cellular and mature pollen stages. Moreover, it was observed in eight promoters, *RMP3 to RMP9,* during the seedling stage, either in immature leaves and cotyledons or roots. To confirm microspore specific expression, the activity of three promoters was further verified through complementation analysis using *Arabidopsis* male-specific gametophytic mutant, *sidecar pollen-2* (*scp-2*), that showed defects in microspore development prior to pollen mitosis I. These results provided strong evidences for demonstrating that SCP driven by *RMP* promoters successfully complemented the *scp-2* mutation, strongly suggesting their potential applications for the manipulation of gene expression on target gene at microspore stage in various plants.

Corresponding author: Tel. 053-950-7751, E-mail: psk@knu.ac.kr

PC-49

A Conserved Oligomeric Golgi Complex Component-Related Protein is Essential for Pollen Development in Arabidopsis

Tien Dung Nguyen, Binbin Li, Sung Aeong Oh, Soon Ki Park*

School of Applied Biosciences, Kyungpook National University, Korea

To identify genes that play critical roles during male gametogenesis in Arabidopsis, we have isolated several pollen morphological mutants from a mutagenized seed pool generated with a T-DNA activation vector. In this study, we have focused on a mutant plant producing ~50% abnormal pollen grains at maturity. The pollen developmental analysis showed that the mutant pollen phenotype was first observed at late bi-cellular stage. Interestingly, the mutation was only maintained as a heterozygote due to the severely reduced genetic transmission through both sexes. TAIL PCR analysis led to the identification of the responsible gene which encodes a Conserved Oligomeric Golgi Complex Component-related protein (COGCC). RT-PCR and GUS-based analysis showed predominant expression of the gene in reproductive organs including developing spores. The gene identity was confirmed by the result that mutant plants harboring a T-DNA containing corresponding wild type gene produced less level of mutant pollen grains. Furthermore, confocal laser scanning microscopy using mature pollen expressing COGCC-RFP driven under the native promoter showed small punctate signals, which are likely to be from the Golgi complex. Further experiments for co-localization of the COGCC-RFP with the Golgi markers, COGCC- ST::GFP are underway.

Corresponding author: Tel. 053-950-7751, E-mail: psk@knu.ac.kr

PC-50

Analysis of Genome-wide Transcripts in Colored-grain Wheat Under Stress Condition

Dae Yeon Kim[1], Min Jeoug Hong[2], Woo Joo Jung[1], Chan-Seop Ko[1], Yong Weon Seo[1*]

[1]Department of Biotechnology, Korea University, Seoul 136-713, Korea
[1]Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, 29 Geumgu, Jeongeup 580-185, Korea

Nutritious and functional foods from crop have received great attention in recent years. Colored-grain wheat contains high phenolic compound and a large number of flavonoid. The anthocyanin and polyphenolic synthesis and accumualtion is generally stimulated in response to biotic or abiotic stresses. Here, we analysed genome wide transcripts in seedling of colored-grain wheat response to ABA and PEG treatment. About 900 and 1500 transcripts (p-value < 0.05) from ABA and PEG treatment were aligned to IWGSC1+popseq DB which is composed of over 110,000 transcripts including 100,934 coding genes. NR protein seqeunce of *Poaceae* from NCBI and protein sequence of transcription factors originated from 83 species in plant transcription factor database v3.0 were used for annotation of putative transcripts. Gene ontology analysis were conducted and KEGG mapping was performed to show expression pattern of biosynthesis genes related in flavonoid, isoflavonoid, flavons and anthocyanin biopathway. Total anthocyanin and phenol compound were measured and expression of flavonoid biosynthesis genes were showed by qRT-PCR to validate the results of RNAseq analysis.

Acknowledgement: This study was supported by the Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ01102102), Rural Development Administration, Republic of Korea.

Corresponding author: Tel. 02-3290-3464, E-mail: seoag@korea.ac.kr

PC-51

Genome-wide Detection of Single Nucleotide Polymorphisms (SNPs) Between Two Korean Tongil Type Rice Varieties

Hyun-Ju Kang[1], Eokkeun Ahn[2], Inchan Choi[1], Hye-Jin Yoon[1], Kyung-Hwan Kim[1], Hyeonso Ji[1*]

[1]Gene Engineering Division, Department of Agricultural Biotechnology, National Institute of Agricultural Sciences, Jeonju 560-500, Korea
[2]Department of Central Area, National Institute of Crop Science, Suwon 441-707, Korea

Closely related cultivars generally used for crossing in breeding lack sufficient known DNA polymorphisms with already developed DNA markers even though they exhibit remarkable phenotype difference in agronomically important traits. However, next-generation sequencing enables the identification of massive DNA polymorphisms such as single nucleotide polymorphisms (SNPs) between highly homologous genomes. We performed whole-genome resequencing of two Korean Tongil type rice varieties, Gayabyeo and Taebaegbyeo, which show remarkable difference in brown planthopper resistance. The sequencing yielded 18.5 X 10^9 bps for Gayabyeo, and 17.9 X 10^9 bps for Taebaegbyeo. After quality trimming and read mapping onto Nipponbare reference sequence, the final effective mapping depth was 27.6x for Gayabyeo and 25.5x for Taebaegbyeo. We detected 473,084 putative SNPs between Gayabyeo and Taebaegbyeo. We are developing CAPS (Cleaved Amplified Polymorphic Sequences) markers based on SNPs which are within restriction enzyme recognition sites. Up to now, 43 CAPS markers were developed and their genetic map was constructed by genotyping 180 F2 plants derived from a cross between Gayabyeo and Taebaegbyeo. More markers will be developed and we are going to map the brown planthopper resistance gene of Gayabyeo based on the developed markers.

Corresponding author: Tel. 063-238-4657, E-mail: jhs77@korea.kr

PC-52

The high-density Genetic Map of Perilla F2 Population by Genotyping-by-Sequencing (GBS)

Ji-Eun Kim[1], Bo Mi Lee[1], Bong-woo Lee[1], Moon Nam[1], Myoung Hee Lee[2], Tae-Ho Kim[3], Sung-Hwan Jo[1], Jeong-Hee Lee[1*]

[1]SEEDERS Inc., #N218, 11-3, Techno-1 ro, Yuseong-gu, Daejeon, 34015, Korea
[2]Legume and Oil Crop Research Division, National Institute of Crop Science, RDA, Miryang 50424, Korea
[3]Department of Agricultural Biotechnology, Genomics Division, Crop Genomics Laboratory, National Academy of Agricultural Science, RDA, Wanju 55365, Korea

For a high-quality reference genome of plant having complex and repetitive sequence, the high-density genetic map is essential. The diploid *P. citriodora* are the wild type collected from Jeju island and *de novo* genome assembly of *P. citriodora* is in progress. To make pseudomolecule of *P. citriodora* genome, we constructed the high density genetic map using *Ape*KI and *Pst*I-*Msp*I for GBS library of 96 F2 lines, derived from a cross between the *P. citrodora* and *P. hirtella*. Among 2,089,544 polymorphic single nucleotide polymorphisms (SNP) between the *P. citrodora* and *P. hirtella*, we picked out 36,365 and 9,607 SNP in *Ape*KI and *Pst*I-*Msp*I for GBS library, respectively, and made each SNP genotyping matrix. A high resolution genetic map was created with 1,205 and 1,326 SNP markers in *Ape*KI and *Pst*I-*Msp*I for GBS library, respectively. The GBS approach presented here provides a powerful method of developing high-density markers in species without a sequenced genome while providing valuable tools for anchoring and ordering physical maps and whole-genome shotgun sequence.

Corresponding author: Tel. 042-710-4035, E-mail: jhlee@seeders.co.kr

PC-53

Characterization of Cytochrome P450 (CYP) Genes Related to Saponin Biosynthesis in *Platycodon grandiflorum*

Sohyeon Park[1], Jemin Yoo[1], Yurry Um[2], Ok Tae Kim[2], Chang Pyo Hong[3], Seong-Cheol Kim[2], Yi Lee[1*]

[1]Department of Industrial Plant Science & Technology, Chungbuk National University, Cheongju 361-763, Korea
[2]Department of Herbal Crop Research, NIHHS, RDA, Eumseong 369-873, Korea
[3]TheragenEtex Bio Institute, Theragen Etex, Suwon 443-270, Korea

Platycodon grandiflorum is a perennial plant and a member of Campanulaceae family. Platycodin D is the richest saponin derived from *P. grandiflorum* and pharmacologically active component. Platycodin D is synthesized from triterpenoids by several kind of enzymes including Cytochrome P450 (CYP). CYP is known to exist in superfamily in plant kingdom, and essential roles in saponin biosynthetic pathway by hydroxylation or oxidation of triterpene skeletons. Recently, next generation sequencing (NGS) technology is rapidly developed as a method to discover target genes. In this study, we tried to identify CYP genes involved in saponin biosynthetic pathway from the various tissues of *P. grandiflorum* using RNA-seq analysis. The sequencing was performed using Illumina HiSeq platform after cDNA library preparation. The produced reads were assembled using CLC Genomics Workbench software (CLC Bio, Inc.). We obteined 122,663 contigs and found out 191 putative CYP genes.

Acknowledgement: This work was carried out with the support of "Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ01035104)" Rural Development Administration, Republic of Korea.

Corresponding author: Tel. 043-261-3373, E-mail: leeyi22@cbnu.ac.kr

PC-54

Analysis of Genetic Diversity in 5 *Codonopsis* Species Based on SSR Markers

Sohyeon Park[1], Serim Kim[1], Jinsu Gil[1], Yurry Um[2], Hee Chung[1], Ok Tae Kim[2], Ho Bang Kim[3], Seong-Cheol Kim[2], Yi Lee[1*]

[1]Department of Industrial Plant Science & Technology, Chungbuk National University, Korea
[2]National Institute of Horticultural and Herbal Science, Rural Development Administration, Korea
[3]Life Sciences Research Institute, Biomedic Co.,Ltd., Bucheon(420-852), Korea

Codonopsis is a flowering plant belongs to the family Campanulaceae. As currently recognized, two other groups, *Campanumoea* and *Leptocodon*, are included in the *Codonopsis*. The enlarged genus *Codonopsis* is distributed in Eastern, Southern, Central, and Southeastern Asia. *C. lanceolata*, *C. clematidea* and *C. pilosula* has many kinds of medicinal properties and this plants are used as medicinal and edible plants. *C. ovata* and *C. mollis* are distributed in Pakistan Kashmir and Himalaya mountains at an altitude of about 3,000 m, and flowers bloom in July to August. In this study, we analyzed the genetic diversity of 5 *Codonopsis* species using 8 SSR markers base on *C. lancelolata* genomic sequences. Samples were obtained from fresh leaves of 5 plants from each species and genomic DNA was extracted using CTAB method. PCR was performed in total 20μ l reaction volume containing 20 ng of DNA template and 5 pmole of primers. The amplified band sizes ranged from 74 to 301 bp, and clearly showed single or doble bands in eletrophoresis. From the phylogenetic analysis, *C. lanceolata* was grouped together, but the others were not grouped together according to the species. Therefore, we concluded that *C. lanceolata* cultivated in Korea is different from the other species, and the eight SSR markers used in this study are able to distinguish *C. lanceolata* from the other species.

Acknowledgement: This work was carried out with the support of "Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ01102202)" Rural Development Administration, Republic of Korea.

Corresponding author: Tel. 043-261-3373, E-mail: leeyi22@cbnu.ac.kr

PC-55

The CRISPR/Cas9-mediated Genome Editing in Banana Cells

Youjin Shin[1], Jin-Soo Kim[1,2], Jae-Young Yun[1*]

[1]Center for Genome Engineering, Institute for Basic Science, Daejeon, Korea
[2]Department of Chemistry, Seoul National University, Seoul, Korea

Bananas (*Musa* spp.) are perennial monocotyledonous herbs and the fourth most important food crop after wheat, rice, and corn. Most of current production relies on a single triploid cultivar called Cavendish. Currently, a lethal disease caused by the Fusarium fungus is a huge problem for Cavendish cultivation. The severity of the problem is attributed to the prevalent practices of tissue clonal propagation, thus making it vulnerable to a single deadly pathogen attack. By CRISPR/Cas9 genome editing, we plan to make Fusarium-resistant Cavendish bananas before this cultivar becomes extinct. The goals are that we identify the 'susceptibility' genes responsible for the fungal infection, and knock them out by using CRISPR/Cas9 to generate resistant 'patched' Cavendish banana. Here, we developed and demonstrated CRISPR/Cas9-mediated genome editing system in Cavendish banana. For "Proof-of-Principle" banana genome editing, we targeted *GA20ox2* and *PPO* genes in Cavendish protoplasts. We prepared mesophyll-originated protoplasts from young Cavendish leaves and delivered to them CRISPR/Cas9 as a ribonucleoprotein (RNP) form in the cells using PEG-transfection. We collected genomic DNA pools from the protoplasts harvested at 24 hours after RNP delivery, and analyzed global levels of targeted genome editing and resulting indel patterns via NGS amplicon sequencing. The data indicate that the efficiencies of CRISPR/Cas9-mediated genome editing, showing up to 13% in banana cells, are comparable to those of other crops' genome editing reported. The genomic indel patterns suggest that Cas9 nucleases were properly guided to target loci and the resulting double strand breaks followed canonical DNA-repair pathways in banana cells.

Corresponding author: Tel. 042-878-8305, E-mail: jae0yun@ibs.re.kr

PC-56

Development of Chloroplast InDel Markers to Distinguish *Angelica* Species

Sohyeon Park[1], Sangik Park[1], Jinsu Gil[1], Yurry Um[2], Hee Chung[1], Seong-Cheol Kim[2], Yi Lee[1*]

[1]Department of Industrial Plant Science & Technology, Chungbuk National University, Cheongju 28644, Korea
[2]National Institute of Horticultural and Herbal Science, Rural Development Administration, Eumseong 27709, Korea

Angelica gigas is a monocarpic biennial or short lived perennial plant. *A. gigas*, also called Dang Gui or Korean Angelica, is a major medicinal herb used in Asian countries such as Korea, Japan and China. In Korea, we are using the roots of *A. gigas*, but, they are using *Angelica sinensis* in China and using *Angelica acutiloba* in Japan to obtain many active constituents such as dercursin, decursinol angelate, nodakenetin, or nodakenin. The plants of *Angelica* genus are used to improve gynecological health. The biggest problem in the using of *A. gigas* would be the confusion with *A. acutiloba* or *A. sinensis.* In this study, we developed chloroplast InDel markers to distinguish *A. gigas, A. acutiloba* and *A. sinensis.* The markers were useful to distinguish *A. gigas, A. acutiloba, A. sinensis* and other *Angelica* species.

Acknowledgement: This work was carried out with the support of "Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ01102202)" Rural Development Administration, Republic of Korea.

Corresponding author: Tel. 043-261-3373, E-mail: leeyi22@cbnu.ac.kr

PC-57

High-throughput transcriptome analysis for identifying genes determining flowering time

Cheol-Won Lee, Yong Weon Seo*

Department of Biosystems and Biotechnology, Korea University, Seoul 136-701, Korea

Although vast factors and various cues related with flowering have been established, the pathway how the environmental cues affect the flowering and how the signals converge and regulate have not be clearly defined and remain complicated. Nevertheless, control of flowering time is a strongly important challenge in the crop improvement not only for fundamental studies but also for breeding aiming for early maturity. In this study, we investigate transcripts' levels relative to different flowering time with the exposed part of the wheat peduncle using two cultivars that have extremely different flowing time as well as maturity. With this, we also identify GO terms which genes specially function in the peduncle relative to different flowering time.

Acknowledgement: This work was carried out with the support of "Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ01103501)" Rural Development Administration. Republic of Korea.

Corresponding author: Tel. 02-3290-3005, E-mail: seoag@korea.ac.kr

PC-58

Candidate Gene Analysis for the Genes Controlling the Yellow Color in *Capsicum annuum* Cultivar Micropep

Ayoung Jung[1], Juhun Lee[1], Jin-Kyung Kwon[1], Suna Kim, Byoung-Cheorl Kang[1*]

[1]서울대학교 농업생명과학대학

Carotenoids are major pigments coloring yellow, orange and red in plants. In *Capsicum*, phytoene synthase (*PSY*), capsanthin-capsorubin synthase (*CCS*), β -Carotene hydroxylase (*Crtz-2*) and lycopene β -cyclase (*Lcyb*) were identified to be involved in the carotenoid synthesis pathway. Orange and yellow colors in pepper can be resulted from mutations in these four genes but the relationship between the colors and the four candidate genes has not been fully elucidated. We examined these four carotenoid biosynthesis genes and measured the carotenoid contents of *C. annuum* Micropep Red (MR), Micropep Yellow (MY) and their F_2 population. Micropep lines have dwarf phenotypes. Mutation of the two candidate genes, *PSY* and *CCS*, were identified in the MY line. These mutations of *PSY* and *CCS* genes cosegregated with the fruit colors in the F_2 population with a phenotypic ratio of 9:6:1(red:orange:yellow). In the F_2 population, red peppers (*PSY/CCS*) accumulate higher levels of total carotenoid than those of yellow peppers (*psy/ccs*). In the orange peppers, we were able to classify the carotenoid content profile according to genotypes of *PSY* and *CCS*. Total carotenoid content in type 1 (*PSY/ccs*) was much higher than that in type 2 (*psy/CCS*) but capsanthin was accumulated more in type 2 than type 1. These results show that *PSY* and *CCS* genes affect the fruit colors of pepper in different ways in the carotenoid pathway. Moreover markers developed in this study can be used to distinguish the fruit colors of pepper.

Corresponding author: Tel. 02-880-4563, E-mail: bk54@snu.ac.kr

PC-59

Identification of New Resistance Sources for *Cucumber mosaic virus* New Isolate-P1 (CMV-P1) in the Germplasm Collection of Capsicum spp.

Seula Choi[1], Myeong-Sook Han[1], Jin-Kwan Jo[1], Joung-Ho Lee[1], Eun-Ho Son[1], Byoung-Cheorl Kang[1*]

[1]Department of Plant Science, Plant Genomics & Breeding Institute, and Research Institute of Agriculture and Life Sciences, Seoul National University, Korea
[2]370, Nongsaengmyeong-ro, Wansan-gu, Jeonju-si, Jeollabuk-do, Korea

Cucumber mosaic virus is responsible for agronomic losses in many important crops worldwide. *Capsicum annuum* 'Bukang' Commercial F1 hybrid shows resistance to CMV-P0 strains (CMV-Kor and CMV-Fny). And the single dominant resistance gene, *Cmr1*, is known to control CMV resistance in 'Bukang'. Recently, a new isolate, CMV-P1, breaking the *Cmr1*-mediated resistance, about was identified in Korea. To find out the resistance sources, two thousands of *Capsicum* germplasm collections comprising cultivated and wild species were screened for resistance to CMV-P1. For the selection of resistance sources, two criteria were established: 1) CMV-P1 inoculated plants were evaluated once a week for a month, compared with susceptible controls ('Jeju' and 'Bukang') and one resistant control *C. annuum* 'LAM'. Symptomless peppers were selected as potential resistance plants. 2) For these candidate plants, CMV accumulation levels were evaluated with a double antibody sandwich (DAS)-enzyme-linked immunosorbent assay (ELISA). Finally 'Kathmandu-1', 'Kathmandu-2a' and 'Kathmandu-2b' have been selected as resistant plants. Taken together, with these newly identified CMV-P1 resistance sources can be used for CMV resistance pepper breeding.

Corresponding author: Tel. 02-880-4563, E-mail: bk54@snu.ac.kr

PC-60

Genetic Mapping of Resistance Sources Against ChiVMV (*Chili veinal mottle virus*) in Hot Pepper

Joung-Ho Lee, Jeong-Tak An, Koeun Han, Seula Choi, Muhammad Irfan Siddique, Byoung-Cheorl Kang*

Department of Plant Science, Plant Genomics & Breeding Institute, and Research Institute of Agriculture and Life Sciences, Seoul National University, Korea

Chili veinal mottle virus (ChiVMV) is the notorious virus affecting the severe loss of pepper production in Asia and Africa. To map the positions of ChiVMV resistance genes, F_2 mapping populations were constructed by crossing each resistance accession, *Capsicum annuum*, 'CV3', 'CV4', and 'CV8' with susceptible *C. annuum*, 'Jeju'. In the 'CV3' and 'CV8' mapping populations, resistance genes were inherited by a single dominant manner and located on the short arm of pepper chromosome 6. The ChiVMV resistance marker reported in the previous study was co-segregated with these genes. Through allelism test of resistance genes from 'CV3' and 'CV8', it was revealed that the resistance gene in each line was originated from the same locus, and we named this gene, *Cvr1* (ChiVMV resistance 1) locus. We developed several SNP markers linked to *Cvr1* using pepper genome information and pepper bacterial artificial chromosome (BAC) sequences. By contrast, the inheritance mode of ChiVMV resistance in CV4 was different from those of CV3 or CV8. The inheritance study showed that two independent complementary genes involved in ChiVMV resistance in CV4. To map the resistance genes in CV4, SNP-based linkage map was constructed by genotyping-by-sequencing (GBS) method. The result of this study will accelerate the ChiVMV resistance research and breeding resistance cultivar to ChiVMV in pepper.

Corresponding author: Tel. 02)880-4563, E-mail: bk54@snu.ac.kr

PC-61

Correcting Population Stratification in Pepper Core Collection for Genome-wide Association Studies (GWAS)

Hea-Young Lee*, Koeun Han, Jin-Kyung Kwon, Byoung-Cheorl Kang*

Department of Plant Science and Vegetable Breeding Research Center CALS, Seoul National University, Seoul 151-921, Korea

Genome-wide association study (GWAS) is an effective approach for identifying genetic variants associated to useful agronomic traits. GWAS has emerged as a powerful approach for identifying genes underlying complex diseases or morphological traits at an unprecedented rate. In such studies, it is very important to correct for population stratification, which refers to allele frequency differences between cases and controls due to systematic ancestry differences. Population stratification can cause false positive findings if not adjusted properly. As we are planning to perform GWAS for various agronomic traits in pepper, a genotyping-by-sequencing (GBS) approach was used to provide dense genome-wide marker coverage (>19,000 SNPs) for a 250 pepper core collection. 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. These results will not only find genetic variants among pepper accessions but also provide powerful evidence for reducing first positive error to perform GWAS in large scale studies.

Corresponding author: Tel. +82-2-880-4563, E-mail: sweettin@snu.ac.kr, bk54@snu.ac.kr

PC-62

Hormone Related Transcriptome Analysis of Wheat During Pre-harvest Sprouting and Exogenous ABA Treatment

Yong Jin Lee, Jae Yoon Kim, Yong Weon Seo*

Division of Biotechnology, Korea University, Seoul 02841, Korea

Wheat is one of the most produced and consumed food crop and its importance is consistently increasing. Nonetheless, the self-sufficiency of wheat in Korea is only 1.1% (except forage). Various unfavorable conditions on cultivating wheat such as abiotic and/or biotic stresses in Korea are the major problems. Especially as harvest of wheat overlaps with the rainy season, the premature germination, pre-harvest sprouting (PHS), is one of the main reason of poor wheat cultivation in Korea. PHS severely reduces yield and end-use quality, and consequently leads large economic losses in cereals. To understand and reveal the phytohormone effects on wheat germination and PHS, we analysed phytohormone biosynthesis and signaling pathway related transcriptome. Two Korean wheat cultivars 'Keumkang' and 'Uri', showing different germination index (GI) were used in this study. PHS and exogenous ABA were treated on the spikes of 35 days after flowering of each cultivar and total RNAs were extracted 1 week after treatment. Using HiSeq 2500, we obtained 104,542 and 98,607 of representative de novo assemblied transcripts for 'Keumkang' and 'Uri', respectively. Among the transcripts, about 780 of phytohormone related genes were isolated and differential expression heatmaps were made. These transcriptome analysis will provide important understandings of molecular mechanisms underlying details of germination and dormancy in cereals.

Acknowledgement: This work was supported by the National Research Foundation of Korea (NRF) grant funded by the Korea government (MSIP) (NRF-2014R1A1A1003621). This work was also carried out with the support of "Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ01103501)" Rural Development Administration. Republic of Korea.

Corresponding author: Tel. 02-3290-305, E-mail: seoag@korea.ac.kr

PC-63

Probing High-yield Traits of Soybean by Transforming Senescence-delay Genes

Hyun Suk Cho[1], Jin Ho Yang[1], Jin Sol Park[1], Hye Jeong Kim[1], Yoon Jeong Lee[1], Jae Seong Kim[1], Hyun Hee Im[1], Ki Jung Lee[1], Dong Hee Lee[2], Young Soo Chung[1*]

[1]Dept. of Genetic Engineering, Dong-A University, Busan, Korea
[2]Venture Bldg 306 Pohang Techno Park Pohang, Kyungbuk, 790-824, Korea

High yield is the most important trait in various agricultural characteristics. Many approaches to improve yield have been tried in conventional agricultural practice and recently biotechnological tools employed for same goal. Genetic transformation of key genes to increase yield is one way to overcome current limitation in the field. We produced transgenic soybean plants through high efficient transformation method by introducing all gene member with AT-hook binding domain, hoping to obtain manageable delay of senescence. Many transgenic soybean plants are growing in greenhouse and GMO field, and will be evaluated their senescence and any association with yield increase.

Corresponding author: Tel. 82-51-200-5683, E-mail: chungys@dau.ac.kr

PC-64

Transformation of Soybean with Improved Agricultural Traits of Insect Resistance and Drought Tolerance

Jae Seong Kim[1], Hyun Suk Cho[1], Hye Jeong Kim[1], Yoon Jeong Lee[1], Jin Ho Yang[1], Jin Sol Park[1], Hyun Hee Im[1], Ki Jung Lee[1], Jeong Il Kim[2], Soon Chun Jeong[3], Dong Hee Lee[4], Young Soo Chung[1*]

[1]Dept. of Genetic Engineering, Dong-A University, Busan, Korea
[2]Department of Biotechnology and Kumho Life Science Laboratory, Chonnam National University, Kwangju 500-757, Korea
[3]Bio Evaluation Center, Korea Research Institute of Bioscience and Biotechnology, Daejeon, Korea
[4]Venture Bldg 306 Pohang Techno Park Pohang, Kyungbuk, 790-824, Korea

Soybean is a crop of importance economically and nutritionally in many parts of the world. Thanks to many new genes brought from genomic research, It is possible to introduce various candidate genes through genetic transformation to see the performance of the genes in field. In our lab, soybean transformations have been tried for last 10 years to probe the possibility of traits improvement by transformation of new gene into soybean. For this purpose, three different genes were transformed into Korean soybean variety, Kwangan. First, the gene that controls early flowering of plant was transformed into Kwangan. Second, a candidate gene for insect resistance was transformed to produce transgenic plants. Third, another candidate gene for drought tolerance was transformed. All the transgenic plants were confirmed for gene introduction and their expression using PCR, real-time PCR, RT-PCR and Southern blot analysis.

Corresponding author: Tel. (82-51): 200-5683, E-mail: chungys@dau.ac.kr

PC-65

An Interspecific Genetic Linkage Map Based on RAPD and SSR in Citrus

Yali Chang[1], Eun-Ui Oh[1], Kyunguk Yi[1], Ho Bang Kim[2], Kwan Jeong Song[1*]

[1]Faculty of Bioscience & Industry, SARI, Jeju National University, Jeju 63243, Korea
[2]Life Science Research Institute, Biomedic Co., Ltd, Bucheon 14548, Korea

Based on double pseudo-testcross theory, a population of 152 F_1 seedlings, which were randomly selected from a cross of maternal 'Fina clementine' (*Citrus clementina* Hort. ex. Tan) and paternal 'Byungkyul' (*C. platymamma* Hort. ex. Tan.), was used to construct a genetic linkage map based on RAPD and SSR. The former species originated from Spain, as a non-apomitc genotype with high yield, easy peeling, and high-content fruit juice, and the latter is a primitive Korean citrus species with cold resistance and polyembryony. These two citrus genotypes, respectively cultivated in two geographically-distant regions in the early of citrus cultivation, are speculated to be highly polymorphism. A total of 840 random decamer oligonucleotide primers, 66 pairs of SSR primers developed from bacterial artificial chromosome end sequences (bSSR), and 150 pairs of genome-SSR (gSSR) primers developed from DNA sequences comparison by next generation sequence (NGS) technique on the platform of Illumina Hiseq 2500, were together screened against two parents and six F_1 seedlings. Next, 64 decamer oligonucleotide primers, 7 pairs of bSSR primers and 50 pairs of gSSR primers were selected for PCR amplification for the full-sib family. Finally, 82 RAPDs, 7 bSSRs and 47 gSSRs were sorted into two data sets and linkage maps for each parent were constructed with JoinMap 4.0 version. The map of 'Fina' clementine contained 41 markers distributed into 13 linkage groups (LGs), owned a whole length of 517.6 cM with an average distance of 12.6 cM. The map of 'Binguyl' included 58 markers distributed into 11 LGs, possessed the total map length of 670.8 cM with the similar average interval of 11.6 cM between markers.

Corresponding author: Tel. 064-754-3328, E-mail: kwansong@jejunu.ac.kr

PC-66

Molecular Characterization of Transgenic Plants Using Next Generation Sequencing and Bioinformatics.

Ji Hye Ohn[1*], Andre Silvanovich[2], Carl Garnaat[2], Colton Kessenich[2], Qing Tian[2]

[1]Monsanto Korea, Ltd, Seoul, Korea
[2]Monsanto Company, St. Louis, Missouri, U.S.A.

Molecular characterization of crops improved through biotechnology has traditionally been conducted using Southern blot analysis which has been used to determine T-DNA copy number, the presence or absence of backbone (sequence outside of the T-DNA) and to demonstrate generational stability of the T-DNA insert. The advancement of high-throughput DNA sequencing (HTS) technology allows efficient characterization of the transgene incorportated into the genome of the plant by rapidly sequencing the entire plant genome. By combining NGS (Next Generation Sequencing) technologies with bioinformatic methods that identify the T-DNA insert derived from the plasmid vector and genome-T-DNA junction sequences, it has been shown that conclusions equivalent to those of a Southern blot are readily obtained. To assure the validity of the conclusions, NGS reads are collected at median coverage depths of >75x across the entire genome, a value 2-3 fold greater than is used for clinical diagnosis of human disease. By mapping the sequence reads to the plasmid vector, and identifying the number of unique junctions, we can confirm insert number, copy number, and absence of backbone, across multiple generations. With the widespread availability of NGS technology and its steadily decreasing costs it is predicted that NGS-based method will easily be adopted for molecular characterization of transgenic plants.

Corresponding author: Tel. 02-3393-3765, E-mail: ji.hye.ohn@monsanto.com

PC-67

A Simple, Rapid and Systematic Method for the Developed T-DNA Insertion Population Rice

Hyemin Lim, A-Ram Kim, Hyun-Ju Hwang, Jung-Il Cho, Hyeonso Ji, Chang-Kug Kim, Soo-Chul Park, Gang-Seob Lee*

National Academy of Agricultural Science, Rural Development Administration, Jeonju 565-851, Korea

We have generated 383 independent transgenic lines for genetically modified (GM) rice that contained *PsGPD* (*Glyceraldehyde-3-Phosphate Dehydrogenase*), *ArCspA* (C*old Shock Protein*), *BrTSR15* (*Triple Stress Resistance 15*) and *BrTSR53* (*Triple Stress Resistance 53*) genes over-expression constructs under the control of the constitutive (CaMV 35S) promoter. TaqMan copy number assay was determined inserted T-DNA copy number. Also flanking sequence tags (FSTs) analysis was isolated from 203 single copy T-DNA lines of transgenic plants and sequence mapped to the rice chromosomes. In analyzing single copy lines, we identified 157 flanking sequence tags (FSTs), among which 58 (36%) were integrated into genic regions and 97 (62%) into intergenic regions. About 27 putative homozygous lines were obtained through multi-generations of planting, resistance screening and TaqMan copy number assay. To investigate the transgene expression patterns, quantitative real-time PCR analysis was performed using total RNAs from leaf tissue of single copy, intergenic region of T-DNA insertion and homozygous T2 plants. The mRNA expression levels of the examined transgenic rice were significantly increased in all of the transgenic plants. In addition, myc-tagged 35S:BrTSR15 and 35S:BrTSR53 transgenic plants were displayed higher levels of transgene protein. These results may be useful for producing of large-scale transgenic plants or T-DNA inserted mutants in rice.

Corresponding author: Tel. 063-238-4791, E-mail: kangslee@korea.kr

PC-68

Expression of a Putatively Stress-related Gene *BrTSR53* Isolated from Chinese Cabbage (*Brassica rapa*)

A-Ram Kim, Hyemin Lim, Hyun-Ju Hwang, Sung Han Park, Chang-Kug Kim, Hyeonso Ji, Jung-Il Cho, Soo-Chul Park, Gang-Seob Lee*

National Academy of Agricultural Science, Rural Development Administration, Jeonju, Jeonlado, Korea

Crops are exposed to various environmental stresses. These have been affecting the growth of crops, resulting in the severe loss of agronomic production in many countries. Therefore, development of new varieties of resistant crops is required to assure the desired productivity of crops in stress conditions. In this study, a putatively stress-related gene *BrTSR53* was isolated from *Brassica rapa*. The *BrTSR53* is 481 bp long and contains ORF region of 234 bp. The expression of *BrTSR53* was determined by quantitative real-time PCR analysis. After 3 hr, the highest quantities of mRNA were revealed in cold and salt stress treatments. In drought stress treatments, there was the highest expression after 36 hr. Therefore, it was confirmed that the ORF in *BrTSR53* should be a gene that confer increased resistance to *B. rapa* growing in different stress conditions. The ORF region of *BrTSR53* gene was cloned into an expression vector, pYES-DEST52, and a new protein with molecular weight of 13 kDa was detected by western blot analysis. Also, stress tolerance tests showed that BrTSR53-ORF transgenic yeast exhibited increased resistance to the salt stresses compared with the control. In conclusion, the present data predicts that novel ORF in *BrTSR53* can serve as an important genetic resource for abiotic stress resistance.

Corresponding author: Tel. 063-238-4791, e-mail: kangslee@korea.kr

PC-69

환경 스트레스 내성 유전자 *ABF3* 도입 국화 형질전환체 개발 및 특성 분석

박진선, 윤여진, 형남인*

충남 천안시 안서동 상명대학교 식물식품공학과

환경 스트레스 내성에 대한 식물의 반응기작에서 가장 중요한 조절인자는 ABA이다. 식물 호르몬인 ABA는 식물의 생장과 발달, 그리고 스트레스 적응에 중요한 많은 유전자들의 발현을 조절한다. ABA 의존성 경로의 전사조절인자 ABA-responsive element binding factor(ABF)는 삼투 스트레스 반응 유전자의 발현을 조절하여 건조 스트레스 내성을 증가시키는 역할을 한다. 애기장대에서 cloning된 *ABF3* 유전자를 CaMV 35S 프로모터와 Ubiquitin1 프로모터의 조절 하에 애기장대와 벼에 각각 이용하여 형질전환체를 만든 결과, 형질전환체가 증산 감소와 건조 내성을 보여주었다. 국내 농작물 중 화훼작물은 경쟁력이 높은 작물로 인식되어 보급이 증가하고 있는 반면, 재배 시 가뭄 홍수, 저온, 고온 등 여러 환경 스트레스 등으로 어려움을 겪고 있다. 따라서 본 연구에서는 *ABF3* 유전자를 도입하여 환경스트레스 내성 형질전환 국화를 개발하고자 하였다. 국화 스탠다드 품종 '신마'를 이용하여, *Agrobacterium tumefaciens*를 매개로 *ABF3* 유전자를 도입한 형질전환체를 개발하고자 실험을 수행하였다. 항시발현 프로모터인 CaMV 35S와 스트레스 유도성 프로모터인 IbSWPA2의 조절 하에 *ABF3*가 위치한 cassette를 pCKLSL에 각각 삽입한 vector를 제작하여 *Agrobacterium* LBA4404와 EHA105에 도입하였다. 잎 절편체에 *Agrobacterium*을 접종한 다음 잎 절편체를 3일동안 재생 배지에서 공동배양하였다. 그리고 공동배양이 끝난 잎 절편체를 phosphinothricin(PPT) 1.5 mg/L와 cefotaxime 250 mg/L가 포함된 선발 배지로 옮겨 주었다. 배양 8주 후, 선발 배지에서 배양한 절편체로부터 형성된 신초를 절단하여 PPT 1.5 mg/L가 포함된 신초신장배지에 옮겨 주었고, 4주마다 계대배양을 실시하였다. 재생된 신초 중 정상적으로 신장하면서 뿌리가 형성된 형질전환 계통을 선발하였다. 국화 '신마'의 형질전환을 통하여 독립적인 29개의 형질전환 계통을 선발하였고, 형질전환 효율은 5.6%로 나타났다. 형질전환 계통의 PCR과 RT-PCR을 통해 *ABF3*와 *bar* 유전자의 도입 및 발현을 확인하였다. 형질전환 계통을 온실에서 재배하여 표현형 분석(초장, 엽수, 경경) 및 건조 스트레스 조건에서의 반응 및 생리학적 특성을 분석하였다.

Corresponding author: Tel. 010-8809-5293, E-mail: nihyung@smu.ac.kr

PC-70

Genome-wide Characterization of Transcription Factors and Transcriptional Regulators in *P. ginseng*

Sang-Choon Lee[1], Murukarthick Jayakodi[1], Beom-Soon Choi[2], Nam-Hoon Kim[1], Junki Lee[1], Woojong Jang[1], Nomar Espinosa Waminal[1], Yun Sun Lee[1], Hyun-Seung Park[1], Ho Jun Joh[1], Jee Young Park[1], Sampath Perumal[1], Nguyen Binh[1], Hana Lee[1], Jinkyung Kim[1], Inseo Kim[1], Yeisoo Yu[2], Hyun Jo Koo[1], Tae-Jin Yang[1*]

[1]Department of Plant Science, Plant Genomics and Breeding Institute, and Research Institute of Agriculture and Life Sciences, College of Agriculture and Life Sciences, Seoul National University, Seoul, Korea
[2]Phyzen Genome Institute, Seongnam, Korea

Panax ginseng is the most famous medicinal plant representing Korea. However, *P. ginseng* is so susceptible to environmental factors such as heat stress that the stable cultivation and production of this plant are very difficult. On this account, to understand stress response mechanism and facilitate molecular study of *P. ginseng,* we identified gene families for transcription factors (TFs) and transcriptional regulators (TRs) from about 59,400 protein-coding genes predicted in *P. ginseng* draft genome sequence. As a result of TF searches based on conserved domains, a total of 3,588 genes were identified and classified into 66 TF gene families, which accounted for 6.1% of total annotated protein-coding genes in *P. ginseng*. The most abundant TF genes belonged to AP2/EREBP, bHLH, and MYB families. In addition, 17 TF genes were also identified to be over-represented in *P. ginseng* genome, compared to genome of carrot, a relative species of *P. ginseng* in the Apiales order. For TR genes, a total of 851 genes identified and classified into 25 TR gene families, which accounted for 1.4% of total annotated genes in *P. ginseng*. The most abundant TR genes belonged to SET, PHD, and SNF2 families. As a case study, heat shock transcription factor (HSF) gene family involved in heat response and tolerance was characterized in detail. This study was carried out with the support of “Cooperative Research Program for Agriculture Science & Technology Development (Project Nos. PJ01100801, PJ01103001)”, Rural Development Administration, Republic of Korea.

Corresponding author: Tel. 02-880-4547, E-mail: tjyang@snu.ac.kr

PC-71

DNA Fingerprinting Analysis of Rice Varieties Using a Core Set of Simple Sequence Repeats(SSR) Markers

Jee-Hwa Hong[1], Yong-Sham Kwon[2*]

[1]Seed Testing & Research Center, Korea Seed & Variety Service, Gimcheon 39660, Korea
[2]Department of Molecular Genetic Engineering, Dong-A University, Busan 49315, Korea

Simple sequence repeats(SSR) markers are one of the most suitable technique for DNA fingerprinting analysis. This marker has great discrimination power for varieties with narrow genetic background because of highly discrimination power, reproducibility of data production and different detection platform, and repeatability of overtime. Therefore, the working group on biochemical and molecular techniques (BMT) of the International Union for the Protection of New Varieties of Plants(UPOV) has recommended the use of SSR markers for genetic characterization of varieties.
The suitability of SSR markers for DNA fingerprint database were evaluated for 325 rice varieties. Of the 600 pairs of SSR primers screened against 11 rice varieties. a core set of 27 primer pairs were selected in accordance with 4 criteria such as high PIC (Polymorphism Information Contents) value, high repeatability, distinct PCR bands and evenly distributed across rice genome. A total of 353 polymorphic amplified fragments were obtained by using 27 SSR markers. The number of alleles per locus ranged from 9 to 22 with an average of 15.5 alleles per locus. The average polymorphism information content (PIC) was 0.734 ranging from 0.555 to 0.886. Three hundred fifty three SSR loci were used to calculate Jaccard's distance coefficients for UPGMA cluster analysis. These varieties were separated into several distinctive groups corresponding to varietal types. Almost all of the varieties were discriminated by SSR marker genotypes. This information may be useful to select comparative variety through comparison of genetic relationship analysis between existing variety and candidate varieties in distinctive tests.

Corresponding author: Tel. 051-200-7521, E-mail: yskwon3@dau.ac.kr

PC-72

들잔디 CIGR 유전자의 분리 및 특성분석

김양지[1], 양대화[2*], 송필순[2], 이효연[1,2*]

[1]제주대학교 생명공학부
[2]제주대학교 아열대원예산업연구소

잔디는 화본과에 속하는 다년생 초종으로, 한국 및 동남아시아, 미국 등에서 경기장, 골프장, 공원 등 다양한 장소에 분포하는 주요 원예작물이다. 잔디는 주로 생육적온에 따라 한지형과 난지형 잔디로 분류된다. 한지형 잔디는 추위에 강한 초종으로 대표적으로 크리핑벤트그래스(*Agrostis stolonifera*), 켄터키블루그래스(*Poa pratensis*) 등이 있다. 난지형 잔디는 여름철 고온 및 건조에 강하며 들잔디(*Zoysia japonica*), 갯잔디(*Zoysia sinica*), 금잔디(*Zoysia matrella*) 등이 속한다. 최근 들잔디는 학교 운동장 및 신도시 공원 조성에 많이 이용되고 있으나, 다른 잔디 품종에 비해 들잔디는 초장이 길어 예초를 자주 해야 하는 단점이 있기 때문에, 초장 및 줄기 길이가 짧은 왜성형질을 갖는 품종 개발이 필요하다. 따라서 우리는 식물 초장에 영향을 미치는 식물 특이적 GRAS protein family인 CIGR(chitin-inducible gibberellin-responsive) 유전자를 cloning 및 유전자 발현분석 중에 있으며, 추후 유전자 기능분석을 수행할 것이다.

Acknowledgements: 본 연구는 농림축산식품부 농림수산식품기술기획평가원 농림축산식품부사업(과제번호: 315025-3), 교육부 한국연구재단(No.2009-0094059)의 지원을 받아 연구되었음

Corresponding author: Tel. 064-754-3347, e-mail: hyoyeon@jeju.ac.kr

PC-73

Pyramiding of Two Rice Bacterial Blight Resistance Genes, *Xa3* and *Xa4,* and a Closely Linked Cold Tolerance QTL on Chromosome 11

Yeon-Jae Hur[1*], Jun-Hyeon Cho[1], Hyun-Su Park[2], Tae-Hwan Noh[2], Dong-Soo Park[1], Ji Yun Lee[1], Young-Bo Sohn[1], Dongjin Shin[1], You Chun Song[1], Young-Up Kwon[1], Jong-Hee Lee[3]

[1]National Institute of Crop Science, RDA, Miryang 50424, Korea
[2]National Institute of Crop Science, RDA, Wanju 55365, Korea
[3]Research Policy Bureau, RDA, Joenju, 54875, Korea

Bacterial blight (BB) caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) is a destructive disease of cultivated rice. Pyramiding BB resistance genes is an essential approach for increasing the resistance level of rice varieties. We selected an advanced backcross recombinant inbred line 132(ABL132) from the BC_3F_7 population derived from a cross between cultivars Junam and IR72 by K3a inoculation and constructed the mapping population (BC_4F_6) to locate the *Xa4* locus. The *Xa4* locus was found to be delimited within a 60-kb interval between InDel markers InDel1 and InDel2 and tightly linked with the *Xa3* gene on chromosome 11. After cold (4°C) treatment, ABL132 with introgressions of IR72 in chromosome 11 showed lower survival rate, chlorophyll content, and relative water content (RWC) compared to Junam. Genetic analysis showed that the cold stress-related quantitative trait locus (QTL) *qCT11* was located in a 1.3-Mb interval close to the *Xa4* locus. One line, ABL132-36, containing the *Xa3* resistance allele from Junam, the *Xa4* resistance allele from IR72, and the cold tolerance QTL from Junam (*qCT11*), was developed from a BC_4F_6populationof250plants. This is the first report on the pyramiding of *Xa3* and *Xa4* genes with a cold-tolerance QTL. This region could provide a potential tool for improving resistance against BB and low temperature stress in rice breeding programs.

Corresponding author: Tel. 063-238-0751, E-mail: ccriljh@korea.kr

PC-74

Genome-wide Transcript Analysis of Colored-grain Wheat During Grain Development

Dae Yeon Kim[1], Min Jeoug Hong[2], Yong Weon Seo[1*]

[1]Department of Biotechnology, Korea University, Seoul 136-713, Korea
[2]Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, 29 Geumgu, Jeongeup 580-185, Korea

Hexaploid wheat is one of the most important cereal crops for human nutrition. Molecular understanding of the biology of the developing grain will assist the improvement of yield for different environments. In addition, colored-grain wheat that contains high phenolic compound and a large number of flavonoid is useful material for the advancement of quality trait. The transcriptome from three different stages of developing caryopses in colored-wheat was determined using RNA sequencing. About 1200 and 3100 of significant transcripts (p-value < 0.05) from middle and late stages of grain development comparing with early stage of grain development were aligned to IWGSC1+popseq DB which is composed of over 110,000 transcripts including 100,934 coding genes. NR protein seqeunce of *Poaceae* from NCBI and protein sequence of transcription factors originated from 83 species in plant transcription factor database v3.0 were used for annotation of putative transcripts. Gene ontology analysis were conducted and KEGG mapping was performed to show expression pattern of biosynthesis genes related in flavonoid, isoflavonoid, flavons and anthocyanin biopathway. The expression profiling of genes related in anthocyanin biosynthesis and MYB transcription factors were conducted to validated the results of RNA sequencing analysis

Acknowledgements: This study was supported by the Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ01102102), Rural Development Administration, Republic of Korea.

Corresponding author: Tel. 02-3290-3464, E-mail: seoag@korea.ac.kr

PC-75

국화흰녹병균 검출용 특이 프라이머 개발

배신철[1*], 전푸름[1], 안호근[1], 안일평[1], 박상렬[1], 황덕주[1], 김정구[2]

[1]전북 전주시 완산구 농생명로 370 국립농업과학원 유전자공학과
[2]전북 전주시 완산구 농생명로 370 국립농업과학원 유전체과

우리나라 절화 국화의 재배면적은 2006년에는 805ha로 정점에 이르렀고 이후 지속적으로 감소하고 있지만, 절화류 중에서는 2012년 기준으로 판매액이 장미에 이어 두 번째로 많아 국내 화훼작물 중 큰 비중을 차지하고 있다. 국내외적으로 국화흰녹병은 국화에 심각한 피해를 주는 병해 중 하나이다. 국화흰녹병은 일단 발병하면 병원균의 특성상 단시간내에 비닐하우스 전체를 감염시키기 때문에 육안으로 병반을 확인하기 이전에 국화흰녹병 감염 여부를 확인하는 것이 병피해를 최소화할 수 있다. 국화흰녹병균 유전체 분석 정보를 이용하여 국화흰녹병균만 선별적으로 검출할 수 있는 프라이머를 선발하였다. 선발된 프라이머를 이용하여 국화에서 발병되는 국화역병균, 균핵병균 등 5종의 국화곰팡이 병원균 게놈 DNA를 대상으로 PCR 분석한 결과 국화흰녹병균만 특이적으로 PCR 증폭되는 것을 확인하였다. 또한 국화흰녹병균 특이적 검출을 위해 선발된 프라이머 세트를 이용하게 되면 국화흰녹병균 게놈 DNA를 20pg까지 검출이 가능하였다. 이는 국화흰녹병균 rDNA를 대상으로 PCR로 검출한 다른 그룹의 연구결과보다 5배 이상 민감도가 높음을 확인하였다. 또한 실시간 PCR을 실시하는 경우 국화흰녹병균 게놈 DNA 6pg까지 검출이 가능하였다.

Corresponding author: Tel. 063-238-4665, E-mail: scbae@korea.kr

PC-76

Sequencing Analysis Can Demonstrate the Presence and Intactness of Transgenic Events in the Biotechnology Stack Product

Andre Silvanovich[1], Bradley Comstock[1], Marianne Malven[1], Will Urquhart[1*], Hye Jung Hyun[2]

[1]Monsanto company, 800 North Lindbergh Boulevard, St.Louis, MO 63167, USA
[2]Monsanto Korea, STower, 82, Saemunan-Ro, Jongno-Gu, Seoul, 110-700, Korea

The breeding stack is developed using conventional breeding, which combines fully characterized and approved single events. Once stably integrated into the genome, the transgenic event behaves the same regarding inheritance and function as endogenous plant genes. Since conventional breeding does not produce new DNA or change the T-DNA sequence, the transgenic events in the stack are not different from those of the parental singles. Therefore, the safety assessment of single events can be directly applied to the safety of the stack since there is no change in the T-DNA or flanks in the stack. In this sense, it is sufficient to confirm that the transgenic events are present and intact in stack to demonstrate the parental lines are maintained in the stack. Historically, Southern blotting was utilized to confirm the T-DNA and flanks presence and intactness in the stack by comparing the fingerprint of the transgenic event from the single to the fingerprint of transgenic events from the stack. Recently, PCR/Sequencing has been performed to confirm the transgenic event's presence and intactness in stack. In this analysis, the sequences of the T-DNA and flanks from the stack are directly compared back to the T-DNA and flank sequences of the singles demonstrating that transgenic events are present and intact in the stack. Therefore, the sequencing analysis produces the equivalent endpoints as Southern blot analysis.

Corresponding author: Tel. 02-3393-3767, E-mail: hye.jung.hyun@monsanto.com

PC-77

Identification and Characterization of the Causal Agent of Gummy Stem Blight (GSB) from Melon, Watermelon and Cucumber in Korea

Md. Zahid Hassan, Hoy-Taek Kim, Jong-In Park, Ill-Sup Nou*

Department of Horticulture, Sunchon National University, 255, Jungang-ro, Suncheon, Jeollanam-do, 57922, Korea

Gummy stem blight (GSB) is one of the most destructive diseases of melon, watermelon and cucumber over the world as well as in Korea. During warm, humid climates in green houses and open field it becomes more destructive and causing serious yield losses. Five isolates (SCNUGSB 1 from melon, SCNUGSB 2 and SCNUGSB 3 from watermelon, SCNUGSB 4 and SCNUGSB 5 from cucumber) of GSB were collected from the field of cultivated region in Korea and cultured on potato-dextrose agar (PDA) medium to identify and characterize the causal agent which causes GSB on melon, watermelon and cucumber. Pathogenicity assays for virulence test and sequence characterization of the rDNA internal transcribed spacer (ITS) were performed of the five isolates. Based on pathogenicity assays the five isolates differed significantly on aggressiveness and rDNA-ITS sequences as well as phylogenetic analysis confirmed the isolates as *Didymella bryoniae*. The rDNA-ITS sequences also revealed that the five isolates were highly identical with the exception of one isolate (SCNUGSB 5) derived from cucumber and which was *Stagonosporopsis cucurbitacearum* (KF386571). We will develop the inoculation system of melon, watermelon and cucumber by using five isolates and molecular markers for the selection of resistant line and cultivars.

Acknowledgements: This research was supported by the Export Promotion Technology Development Program (Grant No. 312065-05-4-HD030) and Golden Seed Project (Center for Horticultural Seed Development, No. 213003-04-4-SB110) Ministry of Agriculture, Food and Rural Affairs (MAFRA), Ministry of Oceans and Fisheries (MOF), RDA and Korea Forest Service (KFS).

Corresponding author: Tel. 061-750-3249, E-mail: nis@sunchon.ac.kr

PC-78

Molecular Dissection of a Rice Nucleus-associated RING Finger Protein and its Potential Role in Salt Stress in *Arabidopsis*

Yong chan Park, Sandeep Chapagain, Dae Gyeom Oh, Cheol Seong Jang*

Plant Genomics Lab., Dept. of Applied Plant Sci., Kangwon Nat' l Univ., Chuncheon 200-713, Korea

As sessile organism, Plants have evolved mechanisms that allow them to adapt and survive periods of various environmental stresses. Among these stresses, salinity is one of the major adverse factors that adversely affect to plant growth and yield potential. Therefore, the ability to enhance the tolerance of crops to salinity stress, and have a potentially huge impact on productivity. In this study, we identified the molecular functions of a rice RING domain E3 ligase, *OsSARFP1* (*Oryza sativa* Salt and ABA induced RING finger protein 1), which is highly induced under salt and ABA conditions. Results of subcellular localization showed that the OsSARFP1 was located in cytosol (66%) and nucleus (34%) under non-treated conditions. However, after salt treatments, the florescence signals of OsSARFP1 was detected in nucleus (60%) higher than in cytosol (30%). Heterogeneous overexpresssion of *OsSARFP1* in *Arabidopsis* exhibited sensitive phenotypes with respect to Salt-responsive seed germination, seedling growth. In ABA conditions, *OsSARFP1* overexpression plants showed highly tolerance phenotypes, such as root length and stomatal closure. These findings might support to sensitive in salts stress via ABA-dependent regulations of related systems. Moreover, these results further demonstrate that the OsSARFP1 Ub E3 ligase might negatively regulate the cellular functions under salt stress conditions in rice

Corresponding author: Tel. 033-250-6416, E-mail: csjang@kangwon.ac.kr

PC-79

Tomato Fruit Ripening has been Delayed through The Regulation of Ethylene Biosynthesis Transcription Factors Under Sound Wave Treatment

Joo Yeol Kim*, Hye Ryun Ahn, Soo In Lee, Jin A Kim, Mi Jeong Jeong*

Department of Agricultural Biotechnology, National Institute of Agricultural Science (NAS), RDA, Jeonju 560-500, Korea

Regulation of tomato fruit ripening may help extend fruit shelf life and prevent losses due to spoilage. Here, tomato fruit were investigated whether sound treatment could delay their ripening. Harvested fruit were treated with low-frequency sound waves (1 kHz) for 6 h, and then monitored various characteristics of the fruit over 14-days at 23±1°C. Seven days after the treatment, 85% of the treated fruit were green, versus fewer than 50% of the non-treated fruit. Ethylene production and respiration rate were lower in the sound-treated than non-treated tomatoes. Furthermore, changes in surface color and flesh firmness were delayed in the treated fruit. The expression level of several ethylene biosynthesis-related genes was also influenced by sound wave treatment. But, there is a change the expression of the ethylene biosynthesis genes under sound wave treatment still remains a question whether the effect is direct or indirect. So, to investigate whether *RIN* and *HB-1* as a major transcription factor can directly activate the transcription of *ACS* and *ACO*, we performed transient assay in *Arabidopsis thaliana* and *Nicotiana tabacum*. The GUS activity of *ACS* and *ACO* by *RIN* was reduced after sound wave treatment and these of *ACS* and *ACO* by *HB-1* was also decreased except *ACO1* and *ACO3*. These results indicated that sound wave treatment was delayed tomato fruit ripening by regulation of ethylene biosynthesis-related genes through modulation of the expression of *RIN* and *HB-1* as a major transcription factor.

*These authors contributed equally to this work

Corresponding author: Tel. 063-238-4617, E-mail: center1097@korea.kr

PC-80

Identification of Genes Involved in Cucurbitacin E Biosynthesis

Young Cheon Kim[1], Sanghyeob Lee[1,2*]

[1]Plant Genomics Laboratory, Department of Plant Biotechnology, College of Life Sciences, Sejong University, 209 Neungdong-ro, Gwanjing-gu, Seoul 143-747, Korea
[2]Plant Biotechnology Research Institute, Sejong University, 209 Neungdong-ro, Gwanjing-gu, Seoul 143-747, Korea

Cucurbitacin E is a biochemical compound from the family of Cucurbitacins. These are found in plants which are member of the family Cucurbitaceae, most of them coming from traditional Chinese medicinal plants, but also in other plants such as pumpkins, wild watermelons and gourds. Cucurbitacin E is a highly oxidated steroid consisting of a tetracyclic triterpene. In this study we are trying to identify the genes involved in cucurbitacin biosynthetic pathway in Citrullus spp.

Acknowledgements: This work was supported by the grants from Korea-China Collaborative Research Program (NRF-2015K2A2A2001928) of NRF (National Research Foundation of Korea).

Corresponding author: Tel. 82-2-3408-4375, E-mail: sanglee@sejong.ac.kr

PC-81

Exploring Resistance Against *PHYTOPHTHORA CAPSICI* in Pepper

Muhammad Irfan Siddique, Koeun Han, Byoung-Cheorl Kang*

Department of Plant Science, Plant Genomics and Breeding Institute, and Vegetable Breeding Research Center, College of Agriculture and Life Sciences, Seoul National University, Seoul 151-921, Korea

Pepper (*Capsicum annuum*) is an economically important vegetable grown in tropical and temperate regions for fresh and processed use. *Phytopthora* blight and root rot caused by the oomycete pathogen *Phytophthora capsici* is the most devastating pepper disease in the world. Although many controlling methods are available including fungicide and resistance cultivars, the pathogen affects yield and quality adversely. Furthermore, breeding resistance against Pc is complicated because of complex mode of inheritance and progressive evolution in pathogen races. In present study, we detected two QTLs; *QTL5-1* and *QTL5-2* on chromosome P5 using an F_2 population cross between resistant accession CM334 and susceptible parent ECW30R, conferring resistance to low and high virulence Pc isolates, respectively, and evaluated their interaction with molecular markers anchoring in close vicinity. In addition, 548 F_4 lines were genotyped with 3 different SNPs markers linked to the two QTLs. Among these, 79 selected lines were subjected to genotyping-by-sequencing (GBS) analysis and screened with highly aggressive Pci solate. As a result, a new genetic linkage map was constructed using 1170 SNPs identified by GBS across 12 pepper chromosomes. QTLs effective against highly aggressive Pc isolate were mapped. The resistant QTLs and linked SNPs will be validated in recombinant inbred line and commercial cultivars. These markers will expedite the breeding programs for resistance introgression in high-yielding Pc susceptible cultivars.

Corresponding author: Tel. 82-2-880-4563, E-mail: bk54@snu.ac.kr

PC-82

The Regulation of *Brassica rapa* GIGANTEA Gene Expression is Available to Improvement of Salt Tolerance in Chinese Cabbage

Ha-eun Jung*, Mi Jeong Jeong, Soo In Lee, Jin A Kim*

Department of Agricultural Biotechnology, National institute of Agricultural Science, Rural Development Administration, 370, Nongsaengmyeong-ro, Wansan-gu, Jeonju-si, Jeollabuk-do, 560-500, Korea

Circadian clocks integrate environmental signals with internal cues to coordinate diverse physiological outputs. 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 show that the *GI* gene in *Brassica rapa* (*BrGI*) is similar to Arabidopsis *GI* in terms of both expression pattern and function. *BrGI* functionally rescued the late-flowering phenotype of the Arabidopsis *gi-201* loss-of-function mutant. RNAi-mediated suppression of *GI* expression in both Arabidopsis Col-0 and *B. rapa* DH03 increased tolerance to salt stress. Our results demonstrate that the molecular functions of GI described in Arabidopsis are conserved in *B. rapa* and suggest that manipulation of gene expression through RNAi and transgenic overexpression would enhance tolerance to abiotic stresses and thus improve agricultural crop production.

Corresponding author: Tel. 063-238-4619, E-mail: jakim72@korea.kr

PC-83

Diurnal Expression of Glucosinolate Genes in Brassica rapa Under Various Light Quality Conditions

Jin A Kim*, Ha-eun Jung, Soo In Lee, Mi Jeong Jeong

Department of Agricultural Biotechnology, National institute of Agricultural Science, Rural Development Administration, 370, Nongsaengmyeong-ro, Wansan-gu, Jeonju-si, Jeollabuk-do, 560-500, Korea

Light is critical importance to plants as a primary source of energy, while light intensity, spectral quality, and duration regulate most stages of plant development and maintain high photosynthetic efficiency. Plants have evolved sophisticated sensory photoreceptors, which coordinately judge the quality, quantity, direction, and duration of light, to regulate diverse photomorphogenic responses throughout their life cycle. To perceive light signal, one of the major environmental triggers, plants have evolved several different classes of photoreceptors to monitor light quality and quantity. Photon flux density, photoperiod, and light quality provided by LEDs affect plant biomass production, leaf and stem structure, growth habit, branching, tillering, or flowering characteristics. In the agricultural industries, LEDs are not used as only supplementary lighting but as main lighting source in the closed cultivation systems. Various light signals, acting through the photo receptors control the growth, affect development and metabolisms of plant. Light period during 1 day also affect various physiologies in plants. Glucosinolates are a major class of secondary metabolites involved in plant defence against pathogens. Recently, the levels of glucosinolates were found to be higher during the day than during the night. Re-illumination of such dark-adapted plants induced accumulation of mRNA for many genes of glucosinolate biosynthesis, leading to increased glucosinolate biosynthesis. We studied how glucosinolate biosynthesis changes in *Brassica rapa*. Seedlings under different light qualities.

Corresponding author: Tel. 063-238-4619, E-mail: jakim72@korea.kr

PC-84

Identification of Drought and Salt Stress-responsive Genes in Poplar (*Populus alba* × *P. glandulosa*)

Seo-Kyung Yoon[1,2], Eung-Jun Park[1], Eun-Kyung Bae[1], Young-Im Choi[1], Kyu-Suk Kang[2], Hyoshin Lee[1*]

[1]Department of Forest Genetic Resources, National Institute of Forest Science, 39 Onjeong-ro, Suwon, 441-847, Korea
[2]Department of Forest Sciences, Seoul National University, 1 Gwanak-ro, Seoul, 151-742, Korea

Drought and salt stresses are the major environmental stresses that adversely affect plant growth and productivity. To comprehensively identify genes responsible for stress tolerance, we analyzed the whole-genome expression profiles of poplar (Populus. alba × P. glandulosa) leaves exposed to drought and salt stresses. Among the genes that were responsive to drought or salt stress, we isolated 20 genes that were significantly expressed in stressed poplar. These genes can be classified into two groups. The first group consists of the genes encoding regulatory proteins. In particular, we identified three families of transcription factors, including NAC, homeodomain and bZIP, which were significantly induced by drought or salt stress. The second group comprised genes encoding functional proteins that act as downstream effectors in the stress response pathway. These included phosphorylase proteins, galactinol synthase (GolS), glutathione S-transferase (GST), a low temperature and salt responsive protein, late embryogenesis abundant (LEA), CAP160 protein and others. Among these, the gene encoding LEA protein was specifically induced under salt stress. Some of the genes were associated with drought and salt stresses, validating our findings. However, the largest group of salt stress induced genes encoded unknown proteins, as in the case of drought stress. Ten of the drought inducible genes were also induced by salt stress, including five genes encoding unknown proteins. These results indicate that some crosstalk takes place between the drought and salt stress responses, and these proteins of unknown function play important roles in the responses to drought and salt stress.

Corresponding author: Tel. 031-290-1174, E-mail: hslee@forest.go.kr

PC-85

Fine Mapping of the Root-Knot Nematode (*Meloidogyne incognita*) Resistance Gene *Me7* in Pepper (*Capsicum annuum*)

Amornrat Changkwian[1], Ji-Woong Han, Joung-Ho Lee, Gyung-Ja Choi[2], Byoung-Cheorl Kang[1*]

[1]Department of Plant Science, Plant Genomics and Breeding Institute, and Vegetable Breeding Research Center, College of Agriculture and Life Sciences, Seoul National University, Seoul 151-921, Korea
[2]Research Center for Biobased Chemistry, Korea Research Institute of Chemical Technology, Daejoen 305-600, Korea

Root-knot nematode (*Meloidogyne incognita*) is an endoparasitic roundworm that causes major damage to chili pepper worldwide. The pepper accession *Capsicum annuum* CM334 is known to carry a single dominant gene (*Me7*) against this parasite. The resistant gene is presumed to be located on the distal end of chromosome 9. In this study, several PCR based *Me*-specific markers as well as newly developed markers have been used to narrow down the target region of the *Me7*. An F_2 population derived from a cross between ECW30R and CM334 was used for construction of a linkage map. One of the *Me7* flanking markers was found to be located on a scaffold belong to chromosome 9 (1.7 Mb) and another one was located on chromosome 0 (0.3 Mb), which is yet to be assigned to a chromosome. The root-knot nematode resistant gene (*Mi*) in tomato belongs to a nucleotide binding and leucine-rich repeat (NB-LRR) gene family. Therefore, additional SNP markers will be developed from mRNA sequences coding for NB-LRR and nematode resistance-like proteins to facilitate mapping of the *Me7*.

Corresponding author: Tel. 82-2-880-4563, E-mail: bk54@snu.ac.kr

PC-86

The Construct of Backcross Inbred Line for *qSTV11*^{Z} Fine-mapping.

Sais-Beul Lee[1*], Yeon-Jae Hur[1], Tae Heon Kim[1], Dongjin Shin[1], Jun-Hyeon Cho[1], Sang-Ik Han[1], Un-Sang Yeo[1], You-Chun Song[1], Jong-Hee Lee[3], Yeong-Up Kwon[1], Kyung-Min Kim[2*], Dong-Soo Park[1*]

[1]National Institute of Crop Science, Miryang 50424, Korea
[2]Kyungpook National University, Daegu 41566, Korea
[3]Research Policy Bureau, RDA, Jeonju, 54875, Korea

Rice stripe virus (RSV) is one of the major constraints to rice production which is transmitted by the small brown planthopper (SBPH; *Laodelphax striatellus*). Typical symptoms of RSV are chlorosis and weakness of newly emerged leaves, white, yellow spot, stripe and necrotic on leaves, necrotic and wilting leaves, plant growth decline and the plants gradually die (Takahashi et al. 1991). Cultivation of resistance cultivar is the most economic and effective way to control RSV. The resistance genes, *Stv-a*, *Stv-b* and *Stv-b*^{i} have been reported in previous studies (Washio et al. 1968a). In this study, fine-mapping using 2100 BC_2F_2 plants derived from a backcross between susceptible recurrent parent, Ilpum and resistant donor parent, Zenith. Chromosome segment introgression lines that were heterozygous at a different region were selected, two type of hetero line was displayed a heterozygous genotype between Sid2 until Sid75 and Indel9 until RM6680. But didn't fined homo lines in the Sid2 until RM6680. We identification of a narrow down, *qSTV11*^{Z} region harboring *Stv-b* from Zenith.

Corresponding author: Tel. +82-55-350-1184, E-mail: parkds9709@korea.kr

PC-87

Analysis of QTL Markers for Drought Tolerance in Maize

Hyochul Kim[1], Kitae Song[1], Seungho Shin[1], Kyung-Hee Kim[1], Jun-Cheol Moon[2], Jae Yoon Kim[3], Byung-Moo Lee[1*]

[1]Department of Life Science, Dongguk University, Gyeonggi, 10326, Korea
[2]Agriculture and Life Sciences Research Institute, Kangwon Nat' Univ., Kangwon, 24341, Korea
[3]College of Life Science and Biotechnology, Korea Univ., Seoul, 02841, Korea

Maize is one of the most important food and cereal crop in the worldwide, but global climate change affects maize production in various ways. Among abiotic stress, drought stress has negative effects on the seedling stage, vegetative and reproductive growth stage, photosynthesis, root proliferation, anthesis-silking interval (ASI), pollination and grain yield. A total of 146 QTL markers related to grain yield, ear weight, kernel number per ear, ASI, root specificity, seedling survival, leaf ABA concentration and drought tolerance index were selected from previous publications. NAM population (B73, CML103, CML228, CML277, CML322, CML69, Ki3, Ki11, Ky21, M37W, Ms71, NC350, Oh43 and Tzi8), Korean commercial (Cheongdaok, Gangdaok, Ilmichal, Kwangpyeongok and Pyeonganok), Southeast Asia commercial (DK9955, LVN-4 and 333) and CML270 were evaluated ASI under drought and well-watered conditions in the greenhouse at Dongguk university. In this report, we performed a genotype-phenotype analysis of ASI and 146 QTL markers that was based on drought tolerance (Ki11) and susceptibility (Ki3). We found three drought tolerance markers and eight susceptible markers. These markers will support molecular breeders to develop drought tolerant maize species.

Acknowledgment: This work was carried out with the support of "Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ009939201)" Rural Development Administration, Republic of Korea.
This research was supported by 213001-04-4-SB920, Ministry of Agriculture, Food and Rural Affairs (MAFRA), Ministry of Oceans and Fisheries (MOF), Rural Development Administration (RDA) and Korea Forest Services (KFS).

Corresponding author: Tel. 031-961-5130, E-mail: bmlee@dongguk.edu

PC-88

Development of Potyvirus Resistance in Non-transgenic Tomato Plants Using CRISPR/Cas9 Technology

Saminathan Subburaj[1], Luhua Tu[1], Yong-Tae Jin[1], Sangsu Bae[2], Geung-Joo Lee[1*]

[1]Department of Horticulture, Chungnam National University, Daejeon 305-764, Korea
[2]Department of Chemistry, Hanyang University, Seoul 133-791, Korea

Tomato (*Solanum lycopersicum* L.) belongs to the Solanaceae, which is economically an important vegetable crop and highly vulnerable to viruses in the potyvirus family. The eukaryotic translation initiation factor *eIF4E* family have been found as major determinants of plant susceptibility to potyviruses. However, the identification and functional characterization of these *eIF4E* genes in important crop is often limited. CRISPR/Cas9 (Clustered Regularly Interspaced Short Palindromic Repeats) system has been emerged as a powerful molecular breeding tool for site directed mutagenesis in higher plants. To investigate the further role of *eIF4E* in virus resistance of tomato we set up a CRISPR/Cas9 system in four different cultivars (Summer King, Sweet King, Minipop and Micro Tom) to mutate normal function of *eIF4E* using direct delivery of purified Cas9 protein and single guide RNA (sgRNA) into isolated protoplast cells. After transient introduction of RNA-guided endonuclease (RGEN) ribonucleoproteins (RNPs) with different sgRNAs targeting *eIF4E*, mutagenesis at the targeted loci of tomato cultivars of protoplast transfectants were confirmed by cloning of *eIF4E* loci and targeted deep sequencing. Small deletions and single nucleotide polymorphisms (SNPs) were observed in the cloned nucleotide sequences of *eIF4E*s of protoplast transfectants, but not in putative off-target sites. Targeted deep DNA sequencing analysis revealed mutation rates produced collectively by the three eIF4E-RGEN target sites were ranged from 2% to 6.8% with an average of 3.8 ± 1.01% in DNA fragments of analyzed protoplast transfectants of Minipop cultivar. Our results demonstrated that direct delivery of RGEN RNPs into protoplast cells of tomato can be exploited as an efficient tool for generating potyvirus resistance genes in important crops without the use of transgenic approaches.

Corresponding author: Tel. +82-42-821-5734, E-mail: gjlee@cnu.ac.kr

PC-89

Fine Mapping and Identification of Candidate Genes for the *sy-2* Locus in a Temperature-sensitive Chili Pepper (*Capsicum chinense*)

Li Liu[1], Jelli Venkatesh[1], Yeong Deuk Jo[1], Sota Koeda[2], Munetaka Hosokawa[2], Jin-Ho Kang[3], Byoung-Cheorl Kang[1*]

[1]Department of Plant Science and Plant Genomics and Breeding Institute, Seoul National University, Seoul 151-921, Korea
[2]Department of Agronomy and Horticultural Science, Graduate School of Agriculture, Kyoto University, Sakyo-ku, Kyoto 606-8502, Japan
[3]Crop Biotechnology Institute/ GreenBio Science and Technology, Seoul National University, Pyeongchang 232-916, Korea

Seychelles-2 ('*sy-2*') is a temperature-sensitive natural mutant of *Capsicum chinense,* which exhibits an abnormal leaf phenotype when grown at temperatures below 24°C. We previously showed that the *sy-2* phenotype is controlled by a single recessive gene, *sy-2*, located on pepper chromosome 1. In this study, a high-resolution genetic and physical map for the *sy-2* locus was constructed using two individual F_2 mapping populations derived from across between *C. chinense* mutant '*sy-2*' and wild-type 'No.3341'. The *sy-2* gene was fine mapped to a 138.8kb region between markers SNP 5-5 and SNP 3-8 at the distal portion of chromosome 1, based on comparative genomic analysis and genomic information from pepper. The *sy-2* target region was predicted to contain 27 genes. Expression analysis of these predicted genes showed a differential expression pattern for *ORF10* and *ORF20* between mutant and wild-type plants; with both having significantly lower expression in '*sy-2*' than in wild-type plants. In addition, the coding sequences of both *ORF10* and *ORF20* contained single nucleotide polymorphisms (SNPs) causing amino acid changes, which may have important functional consequences. *ORF10* and *ORF20* are predicted to encode F-box proteins, which are components of the SCF complex. Based on the differential expression pattern and the presence of nonsynonymous SNPs, we suggest that these two putative F-box genes are most likely responsible for the temperature-sensitive phenotypes in pepper. Virus induced gene silencing was carried out to probe to the candidate gene's function.

Corresponding author: E-mail: bk54@snu.ac.kr

PC-90

Identification and Molecular Characterization of Novel Genes Under Abiotic Stresses from *Triticum aestivum* L.

Jin Seok Yoon[1], Jae Yoon Kim[2], Yong Weon Seo[1*]

[1]Department of Biosystems and Biotechnology, Korea University, Seoul 136-701, Korea
[2]Division of Biotechnology, Korea University, Seoul 136-701, Korea

Wheat is one of the staple crops for mankind in the world. Despite effort of maintenance for productivity and quality, wheat production is adversely affected by multiple environmental stresses such as drought, heat, cold and salinity. To understand and improve the resistance for environmental stress in wheat, gene expression profiles were studied for environmental stress related gene. Recently, abscisic acid-, stress-, and ripening-related genes have been identified in various species of dicot and monocot plants. One novel gene, charperone-like gene, have been reported as transcriptional regulator, related to cell protection and respond to abiotic stresses. In this study, we identified several charperone-like genes in the wheat leaves by database collection from Ensembl Plant database. The phylogenetic analysis revealed that charperone-like genes in wheat classified with two groups. In order to identification of expression profiles, qRT-PCR was performed for these genes with gene specific primers. Generally, charperone-like genes was accumulated the transcripts in the leave, stem, and root. Additionally, their expression was up-regulated with PEG or H_2O_2 treatment, but NaCl treatment. These findings have important implications in the molecular mechanisms of plant response against abiotic stresses.

Acknowledgements: This work was carried out with the support of "Next-Generation BioGreen21 Program for Agriculture & Technology Development (Project No. PJ0110352016)" Rural Development Administration. Republic of Korea.

Corresponding author: Tel. +82-2-3290-3005, E-mail: seoag@korea.ac.kr

PC-91

황기의 계통분류를 위한 유전체기반 분자마커 개발

허목[1*], 엄유리[1], 길진수[2], 박소현[2], 이이[2], 정진태[1], 김연복[1], 김성철[1], 정찬식[1]

[1]농촌진흥청 국립원예특작과학원 인삼특작부 약용작물과
[2]충북대학교 농업생명환경대학 특용식물학과

황기는 식용과 약용으로 사용되는 주요 약초임에도 불구하고 유전체 기반 연구가 미흡한 실정이다. 유전체 분석기반을 통한 약용작물의 유전육종 시스템 도입은 기원정립 뿐만 아니라 기존의 전통육종에 큰 영향을 미칠 것이다. 황기 재료는 국립원예특작과학원 인삼특작부 시험포장에서 재배중인 풍성, 아성과 지역수집종인 제천, 산청 그리고 해외수집종인 중국 길림(총 5계통)을 사용하였다. 각 계통의 잎 100mg에서 DNeasy Plant Mini Kit (QIAGEN GmbH, Hilden, Germany)을 이용하여 DNA를 추출하였다. 이렇게 얻어진 5종의 황기 DNA를 이용하여 시퀀싱을 위한 라이브러리를 제작하였다. 분석장비는 illumina Hiseq2000을 이용하였다. 생산된 염기서열은 *De novo* assembly하여 450,449개의 contig를 얻을 수 있었고 반복서열을 두 개의 염기서열이 2번이상 반복되는 선발기준을 통해 추출하였더니 147,766개의 simple sequence repeat(SSR) 마커 후보를 얻을 수 있었다. CLC genomics workbench 프로그램을 이용하여 5계통의 황기에 대해 변이를 보이는 949개 SSR 마커를 선발하였다. data mining을 통하여 명확한 변이가 추정되는 99개 SSR마커를 우선선발 하였고 이들 중 17개 SSR마커에 대해 프라이머를 제작하여 fragment analysis 한 결과 5계통의 황기에서 유전적 다형성을 확인할 수 있었다. 본 연구의 자료는 향후 순계선발 및 계통육성을 통한 황기 품종 등록 시 표지자로 활용하여 국내 황기 육성 품종에 대한 지적재산권 확보에 크게 기여할 수 있을 것으로 사료된다.

Corresponding author: Tel. 043-871-5562, E-mail: mok0822@korea.kr

PC-92

Development of Genetic Map and QTLs for Stem Diameter Using New CAPS Markers in MGRIL Population

Ye Ji Lee[1], Eun-Ju Byeon[1], Seon-Hwa Bae[1], Hyeonso Ji[2], Gang-Seob Lee[3], Ung-Han Yoon[1], Tae-Ho Kim[1*]

[1]Genomics Division, National Institute of Agricultural Science, RDA, Jeonju, 54874, Korea
[2]Genetic engineering Division, National Institute of Agricultural Science, RDA, Jeonju, 54874, Korea
[3]Biosafety Division, National Institute of Agricultural Science, RDA, Jeonju, 54874, Korea

The rice recombinant inbred lines derived from Milyang23 and Gihobyeo cross were used in genetic mapping and QTL analysis studies. In this study, we developed a new 101 CAPS markers based on the SNPs in the whole genome region between these varieties. As a result, the total genetic distance and average distances were 1,696.97 cM and 3.64 cM, respectively. In comparison to the distance of the previous genetic map constructed based on 365 DNA markers, the new genetic map was found to have a decreased distance. The map was applied for the detection of QTLs on all seven traits relevant to diameter of stem internode, length of culms, length of panicles and the number of panicles including the correlation analysis between each trait. The QTLs results were similar to the report in previous studies, whereas the distance between the markers was narrowed and accuracy increased with the addition of 101 CAPS markers. A total of 9 new QTLs were detected for stem internode traits. Among them, qI1D-6 had higher LOD of 5.1 and phenotype variation of 50.92%. In this experiment, a molecular map was constructed with CAPS markers using next generation sequencing showing high accuracy for markers and QTLs. In the future, developing more accurate QTL information on stem internode diameters with various agriculturally important traits will be possible for further rice breeding.

PC-93

Perilla Genome Sequencing

Seon-Hwa Bae[1], Myoung-Hee Lee[2], Jeong-Hee Lee[3], Ye-Ji Lee[1], Eun-Ju Byeon[1], Ung-Han Yoon[1], Tae-Ho Kim[1*]

[1]Genomics Division, National Academy of Agricultural Science, RDA, Jeonju, 560-500, Korea
[2]Upland Crop Breeding Research Division, National Institute of Crop Science, RDA, Milyang, 627-701, Korea
[3]SEEDERS, INC. Daeduk Industry-Academic Cooperation Building, Daejeon, 305-509, Korea

Perilla is a self-pollinating annual herb plant of the *Laminaceae* family and has been mainly cultivated as an oil crop in East Asia. The Perilla plant has been known to consist of 2 species, cultivar (2n=4x=40) and wild (2n=2x=20), respectively. Recently due to the increased demands for functional foods, the structural and functional characteristics of perilla genome have been heavily focused. Here we report a progress of de novo genome assembly of *P. citriodora.* We undertook a draft de novo genome assembly by combining data from multiple sequencing platforms using various libraries with different insertion sizes. Using total 643.9 Gb (about 985.3 X coverage) merged with two assemblies (platanus and falcon), the genome was assembled into 1,622 scaffolds with 12,325,979 bp (N50). The platanus assembled genome is composed of 22,112 protein coding genes. To verify the assembly of P. *citriodora* genome, BAC clones were constructed with *HindIII* and *BamHI* digestion, yielding insert size of 102 kb and 80 kb, respectively. The results above will provide important information of the genome structure to understand the functional genomics of perilla.

PC-94

Development of Functional Molecular Markers for Cabbage Breeding

Hayoung Song[1], Ill-Sup Nou[2], Yoonkang Hur[1]

[1]Department of Biological Sciences, College of Biological Science and Biotechnology, Chungnam National University, Daejeon, Korea
[2]Department of Horticulture, Sunchon National University, Suncheon, Jeonnam, Korea

Various molecular markers, such as SSRs and SNPs, have been widely used in plant breeding. This type of MAS (marker assisted selection) has long been used in the breeding programs to improve yield, quality, and resistance to abiotic and biotic stresses. Cabbage (*Brassica oleracea*) is important vegetable crops in the world and its importance in Korea gradually increasing. To assist cabbage breeding to develop the most elite lines, we have tried to develop gene-based functional molecular markers associated with important crop traits. As results, we have developed FMMs from intron, exon as well as promoter regions, which are related to quality and resistances to abiotic stresses. In poster, we will discuss all inforations on these markers. [This research was supported by research grants from Golden Seed Project (Center for Horticultural Seed Development, 213003-04-4SB230), Ministry of Agriculture, Food and Rural Affairs (MAFRA), Ministry of Oceans and Fisheries (MOF), and Rural Development Administration (RDA)]

PC-95

Classification of Flowering Time and Maturity Locus Genotyping of Elite Soybean Cultivars in Korea

Kil-Hyun Kim[1*], Min-Jung Seo[1], Myoung-Ryoul Park[1], Chang-Hwan Park[1], Jung-Kyung Moon[2], Byung Joo Kim[1]

[1]National Institute of Crop Science, RDA, Suwon, 16429, Korea
[2]National Institute of Crop Science, RDA, Wanju, 55365, Korea

Flowering time is one of the major agronomic traits because it is critical for plant adaptation to different latitudes and crop productivity. Soybean (Glycine max (L.) Merr.) is controlled by interactions among photoperiod, temperature, and its genotype. To date, nine maturity loci (*E1* to *E8* and *J*) have been reported to control flowering time and maturity in soybean. Although the molecular basis of four major loci (*E1* to *E4*) have been deciphered, genotypes of Korean soybean cultivars have not identified with these loci. In this study, we genotyped 61 cultivars at *E1* to *E4* genes, meanwhile, flowering time of those cultivars were investigated at Suwon in Korea from 2013 to 2014 and further confirmed in 2015. These soybeans were separated into three main groups which were early (35.6±3.8), mid (49.2±2.9), late (59.3±3.3) on the basis of the flowering time. Four loci of 61 Korean soybean cultivars classified by the usages were genotyped by using 15 allele-specific DNA markers. The percentages of recessive alleles at *E1*, *E2*, *E3*, and *E4* loci were 11.5%, 63.9%, 34.4%, and 0%, respectively. These cultivars had diverse flowering time and showed various allelic combinations. Interestingly, there were no Korean soybean cultivars with recessive *e4-sore1* alleles suggested by the importance for adaptation to long days at high latitudes. Also, the recessive allele *e1-as* only existed in early-flowering cultivars. Overall, this study could provide helpful information about development of new cultivars for adaptation to high latitude as well as identification of new genes involved in flowering time and maturity.

Corresponding author: Tel. 031-695-4049, E-mail: pelicks@korea.kr

PC-96

Construction of DNA Marker Sets for Korean Wheat Cultivar Identification

Jae-Han Son*, Chon-Sik Kang, Young-Keun Cheong, Jong-Chul Park, Tae-Il Park, Yang-Kil Kim, Jong-Ho Park, Young-Jin Oh, Bo-Kyeoung Kim

Crop Breeding Division, National Institute of Crop Science, RDA, 55365, Korea

DNA-based markers have been used in various fields that are molecular biology as well as crop breeding program and DNA marker is regarded important to protect genetic resource, proprietary germplasm and quantification of specific cultivar. Various DNA marker technologies like as simple sequence repeat (SSR), single nucleotide polymorphism (SNP) are used for MAS and development of cultivar specific gene or markers. Eleven DNA markers have been developed for Korean wheat cultivar identification in 2013-2014. Using these markers, 27 of 32 Korean wheat were distinguished between each other. Therefore, in this study, we used SSRs and SNPs techniques to develop the additional DNA markers to make complete set for 32 Korean wheat cultivar. Four DNA markers, KWSM0012, KWSM0013, KWSM0012 and KWSM0015, derived from SSR and SNP were developed additionally. Consequently, total 15 DNA markers were developed by this project and 32 Korean wheat cultivar were identified correctly.

Corresponding author: Tel. +82-63-238-5209, E-mail: pathfinder1@korea.kr

PC-97

Expression of Pepper Cytoplasmic Male Sterility-associated Open Reading Frame, *orf*507 in Transgenic Tobacco Plants

Yeaseong Ha, Min-Young Kang, Yeong Deuk Jo, Byoung-Cheorl Kang*

Department of Plant Science, Plant Genomics and Breeding Institute, and Vegetable Breeding Research Center, College of Agriculture and Life Sciences, Seoul National University, Seoul, 151-921, Korea

Cytoplasmic male sterility (CMS) is a mitochondrial inherited trait that prevents a flower from producing normal pollen grains. CMS has widely been used to produce F_1 hybrid seed in pepper. Though the *orf507* gene is known to be associated with CMS in peppers, definitive and direct evidence that ORF507 induces male sterility is still lacking. In this study, a set of chimeric constructs were developed to confirm the hypothesis that ORF507 protein directly causes male sterility in tobacco. Tapetum-specific promoter TA29, mitochondrial transit sequence yeast *cox*IV pre-sequence, *orf*507 and green fluorescent protein (GFP) gene were cloned sequentially and designated as TCOGN (TA29-*cox*IV pre-sequnce-*orf*507-GFP-nos terminator). For developing control vectors, *orf*507 was cloned under TA29 promoter without *cox*IV pre-sequence (TOGN) or *orf*507 was cloned with or without *cox*IV pre-sequence under the constitutive CaMV35S promoter (SCOGN and SOGN). The four constructs (TCOGN, TOGN, SCOGN and SOGN) were used to transform tobacco using leaf disk transformation mediated by agrobacterium. At flowering stage, transgenic plants will be scored for pollen production and viability. This study is expected to provide evidence that the expression of *orf*507 gene in the tapetum might be responsible for male sterility in pepper.

Corresponding author: Tel. 02)880-4563, E-mail: bk54@snu.ac.kr

PC-98

Identification, Molecular Cloning and Characterization of Stress-Induced Genes in *Lilium formolongi*

Jewel Howlader[1], Nasar Uddin Ahmed[1], Namhee Jeong[1], Kanij Rukshana Sumi[2], Jong-In Park[1], Ill-Sup Nou[1*]

[1]Department of Horticulture, Sunchon National University, 255, Jungang-ro, Suncheon, Jeonnam, 57922, Korea
[2]Department of Fisheries Science, Chonnam National University, 50, Daehak-ro, Yeosu, Jeonnam, 59626, Korea

Biotic and abiotic stresses are the major causes of lily crop loss worldwide. Molecular technique offers the most efficient approach to address these concerns. To explore the stress related resistance gene 12 expressed sequence tags (ESTs) were retrieved from NCBI database. Based on homology results from NCBI and qPCR relative expression level of 12 ESTs under different stress treatments we performed RACE PCR and obtained 7 full length sequences. NCBI blast results of these 7 deduced proteins showed high similarity with different proteins of other crop species. Phylogenetic tree distributed these deduced proteins into 5 distinct clades. Accordingly, based on highly conserved domain we named 7 deduced proteins like *L. formolongi* Heat shock protein 70 viz., LfHsp70-1, LfHsp70-2, LfHsp70-3; Heat shock protein 90 (LfHsp90); Ubiquitin protein (*LfUb*); Cytochrome b5-like heme/steroid binding protein (*LfCytb5-like*); and Rab subfamily of small GTPases protein (LfRabGTPase).Organ-specific RT-PCR expression analysis showed that all these 7 genes expressed in roots, stems, leafs, petioles, tepals, stamens and pistils in sinnapal lily. qPCR relative expression of *LfHsp70-1*, *LfHsp70-2*, *LfHsp70-3*, *LfHsp90*, *LfCytb5-like*, and *LfRabGTPase* genes were up-regulated under *Botrytis cinerea* infection in susceptible sinnapal lily compared to control in leaf samples in a time course basis. Likewise, under *Botrytis elliptica* infection *LfHsp70-1*, *LfHsp70-2*, *LfUb*, *LfCytb5-like*, and *LfRabGTPase* were up-regulated in susceptible sinnapal lily and tolerant napal lily. Subsequently, the qPCR expression of the 7 gene were investigated under 4 different abiotic stresses including heat, cold, drought and salt in sinnapal lily in a time course basis. *LfHsp70-1*, *LfHsp70-2*, *LfHsp70-3*, *LfHsp90*, and *LfCytb5-like* were expressed under heat and cold stress except *LfHsp70-1*which was not expressed in cold stress. *LfHsp70-1*, *LfHsp70-2*, *LfHsp70-3*, and *LfHsp90* were up-regulated under drought stress. *LfHsp70-1*, *LfHsp70-2*, *LfHsp70-3*, *LfCytb5-like* and *LfRabGTPase* were responded under salt stress. Taken together, we hope that the stress responsive candidate genes studied herein will be useful resources for functional analysis in the development of stress resistance *L. formolongi*.

Corresponding author: Tel. 061-750-3249, E-mail: nis@sunchon.ac.kr

PC-99

Resistance of transgenic zoysiagrass overexpressed zoysiagrass class II chitinase gene *Zjchi2* against *Rhizoctonia solani* AG2-2 (IV)

Ji-Nam Kang[1*], Mi-Young Park[2], Hong-Gyu Kang[2], Hyeon-Jin Sun[2], Yong-Ik Kwon[2], Suk-Min Ko[2*], Hyo-Yeon Lee[1,2*]

[1]Faculty of Biotechnology, Jeju National University, Jeju 690-756, Korea
[2]Subtropical Horticulture Research Institute, Jeju National University, Jeju 690-756, Korea

Zoysiagrass (*Zoysia japonica* Steud.) is the warm-season turfgrass species. Recently, it is recognized as most important species of turfgrass in Korea, Japan, China, and USA because of it has advantages that resistance to drought, growing well in poor soil and virtually environments. In the zoysiagrass fields, large-patch disease caused by *Rhizoctonia solani* AG2-2 is most important disease. The disease mainly occurs as small patch about 10 cm with sheath blight in warm-season turfgrass and then rapidly expand to 5 or 10 m. So far, a lot of germicides were used to prevent this disease on zoysiagrass fields, but at the same time it caused economical loss and environmental contamination. Therefore, it is necessary that developing new zoysiagrass cultivars possessing antifungal activity using genetic engineering. Plant chitinases can be used as candidate for developing fungi resistance turfgrass because of chitinases are pathogen related (PR) protein induced by many pathogenic fungi and hydrolyzed the chitin which is a very important component in the fungi cell wall. In this paper, we succeeded to generate transgenic zoysiagrass overexpressed class II chitinase gene (*Zjchi2*) using *Agrobacterium*-mediated transformation even though it is monocot plant and is difficult plant regeneration. In addition, southern blot and PCR analysis were performed. Furthermore, antifungal activity was investigated to examine disease resistance to *R. solani* AG2-2 (IV).

Acknowledgement: This work was supported by Basic Science Research Program through National Research Foundation (2009-0094059), and BioGreen 21 Program (PJ01186002), Rural Development Administration, Republic of Korea

***Corresponding authors:** E-mail: hyoyeon@jejunu.ac.kr

PC-100

Use of High Performance Liquid Chromatography to Determine Genetic Factors of Fruit Colors in Tomato

Hee Ju Yoo[1], Gyu Myung Lee[1], Inhwa Yeam[2], Chang-Sik Oh[3], Je Min Lee[1*]

[1]Department of Horticultural Science, Kyungpook National University, Daegu 41566, Korea
[2]Department of Horticulture and Breeding, Andong National University, Andong 36729, Korea
[3]Department of Horticultural Biotechnology, Kyung Hee University, Yongin 17104, Korea

Carotenoids are essential for plants and animals nutrition, and important factors of pigment variation in fruit, leaf, and flower. Tomato is a model crop for fleshy fruit biology and biotechnology, especially for carotenoid biosynthesis. In tomato commercial cultivars and germplasms, visual phenotyping of ripe fruit colors could be easily determined and subsequent analysis of metabolic profiling should be demanded for hypothesizing genetic factors prior to time-consuming genetic analysis. The HPLC coupled with C30 column efficiently resolved six carotenoids and isomers of several carotenoids in ripe fruits. Carotenoids were analyzed in ripe fruits of yellow, orange and red colored tomatoes. A red tomato produced high amount of *trans*-lycopene as expected. Dark orange tomatoes produced high amount of β -carotene or δ -carotene. Orange tomatoes produced pro-lycopene. Yellow tomatoes showed lack of carotenoids. Genetic determinants impacting fruit color variations were able to infer based on the carotenoid profiles. As a case study, a dark orange tomato producing high amount of δ -carotene were selected for further genetic analysis using a candidate gene. Detailed results will be presented.

Corresponding author: e-mail: jemin@knu.ac.kr, Tel. +82-53-950-5723

PC-101

Genome-wide Characterization of AP2/ERF Superfamily in *Panax Ginseng*

Hyun-Seung Park[1], Sang-Choon Lee[1], Murukarthick Jayakodi[1], Junki Lee[1], Tae-Jin Yang[1*]

[1]Department of Plant Science, Plant Genomics and Breeding Institute, and Research Institute of Agriculture and Life Sciences, College of Agriculture and Life Sciences, Seoul National University, Seoul, Korea

AP2/ERF superfamily is a one of the largest gene families in regular plants and involved in various biological responses related to environmental stresses and development processes. This gene family contains AP2 domains with 60 to 70 conserved amino acid residues and is composed of 4 sub-families, AP2, CBF/DREB, ERF, and RAV sub-family, based on the number of AP2 domain and additional protein domains. From protein-coding sequences predicted in *Panax ginseng* draft genome sequence, total 342 putative AP2/ERF gene family members were identified by searching conserved AP2 domain using iTAK 1.6b standalone software with default parameters. Multiple sequence alignment of AP2/ERF protein sequences of *P. ginseng* were conducted with those of *Arabidopsis thaliana, Capsicum annuum, Solanum lycopesicum, Daucus carota,* and *Vitis vinifera* and phylogenetic relationship were inferred. As expected, *P. ginseng* AP2/ERF genes were also divided into 4 sub-families, of which CBF/DREB and ERF sub-family were further divided into 11 subgroups. AP2/ERF gene family members (342) of *P. ginseng* were increased to almost 1.5 fold, compared to carrot (202), a relative species of *P. ginseng* in the Apiales order. In particular, 27 *P. ginseng* genes were clustered closely with 13 carrot genes, which formed Apiales-specific ERF gene cluster. Most *P. ginseng* genes in the cluster showed strong expression under methyl-jasmonate treatment implying that the genes in Apiales-specific ERF gene cluster might play an important role in jasmonate related responses in *P. ginseng*.

Acknowledgement: This study was carried out with the support of “Cooperative Research Program for Agriculture Science & Technology Development (Project Nos. PJ01100801, PJ01103001)”, Rural Development Administration, Republic of Korea.

Corresponding author: Tel. 02-880-4547, E-mail: tjyang@snu.ac.kr

PC-102

Proteome Analysis of the Roots of Sorghum in Response to Copper

Swapan Kumar Roy, Soo-Jeong Kwon, Kabita Sarker, Hyun-Jin Jung, Min-Heon Yun, Sun-Hee Woo*

Department of Crop Science, Chungbuk National University, Cheong-ju 28644, Korea

To better understand the molecular mechanisms involved in copper stress response, the present study was conducted in the roots of sorghum seedlings. The morphological and ionic changes were observed prominently in the roots when the seedlings of sorghum were exposed to different concentrations (0, 100, and 150 μM) of $CuSO_4$. However, the morphological characteristics were reduced by Cu stress and the most significant growth inhibition was observed in plants treated with a combination of the highest concentrations of Cu^{2+} ions (150 μ M). In the proteome analysis, high throughput two-dimensional polyacrylamide gel electrophoresis coupled with MALDI-TOF-TOF mass spectrometry was performed to explore the molecular responses of Cu-induced sorghum seedling roots. Two dimensional gels stained with silver staining, a total of 422 differential expressed proteins ($\geq$ 1.5-fold) were identified using Progenesis SameSpot software. A total of 21 protein spots ($\geq$ 1.5-fold) from Cu-induced sorghum leaf were analyzed by mass spectrometry. Out of 21 differential expressed protein spots from Cu-induced sorghum roots, a total of 9 proteins were up-regulated while 12 proteins were down-regulated. The abundance of most identified protein species from the roots, which function in stress response and metabolism was significantly enhanced while another protein species involved in transcription and regulation were severely reduced. Taken together, these studies revealed the effects of heavy metal on the growth characteristics and ionic toxicities in sorghum seedling roots, and proteome investigation indicates a good correlation among the morphological, ionic and proteome alterations in sorghum seedling roots exposed to excess copper.

***Corresponding author.** Tel. +82-43-261-2515, Email: shwoo@chungbuk.ac.kr

PC-103

Identification of Physiological and Transcriptomal Analysis in Rice Plant (*Oryza sativa* L.) after acute and chronic γ -irradiation

Sung Min Han, Jung Eun Hwang, In Jung Jung, Hong-Il Choi, Soon-Jae Kwon, Si-Young Kang, Jin-Baek Kim*

Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongup, Jeonbuk 580-185, Korea

To identify the effects of γ -ray in rice, physiological responses and antioxidant-related gene expression were investigated according to acute and chronic irradiation. Four difference growth stages of rice plants were exposed to 50, 100, 200, 300 Gy of gamma irradiation in acute manner for 8 hours or in chronic manner for 10 days. Plant height and tiller number in irradiated 200 Gy on tillering stage plants were significantly affected compared to non-irradiated plants. Chlorophyll contents were reduced but four antioxidant enzymes activities such as catalase, peroxidase, ascorbate peroxidase, and superoxide dismutase were induced as the irradiation dose increased. Electron spin resonance signal intensities were increased in acute irradiation but not in chronic irradiation. Total p.g DNA contents was decreased both acute and chronic irradiation. Superoxide scavenging activity was increased in acute and chronic. Many of the rice genes involved in ROS scavenging and signal transduction pathways showed induction or repression that had increased more than two fold by RNA sequencing analysis. Especially, glutaredoxin and thioredoxin related genes were up-regulated in response to acute irradiation but down-regulated in chronic irradiation. ROS scavenging and signal transduction pathways (Myb domain protein, WRKY DNA-binding protein, and Zinc finger protein) related genes were up-regulated in acute irradiation but down-regulated in chronic irradiation. Our results provided that the plant responses and activation of antioxidant systems were totally different from the γ -irradiation pattern.

Corresponding author: Tel. 063-570-3313, E-mail: jbkim74@kaeri.re.kr

PC-104

Genetic Dissection of Immature Fruit Color in Pepper

Gyu Myung Lee[1], Hee Ju Yoo[1], Doil Choi[2], Je Min Lee[1*]

[1]Department of Horticultural Science, Kyungpook National University, Daegu 41566, Korea
[2]Department of Plant Science and Plant Genomics and Breeding Institute, College of Agriculture and Life Sciences, Seoul National University, Seoul 08826, Korea

Pepper fruit quality is a major trait to consumers, and attributes to appearance, taste, flavor, metabolic composition and nutritional value. Among the quality traits, fruit color has a primary importance because the pigments coferring color are associated with nutrition, health and flavor. Unlike mature fruit color, genetic basis of immature fruit color is largely unknown, which hesitates its utilization for pepper improvement. We mined candidate gene(s) impacting immature fruit color using comparative genomics approach between tomato and pepper. Candidate gene function impacting immature fruit color was confirmed by virus induced gene silencing in fruits. We are currently validating its genetic potential in multiple F2 populations and germplasms showing large variation of immature fruit color. We will present detailed results and its utilization in pepper molecular breeding.

Corresponding author: Tel. +82-53-950-5723, E-mail: jemin@knu.ac.kr

PC-105

Genetic Mapping and Marker Development for the *Powdery Mildew Resistance* Gene *PMR1* in Pepper (*Capsicum annuum*)

Jinkwan Jo, Jelli Venkatesh, Koeun Han, Byoung-Cheorl Kang*

Department of Plant Science, Plant Genomics and Breeding Institute, and Vegetable Breeding Research Center, College of Agriculture and Life Sciences, Seoul National University, Seoul, 151-921, Korea

Powdery mildew (*Capsicum annuum*) is a major fungal disease caused by *Leveillula taurica* in greenhouse. Although powdery mildew resistance has a complex mode of inheritance, resistant cultivars have been steadily developed. Therefore, our objective was to map the resistance gene to powdery mildew resistance in a breeding line, *C. annuum* 'VK515 R'. Based genetic analysis of an $F_{2:3}$ families derived from across between the resistant parent 'VK515 R' and a susceptible parent 'VK515 S', the powdery mildew resistant is controlled by a single dominant gene, *PMR1*. Molecular mapping revealed that the *PMR1* locus is located at 1 cM genetic interval between CZ2_11628, and HRM4.1.6 markers on pepper chromosome 0. These results provide a solid foundation for map-based cloning of the *PMR1* gene and development of markers for breeding powdery mildew resistant cultivars. This is the first report showing the localization of resistance genes to powdery mildew in pepper.

Corresponding author: Tel. 02)880-4563, E-mail: bk54@snu.ac.kr

PC-106

Structure of Genetic Diversity in the Apple Germplasm with Genome-wide SNPs Using Genotyping by Sequencing

Youngjae Oh[1,2], Keumsun Kim[1,2], Sewon Oh[1,2], Jungyeon Won[1,2], Hyeondae Han[1,2], Yoon-Kyeong Kim[3], Daeil Kim[1,2*]

[1]Department of Horticulture, Chungbuk National University, Cheongju 28644, Korea
[2]Brain Korea 21 Center for Bio-Resource Chungbuk National University, Cheongju 28644, Korea
[3]Pear Research Station, National Institute of Horticultural & Herbal Science, Rural Development Administration, Naju 58220, Korea

This study was performed to develop the SNP markers for the assessment of genetic diversity and genetic structure in 95 apple germplasm including bud sport cultivars using genotyping-by-sequencing (GBS). Since the advent of GBS, which is a novel application of NGS technologies, it has been shown to be a valid tool for genomic diversity by rapid and low-cost of genome-wide SNP discovery. Using *Ape*KI for GBS library preparation and sequencing on an Illumina Hiseq 2000 paired-end read, 744 Mb of raw reads were yielded with an average length of 101 bp. After aligning each of 95 accessions' trimmed reads to reference genome (*Malus* × *domestica* cv. Golden Delicious 1.0), an average of 5,952,222 reads (78.86%), which covered reference genome with an average of 2.18%, were successfully aligned to reference genome. An average number of mapped region were 78,406 with an average depth of 22.28. The mapped reads from 95 accessions were filtered with a minimal set of initial quality filters, resulting in union matrix of 786,247 SNPs. For the set of union SNP matrix, by applying subsequent filters, 12,014 SNPs were obtained and utilized for construction of phylogenetic trees using MEGA6 with neighbor-joining method. After analyzing genetic relationship between 95 accessions, they were classified into a total of 3 groups. Group I contained 31 cultivars including 'Hongro', 'Gala', 'Golden Delicious', bud sport cultivars of 'Hongro', 'Gala', and 'Golden Delicious', cross cultivars between them, and others. Group II was characterized as 'Fuji'. These group consisted of 32 cultivars, including 'Fuji', its bud sport cultivars, progenies of 'Fuji', and other cultivars. Group III contained 32 cultivars including 'Mcintosh'. The results of research may be utilized for the establishment and management of apple germplasm collection.

Corresponding author: Tel. 043-261-2527, E-mail: dkpomo@cbnu.ac.kr

PC-107

Development of SNP Set for Genetic Linkage Mapping in Interspecific Asian Pear (*Pyrus* spp.)

Hyeondae Han[1,2], Youngjae Oh[1,2], Keumsun Kim[1,2], Sewon Oh[1,2], Jungyeon Won[1,2], Yoon-Kyeong Kim[3], Daeil Kim[1,2*]

[1]Department of Horticulture, Chungbuk National University, Cheongju 28644, Korea
[2]Brain Korea 21 Center for Bio-Resource Chungbuk National University, Cheongju 28644, Korea
[3]Pear Research Station, National Institute of Horticultural & Herbal Science, Rural Development Administration, Naju 58220, Korea

This study was conducted to develop the set of SNPs between 'Whangkeumbae' (*Pyrus pyrifolia*) and 'Minibae' (*P.* hybrid) for constructing genetic linkage map. Using *Ape*KI for GBS library preparation and sequencing on an Illumina Hiseq 2000, a total of 326 Mb of raw reads were yielded with an average length of 101 bp. After aligning each of 93 progenies' trimmed reads to reference genome (*P. bretschneideri* Rehd.), the mapped reads from 93 progenies were filtered with a minimal set of initial quality filters, resulting in union matrix of 204,982 SNPs. And then, for the construction of genetic linkage maps according to the double pseudo-testcross, three genotype combinations were obtained: when one parent is heterozygous and the other is homozygous (i.e., either AA × AB or AB × AA) and when both parents are heterozygous (i.e., AB × AB). Only SNPs following these segregation ratios in the parents were kept. Each SNP was subsequently tested for the expected segregation ratios in the F_1 progeny: heterozygous in 'Whangkeumbae' (1:1); heterozygous in 'Minibae' (1:1); and heterozygous in both parents (1:2:1). SNPs deviating from these ratios according to a chi-squared test with $p \leq 0.01$ were excluded. F_1 genotypes inconsistent with Mendelian inheritance from the parental genotypes were set to missing value. Finally, the set of 2,331 SNP markers was developed. The results of this study indicate that GBS is feasible for discovering and genotyping SNPs in a variety of fruit trees with complicated genetic background.

Corresponding author: Tel. 043-261-2527, E-mail: dkpomo@cbnu.ac.kr

PC-108

Genetic linkage Maps Using GBS Based SNPs in Interspecific Asian Pear (*Pyrus* spp.)

Hyeondae Han[1,2], Youngjae Oh[1,2], Keumsun Kim[1,2], Sewon Oh[1,2], Jungyeon Won[1,2], Yoon-Kyeong Kim[3], Daeil Kim[1,2*]

[1]Department of Horticulture, Chungbuk National University, Cheongju 28644, Korea
[2]Brain Korea 21 Center for Bio-Resource Chungbuk National University, Cheongju 28644, Korea
[3]Pear Research Station, National Institute of Horticultural & Herbal Science, Rural Development Administration, Naju 58220, Korea

This study was conducted to construct the high-density genetic linkage map as a framework map using genotyping by sequencing (GBS). Recently, a novel application of NGS protocols for detecting and genotyping SNPs simultaneously was developed. GBS library was prepared using *Ape*KI and sequenced on an Illumina Hiseq 2000. After creation of 204,982 SNPs from 93 progenies between 'Whangkeumbae' (*Pyrus pyrifolia*) and 'Minibae' (*P.* hybrid) with SNP calling, finally, the set of 2,331 SNP markers was developed and used to construct the genetic linkage mapping according to the pseudo-testcross mapping strategy. The map for 'Whangkeumbae' consisted of 979 loci on 17 linkage groups (LGs) over totals of 1,089.1 cM, with an average distance of 1.11 cM between markers whereas that for 'Minibae' included 855 loci encompassing a genetic distance of 1,090.5 cM, with an average distance of 1.28 cM. The shortest LGs were 3.3 cM in LG14 of both 'Whangkeumbae' and 'Minibae'. However, the longest LGs were 107.7 cM in LG7 of 'Whangkeumbae', whereas 115.2 cM in LG12 of 'Minibae', respectively. The results of study demonstrate that we constructed a saturated linkage map of pear using SNPs developed by the rapid and robust GBS. This genetic map will be continuously integrated with published SSRs for comparative analysis and simultaneously utilized as a basic framework map to localize many traits of agronomic importance such as soluble solid contents, fruit weight, and fruit shape in interspecific Asian pear F_1 population.

Corresponding author: Tel. 043-261-2527, E-mail: dkpomo@cbnu.ac.kr

PC-109

Identification of Flowering-Related Genes Responsible for Differential Expression Between Two Radish Inbred Lines Exhibiting Disparate Bolting Time Through Comparative Transcriptome Analysis

Won Yong Jung[1], Hyun Ji Park[1], Sang Sook Lee[1], Areum Lee[1,2], Youn-Sung Kim[3*], Hye Sun Cho[1,2*]

[1]Molecular Biofarming Research Center, KRIBB, Daejeon, 34141, Korea
[2]Biosystems and Bioengineering Program, University of Science and Technology (UST), Daejeon, 34113, Korea
[3]Department of Biotechnology, NongHyup Seed Anseong, 17558, Korea

A noticeable economic characteristic of radish (*Raphanus sativus* L.), an important *Brassicaceae* root vegetable crops, is late bolting after cold exposure. However, little information is available about flowering-time related genes and mechanism of late flowering-time in radish. To understand molecular mechanism of flowering-time difference between two radish lines, “late bolting radish”(NH-JS1) and “early bolting radish”(NH-JS2) were performed high-throughput RNA sequencing analysis. In total, 71,188 unigenes were identified by reference-guided assembling and it was found that 309, 788 and 980 genes were differentially expressed between the two inbred lines at 0, 15, and 35 days of vernalization, respectively. Two hundred eighteen putative flowering-time related genes homologous to *Arabidopsis* flowering-time genes were identified in the radish and their expression levels were compared in the two radish samples with or without vernalization treatment. Forty nine genes were found to be differentially expressed between the two radish lines. Most of the up-regulated genes in NH-JS1 compared with NH-JS2 were flowering time repressor genes including RsFLC, showing that NH-JS1 has late flowering time. The down-regulated genes in NH-JS1 were relatively less consistent with the late bolting characteristics, however, several flowering time enhancer genes including RsSOC1, a key floral integrator, showed an apposite expression to the late bolting phenotype. In addition, flowering pathway analysis showed that changes of photoperiod and vernalization pathways between the lines and most of differentially expressed genes involved in vernalization pathway well matched with the different bolting time between the lines. These results suggest that vernalization pathway seems to be conserved in radish and *Arabidopsis*.

Corresponding author: Tel. 042-860-4469, E-mail: hscho@kribb.re.kr

PC-110

Genome-wide Identification and Analysis of Rice Endosperm Preferred Genes Conserved in Various Rice Verities

Woo-Jong Hong, Yo-Han Yun, Sun-A Park[1], Sung-Ruyl Kim[1], Ki-Hong Jung[1*]

Graduate School of Biotechnology & Crop Biotech Institute, Kyung Hee University, Yongin, 446-701, Korea

The study of endosperm development in crop is very important in understanding molecular mechanism to produce and metabolize carbohydrates as a main energy source. A significant accumulation of genome-wide transcriptome data enhances the performance of meta-expression data for diverse applications. In this study, we carried out meta-anatomical expression analysis based on 2566 affymetrix array data in rice and indented to identify 400 endosperm preferred genes using gene search tool installed in Genevestigator. The tissue preferred expression pattern was again confirmed by using additional anatomical expression data consisting of 219 Agilent 44K array data. Subsequently, we identified 299 genes showing endosperm preferred expression. Functional significance of these genes was evaluated by using the analysis for 24 genes which have been characterized through previous studies and by validating the tissue specific expression patterns of four genes using GUS reporter system. The latter suggests new tools for manipulating agronomic traits in endosperm. MapMan analysis revealed the metabolism and regulation overview associated with endosperm development. Especially, we found that starch metabolic pathway is very closely related to endosperm development in rice. We hope that our study provides fundamental information to understand the molecular mechanism of rice endosperm development and resulting data will contribute to enhancing the agronomic trait associated with endosperm.

Corresponding author: E-mail: khjung2010@khu.ac.kr

PC-111

Improving and Sharing Computing Algorithms of Genome Analysis, and System Development of Bioinformatics Tools

Kyu-Won Kim[1,2], Ji-Hye Hwang[3], Jung-Kyung Moon[3], Yong-Jin Park[1,2*]

[1]Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 32439, Korea
[2]Center for crop genetic resource and breeding (CCGRB), Kongju National University, Cheonan 31080, Korea
[3]National Institute of Agricultural Science, Rural Development Administration (RDA), JeonJu 54874, Korea

Currently, the area of national agricultural research on crop genomics requires standardized bioinformatics analysis methods to promote the public use of genome information and the expansion of the method. To this end, bioinformatics analysis methods such as Next-generation sequencing data analysis and genome-wide association study (GWAS) are to be standardized. In addition, it is required to develop sharing platform and to train manpower who manage the platform and have analyzing ability. We have standardized the bioinformatics analysis and have developed platform enabled people to use the method. Also, we have established a system to facilitate sharing the bioinformatics methods and the results among researchers in agricultural research sectors. In addition, we are constructing education system that makes researchers practice the standardized analysis method. Through this, we expect researchers' bioinformatics research performance to be improved and researches using bioinformatics analysis methods to be active.

Corresponding author: Tel. 041-330-1201, E-mail: yjpark@kongju.ac.kr

PC-112

Population Genomics Identifies the Origin and Signatures of Selection of Korean Weedy Rice

Qiang He[1], Kyu-Won Kim[1,2], Yong-Jin Park[1,2*]

[1]Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 32439, Korea
[2]Center for crop genetic resource and breeding (CCGRB), Kongju National University, Cheonan 31080, Korea

Weedy rice is the same biological species as cultivated rice (Oryza sativa); it is also a noxious weed infesting rice fields worldwide. Its formation and population-selective or -adaptive signatures are poorly understood. In this study, we investigated the phylogenetics, population structure, and signatures of selection of Korean weedy rice by determining the whole genomes of 30 weedy rice, 30 landrace rice, and 10 wild rice samples. The phylogenetic tree and results of ancestry inference study clearly showed that the genetic distance of Korean weedy was far from the wild rice and near with cultivated rice. Furthermore, 537 genes showed evidence of recent positive or divergent selection, consistent with some adaptive traits. This study indicates that Korea weedy rice originated from hybridization of indica/indica or japonica/japonica. Moreover, weedy rice is not only a notorious weed in rice fields, but also contains many untapped valuable traits or haplotypes that may be a useful genetic resource for improving cultivated rice.

Corresponding author: Tel. 041-330-1201, E-mail: yjpark@kongju.ac.kr

PC-113

Identification of Octoploid Strawberry Cultivar Using High-throughput SNP Genotyping

Hee-Jeong Jung[1], Karpagam Veerappan[1], Sathishkumar Natarajan[1], Namhee Jeong[1], Indeok Hwang[1], Soichiro Nagano[2], Kenta Shirasawa[2], Sachiko Isobe[2], Ill-Sup Nou[1*]

[1]Department of Horticulture, Sunchon National University, 255 Jungangro, Suncheon, Jeonnam 57922, Korea
[2]Kazusa DNA Research Institute, 2-6-7 Kazusa Kamatari, Kisarazu, Chiba, 292-0818, Japan

Cultivated strawberry (*Fragaria* × *ananassa*) is an important commercial crop grown throughout the world. Improved strawberry cultivars have been, and are being, developed to meet the growing needs of consumers and breeders. In general, strawberries are propagated vegetatively through runners, which sometimes leads to mislabeling and misidentification of cultivars. Thus, accurate identification of strawberry cultivars is essential for germplasm maintenance as well as breeding programs. Molecular marker technology has been widely used to distinguish cultivars of other crops. However, the octoploid nature of cultivated strawberry complicates marker development. SNP markers are efficient and widely used DNA markers due to their high-density distribution in the genome. Here, we have utilized previously published high-quality poly high resolution (PHR) SNPs on the 90 K Axiom® SNP array and developed an accurate 24 SNP chip set. The 24 SNP chip set was then screened with 149 octoploid strawberry cultivars and 109 cultivars were successfully genotyped. The 24 SNPs mapped to 6 chromosomes of Fragaria vesca. Our analysis using SNP genotyping was automated and data processing was easy, reliable and compatible between laboratories. Thus, this high-throughput SNP genotyping method will be a useful tool in distinguishing strawberry cultivars.

Acknowledgements: This work was supported by grants from the Export Promotion Technology Development research programs (315047-3) funded by the Ministry of Agriculture, Food and Rural Affairs, Republic of Korea.

Corresponding author: Tel.061-750-3249, E-mail: nis@sunchon.ac.kr

PC-114

Genome-wide Association Study of Cold Stress During Seedling Stage Using Rice (*Oryza sativa* L.) Core Set

Mijeong Kim*, Yoonjung Lee, Giwon Cho, Jisu Choi, Joohyun Lee

Department of Applied Bioscience, Konkuk, University, Seoul 143-701, Korea

Cold stress is one of the most influenced factors to rice yield. In order to identify genes related to cold stress, genome-wide association study (GWAS) was implemented. Seedlings of 129 rice germplasm were cultivated for two weeks in greenhouse and transferred to chamber which was set up to 12℃ of temperature and 70% of relative humidity. After treating for one week, rice seedlings were transferred to greenhouse and we scored the treated rice seedlings. Rice seedlings were scored 1 to 10 through the comparison between control and treatment. The normal rice seedlings were scored 1 and the withered rice seedlings were scored 10. Scores of these rice germplasm to cold tolerance were normally distributed. Norin22 and Avangard were the most tolerant to cold stress while Hatadani was the most sensitive accession. As a result of GWAS with re-sequencing data and phenotype of rice germplasm using genome association and prediction integrated tool (GAPIT), eight single-nucleotide polymorphisms (SNPs) were observed under stress condition by applying a significance threshold of -logP>4.5 determined by QQ plot. The candidate genes to cold stress were on the end of chromosome 1 based on the manhattan plot.

Corresponding author: tel. 02-450-0480, E-mail: skymi6633@naver.com

PC-115

Genome-Wide Association Study of Vitamin E Using Genotyping-By-Sequencing in Sesame (*Sesamum indicum*)

Qiang He[1], Feifei Xu[2], Jie Yu[1], Tae-Sung Kim[1,3], Yong-Jin Park[1,3*]

[1]Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 32439, Korea
[2]Institute of Nuclear Agricultural Sciences, College of Agriculture and Biotechnology, Zhejiang University, Huajiachi Campus, Hangzhou 310029, China
[3]Center for crop genetic resource and breeding (CCGRB), Kongju National University, Cheonan 31080, Korea

Vitamin E occurs in nature ≥ 8 structurally related forms, four tocopherols and four tocotrienols, all of which are potent membrane-soluble antioxidants. In this study, we detected two major isoforms in sesame seed, α tocopherol and β tocotrienol. To investigate the genetic basis of those traits, we performed the genome wide association studies(GWAS) by using 5,962 genome wide markers acquired from 96 core selections of sesame germplasms. 96 samples were clearly clustered into two subpopulations based on structure and phylogenetic studies. We performed GWAS by using two models, generalized linear model (GLM) and mixed linear model (MLM). SLG08_6621957 on chromosome 8 detected has significant association with α tocopherol both by GLM and MLM respectively. Additional 20 loci were also played roles for α tocopherol content in sesame. For β tocotrienol there's no significant loci were identified by two models except the one locus (SLG03_13104062), which has been detected by two models at moderate level. This study supports that GBS based GWAS was effective approach for sesame breeding and genetic studies. The significant associated genes will be useful for improve the vitamin E content in future sesame breeding.

Corresponding author: Tel. 041-330-1201, E-mail: yjpark@kongju.ac.kr

PC-116

Rice Chloroplast Genome Variation Architecture and Phylogenetic Dissection in Diverse Oryza Species Assessed by Whole-genome Resequencing

Wei Tong[1], Tae-Sung Kim[1,2], Yong-Jin Park[1,2*]

[1]Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 32439, Korea
[2]Center for crop genetic resource and breeding (CCGRB), Kongju National University, Cheonan 31080, Korea

Here, we described chloroplast variation architecture of 383 rice accessions from diverse regions and different ecotypes, in order to understand the rice chloroplast genome architecture. A total of 3,677 variations across the chloroplast genome were identified with an average density of 27.33 per kb, where wild rice shows a higher variation than cultivated groups. Chloroplast genome nucleotide diversity investigation indicated a high degree of diversity in wild rice than in cultivated rice. Genetic distance estimation revealed that African rice showed a low level of breeding and connectivity with the Asian rice, suggesting the big distinction of them. Population structure and principal component analysis revealed the existence of clear clustering of African and Asian rice, as well as the indica and japonica in Asian cultivated rice. Phylogenetic analysis based on maximum likelihood and Bayesian inference methods and the population splits test suggested and supported the independent origins of indica and japonica within Asian cultivated rice. In addition, the African cultivated rice was thought to be domesticated differently from Asian cultivated rice. The chloroplast genome variation architecture in Asian and African rice are different, as well as within Asian or African rice. Wild rice and cultivated rice also have distinct nucleotide diversity or genetic distance. In chloroplast level, the independent origins of indica and japonica within Asian cultivated rice were suggested and the African cultivated rice was thought to be domesticated differently from Asian cultivated rice. These results will provide more candidate evidence for the further rice chloroplast genomic and evolution studies.

Corresponding author: Tel. 041-330-1201, E-mail: yjpark@kongju.ac.kr

PC-117

Development of Primer Sets for the Detection and Identification of the *Epimedium* and *Thalictrum* Using Real-time PCR

Jae-Woo Lee, Ju-Hee Kim, Cheol Seong Jang*

Plant Genomics Lab, Department of Applied Plant Sciences, Kangwon National University, Chuncheon 200-731, Korea

Epimedium koreanum Nakai has been using as medicine in Korea. When *E. koreanum* Nakai using commercially, same species with different genus like *Epimedium pubescens* Maximowicz, *Epimedium sagittatum* Maximowicz, *Epimedium brevicornum* Maximowicz have been mixing which are cheaper than *Epimedium koreanum* Nakai and also mixed with different species but similar shape plant like *Thalictrum aquilegifolium*. In this study, to identify this fraudulent mixture, we have developed marker to detect each plant using Real-Time PCR. The study was performed in five species that were *E. koreanum* Nakai and its same spices *E. pubescens* Maximowicz, *E. sagittatum Maximowicz, E. brevicornum* Maximowicz and different spices of *T. aquilegifolium*. For the development of real-time PCR analysis based on Single-nucleotide polymorphisms (SNPs),. SNPs were obtained *trnL-trnF* region and *matK* gene. To obtain information of SNPs within *trnL-trnF* region, we have used primer-BLAST tool at NCBI and found a specific primer of *T. aquilegifolium*. We have performed cloning *matK* gene of five plants based on gene of *E. Koreanum* Nakai and then they sequence was aligned. The specific primer of *E. pubescens* Maximowicz was designed through sequence alignment data. In order to obtain standard curve in this specific primer, we have diluted target DNA From 50ng to 0.005ng and performed Real-Time PCR. *T. aquilegifolium* specific primer was indicatd 91.6% efficiency, correlation coefficient (R^2) 0.999 and slope −3.540 and *E. pubescens* Maximowica specific primer was presented 86.9% eifficiency, R^2 0.994 and slope −3.681. Our result showed that these specific primer have high sensitivity and have nonspecific amplification for other species. Developed primer set based on Real-Time PCR could be used to distinguish mixture of different plants.

Acknowledgements: This research was supported by a grant (14162MFDS971) from the Korea Ministry of Food and Drug Safety.

Corresponding author: Tel. 070-7135-9637, E-mail: csjang@kangwon.ac.kr

PC-118

Genetic Variation Architecture of mitochondrial Genome Reveals the Differentiation in Korean Landrace and Weedy Rice

Wei Tong[1], Yong-Jin Park[1,2*]

[1]Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 32439, Korea
[2]Center for crop genetic resource and breeding (CCGRB), Kongju National University, Cheonan 31080, Korea

Here, we describe mitochondrial variation architecture and our performance of a phylogenetic dissection of Korean landrace and weedy rice. A total of 4,717 variations across the mitochondrial genome were identified with a density of 9.188/kb adjunct with 10 wild rice. Genetic diversity assessment revealed that wild and landrace rice have higher nucleotide diversity than do cultivated and weedy rice, respectively. Genetic divergence was suggestive of a high level of breeding between landrace and weedy rice, with the landrace showing a closer association with wild rice than with weedy rice. Population structure and principal component analyses showed no obvious difference in the genetic backgrounds of landrace and weedy rice in mitochondrial genome level. Overall, our Phylogenetic, population split, and haplotype network evaluations support independent origins of the *indica* and *japonica* varieties.

Corresponding author: Tel. 041-330-1201, E-mail: yjpark@kongju.ac.kr

PC-119

양배추 시들음병 저항성 및 감수성 품종 구별용 분자마커 개발

강송이, 정희정, 황인덕, 노일섭*

순천대학교 원예학과

배추과 작물의 시들음병은 *Fusarium oxysporum* f. sp. *conglutinans*에 의해 발생하며, 병원균이 물관에서 증식하여 잎이 황화되고 말라죽게 하는 병이다. 특히, 양배추의 연작지에서 큰 피해를 주고 있으며, 양배추의 품질과 생산량을 크게 떨어뜨리고 있다. 시들음병에 대한 양배추의 저항성은A type과B type이 알려져 있으며, A type은 온도 등의 환경조건에 관계없이 저항성을 나타내는 단인자 우성 유전을 하는 반면에, B type은 다인자의 지배를 받아25℃까지는 저항성을 나타내나, 그 이상의 고온에서는 저항성을 나타내지 못하여 높은 시들음병 발생을 보이므로실용성이 없어 국내·외에서는A 타입 저항성 양배추 품종이 개발되어 사용되어져 왔다. 최근 양배추 시들음병 저항성인 FocBo1 유전자가 규명되었으며, 4번째 엑손에 InDel 및10번째 엑손의 결실이 보고되었다. 그러나 아직까지 이와 같은 위치를 검정한 결과 표현형과 일치하지 않은 부분이 있어, 이를 보완하여 양배추 시들음병에 대한 효율적인 저항성 및 감수성을 판별할 수 있는 분자표지의 개발이 필요하다. 양배추 시들음병 저항성 품종과 감수성 품종을 판별할 수 있는 새로운 분자마커를 개발하기 위해 연구하던 중, 양배추 시들음병 저항성 유전자인 *FocBo1*의 염기서열을 분석하여 시들음병 저항성 품종과 감수성 품종에서 특이적으로 차별화되어 나타나는 신규한InDel 위치를 발견하였고, 저항성 여부를 판별할 수 있는 InDel 마커를 개발하였다. 본 연구를 통하여 개발한 마커를 이용하여 양배추 품종이 완전히 성숙하기 전에 시들음병 저항성 및 감수성 품종을 간단하고 정확하게 선별할 수 있을 것이다.

Acknowledgements: 본 연구는 농림축산식품부, 해양수산부, 농촌진흥청, 산림청 Golden Seed 프로젝트 사업(원예종자사업단, 과제번호: 213003-04-4-SB110, 213003-04-4-SBa10)에 의해 이루어진 것임.

Corresponding author: Tel. 061-750-3249, E-mail: nis@sunchon.ac.kr

PC-120

Implementation of Rapid Haplotyping Software in Personal Computers for Standalone Users

Kyu-Won Kim[1,2], Yong-Jin Park[1,2*]

[1]Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 32439, Korea
[2]Center for crop genetic resource and breeding (CCGRB), Kongju National University, Cheonan 31080, Korea

After variant calling and finding target genes from NGS data of crop population, one of the most well-used process is haplotyping for the target gene sequences. Those works for large population and lots of genes is time consuming and not easy to conduct by a user task. Generally, researchers try to analyze haplotypes by using public web interface. However, the researchers that use public web interface will meet a different challenge. They might be reluctant to upload their novel data to the public storage for the analysis and would install the web site into their own local computer system, which is often harder to achieve than a user task. Thus, we implemented a haplotyping software for general private researchers which can be executable in a personal standalone system such as Microsoft Windows on a personal computer specification as well as Linux. The software also has a function that user data and the public data can be joined together and analysis for haplotyping. Through this software, we expect haplotyping to be rapidly and easily, and developing molecular markers to be active.

Corresponding author: Tel. 041-330-1201, E-mail: yjpark@kongju.ac.kr

PC-121

Quiescence Vs Elongation Strategy for Direct Seeding Approach in Korean Rice Core Set

Win Htet Oo[1], Tae-Sung Kim[1,2], Yong-Jin Park[1,2*]

[1]Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 32439, Korea
[2]Center for crop genetic resource and breeding (CCGRB), Kongju National University, Cheonan 31080, Korea

Slow seed germination and delayed seedling establishment will become a major problem from rice production in flood-prone low land areas. So sowing method shifts from transplanting to direct seeding. The “quiescent strategy” under control by the quantitative trait locus SUBMERGENCE 1 (SUB1) has been considered as a major mechanism controlling submergence tolerance in rice and this strategy is favorable to rice plants for their survival during temporal flash flood, no more than two weeks. Besides, “elongation escape strategy” mediated by seedling vigor with fast shoot elongation under submergence is considered to be an important strategy for rice particularly in direct seeding cultivation systems. To characterize for “Quiescence Vs Elongation” of the physiological responses, seedlings from Korean Heusristic Set, having a wide genetic diversity, were compared using principle component analysis. Further characterization of contrasting genotypes would help in elucidating the genetic and biochemical regulatory and signaling mechanisms associated with the tolerance. This could facilitate breeding rice varieties suitable for direct seeding systems and guide efforts for improving water logging tolerance in other crop systems.

Corresponding author: Tel. 041-330-1201, E-mail: yjpark@kongju.ac.kr

PC-122

Genome-wide Association Study and Gene Sets Analysis Reveals Candidate Genes Involved in Salt Tolerance at The Rice Seedling Stage

Jie Yu[1], Tae-Sung Kim[1,2], Yong-Jin Park[1,2*]

[1]Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 32439, Korea
[2]Center for crop genetic resource and breeding (CCGRB), Kongju National University, Cheonan 31080, Korea

Salt is the major factor limiting crop productivity in saline soils and is controlled by various genes. The development of salt-tolerant rice through molecular breeding methods is important to meet the needs of rice breeding. We used 295 accessions to perform a genome-wide association study (GWAS) of salt-tolerance-related phenotypes in rice at the seedling stage, obtaining 93 candidate genes with high association peaks across six phenotypes. We constructed a protein interaction network using the candidate genes identified here, and 33 genes were associated. Based on the expression patterns, we found that most of these genes showed a different expression level under control and salt-stress conditions. In addition, haplotype network and sequence analysis of one 'key' gene in the interaction network was investigated to explore its possible role in the network. Our study revealed candidate salt-tolerance-related genes in rice at the seedling stage, and demonstrated the feasibility of using GWAS to identify genetic factors underlying salt tolerance. The data generated here may provide resources for molecular breeding and functional analysis of salt tolerance in rice seedlings.

Corresponding author: Tel. 041-330-1201, E-mail: yjpark@kongju.ac.kr

PC-123

Orthologous and Evolutionarily Accelerated Genes Identified in Sesame (Sesamum indicum) by Deep Resequencing

Jie Yu[1], Kyu-Won Kim[1,2], Yong-Jin Park[1,2*]

[1]Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 32439, Korea
[2]Center for crop genetic resource and breeding (CCGRB), Kongju National University, Cheonan 31080, Korea

Sesame (*Sesamum indicum* L.) is the queen of oil seed crops and is cultivated widely in tropical and subtropical areas. The availability of the sesame genome sequence presents unprecedented opportunities for studying its genetics, genomics, and evolution. In this report, we conducted a genome resequencing-based identification of sesame orthologs; in total, 26,379 CDSs were isolated. Using a reciprocal best hits and phylogenetic-based method, we ultimately identified a total of 639 ortholog sets after one-to-one ortholog extraction across seven *Pentapetalae* plant species. These orthologs were considered to be the most credible between the two species, and in sesame. Furthermore, we performed a branch model-based maximum likelihood estimation of dN/dS of the orthologs, resulting in the identification of 198 evolutionarily accelerated orthologs. After adjusting the threshold with a P-value and FDR < 0.05, 66 positive selected genes were retained. An enrichment analysis based on various aspects of these genes suggested the important functions of the orthologs in sesame and in other plant species. The method we used here provides a case study for identifying orthologous genes in sesame and other plants species that are distributed in equilibrium phylogenetically, which can be used in other plants.

Corresponding author: Tel. 041-330-1201, E-mail: yjpark@kongju.ac.kr

PC-124

Gene Expression Profiling Through de novo Transciptome Sequencing Provide Insights for the Mechanisms Underlying Side Branch Suppressions That Enhance The Production Quality of The Standard Chrysanthemum Cultivars (Dendranthema grandiflorum Ramat.)

Tae-Sung Kim[1,2], Jie Yu[1], Ha-Seung Park[3], Chang-Pyo Hong[4], Hojin Ryu[5], Yong-Jin Park[1,2*]

[1]Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 32439, Korea
[2]Center for crop genetic resource and breeding (CCGRB), Kongju National University, Cheonan 31080, Korea
[3]Yesan Flower Research Station, Chungnam Provincial Agricultural Research Extension Services, Yesan 32425, Korea
[4]THERAGEN ETEX Bio Institute, Gwanggyo-ro, Yeongtong-gu, Suwon-si, Gyeonggi-do 16229, Korea
[5]Department of Biology, Natural Science, Chungbuk National University, Cheongju 286544, Korea

Chrysanthemum, native to Aisa and northeastern Europe, includes one of the most economically important ornamental crops worldwide. The standard type chrysanthemums (or standard mum), having a single stem with one or few inflorescence(s), is a greatly favored chrysanthemum type in the cut flower markets of Asia including Korea and many others, covering 50~60% of the domestic chrysanthemum explant production. However, the shoot branching in the standard mum has been a critical problem, wasting 30-40% of the total labor cost from the manual decapitation of lateral branches. Thus, effective solutions need to be established urgently. Seiko No issei (Dendranthema grandiflorum Ramat.) is one of popular standard mums in Korea and Japan. In this cultivar, fewer leaves are initiated in the axillary meristems but the outgrowths of buds are significantly arrested, suppressing following shoot branching processes. In contrast, standard type crysanthemum 'Jeongwoon' (Dendranthema grandiflorum Ramat.) shows strong shoot branching phenotypes. De novo transcriptome sequencing has provided effective means to comprehensively analyze gene expression profiles under various cellular functions in non model plants. The characterizations of the differentially expressed genes that are involved in bud inactivation/activation using 'Seiko No issei' and 'Jeongwoon' may help elucidate the naturally shaped regulatory mechanisms underlying the plant architecture in the context of current shoot branching researches. The results of this study may serve as a guide to develop breeding strategies that aid lateral branching problem in the standard mum improvement programs.

Corresponding author: Tel. 041-330-1201, E-mail: yjpark@kongju.ac.kr

PC-125

Genome-wide Association Studies(GWAS) of Related Genes for Flowering Time in Rice Core Set

Min-Young Yoon[1,2], Yong-Jin Park[1,2*]

[1]Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 32439, Korea
[2]Center for crop genetic resource and breeding (CCGRB), Kongju National University, Cheonan 31080, Korea

This work is mainly focused on identifying candidate genes and alleles associated with rice flowering time using GWAS and evolutionary study. The Korean authentic population of 295 rice accessions, including a core set with 137 accessions, was resequenced. Those generated SNPs/Indels were analyzed GWAS with flowering time phenotype. Total 7 genes, *Os01g0773350* and *Os01g0773400* in chromosome 1, *Os06g0259850*, *Os06g0259901*, *Os06g0260000* in chromosome 6, *Os09g0424850* and *Os09g0425200* in chromosome 9 were significantly associated with flowering time according to GWAS results with -log10 (*P*-value) > more than 5. On the other hand, total 68 genes were positively selected form the McDonald-Kreitman test, which were investigated using 10,887 orthologous genes between Rice (*Oryza sativa* L.) and *Brachypodium distachyon* (outgroup) based on different phenotypic groups in 295 accessions. Long flowering time (group 1), medium flowering time (group 2) and short flowering time (group 3) were three grouped by flowering time phenotypes and each group was examined with the outgroup for MKT. Three candidate genes (*Os04g0201900*, *Os08g0159500*, *Os11g0689300*) functionally annotated by DAVID and Q-TARO database were turned out to be under fast evolutionary processes. Then we proceeded GLM test to verify which SNPs are most significantly associated with the flowering phenotype. As a result, we found that a C/T SNP at *Os11g0689300* was significantly associated with flowering time. These results support that GWAS and the evolutionary studies using the genomic resources will be useful as a fundamental research material to improve breeding efficiency on developing new varieties and also useful for further functional studies.

Corresponding author: Tel. 041-330-1201, E-mail: yjpark@kongju.ac.kr

PC-126

유전체 기반 분자육종시스템 구축

이현오, 최범순, 이승욱, 최아영, 신지언, 박미소, 강경대, 유의수*

파이젠 유전체 연구소, ㈜ 파이젠, 13558, 경기도 성남시 분당구 성남대로 331번길, 백궁프라자1 빌딩 605호

다양한 차세대 유전체 데이터로 인해 많은 식물들의 신규 유전체 정보가 생산 되고 있다. 그러나 효율적인 관리, 분석, 가시화 시스템은 미비한 실정이다. 이에 차세대바이오그린21 식물분자육종사업단의 지원을 받아 작물 통합 유전체 정보 관리 시스템을 구축하고자 하였다. 유전체 정보 및 분자 육종에 필요한 정보의 체계적 생산 및 관리를 유도하고, 효율적인 NGS 데이터 분석 시스템 구축으로 resequencing 및 GBS 데이타를 효율적으로 분석, 가공하는 파이프라인을 개발하여 유전변이 데이터의 생산과 효율적인 분자마커 개발을 진행하였다. 우선 벼에서는 *japonica*, *indica*, *aus* 3종의 *Oryza sativa* 표준유전체와 *O. glaberrima* 및 야생종 AA (6종), BB (1종), FF (1종), outgroup (1종) 표준유전체를 DB화 하였고, 배추 및 양배추에서는 *Brassica rapa* (1종), *B. oleracea* (2종)을 DB화 하였다. 또한 토마토, 고추, 애기장대 등 총 10종의 비교유전체용 기타작물 유전체를 DB화 하였고, 더불어 IRRI 벼 3000 계통의 resequencing data를 genbank에서 다운로드 받을 수 있도록 테이블 형태로 관리하며, 71 표현형정보를 분석에 활용 중에 있다. 표준 유전체와의 비교를 통한 유전체 상세 비교모듈 개발로는 1) 유전체서열, 유전자, repeat의 비교정보를 나타내는 Comparative alignment viewer (CAV). 2) GBS 실험 전에 표준유전체를 기반으로 하여 제한효소 선정과 GBS fragment의 수, 사이즈, 빈도 등을 미리 알아 볼수 있는 GBSPreViewer (GBS pattern of restriction viewer). 3) BWA, samtools, picard, GATK등의 대중적인 분석 방법들을 이용하여 reseq, GBS 의 NGS 데이터를 mapping하고 SNP, indel을 찾는 web 기반의 Variant Discovery Pipeline. 4) 유전변이 정보와 표현형 정보를 이용하여 GAPIT, Plink 이용 형질연관 분석을 하는 GWAS 분석 5) SNP 정보와 유전체 정보를 DB화하고 연동하여 각 염색체, 유전자 연관 SNP을 통합적으로 검색하고 특정 SNP지역에서 마커를 개발 할수 있도록 구성하였다. 이 연구의 성과는 비교유전체 분석, 전사체 발현 분석, 유전변이 분석, 형질연관 분석, 분자마커 개발 등 분자육종에 직, 간접적으로 이용할 수 있는 데이터의 생산, 가공에 편리성, 효율성을 증대 시킬 것으로 기대된다.

Corresponding author: Tel. 031-716-0041, E-mail: yeisooyu@phyzen.com

PC-127

The Complete Mitochondrial Genome Sequence of *Senna tora* L.

Choi Ah Young[1], Hyun Oh Lee[1], Ji Eon Shin[1], Mi So Park[1], Yeisoo Yu[1], SeungWook Lee[1], Kyoung Dae Kang[1], Sang-Ho Kang[2], Beom-Soon Choi[1*]

[1]Phyzen Genomics Institute, Seongnam-si, Korea and
[2]National Academy of Agricultural Science, Rural Development Administration, Jeonju-si, Korea

Senna tora L. is a medicinal plant belonging to Fabaceae family, which is economically important and the third-largest family in land plant. *S. tora* has been well known for enhancing eye-sight and used as oriental traditional medicine in East Asia. Mitochondrial (mt) genome is maternally inherited and has 100-10,000 copies in a plant cell. Mt genome of animals contains about 14-20kb DNA information and presents as a single circular molecule, which is relatively simpler formation. Nevertheless, completion of plant mt genome sequence is difficult due to high variability of genome size and gene order caused by recombinations among the copies in many land plants. We recently assembled a complete mt genome sequence of *S. tora* using a hybrid approach of Illumina and PacBio data. First, initial contigs were generated using *de novo* assembly of Illumina PE data and were compared with GenBank mt references to select the contigs derived from mt. The selected contigs, then, were went to gap-filling procedures in order to extend sequences from the termini of contigs and join contigs using error-corrected and assembled PacBio data. The completed mt genome of *S. tora* is 566,589 bp in length with a 45.23% GC content. A total of 63 genes was annotated including 36 protein-coding genes, 22 tRNA genes and 5 rRNA genes. The annotated protein-coding sequence (exon only) is account for 6% of the mt genome and an average gene length was 35,750bp (including introns). Along with chloroplast genome sequence, this study will contribute to develop molecular markers for germplasm classification, authentication and S. tora breeding.

Corresponding author: Tel. +82-31-716-0041, E-mail: bschoi@phyzen.com

PC-128

산초나무(*Zanthoxylum schinifolium* S. et Z.) Microsatellite 표지 개발 및 유전변이 분석

김영미[1*], 조아르나[1,2], 신유승[1], 정지희[1], 김호방[3]

[1]국립산림품종관리센터
[2]고려대학교
[3]㈜바이오메딕 생명과학연구소

산초나무(*Zanthoxylum schinifolium* S. et Z.)는 운향과에 속하는 자생식물로 우리나라 중부이남, 일본, 중국에 분포하고 있다. 과피나 수피, 잎 등에 독특한 향이 있고 항균성분이 있어 향신료와 민간요법에 이용되어져 왔다. 최근 산초나무 항균, 항암, 항염증의 효과가 입증되면서 약리적 천연물질을 생산하는 자원으로서 새로이 주목 받고 있다. Microsatellite 표지는 임목의 육종 프로그램의 관리와 유전자원 보존에 선호되는 표지로서 본 연구에서는 산초나무에서 다형성을 보이는 microsatellite 표지를 개발하였다. Glenn과 Schable (2005) 방법에 따라 microsatellite enrichment 라이브러리를 작성하였다. 이를 기반으로 microsatellite repeat을 가지는 182개 contig 서열(Genebank Acc. KU884701-KU884883)을 확보하고 20개의 후보 프라이머를 제작하였다. 충북 충주(38), 진천(34), 그리고 경기 남양주(32) 지역에서 수집된 104개의 산초나무 표본에서 증폭양상을 확인할 결과 모든 프라이머에서 증폭산물이 관찰되었으며, 그 중 16개 프라이머가 다형성을 보이며 4개의 프라이머가 단형성으로 확인되었다. 다형성을 보이는 16개 프라이머 중 2개에서 분석오류를 발생시키는 요소(multi-copy, motif mismatches)가 확인되어 최종 14개 프라이머가 유전변이 분석에 이용 가능한 프라이머로 선발되었다. 최종 선발된 14개 프라이머의 특성을 확인한 결과 각 프라이머에서는 2개에서 8의 대립유전자(A)가 확인되었다. 이형접합도 관측치(H_o)와 기대치(H_e)는 각각 0.075-0.532과 0.093-0.696의 범위에서 확인되었다. 유효대립유전자 수(A_e)는 1.099에서 3.224으로 확인되었고 PIC 값은 0.086에서 0.646으로 산출되었다. 14개 유전자좌에서 3개 집단의 유전다양성을 분석한 결과 유효대립유전자 수(A_e), 이형접합도 관측치(H_o)와 기대치(H_e)는 각각 1.813, 0.291, 0.369로 확인되었다. 각 집단이 보유하고 있는 평균 고유대립유전자 수(A_p)는 남양주에서 가장 많은 0.643이며 진천과 충주는 각각 0.0500과 0.286으로 확인되었다. 본 연구를 통해 개발된 microsatellite 표지는 산초나무의 유전다양성 평가와 육종연구에 유용할 것으로 기대된다.

PC-129

이미지 센싱 기반으로 한 벼 생육 표현형 분석

이홍석*, 김송림, 이은경, 최인찬, 지현소, 윤혜진, 김경환

전라북도 전주시 완산구 농생명로 370, 국립농업과학원 농업생명자원부 유전자공학과

쌀은 세계 3대 작물 중 하나인 주요 식량자원으로 벼 염색체 완전해독연구 이후 세계 각국은 3만여 개 이상의 유전자 기능을 밝히고 유용 형질 유전자의 개발에 박차를 가하고 있다. 유용 형질 유전자의 개발과 기능분석을 위해서는 형질 전환기술, 표현체 분석, 대사체 분석 등의 기반 기술이 요구된다. 이러한 기술은 육종기간 단축, 다양한 유전 형질 도입 등을 통한 생산량 증대, 기능성 증진 등을 통한 품종육성에 기여 할 수 있다. 벼의 새로운 우수 형질 개발, 유전자 기능 연구, 유전자원 선발 등을 위해 다양한 형질의 미세변화를 관찰 하기 위해, 벼의 많은 생육특성 파라미터를 측정할 필요가 있다. 이미지 센싱을 기반으로 한 표현형 분석은 식물 형태, 생리 및 생화학적 현상을 정량적으로 분석할 수 있다. 표현체 기반 비파괴검사 방법 중 3D 스캔과 근적외선(NIR) 영상장치를 통해 표현형 분석을 하였다. 먼저 RGB카메라를 이용하여 벼의 이미지를 획득하고 RGB이미지를 Lab와 HCL이미지로 변환하였다. RGB이미지 관심영역을 추출한 후 HCL 이미지로 변환하여 배경(Background)을 제거 한다. 배경이 제거된 이진화(Binary)영상과 관심영역추출이미지를 연산하여 벼의 영역만을 추출할 수 있다. 추출된 이미지의 전체 픽셀을 카운팅하여 잎의 총 면적을 측정할 수 있으며, 식물의 키와 분리된 식물의 3D 이미지를 획득할 수 있다. 또한 Lab색차계 채널 중 a*채널은 노란색과 초록색의 정도를 표현하기 적합하므로 엽록소에 따른 잎의 색을 정량적으로 측정할 수 있다. 근적외석 영상장치를 이용하여 벼의 다양한 표현형 분석 실험은 진행 중이며 벼의 성장에 따른 지속적인 측정은 아직 미흡한 단계이다. 본 연구에서는 지속적으로 근적외선 영상장치를 통해 벼의 단백질, 질소, 아밀로스 함량 등의 다양한 형질을 정량적 측정이 가능하도록 이미지 센싱 기반의 벼 생육 표현형을 분석하고자 한다.

Corresponding author: Tel. 063-238-4687 E-mail: ehg117@gmail.com

PC-130

Identification and Characterization of Grain Weight Trait Candidate Genes in a Cross between *Oryza sativa* and *O. rufipogon*

Yun-A Jeon, Dong-Min Kim, Hyun-Sook Lee, Ju-Won Kang, Yun-Joo Kang, Sang-Nag Ahn*

[1]Department of Agronomy, College of Agriculture and Life Sciences, Chungnam National University, Daejeon 305-764, Korea
[2]Seed Testing and Research Center, Korea Seed and Variety Service, Gimcheon 740-220, Korea

Grain weight is important component determining rice grain yield, and it is controlled by quantitative trait loci (QTLs). In a previous study, a high-resolution physical map targeting a cluster of yield-related QTLs for grain weight, spikelets per panicle has been cultivated using series of BC_3F_4 nearly isogenic lines (NILs) derived from a cross between the Korean *japonica* cultivar Hwaseong and *O. rufipogon*. The QTLs including grain weight trait have been mapped in a 25.5kb region containing six genes. These candidate genes (MYB family transcription factor, expressed protein, male sterility 5, similar ascorbate peroxidase, glutelin family protein and NTMC2 type protein) have been identified from publicly available databases of website servers. The information of genes including GenBank accession number, the length of the open readign frame (ORF), and the number of exon has been searched. To identify functions we used for RNA preparation and rice was used for rice transformation. Total RNAs were isolated from various tissues (2-week seedling, flag leaf, root and initiation panicle and five developmental stages) and to investigate the candidate genes pattern in different tissues we performed RT-PCR and qRT-PCR using the gene specific primers. The cDNAs of *OsApx* gene from the parental lines Hwaseong and NIL-*gw9* were cloned. For rice transformation, we constructed using in vector of over-expression and RNAi knock-down of genes with constitutive promoter.

Acknowledgements: This work was supported by the grant from the Next-Generation Biogreen 21 Program for Agriculture & Technology Development (Project No. PJ011048012016), Rural Development Administration, Republic of Korea.

Corresponding author: Tel. 042-821-7038, E-mail: ahnsn@cnu.ac.kr

PC-131

Genetic Diversity and Barcodes of *Taraxacum* Species Based on Complete Chloroplast Genome Sequences

Jin-Kyung Kim[1], Jee Young Park[1], Yun Sun Lee[1], Hyun Oh Lee[2], Hyun-Seung Park[1], Sang-Choon Lee[1], Shin-Jae Kang[1], Jung Hwa Kang[3], Taek Joo Lee[3], Tae-Jin Yang[1*]

[1]Department of Plant Science, Plant Genomics and Breeding Institute, and Research Institute of Agriculture and Life Sciences, College of Agriculture and Life Sciences, Seoul National University, Seoul, Korea
[2]Phyzen Genome Institute, Seongnam, Gyeonggi-Do, Korea
[3]Hantaek Botanical Garden, Yongin, Gyeonggi-Do, Korea

The genus *Taraxacum* comprising over 2,500 perennial plant species belongs to the family Asteraceae, the largest family of flowering plants. *Taraxacum* species have long been utilized for traditional medicinal herbs due to their various pharmacological activities including diuretic, choleretic and anti-inflammatory activities. The genus *Taraxacum* shows taxonomic complexity because of the presence of agamospermy, complex hybridity and polyploidy, which make taxonomic studies of this genus difficult. On this account, the complete chloroplast (cp) genomes of seven *Taraxacum* species were determined by *de novo* assembly with whole genome sequencing data, which is the first comprehensive cp genome analysis on the genus *Taraxacum.* The seven *Taraxacum* cp genomes ranged from 151,173 bp to 151,451 bp in size and exhibited typical circular quadripartite structure with conserved gene content and order. Polymorphic sites such as copy number variation of repeats, SSRs, InDels and SNPs were identified at inter-species level and examined as molecular markers to discriminate each of the seven *Taraxacum* species. Complete cp genomes obtained in this study will provide valuable genetic information for further molecular study, phylogenetic analysis, and authentication of *Taraxacum* species as well as for others in the family Asteraceae. This study was supported by “15172MFDS246, 16172MFDS229” from Ministry of Food and Drug Safety in 2015 and 2016 respectively, Republic of Korea.

Corresponding author: Tel. 02-880-4547, E-mail: tjyang@snu.ac.kr

PC-132

식물표현체 기술을 통한 벼 생육 시 질소원이 생장에 미치는 영향 분석

김송림*, 이홍석, 이은경, 임철희, 최인찬, 윤혜진, 지현소, 김경환

전북 전주시 완산구 농생명로 370, 국립농업과학원 농업생명자원부 유전자공학과

Phenomics (표현체학)은 유전자형과 표현형을 시스템적으로 분석하여 작물의 품종 육성에 활용할 수 있는 High-throughput phenotyping (HTP)시스템이다. 본 연구에서는 벼가 질소원 결핍 시 보이는 생육 특성 및 형질 분석에 식물 표현체 기술을 활용하고자 하였다. 질소는 식물의 생장과 발달에 요구되는 가장 대표적인 macronutrients중 하나로써, 질소에 대한 식물의 발달 양상을 조사하기 위해서 동진 벼를 Yoshida 용액을 기준으로 Nitrogen 0.25배에서 2배 사이의 농도에 따라 재배하고 표현형 관찰은 LemnaTech. 3D scanalyzer에서 획득한 이미지 데이터를 이용하였다. 식물체의 크기 측정은 질소 농도에 따라 생장한 식물체로부터 찍은 이미지를 배경과 분리한 후 skeleton화 시켜 잎의 모양을 선형화시켜 측정하였다. 이를 통해 저농도 보다 고농도의 질소원에서 생장한 식물체가 24% 크게 생장한 것을 관찰하였다. 질소원 결핍은 벼의 잎 색깔에도 영향을 주는데, 잎 색깔 분석은 3D scanalyzer로 찍은 이미지 영상을 Lab 색차계 중 a* 채널을 이용하여 변환시켜 관찰 할 수 있었다. 그 결과, 저농도 보다 고농도의 질소원에서 30% 이상 높은 녹색화 보였고, 질소 결핍 시 엽록소의 생성이 저해되는 양상을 반영하였다. 식물체를 촬영한 이미지의 픽셀의 개수는 잎의 표면적을 측정하기에 용이하였는데, 이것 역시 고농도의 질소원에서 잎 면적이 30% 이상 증가한 것을 알 수 있었다. 요컨대, 이미지 장비를 통한 식물체의 키, 잎 색깔, 잎 면적 측정 방법들은 질소원 결핍 시 식물의 생장에 미치는 식물생리학적 특성들을 잘 보여 주었다. 결국, 본 연구는 벼의 형질을 대량으로 분석하는 시스템에 활용 가능할 것이며, 향후 목적 형질의 조기 선발, 작물육종 등에 활용 할 수 있을 것으로 기대된다.

Corresponding author: Tel. 063-238-4672, E-mail: greenksl5405@korea.kr

PC-133

Identification of QTL Associated with Low-temperature Germinability in NILs Derived from an Interspecific Cross in Rice

Quynh Anh Le[1], Yun-Joo Kang[1], Kyu-Chan Shim[1], Yun-A Jeon[1], Yeo-Tae Yun[2], Ju-Won Kang[1,3], Hyun-Sook Lee[1], Sang-Nag Ahn[1*]

[1]Department of Agronomy, College of Agriculture & Life Sciences, Chungnam National University, Daejeon 305-764, Korea
[2]Chungcheongnamdo Agricultural Research and Extension Services, Yesan 340-861, Korea
[3]Present address: Department of Southern Area Crop Science, National Institute of Crop Science, Milyang 50424, Korea

High germination rate under low-temperature condition is one of the most important factor of growing in rice. From an advanced backcross progeny, one BC_3F_7 line (TR5) which is containing the target QTL region for the homozygous alleles of *O. rufipogon* in the Hwaseongbyeo background was selected as a beginning material for determine mapping of low-temperature germinability. Quantitative trait loci (QTL) controlling low-temperature germinability in rice were confirmed, using 21 NILs derived from the backcross between TR5 and Hwaseongbyeo as a recurrent parent. The experiments for low-temperature germinability at 15 °C were conducted, recorded at 8th day after incubation and used for QTL analysis. Percentage of germination for Hwaseongbyeo, TR5 and *O. rufipogon* was 21.7%, 88.3% and 100%, respectively. And that of NILs ranged from 13.3 to 93.3%. 52 SSR markers located on chromosome 1 and 24 SSR markers located on chromosome 10 were used to construct the linkage map. 6 of 52 (11.54%) and 5 of 24 (20.83%) markers on chromosme 1 and 10 showed polymorphism between Hwaseongbyeo and *O.rufipogon*, respectively. There were 2 putative QTLs, qLTG1 and qLTG10, linkaged with low-temperature recognized on chromosome 1 and 10. The highest effects qLTG1 explained 62.23% of the total phenotypic variation. qLTG10 explained 27.18% of the total phenotypic variation. We confirmed that *O.rufipogon* alleles in those QTLs loci risen the low-temperature germinability.

Acknowledgement: This work was supported by a grant from the Next-Generation BioGreen 21 Program (Project No. PJ011048012016), Rural Development Administration, Republic of Korea.

Corresponding author: E-mail: ahnsn@cnu.ac.kr

PC-134

The Grain Shape QTL, *GW2* is Associated with Chlorophyll Content and First Internode Diameter in Rice

Lu Xin[1], Kyu-Chan Shim[1], Ju-Won Kang[1,2], Hyun-Sook Lee[1], Sang-Nag Ahn[1*]

[1]Department of Agronomy, College of Agriculture & Life Sciences, Chungnam National University, Daejeon 305-764, Korea
[2]Present address: Department of Southern Area Crop Science, National Institute of Crop Science, Milyang 50424, Korea

GW2, a major QTL associate with grain shape and grain weight in rice, was mapped on chromosome 2 in the previous study. Besides, the difference was also found in several other agronomic traits in the gw2 near-isogenic lines (NIL) like chlorophyll content and stem diameter. To know whether *GW2* is associated other agronomic traits, a F_3 population derived from a backcross between japonica *cv. Hwaseong* and CR7501 (One near-isogenic lines from a cross between gw2-NIL and gw8-NIL) was performed in this study. Simple sequence repeat (SSR) analysis was performed of the F_2 and F_3 population, respectively. Phenotypic evaluate was performed including: grain length, grain width, 1000-grain weight, plant height, culm length, No. of panicle, first internode diameter, stem diameter, chlorophyll content, No. of primary branches, No. of secondary branches, spikelets per panicle and grain yield per 5 plants. 79 known SSR markers were chose depend on our previous study to detected *O. grandiglumis* segments. Our study showed that *GW2* is positively associated with first internode diameter and chlorophyll content. Inaddition, a total of 19 QTLs were identified at 4 regions. The phenotypic variation explained by each QTL ranged from 4.7 to 47.8%.

Acknowledgement: This work was supported by a grant from the Next-Generation BioGreen 21 Program (Project No. PJ011048012016), Rural Development Administration, Republic of Korea.

Corresponding author: E-mail: ahnsn@cnu.ac.kr

PC-135

PagBEE3L 형질전환 포플러의 바이오매스 증대 효과

최현모, 최영임*, 노설아, 박응준, 윤서경, 신주희, 배은경, 이효신

경기도 수원시 권선구 온정로 39 국립산림과학원 산림유전자원부

브라시노스테로이드(BR)는 세포 신장 및 형성층 활성 조절에 관여하는 식물 호르몬으로서 식물의 생장과 발달에 중요한 역할을 하는 것으로 알려져 있다. 이러한 BR 호르몬에 의해 발현되는 것으로 알려진 *BEE3* 유전자는 BR 반응을 매개하는데 필요한 전사인자로 알려져 있다. 이에 본 연구실에서는 basic helix-loop-helix 도메인을 갖는 *BEE3* 상동유전자 *PagBEE3L*를 포플러 (*Populus alba* x *P. glandulosa*) 에서 동정하였고, 이 유전자가 포플러의 생장과 발달에 영향을 주어 바이오매스 증대에 기여할 수 있는지 조사하고자 하였다.
유전자의 발현을 조사한 결과, 줄기에서 주로 *PagBEE3L* 유전자의 발현량이 높은 것을 알 수 있었으며 특히 절간보다는 마디에서 발현량이 높은 것을 확인하였다. 바이오매스 증대와 관련된 유전자의 기능과 특성에 대한 연구를 위하여 *PagBEE3L* 과발현 형질전환체 포플러를 제작하였고 표현형을 분석한 결과, *PagBEE3L* 과발현체가 야생형 포플러보다 굵고 긴 줄기를 가지고 있었고, 물관층이 횡적으로 확장된 것을 관찰할 수 있었다. 특히 물관에서 조직특이적으로 *PagBEE3L* 유전자가 발현되고, 물관이 발달될수록 더욱 높게 발현되는 것을 알 수 있었으며, 마이크로어레이를 이용한 유전자 발현 분석 결과, 세포 분화 및 발달에 관련된 유전자들의 발현이 변화되었음을 확인하였다.
본 연구를 통하여 *BEE3L* 유전자가 포플러의 바이오매스 증대에 효과가 있다는 것을 확인할 수 있었고, 이러한 바이오매스 증대는 과발현된 *BEE3L* 유전자가 목질부 세포의 증가에 관여하면서, 물관 발달이 촉진되고, 이에 따라 줄기의 초기 생장이 증대되었기 때문이라는 것을 연구 결과들을 토대로 추정할 수 있다.

Corresponding author: Tel. 031-290-1173, E-mail: yichoi99@korea.kr

PC-136

Cloning of WRKY Genes, Induced by Stresses in Zoysia japonica Steud.

Woo-Nam Kim[1], Yong-Ik Kwon[2], In-Ja song[2], Bo-Hwa Hwang[2], Dong-Sun Lee[1], HyoYeon Lee[1,2*]

[1]Faculty of Biotechnology, Jeju National University, 690-756, Korea
[2]Subtropical Horticulture Research Institute, Jeju National University, Jeju 690-756, Korea

WRKY transcription factor genes belong to large gene families. This family is defined by a domain of 60 amino acids, contains the amino acid sequence WRKY at its amino-terminal end and a putative zinc finger motif it carboxy-terminal end. Some of the WRKY proteins contain two WRKY domains, while others have only one. WRKY transcription factors participated various biotic stress responses such as drought, salt, cold, and high temperature.
Zoysiagrass (Zoysia japonica Steud.) is used primarily useful for the garden or the golf course. However, the zoysiagrass is warm season grass, the resistance to low-temperature stress is required. Recently, it was reporterd that overexpression of OsWRKY76 increased the low temperature resistance, and AtWRKY28 been reported to be related to the environmental stress. But WRKY, environmental stress-related gene, is unknown in zoysiagrass. Here, we report the analyzing of WRKY genes and response by cold, dehydration and senescence stresses in zoysiagrass. Three WRKY gene (ZjWRKY3, ZjWRKY5, ZjWRKY7) cloning from zoysiagrass. It will be transfer into arabidopsis, zoysiagrass and analyze the functions.

Acknowledgements: This work was supported by Basic Science Research Program through the National Research Foundation (2009-0094059), and BioGreen 21 Program (PJ01186001), Rural Development Administration, Republic of Korea

Corresponding author: Tel 064-754-3396, E-mail, hyoyeon@jejunu.ac.kr

PC-137

작물육종 효율 극대화를 위한 식물표현체 플랫폼 구축

이은경*, 이홍석, 임철희, 김송림, 최인찬, 윤혜진, 지현소, 김경환

전라북도 전주시 완산구 농생명로 370 국립농업과학원 농업생명자원부 유전자공학과

식물표현체 플랫폼은 육종가의 주관적 판단에 의한 형질분석을 디지털 영상을 활용해 대량, 신속, 객관적 분석이 가능하게 한 융·복합형 차세대 육종 기술로, 표현형질을 체계적으로 관찰하고 대량으로 분석할 수 있도록 설계된 공장형 진단 장비다. 장비의 구성은 식물재배환경 조절이 가능한 최첨단 온실과 RGB·열화상·형광·근적외선카메라 등의 이미지 획득 장치, 시료를 대량으로 분석하기 위한 식물 운송 컨베이어 시스템으로 되어 있다. 현재 작물 생육을 위한 정밀환경조절 온실을 건축 후, 3D 가시광 이미지 분석장비와 500화분 규모의 자동 이송장치를 설치하고, 근적외선, 적외선 이미지 장비와 추가로 500화분 규모의 이송장치를 도입할 예정이다. 2017년까지 실험실내 3차원 분석실과 포장 단위 정밀검정 시설을 구축하면, 실내, 온실, 포장에서 표현형을 분석할 수 있는 식물표현체 분석 플랫폼이 완료된다. 식물표현체 플랫폼을 이용하면 육안으로 판독하기 어려운 여러 형질들을 정밀하게 측정 가능하고, 고속 대량으로 데이터를 수집해 정확한 분석을 할 수 있다. 분석된 정보는 식물 육종가나 연구자에게 제공돼 신품종 종자 연구 개발 및 기후변화에 적합한 재배 품종 예측, 유전자 기능 대량 검정 등 다양한 분야에 활용될 수 있다.

Corresponding author: Tel. 063-238-4672, E-mail: wowlek44@gmail.com

PC-138

$F_{2:3}$ 집단을 이용한 '대립벼 1호' 종자 형태를 조절하는 유전자 탐색

심규찬, 강주원, 이현숙, 안상낙*

대전광역시 유성구 궁동 충남대학교 농업생명과학대학 농학과

종자중은 수당립수와 함께 가장 중요한 벼 수량 구성 요소이며, 종자의 길이, 폭, 두께에 큰 영향을 받는다. 대립벼 1호는 매우 큰 종자를 갖고 있으며, 종자 형태를 목표로하는 육종에서 유전 재료로 많이 사용되어져 왔다. 본 연구에서는 대립벼 1호에 종자 형태를 조절하는 유전자를 탐색하기 위해 수행되었다. 보석흑찰을 모본, 대립벼 1호를 부본으로 하여 육성한 $F_{2:3}$ 세대를 이용하여 유전분석을 수행하였다. 선행연구에서 동정된 5개의 유전자와 fine mapping된 2개의 QTL을 선정하였고, 이에 밀접하게 연관된 SSR마커를 이용하여 종자 형태 특성과 분산분석을 하였다. 그 결과 *GW2*, *GS3*, qGL6 근처 SSR마커에서 $F_{2:3}$ 세대 모두 유의한 QTL들이 발견되었다. 발견된 QTL들이 *GW2, GS3*에 의한 변이가 맞는지 확인하기 위해 염기서열 분석이 수행되었다. 그 결과 대립벼 1호의 *GW2* 유전자에서 1-bp 결실이 발견되었는데, 이는 선행연구의 'WY3' 계통과 동일한 돌연변이였다. 1-bp 결실로 인하여 아미노산 번역이 조기에 종결되고, *GW2* 유전자가 기능을 잃으면서 종자의 폭과 두께가 증가한다고 보고되었다. *GS3* 유전자 염기서열분석 결과 보석흑찰에서 GS3 유전자 2번째 exon지역에서 C-to-A 돌연변이가 관찰되었고, 대립벼 1호에서는 발견되지 않았다. C-to-A 돌연변이는 종자의 길이를 증가시키는 것으로 보고되었으며, 이 돌연변이가 보석흑찰의 종자 길이를 증가시킨 것으로 확인되었다. qGL6는 6번 염색체에 위치하고 있으며, Wx 유전자와 3Mb 거리에 연관되어 있다. qGL6는 대립벼 1호의 염색체 단편에 의해서 종자의 길이가 길어지는 것으로 나타났다. 결과적으로 GW2 유전자와 qGL6가 대립벼의 종자 크기를 증가시키는 유전자로 확인되었다.

Acknowledgement: 본 연구는 농촌진흥청 차세대바이오그린21사업 (과제번호: PJ011048012016)의 지원에 의해 수행되었습니다.

Corresponding author: Tel. 042-821-7038, E-mail: ahnsn@cnu.ac.kr

PC-139

Characterization of Grain Weight QTL, *gw8*

Yun-Joo Kang[1], Yun-A Jeon[1], Ju-Won Kang[1,2], Hyun-Sook Lee[1], Sang-Nag Ahn[1*]

[1]Department of Agronomy, College of Agriculture & Life Sciences, Chungnam National University, Daejeon 305-764, Korea
[2]Present address: Department of Southern Area Crop Science, National Institute of Crop Science, Milyang 50424, Korea

Rice is one of the most important cereal crop in Asia. In rice breeding, one of the major goal is grain yield which affected by grain weight. In previous studies, high-density maps for two grain weight QTLs, *tgw2* and *gw8.1*, were constructed using progeny derived from crosses between the *japonica* cultivar Hwaseong and *Oryza grandiglumis* (IRGC101154), and Hwaseong and *O. rufipogon* (IRGC105491), respectively. These wild alleles increased grain weight at two loci. To know how these two QTLs interact, an F2 population were developed by crossing two near isogenic lines(NILs) harboring *tgw2* and *gw8.1*. Simple sequence repeat(SSR) markers tightly linked to the QTLs were used to select F3 QTL-NILs from the F2 population. 1,000 grain weight of homozygous plants with wild alleles at the two loci was significantly higher than that of plants with a single QTL. These results indicate that two QTLs act additively, in distinct or complementary pathways in controlling grain weight. *gw8.1* QTL was further mapped between two SSR markers, RM23201 and RM23211, which are 231.6 kb apart using a series of NILs. Within 231.6 kb region, including RING H2 finger protein, 34 genes were detected. We sequenced 228 kb region harboring *gw8.1* of *O. rufipogon* and Keumobyeo (Hwaseongbyeo) and compared the sequence of the 34 genes. Semi-quantitative RT-PCR and qRT-PCR using samples from panicle developmental stages to analyze candidate genes for *gw8.1* is underway.

Acknowledgement: This work was supported by a grant from the Next-Generation BioGreen 21 Program (Project No. PJ011048012016), Rural Development Administration, Republic of Korea.

Corresponding author: E-mail: ahnsn@cnu.ac.kr

PC-140

Principal Component Analysis of Primary Pears and Korean Native Pears (*Pyrus* spp.) Using a Set of Microsatellite Reference Alleles

Keumsun Kim[1,2], Youngjae Oh[1,2], Sewon Oh[1,2], Jungyeon Won[1,2], Hyeondae Han[1,2], Yoon-Kyeong Kim[3], Seolah Kim[1,2], Daeil Kim[1,2*]

[1]Department of Horticulture, Chungbuk National University, Cheongju 28644, Korea
[2]Brain Korea 21 Center for Bio-Resource Chungbuk National University, Cheongju 28644, Korea
[3]Pear Research Station, National Institute of Horticultural & Herbal Science, Rural Development Administration, Naju 58220, Korea

This study was conducted to identify primary species by using 12 microsatellite markers, and to evaluate the usefulness of these microsatellites for classifying the genotypes of the primary species. In total, 43 pear accessions (7 primary pears, 5 Asian pears, 29 Korean pears, and 2 reference pears) were analyzed with 12 primers covering whole pear genome. All pear accessions were successfully classified along with their pedigrees. In PCA results based on the genetic distances of 7 primary pear species, 5 Asian pears, and 2 reference pears using 12 microsatellite markers, the eigenvalue of the first principal component was 5.7714 - a higher score than the eigenvalues derived from Korean pears. The proportion of the first principal component was the highest, at 0.9619. The cumulative percentage of the first 2 principal components was over 99%. The eigenvalue and difference score of the first principal component in 35 pear accessions were 4.6830 and 3.5697, respectively. The proportion of the first principal component was 0.7908. The eigenvalue of the second principal was 1.1134. The proportion of the second principal component was 0.1856, and the cumulative of the first 2 principal components was 0.9661. Considering the proportion scores from the PCA, the classification was almost elucidated by the first principal component. Our results indicate that this standard set of microsatellite markers is for the classification of Korean native pears, and suggests that this data could be useful for developing a core collection of pear genetic data.

Corresponding author: Tel. 043-261-2527, E-mail: dkpomo@cbnu.ac.kr

PC-141

Identification of Changes in Cold Hardiness and Soluble Sugars on Response to Experimental Deacclimation in Peachs (*Prunus persica*)

Keumsun Kim[1,2], Sewon Oh[1,2], Hyunsuk Shin[1,2], Youngjae Oh[1,2], Jungyeon Won[1,2], Hyeondae Han[1,2], Daeil Kim[1,2*]

[1]Department of Horticulture, Chungbuk National University, Cheongju 28644, Korea
[2]Brain Korea 21 Center for Bio-Resource Chungbuk National University, Cheongju 28644, Korea

Recently, the global mean temperature is predicted to increase by 3-5°C over a 100-yaer period because of enhanced atmospheric CO_2 concentration. Although temperate winters have become a little milder, the temperature patterns may become increasingly irregular with untimely warm spells. Thus, more adaptable cultivars to unexpected changes of temperatures are needed than very hardy cultivars tolerating extremely low temperatures. Several roles to carbohydrates in protecting cells from freezing injury have been proposed, including functioning as freezing point depression and stabilization of cell membrane from freezing-induced dehydration. Thus, the present study was conducted to estimate changes in cold hardiness by electrolyte leakage analysis in the shoot of the 10 peach cultivars (‘Aikawanakajima’, ‘Chiyomaru’, ‘Daewol’, ‘Janghowon Hwangdo’, ‘Kiraranokiwami’, ‘Mihong’, ‘Misshong’, ‘Soomee’, ‘Suhong’, and ‘Sun Gold’). Changes in soluble sugars contents were also analyzed using a HPLC. ‘Chiyomaru’ was the cold-tolerant cultivar, whereas ‘Kiraranokiwami’ was the cold-susceptible cultivar. Cold hardiness of all cultivars gradually decreased during an experimental deacclimation. At the same time, total soluble sugars, glucose, fructose, and sucrose contents decreased during the deacclimation in all peach cultivars. However, sorbitol contents declined in nine cultivars, except for ‘Suhong’ which showed an increase during deacclimation. Our results suggest that the cold hardiness and soluble sugars contents presented the decreasing similar patterns during deacclimation.

Corresponding author: Tel. 043-261-2527, E-mail: dkpomo@cbnu.ac.kr

PC-142

배추과 작물의 엽록체 유전체 서열을 활용한 종간 구분 InDel 마커 개발

양기웅, 정지윤, 정남희, 박종인, 노일섭*

국립순천대학교 생명산업과학대학 원예학과

배추과 작물은 유채, 겨자, 갓, 양배추, 브로콜리, 콜리플라워, 배추, 청경채 등과 같은 주요재배 식물들을 포함하여 전 세계적으로 약 3,500여종에 이르는 매우 중요한 원예 작물이다. 이러한 배추과 작물은 매우 다양하여 정확한 분류가 어려운 상황이다. 현재 배추과 작물의 종간 구분은 많은 부분이 표현형으로 분류되어 있다. 현재에는 유전학적으로 종간 분류를 위해 엽록체 유전체를 많이 활용한다. 식물세포의 엽록체는 광합성을 책임지는 주요 기관으로 세포질 유전체를 대표하기 때문에 전체 식물 유전체의 다양성과 진화에 대한 중요한 정보가 된다. 또한 엽록체 유전체의 크기는 120~217kb로 약 130개의 유전자가 작은 변이로 보존 및 유지되어 있다. 본 연구는 현재 NCBI에 등록되어 있는 배추과 작물의 다양한 엽록체 유전체를 확인하였다. *B. napus* 엽록체 유전체 3 종류 (KM454973; 153,531 bp, KJ872515; 153,533 bp, KP161617; 153,454 bp), *B. nigra* (IT119326; 153,633 bp), *B. juncea* (KT581449; 153,483 bp), *B. oleracea* (KR233156; 153,366 bp), 및 *B. rapa* (DQ231548; 153,482 bp)의 엽록체 유전체의 전반적인 변이를 탐색하였고, 다양한 변이 중 아가로스 겔에서 쉽게 구분할 수 있는 16점의 InDel 마커를 제작하여 68종의 Brassicacea에서 종간 구분이 가능한지 확인하였다. 결과적으로 본 연구는 완성된 Brassicacea 엽록체 서열을 바탕으로 종간 식별이 가능한 16점의 InDel 마커를 개발하였고, 이는 다양한 배추과 작물의 분류 및 계통 분석에 많은 기여를 할 것이라고 예상된다.

Acknowledgement: 본 연구는 농림축산식품부, 해양수산부, 농촌진흥청, 산림청 Golden Seed 프로젝트 사업(원예종자사업단, 과제번호: 213003-04-4-SB110)에 의해 이루어진 것임.

Corresponding author: Tel.061-750-3249, E-Mail: nis@sunchon.ac.kr

PC-143

Development of Molecular Marker for Characterizing Early and Late Bolting Genotypes of *Brassica oleracea* var. *capitata*

Md. Abuyusuf[1], Ujjal Kumar Nath[1], Jong-In Park[1], Mi-Young Chung[2], Ill-Sup Nou[1*]

[1]Department of Horticulture, Sunchon National University, 255, Jungang-ro, Suncheon, Jeonam 57922, Korea
[2]Department of Agriculturaln Education, Sunchon National University, 255, Jungang-ro, Suncheon, Jeonam 57922, Korea

Cabbage belonging to the family *Brassicaceae* is popular and cultivated as vegetables, with an exception of seed production. However, flowering is known as bolting which tremendously reduce the quality of cabbage as vegetables. Therefore, late bolting type genotype is expected to growers for ensuring economic values as vegetables. Whereas, early flowering is an important trait for higher and quality seed yield for next generation. Thereby, it is necessary to predict the genotypes whether they are early bolting or late-bolting type before planting using markers, especially suitable molecular markers. Molecular markers would be helpful to select the genotypes of early bolting and late-bolting type. In flowering plants, the alteration from vegetative to reproductive phase is a major conversion controlled by flowering pathway genes and environment together. The major flowering pathway interacting genes are *VRN*, *FRIGIDA* and *FLC* in cabbage. Among them, the direct contributor in flowering is known as Flowering Locus Control (*FLC*). The other two genes are contributed to flowering indirectly through *FLC* genes. Therefore, we have given emphasis primarily only to the FLC genes of *Brassica oleracea* for molecular markers development. We have identified 8 *FLC* genes from Bolbase database that are responsible for flowering in *Brassica oleracea*. To develop the effective molecular markers for separating early and late bolting genotypes, a cross was done between a late bolting inbred line BN4730 (♀) and early bolting inbred line BN7115 (♂). One hundred and forty one (141) F_2 plants are produced after selfing of F_1 and grouped them according to early and late bolting type. DNA was extracted from all the F_2 plants along with their parents. Gene specific markers of the above mentioned *FLC* genes have been developed covering UTR (untranscribed region), promoter and first exon-intron. PCR (Polymerase Chain Reaction) is continuing to find out the variation between early and late bolting type F_2 and parents. According to the consistency of the PCR results we will select the effective primer including more genotypes in this trial for separating as early and late bolting type of cabbage. Finally, we will confirmed those primers and designated as markers for identifying early and late bolting cabbage genotypes for growers, researchers and other interested end-users.

Acknowledgement: This research is supported by Golden Seed Project (Center for Horticultural Seed Development, No. 213003-04-4-SB110) Ministry of Agriculture, Food and Rural Affairs (MAFRA), Ministry of Oceans and Fisheries (MOF), RDA and Korea Forest Service (KFS).

Corresponding author: Tel. 061-750-3249, E-mail: nis@sunchon.ac.kr

PC-144

Identification and Expression Profiling of Rapeseed (*Brassica napus*) Genes Involved in Lipid Metabolism During Silique Development

Hankuil Yi[1*], Eunyoung Cho[1], Kyung Hee Roh[2], Ho Bang Kim[3,4]

[1]Department of Biological Sciences, Chungnam National University, Daejeon 34134 , Korea
[2]Department of Agricultural Biotechnology, National Academy of Agricultural Science, Jeonju 54874, Korea
[3]Life Sciences Research Institute, Biomedic Co., Ltd., Bucheon 14548, Korea
[4]Faculty of Biotechnology, Jeju National University, Jeju 63243, Korea

Here we provide an updated annotation and expression patterns of rapeseed (*Brasica napus*) genes, which are confirmed or expected to be involved in lipid metabolism and expressed in developing siliques. Rapeseed is cultivated world-wide for oil production from its seeds and provides the third largest sources for plant-based oil production. With the recent completion of rapeseed genome sequencing, comprehensive genome-level monitoring of gene expression changes became feasible. Through RNA sequencing of developing rapeseed siliques at three developmental stages with different lipid biosynthesis activities using Korean cultivar *Youngsan*, genes that are used in lipid biosynthesis during silique development were identified and the expression changes and relative contribution of various homeologs in this allotetrapolid plant were assessed. In addition, sequence polymorphisms between *Youngsan* and *Damor bzh* reference lines, are being uncovered, along with the several incorrect gene structure predictions.

Acknowledgement: This work was carried out with the support of “Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ01115102),” Rural Development Administration, Republic of Korea.

Corresponding author: Tel. 042-821-6410, E-mail: hankuil.yi@cnu.ac.kr

PC-145

BrPATL4 gene from *Brassica rapa* Expresses Small Seed and Erect Panicle in Transgenic *japonica* Rice

Joonki Kim[1†], Hye-Jung Lee[1,2†], Franz Marielle Nogoy[1], Dal-A Yu[1], Me-Sun Kim[1], Kwon-Kyoo Kang[3], Illsup Nou[4], Yong-Gu Cho[1*]

[1]Department of Crop Science, Chungbuk National University, Cheongju 28644, Korea
[2]Current Address, Korea Seed & Variety Service, Kimchon 39660, Korea
[3]Department of Horticulture, Hankyong National University, Anseong 17579, Korea
[4]Department of Horticulture, Sunchon National University, Suncheon 57922, Korea

A cDNA clone encoding Sec14-like protein, Patellin 4 was isolated from *Brassica rapa*. The *BrPatellin 4* gene encodes a cDNA (LOC103840314) consisting of 1,695 bp long with 67 bp of the 5' UTR, 1,488 bp of the coding region and 140 bp of the 3' UTR. The open reading frame encodes a polypeptide of 495 amino acids with a calculated mass of 55.7 kDa. *BrPATL4* has highly conserved Sec14-like lipid binding domain with several phospholipid binding pocket and salt bridge. The overexpression of *BrPATL4* in rice resulted in pleiotropic effects on general architecture including small seed size, erected panicles, decreased grain weight, reduced plant height, and increased sterility, which are common to other mutants deficient in GA biosynthesis. To test whether *BrPATL4* overexpressed line has defects in GA signal transduction, we compared the relative expression of GA related gene and the growth rate of second leaf sheath under the applying exogenous GA_3. Consequently, we may conclude that the overexpression of *BrPATL4* did not affect the GA biosynthesis or signaling pathway because of the same response under GA treatment compare to the wild type. However, the causal genes, *D1*, *SRS1*, and *SRS5* for the small seed phenotype and the erection of panicles showed the significantly decreased levels in mRNA accumulation compare to the wild type. These results suggest that the overexpression of *BrPATL4* can control the seed size through the suppression of those genes related to the seed size regulation. Although the molecular function of *BrPATL4* is not clear for small seed and elected panicles of *BrPALT4* overexpression line and its functions remains to be elucidated, this study will provide the clues about the genetic engineering of rice architecture.

[†] These authors contributed equally to this work.

Corresponding author: ygcho@cbnu.ac.kr

PC-146

Functional Characterization of Two NAC Transcription Factors of *OsNAC300* and *OsNAC75* in Rice (*Oryza sativa*)

Shadi Rahimi[1§], Yu-Jin Jung[2§], Me-Sun Kim[1], Eun-Ju eung[1], Kwon Kyoo Kang[2], Illsup Nou[3], Yong-Gu Cho[1*]

[1]Department of Crop Science, Chungbuk National University, Cheongju 28644, Korea
[2]Department of Horticulture, Hankyong National University, Ansung 17579, Korea
[3]Department of Horticulture, Sunchon National University, Sunchon 57922, Korea

Here, we present the identification of two NAC transcription factors in rice (*Oryza sativa*) named as *OsNAC300* and *OsNAC75* located on chromosome 12 and 1, respectively. The conserved domains were found by the sequence alignment of two proteins and their homologues from other plant species. The N-terminus of NAC proteins contains a highly conserved region of DNA binding domain that is around 150 amino acids in length and it was found in both of OsNACs. *OsNAC300* and homologue proteins from some other plant species form an out-group to the *OsNAC75* and homologue proteins by neighbor joining phylogenic analysis. Nuclear localization signal was predicted in *OsNAC75*. RT-PCR analysis was used to show the transcription level of these genes in different rice organs and in response to the different abiotic stresses. To understand the function of *OsNAC75* in response to abiotic stress, transgenic rice plants with overexpressing *OsNAC75* were investigated with the effect of heat stress on wild-type (WT) and overexpression rice lines. Our results demonstrated that the overexpression of *OsNAC75* in rice enhanced tolerance to heat stress. We also measured the effect of heat stress on the electrolyte leakage, which is an indicator for the damage caused by abiotic stress. Under stressed condition, a lower relative electrolyte leakage was observed for the transgenic plants than WT. The mechanisms underlying the changes in tolerance of the transgenic rice plants to abiotic stresses were explored by measuring free proline (Pro) in WT and transgenic plants. These results suggested that *OsNAC75* might play crucial role in plant responses to abiotic stresses.

[§]These authors contributed equally.

Acknowledgement: This work was supported by a grant from the Next-Generation BioGreen 21 Program (PJ01191601), RDA, Republic of Korea.

Corresponding author: E-mail: ygcho@cbnu.ac.kr

PC-148

GM Cabbage Resistant to Diamondback Moth

Yi Re Lee[1], Min Jung[1], Jong Sup Shin[2], Soon-Chun Jeong[3], Chee Hark Harn[1*]

[1]Biotechnology Institute
[2]Breeding Institute, Nongwoo Bio Co., Yeoju, Gyeonggi, Korea
[3]Bio-Evaluation Center, KRIBB, Chungbuk, Korea

GM crops producing *B. thuringiensis* toxins have been on the market for last 19 years or so creating a huge GMO industry. This is a result of *Bt* gene transformation to crops such as corn, soybean and cotton. However, the application to vegetable crops have not been on the market yet. One of the notorious pests in brassica crops is diamondback moth (DBM). In order to protect the insect plague of crops from DBM, 4-5 billion dollars have been wasted annually for applying integrated measures in worldwide. Major prevention is use of pesticides that may build the contamination level of chemicals in the ground and this practice threats the environment and ecosystem. Therefore, as an alternative, we have developed GM cabbages resistant DBM using *bt* gene. GM cabbages were tested for resistance and independent GM cabbages resistant to DBM were selected. Molecular analysis was conducted to find if GM cabbages hold one copy transgene in the intergenic insertion region of the cabbage genome. Finally we found two independent GM cabbages (C85-1 and C95) as events and those have been self-crossed for two generation. Also we are working the development of GM cabbage with a different vector that contains *bar* gene as a selection marker. Recently 5 T_0 cabbages have been obtained with *bar* selection, and Southern blot analysis confirmed that B13 line and B10 line contained one copy transgene.

Corresponding author: Tel. 031-887-6540, E-mail: chharn@nongwoobio.co.kr

PC-149

Genome-wide Identification of Sequence and Structural Variations from The Bacterial Canker of Kiwifruit *Pseudomonas syringae* pv. *actinidiae* (PSA) Pathovars and Their Application to Pathovar Genotyping

Chang Jae Oh[1], Jin-Kyu Woo[1], Ji-Hyeon Kim[1], Hye-Young Lee[1], Mee Hyang Hong[1], Gyoung Hee Kim[2], Young Sun Lee[3], Jae Sung Jung[3], Young Jin Koh[2], Ho Bang Kim[1,4*]

[1]Life Sciences Research Institute, Biomedic Co., Ltd., Bucheon 14548, Korea
[2]Department of Biology, Sunchon National University, Suncheon 57922, Korea
[3]Department of Plant Medicine, Sunchon National University, Suncheon 57922, Korea
[4]Faculty of Biotechnology, College of Applied Life Sciences, Jeju National University, Jeju 63243, Korea

A recently emerged plant disease, bacterial canker of kiwifruit (*Actinidia deliciosa* and *A. chinensis*), is caused by *P. syringae* pv. *actinidiae* (PSA). The disease was first reported in China and Japan in the 1980s. A severe outbreak of PSA began in Italy in 2008 and has spread to other countries, which recently causes severe economic losses to kiwifruit cultivations in South Korea, southern Europe, Chile, and New Zealand. PSA manifests as brown leaf spots with chlorotic haloes, brown discoloration of buds, cankers with exudates on trunks and twigs, collapsed leaders and eventually the death of the plant. In 2011, an Italian research group reported draft genome sequences of PSA strains. In order to study the evolution of PSA pathovars and analyse the transmission of PSA between countries, we generated genome-wide Illumina sequence data of 15 PSA strains covering three major biovars (PSA1, PSA2, and PSA3) and performed comparative genome analysis to mine sequence and structural variations (SNP, PAV etc.) among the biovars and intrapathovars. We identified pathovar-specific variations from the comparative analyses and optimized them as molecular markers to diagnose biovars and intrapathovars for the efficient biocontrol of PSA.

Acknowledgments: This work was supported by the Bio-Industry Technology Development Program grant, funded by IPET, Republic of Korea (grant no. 315019-02-1-HD030 to HBK).

PC-150

Functional Characterization of Alfalfa (*Medicago sativa* L.) DNAJ Gene (MsDNAJ) Involved in Abiotic Stress Defense

Ki-Won Lee*, Md. Atikur Rahman, Sang-Hoon Lee, Ki-Yong Kim, Hee Chung Ji, Tae Young Hwang

Grassland and Forages Division, National Institute of Animal Science, RDA, Cheonan, Korea

The DNAJ-genes have critical functions to abiotic stress response in plants, but their molecular analyses related to stress tolerance are poorly documented. This study was investigated the function of alfalfa DNAJ gene using transgenic tobacco. The annealing control primer based polymerase chain reaction showed that alfalfa-DNAJ expression was triggered by abiotic stresses. Ectopic expression of alfalfa-DNAJ in transgenic tobacco reduced the accumulation of hydrogen peroxide (H_2O_2) under abiotic stresses. The photochemical efficiency of photosystem II (Fv/Fm) was relatively higher in transgenic tobacco plants. The tobacco transgenic plants shows better growth, higher chlorophyll content, and low level of malondialdehyde (MDA) accumulation and relative electrolyte leakage (REL) response to abiotic stresses. In addition, overexpression of alfalfa-DNAJ improved tolerance to abiotic stresses in transgenic tobacco plants. These results indicate that overexpression of alfalfa-DNAJ gene exhibits tolerance to abiotic stresses in transgenic tobacco plants.

Corresponding author: Tel. 041-580-6757, E-mail: kiwon@korea.kr

PC-151

Study About Gene Flow and Stability Assessment in GM Rice (*Oryza sativa* L.)

Jun-Hoi Kim, Jin-Hee Kim, Kyung-Min Kim*

Division of Plant Biosciences, School of Applied Biosciences, College of Agriculture & Life Science, Kyungpook National University, Daegu, 41566, Korea

Rice is very an important crop for food. Especially, the importance of transgenic rice has increased. According to the Food and Agriculture Organization (FAO) statistics, GM crops are now commercially planted on about 100 million hectares in some 22 developed and developing countries. Therefore the significance of environment change and genetic safety has been recently demanded by the commercialization of GM (genetically modified). In this study, we evaluated the agricultural safety of drought-tolerant GM rice and to identify and assess environmental risks. The drought-tolerant GM rice including the donor plant, Ilmi, and four cultivars were analysed for agronomic characters, weediness potential, survival ability in the natural environment, and pollen-mediated gene flow in GM crop fields. There was no statistically significant difference in agronomic characters between the drought-tolerant rice and the donor plant, Ilmi. There was also no statistically significant relationship between the weediness potential and survival ability in the natural environment. These results indicate that drought-tolerant GM rice may be used to detect genetic safety and evaluation standards.

Corresponding author: Tel. 053-950-5711, E-mail: kkm@knu.ac.kr

PC-152

해충저항성 Bt벼의 개발과 안전성평가

임명호[1*], 박순기[2], 조현석[1]

[1]전라북도 전주시 완산구 농생명로 370 국립농업과학원 생물안전성과
[2]대구광역시 북구 대학로 경북대학교 농업생명과학대학 응용생명과학부

해충저항성 Bt벼는 토양미생물 *B. thuringiensis* 유래의 살충성 유전자 *Cry1Ac1*의 염기서열을 식물체 발현에 적합한 코돈으로 변형한 *mCry1Ac1* 유전자를 동진벼에 도입하여 개발한 유전자변형 벼이다. 유전자 도입을 위한 벡터(pZR3TP-Cry1Ac-Bar)는 양 말단의 border 서열 사이에 *rbcS3* 프로모터와 transit peptide에 의하여 조절되는 *mCry1Ac1* 유전자와 *CaMV 35S* 프로모터에 의하여 조절되는 선발마커 *bar* 유전자를 삽입하여 제작하였다. 벼 캘러스와 *Agrobacterium*을 공동 배양하여 형질전환을 수행한 후 105개 T0 식물체의 Southern blot 분석, 주변염기서열 분석, 표현형 조사를 수행하여 유전자가 single intergenic 형태로 삽입된 개체 14개를 확보하였다. 이들 중 도입유전자가 안정적으로 유전되고 생리학적 재배학적 형질이 양호한 4 계통을 선발하여 GMO 격리포장에 전개하여 농업형질, 농업환경 적응성, 생물검정을 통한 내충성, 목적 단백질의 발현 등을 평가하였다. 혹명나방 애벌레의 섭식실험 결과, 4 계통 모두 비슷한 정도의 내충성을 나타내었고, 포장에서의 수량성은 Bt-T07 계통이 대조구인 동진벼 대비 90-95% 정도를 나타내었다. 벼 종자의 영양성분을 분석한 결과 구성 성분과 함량이 동진벼와 실질적으로 동등하다고 평가되었고 농업환경에서의 전반적인 재배학적 특성도 동진벼와 별 다른 차이를 보이지 않았다. 이들 결과를 종합하여 1개 계통을 최종적으로 선발하여 우수 재배종과의 여교배 선발을 진행하고 있으며 향후 이를 이용한 안전성평가 연구를 수행 할 예정이다. 이번 발표는 해충저항성 Bt벼의 개발 과정, 계통 증식과 선발, 평가 등의 연구 수행 결과를 보고하고 향후 진행될 안전성평가에 대한 조언을 구하는 기회로 삼고자 한다.

Corresponding author: Tel. 063-238-4705, E-mail: mlim312@korea.kr

PC-153

CRISPR/Cas9-mediated Multiplex Genome Editing in Plants

Hyeran Kim, Sang-Tae Kim, Min Kyung Choi, Jahee Ryu, Jin-Soo Kim, Sang-Gyu Kim

Plant team, Center for Genome Engineering, Institute for Basic Science, Daejeon, 34047, Korea

The CRISPR-Cas9 system allows us to mutate the targeted gene in plant genome. Our team in the Center for Genome Engineering (IBS), has been developed a simple, flexible and high-throughput vector system for plant genome editing; 1) Cas9 proteins and sgRNAs are expressed under the control of CaMV 35S and U6/U3 promoter, respectively, 2) two-step cloning procedures facilitate the high production of the positive clones. We here introduce the binary vector system and a crucial strategy to generate multiple knockout mutants in *Arabidopsis thaliana* with Cas9 protein and a single guide RNA (sgRNA). All candidate sgRNAs, which guide Cas9 proteins to multiple loci in *A. thaliana* genome, were designed by Cas-Designer program in CRISPR RGEN Tools (http://rgenome.ibs.re.kr). In this study, we successfully generated a double, triple, quadruple, or quintuple knockout mutant of the selected NLRs, plant immune receptors.

Corresponding author: E-mail: mkchoi@ibs.re.kr

PC-154

Allelic Analysis of Low-molecular-weight Glutenin Subunits Using 2-DGE in Korean Wheat Cultivars

Hye-Rang Beom[1*], You-Ran Jang[1], Susan B Altenbach[2], Sun-Hyung Lim[1], Young-Mi Kim[1], Jong-Yeol Lee[1]

[1]National Academy of Agricultural Science, RDA, Jeonju, 560-500, Korea
[2]USDA-ARS, Western Regional Research Center, 800 Buchanan Street, Albany, CA 94710

The reliable identification of alleles for low molecular weight glutenin subunits (LMW-GS) is essential for breeding efforts aimed at improving wheat flour quality. Two-dimensional gel electrophoresis (2-DGE) was used to determine the allelic compositions of LMW-GS in 32 Korean wheat cultivars. Protein patterns generated by 2-DGE from each cultivar were compared to patterns from standard wheat cultivars for each allele. At the *Glu-A3* locus, thirteen *c*, twelve *d*, three *e* (null), two g and two new alleles were identified. At the *Glu-B3* locus, one *b*, nineteen *d*, four *h*, one *i* and five *ad* alleles were identified. At the *Glu-D3* locus, twenty-three *a,* four *b*, four c and one *l* alleles were identified. The alleles of *Glu-B3* LMW-GS were confirmed with SDS-PAGE analysis of omega 5-gliadin (*Gli-B1* locus) which is tightly linked with *Gli-B3* locus. When compared to results obtained previously using SDS-PAGE, there were discrepancies in the allelic designations of 10 of 32 cultivars (31%). While SDS-PAGE is a rapid and relatively simple method for assessing LMW-GS composition, the similar mobilities of the proteins makes it difficult to discriminate certain alleles. 2-DGE is a more complicated technique, but provides a more accurate picture of the complement of the LMW-GS in a given cultivar. In addition to providing essential information for wheat breeders, the 2-DGE reference maps generated in this study also make it possible to study the contributions of individual LMW-GS to flour quality.

Corresponding author: E-mail: gpfkd0629@jbnu.ac.kr

PC-155

Comprehensive Characterization of Low-Molecular-Weight Glutenin Subunit Genes and Their Protein Products in Common Wheat

Jong-Yeol Lee[1*], Hye-Rang Beom[1], Susan B Altenbach[2], Sun-Hyung Lim[1], Young-Mi Kim[1]

[1]National Academy of Agricultural Science, RDA, Jeonju, 560-500, Korea
[2]USDA-ARS, Western Regional Research Center, 800 Buchanan Street, Albany, CA 94710

Although it is well known that low-molecular-weight glutenin subunits (LMW-GS) affect bread and noodle processing quality, the function of specific LMW-GS proteins remains unclear. It is important to find the genes that correspond to individual LMW-GS proteins in order to understand the functions of specific proteins. The objective of this study was to link LMW-GS genes and haplotypes characterized using well-known *Glu-A3*, *Glu-B3* and *Glu-D3* gene specific primers to their protein products in a single wheat variety. A total of 36 LMW-GS genes and pseudogenes were amplified from the Korean cultivar Keumkang. These include 11 *Glu-3* gene haplotypes, two from the *Glu-A3* locus, two from the *Glu-B3* locus and seven from the *Glu-D3* locus. To establish relationships between gene haplotypes and their protein products, a glutenin protein fraction was separated by two-dimensional gel electrophoresis (2-DGE) and 17 individual protein spots were analyzed by N-terminal amino acid sequencing and tandem mass spectrometry (MS/MS). LMW-GS proteins were identified that corresponded to all *Glu-3* gene haplotypes except the pseudogenes. This is the first report of the comprehensive characterization of LMW-GS genes and their corresponding proteins in a single wheat cultivar. Our approach will be useful to understand the contributions of individual LMW-GS to the end-use quality of flour.

Corresponding author: E-mail: jy0820@korea.kr

PC-156

Simultaneous Suppression of Seed Storage Proteins in Rice Seed Using RNA Interference Induces ER-Stress Responses and Germination Delay

Kyoungwon Cho*, Hye-Jung Lee, Yeong-Min Jo, Jong-Yeol Lee, Young-Mi Kim

Department of Agricultural Biotechnology, National Academy of Agricultural Science, Rural Development Administration, Wanju-gun, Jeollabuk-do 565-851, Korea

Seed storage proteins (SSPs) such as glutelin, polamin and globulin are abundant components within the most widely consumed food cereals in the world. Synthesized at the rough endoplasmic reticulum (ER), the SSPs are translocated to protein bodies. Prolamins are located at the spherical protein body I derived from ER, whereas glutelins and globulin are accumulated in the irregular shape protein body derived from vacuole. Our previous studies have shown that the individual suppression of glutelins, 13-kDa prolamins and globulin caused compensative accumulation of other SSPs. Herein, to investigate phenotypic and molecular features on SSPs deficiency, GPGb-RNAi transformants suppressing all of glutelin A, cysteine-rich 13-kDa prolamis and gluobulin were generated through RNA interference (RNAi) approach. We found that glutelin A, cysteine-rich 13-kDa prolamin and gluobulin are less accumulated but glutelin B and ER chaperones such as binding protein 1 and protein disulfide isomerase-like 1-1 are more accumulated at transcript and protein levels in the GPGb-RNAi seeds than those in the wild-type. Further, transcription of starch synthesis-related genes was reduced in immature seeds at two-week after flowering and starch granules were loosely packaged with various sphere sizes in the GPGb-RNAi seed endosperms, resulting from a floury phenotype. Interestingly, the rates of spouting and reduced sugar accumulation in the GPGb-RNAi seeds during germination were found to be delayed compared to the wild-type, providing new information toward understanding the role of SSPs in the formation of intracellular organelles and in germination.

Corresponding author: E-mail: kw.cho253@gmail.com

PC-157

Identification of a Novel Rice B-box Zinc Finger Protein Involved in Regulation of Anthocyanin Biosynthesis

Da-Hye Kim[1*], SangKyu Park[1], MinJi Choi[1], Sun-Hwa Ha[2], Jong-Yeol Lee[1], Sun-Hyung Lim[1*]

[1]National Academy of Agricultural Science, Rural Development Administration, Jeonju, 54874, Korea
[2]Department of Genetic Engineering and Graduate School of Biotechnology, Kyung Hee University Graduate School of Biotechnology, Kyung Hee University, Yongin, 17104, Korea

The B-box zinc finger proteins have been known to play an important role in plant growth and development. In this study, we identified a novel B-box zinc finger protein (OsDBB3b) that is highly expressed in black rice grain containing abundant anthocyanins in pericarp through RNA-seq analysis. To understand its physiological roles in plant, the *OsDBB3b* gene was transformed into wild type and the *transparent testa 1* mutant of *A. thaliana* (*tt1*) which is deficient in WIP-type zinc finger protein involved in the positive regulation of *AtANR* (anthocyanidin reductase) by interacting with MYB-bHLH-WD40 regulon. The OsDBB3b-overexpressing wild type and *tt1* transgenic plants showed increased red pigmentations in midrib near petioles of leaves and delayed-bolting phenotype. In agreement with the phenotype, total anthocyanin contents were elevated in rosette leaves of both transgenic plants compared to corresponding non-transgenic plants. Gene expression analysis revealed that *OsDBB3b* overexpression activated overall genes in shikimate pathway as well as genes in flavonoid pathway. These results indicate that OsDBB3b is a novel transcription factor involved in regulation of plant growth and metabolic flow from shikimate pathway to anthocyanin and proanthocyanidin pathway.

PC-158

Cloning and Characterizations of Flavonol Synthases Isolated from Yellow and Red Onion

SangKyu Park[1*], MinJi Choi[1], Da-Hye Kim[1], Sun-Hwa Ha[2], Jong-Yeol Lee[1], Sun-Hyung Lim[1*]

[1]National Academy of Agricultural Science, Rural Development Administration, Jeonju, 54874, Korea
[2]Department of Genetic Engineering and Graduate School of Biotechnology, Kyung Hee University Graduate School of Biotechnology, Kyung Hee University, Yongin, 17104, Korea

The major class of flavonoids in edible part of onion (*Allium cepa L.*) is flavonol (quercetin glucosides). Flavonols are synthesized from dihydroflavonols through the action of flavonol synthase (FLS) which belongs to a family of 2-oxoglutarate-dependent dioxygenases. We isolated coding regions of cDNAs encoding *AcFLS* from yellow onion breeding line ('HRB') and red onion doubled haploid line ('H6'). There were two differences of amino acids sequences at position 65 and position 213 between AcFLS from HRB (AcFLS-HRB) and AcFLS from H6 (AcFLS-H6). Position 213 was located between proposed residues involved in substrate and 2-oxoglutarate binding. Flavonoids pathway genes including *AcFLS* were predominantly expressed in sheath tissue. Expression levels of *AcFLS* in sheath were similar between HRB and H6, but those of other genes in sheath of H6 were relatively high compared to HRB. Particularly, dihydroflavonol 4-reductase was exclusively expressed in sheath of H6. Quercetin content in H6 was 1.5-fold higher than in HRB. Kinetic analysis conducted with recombinant GST-AcFLS-H6 and GST-AcFLS-HRB revealed that GST-AcFLS-H6 exhibited about 2-times lower catalytic efficiencies for dihydrokaempferol and dihydroquercetin than GST-AcFLS-HRB, and the optimal substrate for these recombinant enzymes is dihydroquercetin rather than dihydrokaempferol.

농생물게놈활용연구사업단

주요 작물에서 유전체 정보활용 육종가 친화형 인터페이스 연구 소개

(Introduction of genomics integrated Interfaces for breeders in major crops)

주요 작물에서 유전체 정보활용 육종가 친화형 인터페이스 연구 소개

(Introduction of genomics integrated Interfaces for breeders in major crops)

- 일시 : 2016년 7월 1일(금), 09:00 ~ 10:40
- 장소 : 라마다플라자 청주호텔 그랜드볼룸
- 주관 : 농생물게놈활용연구사업단

좌장 : 유의수 ((주)파이젠)

시간	발표 내용
09:00~09:25	▸가지과 유전체 활용을 위한 생물정보분석 파이프라인 및 데이터베이스 TGsol 현황 - 조성환 박사 ((주)씨더스)
	▸Development of Bioinformatics pipeline and web database for Solanaceae genome application - SungHwan Jo (SEEDERS)
09:25~09:50	▸두과작물 유전체정보 기반 분자육종 활용을 위한 플랫폼 개발 - 최홍규 교수 (동아대학교)
	▸Constructing a Genomics-Assisted Bioinformatic Platform for Legumes - Hong-Kyu Choi (Dong-A University)
09:50~10:15	▸콩 유전체 육종 지원용 Korean Soya Base 소개 - 김남신 박사 (한국생명공학연구원)
	▸Genomics Integrated Breeding Platform for Soybean: Korean Soya Base - Namshin Kim (Korea Research institute of Bioscience and Biotechnology)
10:15~10:40	▸벼 유전체육종 연구의 진전 및 소규모 연구실간의 Resource 공유체계 구축 : 재료 정보 프로그램 연구경험 공유 - 박용진 교수 (공주대학교)
	▸Research Updates of Rice Breeding Activities using Genome Information, and Development of Resources-Sharing Systems: Seed Materials, Genomic Information, Software and Research Experience - Yong-Jin Park (Kongju National University)

OD-01

가지과 유전체 활용을 위한 생물정보분석 파이프라인 및 데이터베이스 TGsol 현황

이봉우, 김지은, 오재은, 최준경, 이정희, 조성환*

대전광역시 유성구 테크노1로 11-3, ㈜씨더스

TGsol은 가지과 작물(토마토, 고추, 감자)의 GAB(Genome Assisted Breeding)를 구현하도록 돕는 것을 목적으로 하고 있다. GAB를 구현하기 위해서는 게놈 전체를 아우르는 마커와 주요 형질 관련 유전자 및 분자마커를 확보하고, MAS와 MAB 및 genomic selection을 실시할 수 있도록 지원할 수 있는 tool이 필요하다. 이에 따라 TGsol은 GAB 구현에 필요한 핵심데이터 및 tool을 개발하고, 공유하면서 발전해가고 있는 웹 데이터베이스이다. 현재 250여 계통의 토마토 유전자원 resequencing 결과 및 고추의 RIL resequencing 결과를 이용하여 genome-wide SNP를 분석하였고, 이용자가 검색하여 사용할 수 있도록 제공하고 있다. 또한 기능연구를 지원하기 위하여 토마토, 고추, 감자, 애기장대 간 ortholog 분석 및 synteny 검색 도구를 개발하여 유전자 기능연구에 활용되도록 지원하고 있다. 더불어 문헌검색을 통하여 내병성 관련 유전자(256개), 과실관련 유전자, 토마토 유용 대사산물 관련 유전자를 수집하여 형질별, 작물별 MAS(Marker-assisted Selection) 용 마커 개발과 토마토 MAB(Marker-assisted Backcrossing) 후보 마커를 선발하여 제공하는 tool을 개발하여 시연하고 있다. 육종 모델링 tool 구현을 위해서는 230여 계통의 토마토 resequencing 데이터를 수집하여 유전자 별 SNP를 기반으로 haplotype을 확보하여 단순화, 시각화를 구현하고 있으며 향후 표현형 정보와 연계하여 육종 선발을 위한 의사결정시스템을 개발하는데 이용하고자 한다. 이러한 결과들은 유전체 데이터를 공유하고 활용하는 것을 지원해 주신 연구자의 노력이 출발점이 되었으며 앞으로 GAB를 구현하는 연구진과의 활발한 의사소통을 통해 활용도가 높은 데이터베이스를 구축해 가고자 한다. (TGsol website: http://tgsol.seeders.co.kr)

Corresponding author: E-mail: shjo@seeders.co.kr

OD-02

Constructing a Genomics-Assisted Bioinformatic Platform for Legumes

Jin-Hyun Kim[1], Joo-Seok Park[2], Chaeyoung Lee[1], Hong-Kyu Choi[3*]

[1]Department of Medical Bioscience, Dong-A University, Busan, Korea
[2]Department of Applied Bioscience, Dong-A University, Busan, Korea
[3]Department of Genetic Engineering, Dong-A University, Busan, Korea

In recent years, genomic information has increasingly become important for applications in crop breeding, mainly due to the advancement of NGS technology and rapid accruement of the genome data. We are developing and constructing a bioinformatic platform for legume genomics-assisted breeding (TGIL: translational genomics interface for the legumes, http://tgil.donga.ac.kr). Six fully sequenced legume genome information, including *G. max*, *M. truncatula*, *L. japonicus*, *P. vulgaris*, *C. arietinum* and *V. radiata*, plays a pivotal role as the fundamental resources. The platform consists of three major modules, database, analysis 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 genic 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’

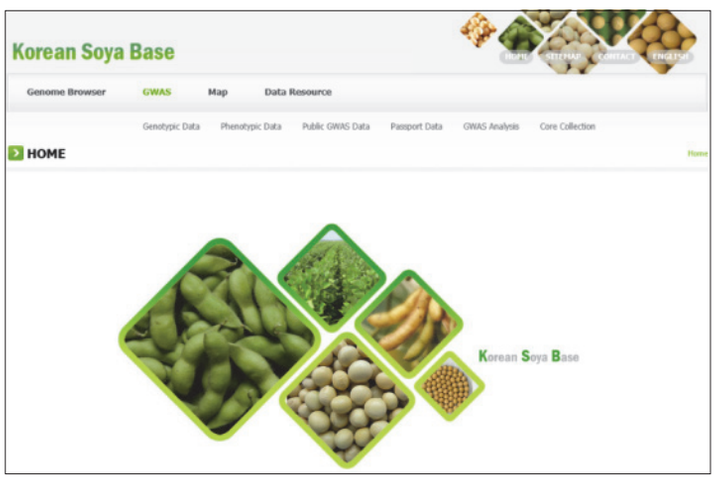
Corresponding author: E-mail: hkchoi@dau.ac.kr

OD-03

Genomics Integrated Breeding Platform for Soybean: Korean Soya Base

Namshin Kim

Korea Research institute of Bioscience and Biotechnology



We have been developing Korean Soya Base, curren tly available at http://www2.nics.go.kr/koreansoyabase /, to provide with genomics information from variou s collection of soybean accessions, such as SNPs & INDELs, genotypes & phenotypes, GWAS results, g enetic maps. Also, we had integrated a few software to help one to use it on the web. Genocore is recen tly developed to incorporate huge genomic data fro m high-density microarray and next-generation seque ncing data. Traditionally, core collection is made fro m a small set of markers, but recently researchers g enerate a huge genotype data. Genocore will be the only software that can handle giga-bytes genomic da ta.

We have generated Affymetrix SoyaSNP 180k SNP-chip from more than 4 thousands soybean accessions and 239 NGS resequencing data from core collection V1. All the genotype information from those accessions will be available at Korean Soya Base after we finish data analysis. Also, genotype and phenotype information from 800 core collections (V2; 407 G. max and 393 G. soja) will be available.

Korean Soya Base is still under development and we hope we could add more information soon.

Corresponding author: E-mail: deepreds@kribb.re.kr

OD-04

Research Updates of Rice Breeding Activities using Genome Information, and Development of Resources-Sharing Systems: Seed Materials, Genomic Information, Software and Research Experience

Yong-Jin Park[1,2*], Tae-Sung Kim[1], Kyu-Won Kim[1], Min-Young Yoon[1], Il-Pyung Ahn[3], Yong-Soo Choi[4], Won-Il Kim[3], Jung-Kyung Moon[3]

[1]Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 32439, Korea
[2]Center for crop genetic resource and breeding (CCGRB), Kongju National University, Cheonan 31080, Korea
[3]National Institute of Agricultural Science, Rural Development Administration (RDA), Wan-Joo 55365, Korea
[4]Natural Products Research Center, Korea Institute of Science and Technology, Gangneung 25451, Korea

Rice (Oryza sativa L.) is one of the most important staple crops in the world, providing a primary energy source for more than half of the world's population. Currently, the amount of land suitable for agriculture is decreasing due to a variety of factors such as rapid climate changes and industrialization, while rice-eating human populations continue to grow. On the other hand, especially in developed countries, people tend to favor rice with high nutritional and functional qualities. To meet the global nutritional and socio-economic demands, modern rice need to exploit available genomics resources/tools to develop superior rice varieties, efficiently accumulating and combining beneficial alleles from rice germplasm. Here, we'd like to present our progress of the genomics assisted breeding research in rice. Especially, in the 2nd phase of BioGreen research project since ´2015, we have been establishing GWAS (Genome-wide association study) pipelines to integrate Omics data to mine useful alleles underlying the rice milky stage, which are predicted to significantly influence the rice morphological, chemical and nutritional properties. To do so, we have been profiling transcriptome/proteome/ionome data from 15-day-old rice grains of 150 accessions of rice core population, in order to utilize this high through-put information as individual phenotypes. We'll also discuss about our preliminary approaches in the association mapping, linking the transcriptome and ionome of the rice germplasm on rice eating quality and ion uptake rate respectively. In addition, we are going to extend our discussion to the case studies of genome assisted breeding researches, happening in our laboratory, to improve many important agricultural traits in rice including abiotic stress resistances as well as eating and functional qualities. In the end, we'd like to introduce the mechanisms to share our experiences for managing genome resources through sophisticated software systems, which can fluently extract valuable genomic Information from rice germplasm materials to assist genomics-based crop breeding including rice.

Corresponding author: E-mail: yjpark@kongju.ac.kr

GM작물개발사업단
&
식물분자육종사업단

"Genome editing and molecular farming"

Genome editing and molecular farming

- 일시 : 2016년 7월 1일(금), 09:00 ~ 10:40
- 장소 : 라마다플라자 청주호텔 그랜드볼룸
- 주관 : GM작물개발사업단(NCGC) & 식물분자육종사업단(PMBC)

좌장: 조현석 (국립농업과학원)

시간	구분	내용
09:00~09:10	개회사 / 사업단장 인사말	
09:10~09:30	격려사	▸국가 농생명산업 발전과 식물생명공학 - 정광용 (전 농촌진흥청 차장)
09:30~10:05	주제발표 1	▸Versatile application of CRSPR/Cas9 system in plant research - 배상수 교수 (한양대학교)
10:05~10:40	주제발표 2	▸Transgenic plants producing green-vaccine for CSFV(classical swine fever virus) lead on plant biotechnology-based product on market - 손은주 박사 ((주)바이오앱)

OE-01

식물연구에서 크리스퍼 유전자가위의 다양한 적용

배상수

서울시 성동구 왕십리로 222, 한양대학교 화학과

유전자가위는 1세대인 ZFN, 2세대인 TALEN을 거쳐 3세대인 크리스퍼 유전자가위가 개발되었는데, 이를 이용하면 인간, 동물 및 식물 등 매우 다양한 종에서 특정 유전자 녹아웃이나 녹인을 매우 정교하게 원하는 곳에서만 일으킬 수 있다. 크리스퍼 유전자가위는 단백질 모듈 연결을 통해 타겟 DNA를 인식하는 ZFN, TALEN과는 다르게, 가이드 RNA 서열에 따라 타겟 DNA를 구분할 수 있다. 이렇게 RNA만 바꾸어 줌으로써 Cas9 또는 Cpf1 크리스퍼 단백질이 타겟 DNA에 작용하여 절단을 일으킬 수 있기 때문에, 사용하기가 매우 쉽고 가격 또한 저렴하다. 그래서 기존의 유전자가위들에 비해 매우 폭발적으로 널리 사용되고 있다. 최근에는 DNA를 사용하지 않은 크리스퍼 유전자가위 기술이 개발되었는데, 이는 플라스미드 대신 정제 단백질과 RNA를 뽑아서 사용하는 방식이다. 이를 식물에 적용할 경우, 외부 DNA를 사용하지 않기 때문에 현재 제도적인 GMO 규제 논란에서 자유로울 가능성이 있다. 본 발표에서는 누구나 쉽게 크리스퍼 유전자가위를 식물에서 사용할 수 있도록 오작동 가능성이 적은 타겟을 선정하는 웹툴에 대해 설명하고자 한다. 그리고 더 나아가, 다재다능한 크리스퍼 유전자가위를 이용하여, 애기장대에서의 유전체 편집과 페튜니아에서의 유전체 변이 및 미세조류인 클라미도모나스에서의 형질전환체 유도 방법에 대해 설명하고자 한다.

Corresponding author: Tel. 02-2220-2618, E-mail: sangsubae@hanyang.ac.kr

Versatile application of CRISPR/Cas9 system in plant research

Sangsu Bae

Department of Chemistry, Hanyang University, Seoul 133-791, Republic of Korea

Programmable nucleases, which include zinc finger nucleases (ZFNs), transcription-activator-like effector nucleases (TALENs), and RNA-guided engineered nucleases (RGENs) derived from CRISPR/Cas9 or CRISPR/Cpf1 system enable targeted gene editing such as gene knockout or knock-in at desired target loci of various eukaryotic cells, animals, and plants. Unlike ZFNs and TALENs whose DNA specificities are determined by DNA-binding proteins, CRISPR nucleases use complementary base pairing to recognize target sites. CRISPR nucleases are widely used due to the ease of use and inexpensive cost; researchers can induce gene editing at different sites by simply altering the guide RNAs. Recently, DNA-free CRISPR nucleases, the delivery of preassembled Cas9 protein-gRNA ribonucleoproteins (RNPs), has been introduced in various organisms including plants. It could be exempt of regulation that applies to genetically modified organisms (GMO) due to the absence of foreign DNA sequences in the transformant cells. Here I present web-based design tools for CRISPR nucleases including a novel potential off-target searching method. Furthermore, I introduce versatile applications of CRISPR nucleases - genome editing in *Arabidopsis thaliana,* site-directed mutagenesis in *Petunia x hybrida,* and one-step transformation of *Chlamydomonas reinhardtii* by the DNA-free CRISPR-Cas9 method.

Corresponding author: Tel. 82-2-2220-2618, E-mail: sangsubae@hanyang.ac.kr

OE-02

Transgenic Plants Producing Green-vaccine for CSFV(classical swine fever virus) Lead on Plant Biotechnology-based Product on Market

Minhee Park[1], Kyungmin Min[1], Sungmin Gu[1], Soo-Hong Park[1], Nam-Hyung Kim[1], Hyunsook Lee[1], Hyewon Kim[1], Yongjik Lee[1], Seong-In Lim[4], Hye-Young Jeong[4], Dong-Jun An[4], Jaeyoung Song[4], Inhwan Hwang[2,3], Eun-Ju Sohn[1,3*]

[1]BioApp Inc., Business Incubation Center
[2]Department of Life Science
[3]Division of Integrative Biosciences and Biotechnology, Pohang University of Science and Technology, Pohang 37673, Korea
[4]Animal and Plant Quarantine Agency, Gimchen, 39660, Korea

Classical swine fever (CSF) is a highly contagious and important disease in pork industry worldwide including South Korea. Recently, OIE put in place a procedure for official CSF-free country recognition. There are two major ways to control the CSF outbreaks and economical loss, one is a non-vaccination stamping-out policy toward “disease-free status” and the other is a systemic prophylactic vaccination policy. The prophylactic live vaccine is a strong obstacle for pork and pork products trade between countries. In order to help controlling CSF and promoting the pork international trade, we utilized the plant expression system to produce the CSF E2 protein for subunit marker vaccine which confers differentiation between infected and vaccinated animals (DIVA). CSF E2 is known as GP55 (glycoprotein 55) for being highly glycosylated. In design of expression vector, signal peptide of BiP drives E2 into ER and HDEL sequence retains E2 protein in the ER for glycosylation and accumulation. Transgenic Arabidopsis and Nicotiana show high expression levels greater than 1% of TSP. The plant-made E2 (pmE2) proteins were purified by affinity chromatography in cost-effective proprietary methods. Based on commercially available CSF antigen detection ELISA kit from a company, purified pmE2 has strong positive values with less than 5 ng coated. Purified pmE2 proteins induced a strong immune response for neutralizing antibody formation in mice by twice injection at dose of 0.2 μg. The pmE2 were injected in accordance with CSF vaccine protocol 40-day and 60-day old piglets. The pmE2 injection generated neutralizing antibody with 512 of VNT (virus neutralizing test) in piglets and protected immunized piglets from strong virulent CSF strain challenge at 10^6 TCID 50/ml. In summary, pmE2 were able to induce protective immunity.

Corresponding author: Tel. 054-279-8761, E-mail: ejsohn@postech.ac.kr

GSP 채소종자사업단
&
GSP 원예종자사업단

GSP 채소종자사업단

- 일시 : 2016년 7월 1일(금), 09:00 ~ 10:40
- 장소 : 라마다플라자 청주호텔 그랜드볼룸
- 주관 : GSP 채소종자사업단 & GSP 원예종자사업단

▸좌장 : 임용표 단장 (채소종자사업단)

내용
▸육성가 권리보호와 종자산업의 발달 - 이승인 박사 (국립종자원)
▸종자검정서비스 확대를 위한 국립종자원의 전략 - 소은희 박사 (국립종자원)

GSP 원예종자사업단

▸좌장 : 노일섭 단장 (원예종자사업단)

내용
▸Breeding for Pyramiding Target-genes and Selection of F1 Hybrids by Marker Assisted Selection in Tomato - 김명권 박사 (토마토생명공학연구소)
▸Gene Identification, Expression Analysis and Breeding for Enhanced Glucosinolate Biosynthesis in Brassica - Dr. Arif Hasan Khan Robin (Sunchon National University)

OF-01

육성가 권리보호와 종자산업의 발달

이승인

국립종자원

품종보호제도는 식물의 신품종 육성가에게 상업적 실시의 배타적인 독점권을 법적으로 보장하여 주는 지식재산권 제도이다. 이 제도는 「종자산업법」이 발효(1997.12.31.)되면서 도입·시행되었으며, 2012년 「식물신품종보호법」으로 관련법이 분리·정비 되었다. 품종보호는 육성가의 권리를 보호함으로써 우수품종의 육성의욕을 고취하는 것이 목적이다. 이를 통하여 우량종자의 보급을 촉진하고 농업생산성의 향상과 소득증대를 도모함으로써 궁극적으로 종자산업의 발전을 지향한다.

우리나라에는 국립종자원(농·원예작물)을 비롯하여 국립산림품종관리센터(산림작물)와 수산식물품종관리센터(수산식물)의 3곳의 품종보호제도 운영기관이 있다. 우리나라는 UPOV 회원국 중 세계 7위 수준의 출원국이며, 작년에 총 799품종의 출원을 기록하였다. 우리나라 품종보호는 제도 도입 이래 지난 19년 사이 UPOV 내에서 전례 없는 양적 성장을 이룩하였으나 질적인 면에서는 여러 해결해야 될 과제를 안고 있다. 이는 크게 심사의 품질과 국가 전체적인 권리의 보호수준, 그리고 권리 유지와 실시 측면에서의 건전성 요인 등으로 살펴볼 수 있다.

국립종자원의 조사에 따르면 2014년 1개년 기준 우리나라 품종보호 등록품종의 실시율은 40.7%로, 종자업체가 61.7%로 가장 높고 기관의 실시율은 33.2%로 가장 낮다. 또한 최근 문제가 되고 있는 一품종 異명칭 사례에서 보듯이 효과적인 권리보호를 위해서는 제도적 장치뿐만 아니라 무분별한 유사품종을 남발하는 일이 없도록 사회적인 동의와 성숙도가 매우 중요한 요소이다. 이를 위하여 심사기관은 품종보호 출원품종의 등록요건을 명확히 판단하여 자격이 없는 품종과 출원인의 권리화를 방지함으로써 제도의 신뢰성을 유지하여야 하며, 법적·기술적 제도 운용에서 충분한 전문성을 확보하는 것이 중요하다.

품종보호는 농산업분야의 대표적인 지식재산제도로서 국산품종 육성 확대뿐만 아니라 우수한 외국 품종과 자원의 도입, 수출 확대, 그리고 국민의 소비 만족과 영양가치를 높이고 행복하고 풍요로운 생활로 이끄는 종자산업의 핵심요소이다.

OF-02

Current condition and strategy for expansion of seed testing service in KSVS

Eun Hee Soh

Korea Seed & Variety Service

국립종자원은 종자수출지원을 위해 2011년부터 국제종자검정협회(ISTA) 인증실험실을 운영중에 있다. ISTA 인증실험실이란, 국제종자분석증명서 발급기능을 보유한 실험실로서 해외로 수출할 종자에 대한 품질을 국제규정에 맞게 검정할 능력과 시스템을 갖춘 실험실을 의미한다. 현재 산림종자를 제외한 모든 작물을 대상으로 발급가능하며, 순도, 발아, 수분 등 7개 검정항목에 대한 품질분석이 가능하다. 향후 전작물을 대상으로 7개항목외 건전도 및 GMO검정에 대한 인증범위를 확대할 계획이다. 국립종자원은 신품종 심사지원 및 종자침해, 종자분쟁 및 일품종이명칭 등 종자유통관리를 위한 종자품질검정, 유전자분석 및 건전도검정을 수행하고 있다. 특히 종자분쟁건의 대부분을 차지하고 있는 품종유사성 해결을 위해 품종식별용 DNA DB를 구축해왔고 현재 27작물 약 4,700품종을 구축 중에 있다. 그 밖에도 직접적인 종자검정서비스 외에 민간대상의 다양한 종자검정교육운영을 통해 전문인력양성 추진하고 있으며 산·학·관·연과 협동하여 다양한 연구과제(페노믹스를 활용한 품종 DB 구축, 국가표준 DB구축, 종자가공처리 신기술개발)를 통한 종자검정 서비스를 확대해 나갈 계획이다. 이외에도 향후 과수무독묘 품질인증 서비스업무 및 국제종자생명교육센터를 설립('18)하여 종자산업에 종사할 전문가를 육성할 계획이다.

OF-03

Breeding for Pyramiding Target-genes and Selection of F_1 Hybrids by Marker Assisted Selection in Tomato

김명권

충북 청주시 흥덕구 강내면 월곡길, 토마토생명과학연구소

토마토 육종에서 과품질과 내병성이 중요한 요소이다. 내병성, 과품질, 과색 관련 유전자를 분자마커로 계통선발과 F_1 Hybrid 선발에 활용하였다. 내병성 마커로 토마토황화잎말림바이러스(Ty1, Ty2, Ty3), 토마토모자이크바이러스(Tm2a), 토마토반점시들음바이러스(Sw5), 시들음병(I2, I3), 반신위조병(V), 근부위조병(Forl), 역병(Ph3), 잎곰팡이병(Cf9), 선충(Mi1) 등을 검정하였고, 저장성 마커로 Rin gene, 과색 마커로 Orange, Yellow, Brown, Pink color 등을 검정하여 유묘기에 1차로 선발하고, 정식포장에서 최종선발된 계통과 F_1 hybrid를 다시 확인하였다. Marker Assisted Selection으로 육성한 토마토 6품종을 개발하여 농가에 보급 판매하고 있다.

Corresponding author: Tel. 043-235-3368, Fax. 043-235-3369, E-mail: mkkim207@naver.com

OF-04

Gene Identification, Expression Analysis and Breeding for Enhanced Glucosinolate Biosynthesis in *Brassica*

Arif Hasan Khan Robin, Go-eun Yi, Rawnak Laila, Kiwoung Yang, Jong-In Park, Ill-Sup Nou*

Department of Horticulture, Sunchon National University, Suncheon 57922, Korea

Glucosinolates are the biochemical compounds anti-carcinogenic to animals as they prevent prostate cancer and anti-oxidative to pests and herbivores of plants. Glucosinolates are abundant in *Brassica* vegetables and oils. In this study, we have identified 84 glucosinolates biosynthetic genes from *B. oleracea* genomic database, obtained their encoding DNA sequence and designed primer for both semi-quantitative (RT-PCR) and quantitative PCR (qPCR) analysis in four different subspecies: cabbage, kale, kohlrabi and cauliflower. In the first experiment, 84 glucosinolate biosynthetic genes were differentially expressed in four different subspecies of *B. oleracea*. A total of 14 different glucosinolates were identified in the edible organs of four subspecies. According to RT-PCR analysis, all genes were not expressed in the same edible organ of a subspecies. In our second experiment, under exogenous methyl jasmonate (MeJA) and salicylic acid (SA) treatment the sub-species specific effects of those two phyto-hormones were observed. MeJA and SA treatment enhanced accumulation of aliphatic glucoiberin in cabbage. Upregulation of *CYP81F3* (Bol028919) gene and *MYB51* (Bol030761) gene increased NGBS accumulation in kale. *CYP81F4* was highly expressed in all three subspecies. MeJA was more effective elicitor compared to SA for indolic GBS and NGBS accumulation. Kale leaves exhibited the highest progoitrin, sinigrin, gluconapin that might be associated with comparatively higher upregulation of *MYB28* (Bol036286), *ST5b*, *ST5c* and *AOP2* genes. In our third experiment, the content and expression of genes were genotype-specific in cabbage inbred lines. As *B. fruticlosa* contains glucosinolate high in amount, therefore our ongoing experimentation is increasing the content of glucosinolate in *B. oleracea* lines through breeding approaches.

Corresponding author: E-mail: nis@sunchon.ac.kr

GSP 식량종자사업단

GSP 식량종자사업단

- 일시: 2016년 7월 1일(금), 09:00 ~ 10:40
- 장소: 라마다플라자 청주호텔 우암홀
- 주관: GSP 식량종자사업단

좌장 : 조영찬 박사 (국립식량과학원)

발표 내용
▸Specialty Corn Breeding at Sweet Seeds in Thailand to The Tropical World – Dr. Taweesak Pulam (Sweet Seeds Co., Ltd., Thailand)
▸The Status of Rice Production and Breeding in China – Dr. Han Longzhi (Institute of Crop Sciences of Chinese Academy of Agricultural Sciences, China)
▸Application of Biotechnology in Developing New Rice Varieties For High Temperature Tolerance in the Philippines – Dr. Norvie Manigbas (PhilRice, Philippines)
▸Introduction of rice in rice production and the change of major diseases in rice during the period of climate change in Vietnam – Dr. Lai Tien Dung (Plant Protection Institute Research, Vietnam)

OG-01

Specialty Corn Breeding at Sweet Seeds in Thailand to The Tropical World

Tweesak Pulam

Sweet Seeds Co., Ltd., Thailand

We have been doing sweet corn and waxy corn breeding since 1990 for Thailand. During the past 25 years we use classical method of inbred hybrid to develop hybrids for Thailand later South East Asia and other areas of the tropical world.
On the long term basis, we have developed unique sweet corn populations using old genetic diversity and biotechnology techniques for genetic distance. These populations have given us successes in sweet corn hybrids for our market and export market.
We initiated development of several germplasm for various kind of specialty corn including the first red super sweet of the world.
The discussion includes expansion of seed export to other countries in tropical areas.

OG-02

The Status of Rice Production and Breeding in China

Longzhi Han

Institute of Crop Science, Chinese Academy of Agricultural Sciences, Beijing 100081, China

China is one of the biggest country of rice production, and also a large country of rice consumption, more than 50% of Chinese population relay on rice as the staple food. With the increasing of population and the opening of world grain market, demand for rice will continue to grow. Therefore, it is necessary to emphasis the important role of rice production and rice breeding in agriculture sustainable development, which have important strategic significance to solve the contradictory between food supply and demand in China and even the world, and ensure national food security.

1. Rice production

China's superiority rice cultivation regions are mainly distributed in the Yangtze River Basin, the southeast coast areas and the northeast region. In 2014, the rice cultivation area in China was 30.309 million hm^2, accounted for 26.9% of the total area of grain crops. With the demand of rice consumers for high-quality Japonica rice increasing, the cultivation area of Japonica rice tends to increase year by year, which accounted for about 32% of the total rice area. In 2014, the hybrid rice cultivation area (the total area of varieties with annual cultivation area of more than 6 667 hm^2) was 12.798 million hm^2, decreased by 14.4% compared to 2005, while the conventional rice area was 11.129 million hm^2, increased by 41.1% compared to 2005. The area of hybrid rice accounted for 53.5% of the total rice area in 2014. Two-line hybrid rice cultivation area has been gradually increased, its accounted for the proportion of hybrid rice area increased to 22.5% of 2010 and 34.4% of 2014 from 0.92% of 1996. The increase of conventional rice cultivation area was mainly due to the increase of Japonica rice area in northeast China, especially the Japonica rice in Heilongjiang province. Rice yield per unit area and total yield increased year by year, the rice total yield reached 206.5 million ton in 2014, accounting for 34% of total grain output, increased by 9.9% compared to 2000; rice yield per unit area was 6813.2 kg/hm^2, increased by 8.64% compared to 2000. The continuous increase of rice yield per unit area and total yield has played an important role in the development of China's social and economic stability.

2. Rice breeding

During the 1950s and 1960s, China has successfully bred dwarf rice varieties including Aijiaonante, Guangchangai, Taizhongzailai 1 and so on, which were applied in production and promoted the rice yield increased by 30%-50%, also solved the reduction of rice yield caused by lodging as well as food self-sufficiency. In 1964, China took the lead role in rice heterosis utilization research. In 1973, the male sterility of wild rice resources was used and to achieve the "three lines matching" in China, which applied in production and promoted the rice yield per unit area increased by more than 20% compared to dwarf varieties, known as "The Second Green Revolution" of rice production. China's hybrid rice is a major achievement in the history of agricultural development in the world, it has made an important contribution to the development of rice industry in China and even the whole world. However, in the middle of 1980s, China's rice breeding was in the climbing stage, rice yield per unit area failed to make progress in more than ten years. In order to achieve the breakthrough in rice breeding, Chinese government started the project of super-high-yield rice breeding in 1996, established the breeding goal in three periods, the average of yield per unit of single cropping rice every 2-years could achieve 10.5 t/hm^2, 12.0 t/hm^2 and 13.5 t/hm^2 in 2000, 2005 and 2010 respectively. In the breeding of northern Japonica rice, many super rice varieties of northern Japonica such as Shennong 265, Shennong 606, Jijing 88, Jijing 83, Longjing 21, Longjing 31 and so on had been successfully bred through the methods of sub-species hybridization and geographically distant hybridization, taking multiple cross and backcross, combining the new plant type and strong heterosis, optimizing the combination of traits, aggregating favorable genes. In the breeding of hybrid rice, many super hybrid rice combinations including Liangyoupeijiu, Fengliangyou 1, Yangliangyou 6, Y liangyou 1, Shenliangyou 5814, Y liangyou 900 and so on had been successfully bred by the methods of two-line hybrid, taking the advantage of wide compatibility materials and

PTGMS materials, combining the improvement of morphological and heterosis level, which exceeded the expected target of super high yield breeding plan in 2000, 2004 and 2011 respectively. In the 2010-2014, the average of national rice yield per unit area (6.74 t/hm^2) increased by 6.42% compared to 2000-2004 (6.20 t/hm^2); In the 2010-2014, the average of northeast Japonica rice yield per unit area (7.56 t/hm^2) increased by 12.62% compared to 2000-2004 (6.60 t/hm^2).

Up to now, China has achieved excellent achievement in rice breeding, however, the genetic basis of parental materials used in breeding is narrow at present, which is one of the biggest "bottleneck" in the sustainable development of rice breeding. In the future, we should actively explore elite germplasms of rice landraces and wild rice carried with beneficial genes, and these germplasms could be applied for breeding to broaden the genetic base of breeding materials; at the same time, in order to meet the demand of Chinese rice farmers and rice consumers for rice varieties, we should combine the conventional breeding technique and molecular breeding technology, and improve the comprehensive resistance and grain quality of rice improved varieties, including the resistance to disease, insect, and the resistance to natural stress as well as the ecological environmental adaptability.

OG-03

Application of Biotechnology in Developing New Rice Varieties For High Temperature Tolerance in the Philippines

Norvie L. Manigbas[1*], Luvina B. Madrid[1], Jupiter L. Grospe[1], Young-Chan Cho[2]

[1]Plant Breeding and Biotechnology Division, Philippine Rice Research Institute (PhilRice), Science City of Muñoz, Nueva Ecija, Philippines
[2]National Institute of Crop Science, RDA, Wanju 55365, Rep. of Korea

Rice is grown mainly in tropical and subtropical zones where increasing temperatures can severely affect crop growth. High temperatures at reproductive stage can induce floret sterility and limit rice yields. In the Philippines, second or third crop planting of rice in February is most vulnerable because reproductive stage occurs in April-May which is the hottest period of the year (37-40 oC, 80-85 % RH). With occurrence of increasing temperature, new rice varieties should adapt and thus, breeding for high temperature tolerance is imperative. In 2007 experiments, PhilRice has identified donors for heat tolerance and breeding started. Full implementation of the breeding program took off in 2010 under the ASEAN-Korea funded project. Since then, hundreds of lines were developed and were tested under high temperature environments. Biotechnology was applied in the program namely, marker-assisted selection (MAS) and identification of QTLs. To identify QTL for high-temperature tolerance, progeny of BC2F4 derived from cultivar NSICRc150 and Dular were crossed and phenotyped in 2014 DS under glasshouse conditions. There were 3 minor and 6 major QTLs detected associated with high temperature tolerance in chromosomes 1, 3, 4, 5 and 10. One elite breeding line PR44500-A3-3-2-2 from a backcross NSIC Rc160*4 x Dular selected using MAS was entered into the National Cooperative Test (NCT) in 3 high temperature locations in the Philippines. NCT is a multi-location field performance evaluation of promising lines for variety release in the Philippines. There are other 111 advanced breeding lines developed and incorporated into the breeding program for testing and germplasm utilization.

Acknowledgement: This work was supported by a fund from the Technology Cooperation Bureau, Rural Development Administration, Rep. of Korea and the Department of Agriculture-Philippine Rice Research Institute.

Corresponding author: E-mail: norviem@yahoo.com, nl.manigbas@philrice.gov.ph

OG-04

Introduction of rice in rice production and the change of major diseases in rice during the period of climate change in Vietnam

Lai Tien Dung

Plant Protection Institute Research

In recent years, Vietnam's rice farming continuous development of area, yield and production, making Vietnam from imported countries become rice exporting nations on world's No2. Besides, Vietnam is also one of the countries most strongly affected by climate change and rising sea water made imbalance on production as droughts, floods, salinity and extremely weather has increased the seriously level of the major diseases' as blast, neck blast, bacteria blight and sheath blight. The appearance of some new species as virus disease has caused significantly reduced yields in the Red River Delta and the Mekong Delta region.

Review on survey and evaluation results epidemic in 40 years (from 1976-2015) can be found there has been a change in the level of appearing harmful pests of rice in a trend that recent years appear harmful levels of many species increase, especially viral species and species ratio high natural increase.

In order to ensure national food security, maintain sustainable growth in rice production, to respond to climate change, Vietnam will face many challenges. In which, research on rice varieties resistant to seriously disease and adapt to the adverse conditions of climate change are urgently required.

2016 한국육종학회 학회상 시상

2016 한국육종학회 학회상 시상

○ 일시 및 장소 : 2016년 6월 30일(목), 17;40

○ 시상내용

1. 농우육종학회상

- 수 상 자 : 황영현 (소이벤처)
- 선정사유 : 세계최고 기능성 콩인 아가콩을 포함 31개의 두과 신품종을 육성하였다. 특히 대학에서 "이소플라본"의 함량이 기존 콩의 5-7배 이상인 콩 신품종을 다수 육성하였고, 이를 상품화하기 위해 소이벤처(주)를 설립하여 다양한 건강기능성 콩 제품 개발 및 판매를 통해 학생들에게 작물 육종의 중요성과 민간육종에 의한 상품화 전 과정에 대한 교육으로 젊은 육종가를 배출하는데 기여하였으며, 또한 직접 육종한 콩을 농가에 계약 재배하여 상품화함으로써 농가 소득증대에 크게 기여하였음

2. 한국육종학회상 연구부문

- 수 상 자 : 윤해근 (영남대학교 자연자원대학 원예생명과학과)
- 논문제목 : Differential Expression Screening of Defense Related Genes in Dormant Buds of Cold-Treated Grapevines (Plant Breeding and Biotechnology 2013;1:14-23)

3. 한국육종학회상 품종부문

- 수 상 자 : 이종희 (농촌진흥청 연구운영과), 작물과
- 품 종 명 : 새일미 (제5215호, 2014.12.11.)
- 논문제목 : 분자육종기술(MAS)을 이용한 선발 및 여교배를 통하여 일미벼의 장점은 살리고 단점은 보완한 수요자 맞춤형 품종 "새일미" 개발
(Plant Breeding and Biotechnology 2015;3:1-10)

4. 우수논문상 다피인용부문

- 수상자(1) : 이진석 (국립식량과학원 전작과)
- 논문제목 : 맛과 당도가 뛰어난 단옥수수 신품종 '구슬옥'
(Korean Journal of Breeding Science 2013.45.4.416)

- 수상자(2) : Michael J. Thomson
- 논문제목 : High-Throughput SNP Genotyping to Accelerate Crop Improvement
(Plant Breeding and Biotechnology 2014;2:195-212)

5. 우수논문상 다수논문게재부문

- 수상자(1) : 배석복 (국립식량과학원 남부작물부 밭작물개발과)
- 수상자(2) : 정종욱 (국립농업과학원 농업유전자원센터)

6. 한국육종학회 공로상

- 28대 학회장 서용원 (고려대학교)

색인

■ 영 문 ■

Name	Page
A	
Abdul Kayum	23, 24, 46
Abigail Rubiato Cuyacot	171
Abuyusuf	303
Ahn Eokkeun	212
Ahn Hye Ryun	239
Ahn Il-Pyung	18, 324
Ahn Joon-Woo	117, 120, 178, 183
Ahn Sang-Nag	39, 290, 293, 294, 299
Ahn Yul-Kyun	163, 192, 193, 206, 207
Akbota Makulbekova	71, 118
Amornrat Changkwian	245
An Dong-Jun	328
An Gynheung	208
An Jeong-Tak	220
Andre Silvanovich	226
Arif Hasan Khan Robin	25, 333
Arya K	65
Ashokraj Shanmugam	21
Atikur Rahman	161, 310
B	
Bae Eun-Kyung	244
Bae Sangsu	248, 327
Bae Seon-Hwa	252, 253
Bae Shin-Chul	18
Bae Suk-Bok	81
Beom Hye-Rang	313, 314
Binod P. Luitel	86, 94, 150, 162
Byeon Eun-Ju	252, 253
C	
Carl Garnaat	226
Chae Won-Byoung	52
Chang Ancheol	181, 195
Chang Sungyul	157
Chang Yali	225
Cheong Young-Keun	256
Chin Joong Hyoun	32
Cho Eunyoung	304
Cho Giwon	274
Cho Hye Sun	269
Cho Hyun Suk	223, 224
Cho Hyun-Suk	181
Cho Ji-Hong	166
Cho Jun-Hyeon	233, 246
Cho Jun-Hyun	38
Cho Jung-Il	227, 228
Cho Kwang-Soo	166
Cho Kyoungwon	315
Cho Mijung	14
Cho Seong-Woo	146
Cho Shin-Hwan	192
Cho Yang-Hee	152, 153, 154
Cho Yong Gu	200, 202
Cho Yong-Gu	80, 158, 159, 160, 204, 305, 306, 307
Cho Yoo-Hyun	18
Cho Young-Chan	340
Choi Ah Young	287
Choi Beom-Soon	230, 287
Choi Doil	45, 264
Choi Gi Jun	161
Choi Gyung-Ja	245
Choi Hong-Il	109, 117, 120, 263
Choi Hong-Kyu	43, 179, 194, 322
Choi Inchan	212
Choi Jisu	274
Choi Mi Na	196
Choi Min Kyung	313
Choi Min-Seon	170
Choi MinJi	316, 317
Choi Sang-Woo	124
Choi Sena	193
Choi Seula	219, 220
Choi Yong-Soo	324
Choi Yoram	43, 179, 194
Choi Young-Im	244
Chung Hee	215, 217
Chung Jong-Il	124
Chung Mi-Young	303
Chung Young Soo	223, 224
Chung-Jui Tsai	10
Chunying Zhang	37
Colton Kessenich	226
CuifengTang	33
D	
David A. Brummell	7
Di Cui	33
E	
Eung Eun-Ju	306
F	
Feifei Xu	275
Feng Peng Li	18
Franklin Hinosa Mancia	171
Franz Marielle Nogoy	158, 160, 204, 305
Franz Nogoy	159
G	
Gho Yunsil	208
Gil Jinsu	215, 217
Gu Sungmin	328
H	
Ha Bo-Keun	113, 115, 182
Ha Sun-Hwa	316, 317
Ha Yeaseong	257
Ham Tae-Ho	30
Han Hyeondae	266, 267, 268, 300, 301
Han Ji-Woong	245
Han Koeun	45, 123, 220, 221, 241, 265
Han Muho	196
Han Myeong-Sook	219
Han Sang-Ik	38, 246
Han Sung Min	120, 263
Han Sung-Jin	124
Harn Chee Hark	308
Harshavardhanan Vijayakumar	27
Heo Jong Seok	32
Heu Sung-Gi	122
Hisashi Tsujimoto	146
Hong Chang Pyo	214
Hong Chang-Pyo	284

Name	Page
Hong Jee-Hwa	231
Hong Jong-Pil	192, 206, 207
Hong Jongpil	163
Hong Mee Hyang	309
Hong Min Jeoug	183, 211, 234
Hong Min-ji	35
Hong Su-Young	166
Hong Sung-Gil	30
Hong Woo-Jong	270
Hur Yeon-Jae	233, 246
Hur Yoonkang	254
Hwang Bo-Hwa	296
Hwang Duk-Ju	18
Hwang Hyun-Ju	227, 228
Hwang In-Taek	173
Hwang Indeok	28, 273
Hwang Inhwan	328
Hwang Ji-Hye	271
Hwang Jung Eun	117, 120, 263
Hwang Sun-Goo	172
Hwang Tae Young	161, 310
Hwang Yoon-Jung	171
Hyun Jong Nae	185

I

Name	Page
Im Hyun Hee	223, 224
Im Ju-Seong	166
Im Juhyun	113, 115, 182
In Min-Sik	73
Inès Yacoubi	187

J

Name	Page
Jagadeesh Sundaramoorthy	60, 197 198
Jang Cheol Seong	238, 277
Jang Ji-Young	50
Jang Soo-In	30
Jang Su	125
Jang Suk-Woo	52
Jang Suyeon	30
Jang Woojong	230
Jang You-Ran	313
Jang Young Eun	117, 120
Jelli Venkatesh	249, 265
Jeon Jae-Heung	50
Jeon Jong-Seong	204
Jeon Yun-A	290, 293, 299
Jeong Eun Ji	115
Jeong Eun-Ju	159
Jeong Hee-Jin	45
Jeong Hye-Young	328
Jeong Jae-Eun	13, 71, 118
Jeong Jong-Min	40
Jeong Kyumi	174, 177, 186
Jeong Mi Jeong	239, 242, 243
Jeong Na-Rae	173
Jeong Namhee	46
Jeong Namhee	258, 273
Jeong Sang Wook	108, 111, 178
Jeong Sang-Wook	109
Jeong Soon Chun	224
Jeong Soon-Chun	113, 308
Jewel Howlader	46, 258
Ji Hee Chung	161, 310
Ji Hyeonso	212, 227, 228, 252
Jian Feng Ma	4
Jin Yong-Ik	166
Jin Yong-Tae	248
JinmeiLi	33
Jo Han Jig	182
Jo Jin-Kwan	219
Jo Jinkwan	265
Jo Sung-Hwan	213
Jo Yeong Deuk	120, 249, 257
Jo Yeong-Min	315
Joh Ho Jun	230
Ju Jung-Il	73
Ju Yoon-Ha	171
Jun Tae-Hwan	193
Jung Ayoung	218
Jung Chan-Sik	64, 81
Jung Ha-eun	242, 243
Jung Hee-Jeong	28, 273
Jung Hyun-Jin	262
Jung In Jung	117, 263
Jung Injung	120
Jung Jae Sung	309
Jung Jin Kyo	14
Jung Ki Hong	41, 209
Jung Ki-Hong	208, 270
Jung Kun-Ho	122
Jung Min	308
Jung Won Yong	269
Jung Woo Joo	190, 191, 211
Jung Yeo Jin	200
Jung Yu Jin	200, 201, 202
Jung Yu-Jin	158, 204, 306, 307
Jupiter L. Grospe	340

K

Name	Page
Kabita Sarker	262
Kang Byoung-Cheorl	45, 123, 218, 219, 220, 221, 241, 245, 249, 257, 265
Kang Chon-Sik	256
Kang Dae Bong	196
Kang Dong-Hui	124
Kang Hanna	30
Kang Hong-Gyu	149, 259
Kang Hong-Kyu	35
Kang Hyun-Ju	212
Kang Ji-Nam	259
Kang Jin-Ho	173, 249
Kang Ju-Won	39, 290, 293 294, 299
Kang Jung Hwa	291
Kang Kwon Kyoo	200, 201 202, 306, 307
Kang Kwon-Kyoo	158, 159 160, 204, 305
Kang Kyoung Dae	287
Kang Kyu-Suk	244
Kang Kyung-Ho	40
Kang Min-Young	123, 257
Kang Sang-Ho	287
Kang Shin-Jae	291
Kang Si-Yong	108, 109, 111 117, 120, 178, 182
Kang Si-Young	263
Kang Song-I	28
Kang Sung-Min	45
Kang Sungtaeg	14, 113
Kang Yong-Min	164
Kang Yun-Joo	39, 290, 293, 299
Kanij Rukshana Sumi	258
Karpagam Veerappan	273
Kenta Shirasawa	273
Khadiza Khatun	24

Name	Page
Khin Thanda Win	22
Kim A-Ram	227, 228
Kim Backki	125
Kim Bo-Kyeoung	256
Kim Bo-Kyung	40
Kim Bongju	44
Kim Byung Joo	255
Kim Chang-Kug	227, 228
Kim Cheol-Woo	170
Kim Chung-Guk	122
Kim Da-Hye	316, 317
Kim Dae Yeon	185, 188, 211, 234
Kim Daeil	266, 267, 268, 300, 301
Kim Dea Yeon	183
Kim Do-Sun	192
Kim Dong-Min	290
Kim Ee Yup	182
Kim Eun-Young	170
Kim Eunsil	14
Kim Gyoung Hee	309
Kim Haein	174, 177, 186
Kim Hee Dae	52
Kim Ho Bang	215, 225, 304, 309
Kim Hoy-Taek	19, 21, 23
	202, 236, 237
Kim Hye Jeong	223, 224
Kim Hyeran	313
Kim Hyewon	328
Kim Hyochul	247
Kim HyoungSeok	157
Kim Hyun Uk	5
Kim Hyun-Ho	73
Kim Hyun-Soon	50
Kim Inseo	230
Kim Jae Seong	223, 224
Kim Jae Yoon	188, 205
	222, 247, 250
Kim Jae-Hee	105
Kim Jeong Ho	163, 192
Kim Jeong Hoe	197
Kim Jeong Il	224
Kim Jeong-Ho	193, 206, 207
Kim Jeong-Hwa	116
Kim Ji-Eun	213
Kim Ji-Hyeon	309
Kim Jin A	239, 242, 243
Kim Jin-A	124
Kim Jin-Back	111
Kim Jin-Baek	108, 109
	117, 120, 178, 263
Kim Jin-Beak	183
Kim Jin-Hee	192, 193, 311
Kim Jin-Hyun	43, 179, 194, 322
Kim Jin-Kyung	291
Kim Jin-Soo	9, 216, 313
Kim Jinhee	163, 206, 207
Kim Jinkyung	230
Kim Jong Hee	200, 201
Kim Joo Yeol	239
Kim Joo Yong	167, 169
Kim Joonki	159, 160, 305
Kim Ju-Hee	277
Kim Jun-Hoi	311
Kim Juyoung	25
Kim Keumsun	266, 267
	268, 300, 301
Kim Ki-Hyun	80
Kim Ki-Yong	161, 310
Kim Kil-Hyun	255
Kim Kyu-Won	18, 271, 272
	280, 283, 324
Kim Kyung Hun	185
Kim Kyung Hye	14
Kim Kyung-Hee	247
Kim Kyung-Hwan	212
Kim Kyung-Min	246, 311
Kim Kyunghee	44
Kim Me-Sun	158, 159
	160, 305, 306
Kim Mijeong	274
Kim Minsu	13, 71, 116, 118
Kim Myong Kwon	202
Kim Myoung Kwon	201
Kim Myung-Sik	81
Kim Nam Soo	175
Kim Nam-Hoon	230
Kim Nam-Hyung	328
Kim Namshin	323
Kim O Gyeom	101
Kim Ok Tae	214, 215
Kim Sang Hoon	120, 178, 183
Kim Sang Heon	187
Kim Sang-Gyu	313
Kim Sang-Min	90
Kim Sang-Tae	313
Kim Sang-Woo	80
Kim Sanghun	182
Kim Sea-Hyun	105
Kim Seolah	300
Kim Seong-Cheol	214, 215, 217
Kim Serim	215
Kim Seungill	45
Kim Sin Ji	115
Kim Su-Dong	73
Kim Suk-Man	40
Kim Suna	218
Kim Sung-Gook	122
Kim Sung-Il	51, 167, 168, 169
Kim Sung-Ruyl	270
Kim Sung-Up	64, 81
Kim Sunggil	44, 170
Kim Tae Heon	246
Kim Tae-Heon	38
Kim Tae-Ho	213, 252, 253
Kim Tae-Sung	275, 276
	281, 282, 284, 324
Kim Un-Ji	52
Kim Won-Il	324
Kim Woo-Nam	35, 296
Kim Wook	147
Kim Wook-Jin	164
Kim Woon Ji	113, 115, 182
Kim Yang-Kil	256
Kim Yoon-Kyeong	266, 267
	268, 300
Kim Youn-Sung	269
Kim Young Cheon	240
Kim Young-Mi	313, 314, 315
Kim Yu Ri	113
Kim Yuri	115
Kishor D S	65
Kiyomi Abe	35
Ko Chan Seop	185
Ko Chan-Seop	211
Ko Ho-Cheol	181
Ko Suk-Min	259
Ko Sun-Bo	52
Koh Eunbyeol	126
Koh Hee-Jong	32, 33
	65, 125, 126
Koh Young Jin	309

Name	Page
Koo Hyun Jo	230
Krishnanand P. Kulkarni	13, 116
Kshirod Jena	40
Kwak Jun Soo	167, 168
Kwak Youngshin	195
Kweon Young Up	185
Kwon Jin-Kyung	218, 221
Kwon Soo-Jeong	80, 262
Kwon Soon-Jae	108, 109
	111, 117, 120, 178, 263
Kwon Yeong-Up	38, 246
Kwon Yong-Ik	35, 259, 296
Kwon Yong-Sham	231
Kwon Young-In	30
Kwon Young-Up	233

L

Name	Page
Lai Tien Dung	341
Lee Areum	269
Lee Bo Mi	213
Lee Bo-Hee	73
Lee Bong Choon	90
Lee Bong-woo	213
Lee Bumkyu	181, 195
Lee Byung-Moo	172, 247
Lee Chaeyoung	43, 179, 194, 322
Lee Cheol-Won	189, 217
Lee Chul-Won	80
Lee Dong Hee	223, 224
Lee Dong-Ho	71, 118
Lee Dong-Sun	296
Lee Dongryung	32
Lee Eun Su	163, 206, 207
Lee Eun-Su	192, 193
Lee Gang-Seob	181, 227, 228, 252
Lee Geung-Joo	50, 248
Lee Gi-An	152, 153, 154
Lee Gileung	126
Lee Gyu Myung	260, 264
Lee Hana	230
Lee Hea-Young	221
Lee Hee-Bong	178
Lee Heo Ju	201
Lee Hong Gil	203
Lee Hye-Eun	163, 206, 207
Lee Hye-Jung	158, 159,
	160, 305, 315
Lee Hye-Young	309
Lee Hyo Ju	202
Lee Hyo-Ryeon	196
Lee Hyo-Yeon	35, 149, 259
Lee Hyoshin	244
Lee HyoYeon	296
Lee Hyun Oh	287, 291
Lee Hyun-Sook	39, 290, 293
	294, 299
Lee Hyunsook	328
Lee Jae-Woo	277
Lee Je Min	260, 264
Lee Jeong-Dong	13, 14, 60, 71
	116, 118, 197, 198
Lee Jeong-Hee	213, 253
Lee Ji Yun	233
Lee Jong Yeol	132
Lee Jong-Hee	233, 246
Lee Jong-Nam	52
Lee Jong-Ro	153, 154
Lee Jong-Yeol	313, 314, 315
	316, 317
Lee Joohyun	274
Lee Joung-Ho	219, 220, 245
Lee Ju Kyong	99, 100, 101, 165
Lee Ju Seok	14
Lee Juhun	218
Lee Jundae	174, 177, 186
Lee Jung-Ro	152
Lee Jung-Yun	30
Lee Junki	230, 261
Lee Ki Jung	223, 224
Lee Ki-Won	161, 310
Lee Kyeong-Ryeol	181
Lee Kyounghee	199
Lee Kyung Jun	152, 153, 154
Lee Man Bo	142
Lee Min Kyu	108, 109
Lee Min-Jeong	52
Lee Min-kyu	111
Lee Minkyu	178
Lee Myoung Hee	213
Lee Myoung-Hee	253
Lee Myung-Hee	64, 81
Lee Ok Ran	59
Lee Sais-Beul	246
Lee Sang Sook	269
Lee Sang-Choon	230, 261, 291
Lee Sang-Hoon	161, 310
Lee Sanghyeob	12, 22, 37, 240
Lee Seokhyung	60, 197, 198
Lee SeungWook	287
Lee Soo In	239, 242, 243
Lee Su-Jin	124
Lee Sung-Il	175
Lee Taek Joo	291
Lee Unseok	157
Lee Won-Ju	146
Lee Ye Ji	252
Lee Ye Rin	174, 177, 186
Lee Ye-Ji	253
Lee Yeon-Hee	181
Lee Yi	214, 215, 217
Lee Yi Re	308
Lee Yong Jin	222
Lee Yongjik	328
Lee Yoon Jeong	223, 224
Lee Yoonjung	274
Lee Young Sun	309
Lee Young-Hee	64
Lee Youngsook	36
Lee Yun Sun	230, 291
Lee Yunjoo	126
Li Binbin	210
Li Hong-yu	149
Li Liu	249
Lim Hyemin	227, 228
Lim Ki-Byung	171
Lim Min-Ji	175
Lim Seong-In	328
Lim Sun-Hyung	313, 314, 316, 317
Longzhi Han	33, 338
Lu Xin	294
Luhua Tu	248
Luvina B. Madrid	340

M

Name	Page
Ma Kyung-Ho	152, 153, 154
Ma Shi Jun	99
Manosh Kumar Biswas	46
Marjohn Nino	159
Maurice Molony	8

Name	Page
Min Kyungmin	328
Mirwais Ghani	71, 118
Moon Byeong-Cheol	164
Moon Dahyun	147
Moon Jun-Cheol	172, 247
Moon Jung-Kyung	113, 255, 271, 324
Moon Sunok	208, 209
Muhammad Irfan Siddique	220, 241
Muhammad Qudrat Ullah Farooqi	99, 100
Munetaka Hosokawa	249
Murukarthick Jayakodi	230, 261

N

Name	Page
Nam Bo Mi	183
Nam Moon	213
Nasar Uddin Ahmed	258
Neha Roy	175
Ngoc Quy Nguyen	59
Nguyen Binh	230
Nino Marjohn	158
Noh Tae-Hwan	233
Nomar Espinosa Waminal	230
Norvie L. Manigbas	340
Nou Ill Sup	200, 201, 202
Nou Ill-Sup	19, 21, 23, 24, 25, 27, 28, 46, 204, 236, 237, 333, 254, 258, 273, 303
Nou Illsup	158, 160, 305, 306

O

Name	Page
Oh Chang Jae	309
Oh Chang-Sik	260
Oh Dae Gyeom	238
Oh Eun-Ui	225
Oh Eun-Young	64, 81
Oh In-Seok	64, 81
Oh Sewon	266, 267, 268, 300, 301
Oh Sung Aeong	41, 208, 209, 210
Oh Sung-Dug	181
Oh Sung-dug	195
Oh Young-Jin	256
Oh Young-Ju	181
Oh Youngjae	266, 267, 268, 300, 301
Ohn Ji Hye	226
Oo Moe Moe	209
Ouk Sothea	158, 159

P

Name	Page
Pae Suk-Bok	64
Park Chang-Hwan	255
Park Cheol-Woo	13, 118
Park Chul-Woo	71
Park Daesu	195
Park Dong-Soo	233, 246
Park Eung Jun	196
Park Eung-Jun	244
Park Gyu Tae	60, 197, 198
Park Ha-Seung	284
Park Hyeong-Jun	80
Park Hyun Ji	269
Park Hyun-Seung	230, 261, 291
Park Hyun-Su	233
Park Inkyu	164
Park Jee Young	230, 291
Park Jin Sol	223, 224
Park Jong-Chul	256
Park Jong-Ho	256
Park Jong-In	19, 21, 23, 24, 25, 27, 46, 236, 237, 258, 303, 333
Park Jonghwa	32
Park Joo-Seok	43, 179, 194, 322
Park Kyong-Cheul	165
Park Mi So	287
Park Mi-Young	259
Park Minhee	328
Park Myoung-Ryoul	255
Park Nam-il	165
Park Sang-Ryeol	18
Park Sangik	217
Park SangKyu	316, 317
Park Sohyeon	214, 215, 217
Park Soo-Chul	227, 228
Park Soo-Hong	328
Park Soo-Kwon	113
Park Soon Ki	41, 208, 209, 210
Park Su-Hyoung	52
Park Sumin	14
Park Sun-A	270
Park Sung Han	228
Park Tae-Il	256
Park Yong chan	238
Park Yong-Jin	18, 271, 272, 275, 276, 278, 280, 281, 282, 283, 284, 285, 324
Park Young-Chun	73
Park Youngki	105
Paulina Calderón Flores	132

Q

Name	Page
Qiang He	272, 275
Qing Tian	226
Quynh Anh Le	293

R

Name	Page
Ra Ji-Eun	90
Ra Won-Hee	18
Rahul Vasudeo Ramekar	99, 165
Rawnak Laila	24, 25, 333
Roh Kyung Hee	304
Rupesh Tayade	41, 209
Russell Reinke	40
Ryu Hojin	284
Ryu Jahee	313
Ryu Jai Hyunk	108
Ryu Jaihyunk	109, 111, 178
Ryu Su-Noh	30

S

Name	Page
Sa Kyu Jin	99, 101, 165
Sachiko Isobe	273
Saminathan Subburaj	248
Sampath Perumal	230
Sandeep Chapagain	238
Sandeep Karna	193
Sathishkumar Natarajan	273
Sebastin Raveendar	152, 153, 154
Seiichi Toki	35
Senthil Kumar Thamilarasan	27
Seo Hak Soo	51, 60, 167

Name	Page
	168, 169, 197, 198
Seo Jeonghwan	33
Seo Min-Jung	255
Seo Myeong-Hoon	52
Seo Pil Joon	199, 203
Seo Yong Weon	114, 131, 132
	142, 183, 185, 187, 188
	190, 191, 205, 211, 217
	222, 234, 250
Seo Yong-Weon	189
Shadi Rahimi	306, 307
Shim Kang-Bo	122
Shim Kyu-Chan	293, 294
Shin Dongjin	38, 233, 246
Shin Hyunsuk	301
Shin Ji Eon	287
Shin Jong Sup	308
Shin Myoung-Jae	152, 153, 154
Shin Seong-Hyu	122
Shin Seungho	247
Shin Youjin	216
Si-Yong Kang	183
Soh Eun Hee	332
Soh Moon-Soo	208, 209
Sohn Eun-Ju	328
Sohn Soo-In	181
Sohn Soo-in	195
Sohn Young-Bo	233
Soichiro Nagano	273
Son Eun-Ho	219
Son Jae-Han	256
Song Deok-Young	64
Song Hayoung	254
song In-Ja	296
Song Jae-Young	159
Song Jaeyoung	328
Song Jong Tae	13, 60, 71, 116
	118, 197, 198, 208, 209
Song Kitae	247
Song Kwan Jeong	225
Song Sun-Kyeong	307
Song Won-Yong	36
Song You Chun	233
Song You-Chun	38, 246
Sota Koeda	249
Sovetgul Asekova	71, 116, 118
Sovetgul Asekovaa	13

Name	Page
Suh Hye-Young	206
Suh Mi Chung	25
Sun Hyeon-Jin	149, 259
Susan B Altenbach	313, 314
Swapan Kumar Roy	80, 262
T	
Thanda Win	37
Tien Dung Nguyen	41, 208,
	209, 210
Tweesak Pulam	337
U	
Ujjal Kumar Nath	24, 46, 303
Um Yurry	214, 215, 217
V	
Van Ngoc Tuyet Nguyen	208
Vijaya Vardhana Reddy. Chaikam	3
Vinod Kumar	65
W	
Wei Tong	276, 278
Win Htet Oo	281
Won Hong-Sik	166
Won Jungyeon	266, 267
	268, 300, 301
Woo Jin-Kyu	309
Woo Mi-Ok	126
Woo Sun-Hee	80, 146, 262
Woo Sunmin	125
Y	
Yang Eun-Young	193
Yang Hee-Bum	45
Yang Jin Ho	223, 224
Yang Kiwoung	25, 333
Yang Tae-Jin	44, 230, 261, 291
Yashoda	65
Yeam Inhwa	260
Yeo Sang-Min	164
Yeo Un-Sang	81, 246

Name	Page
Yi Go-eun	333
Yi Hankuil	304
Yi Kyunguk	225
Yin Min-Sik	52
Yogeesh K J	65
Yoo Hee Ju	260, 264
Yoo Hong-Seob	166
Yoo Jemin	214
Yoon Hye-Jin	212
Yoon Jin Seok	114, 131, 205, 250
Yoon Min-Young	285, 324
Yoon Seo-Kyung	244
Yoon Ung-Han	252, 253
Yoon Young-Nam	81
Yoye Yu	33
Yu Dal-A	159, 160, 305, 307
Yu Je-Hyeok	80
Yu Jie	275, 282, 283, 284
Yu Yeisoo	230, 287
Yun Doh-Won	181, 195
Yun Jae-Young	216
Yun Min-Heon	262
Yun Tug-Sang	73
Yun Yeo-Tae	293
Yun Yo-Han	270
Z	
Zach Lippman	6
Zahid Hassan	237
Zhang Chunying	12, 22
Zhuo Jin	33

■ 국 문 ■

ㄱ	
강경대	286
강경호	31, 34, 66, 78, 151
강범규	84, 85
강성택	15
강송이	279
강시용	130
강위금	61
강주원	298
강천식	16, 49, 67, 76, 82,

Name	Page
	83, 95, 96, 141
강현중	67
고산	54
고재권	34, 53, 138, 151
고종민	84, 85
고종철	66, 134
고지연	66, 134
고호철	86, 94, 150, 162
곽도연	66, 134
곽상철	192
구성철	84
구자환	61
권순욱	74, 79, 130, 139, 154, 155
권순종	61, 180
권영업	56, 57, 58, 68, 107, 136, 140
권오덕	56
권오창	98
권혁	148
길진수	251
김경민	68, 140
김경혜	15
김경호	16, 29, 67, 76, 82, 83, 141
김경화	129
김경환	289, 292, 297
김경훈	16, 68, 140
김경희	70, 75, 127
김광수	54
김기영	17, 66
김기용	55
김길현	69
김도국	104
김도순	75, 137
김동용	155
김둘이	42
김명권	20, 332
김명기	61, 63, 66, 72, 78
김미선	104
김미진	103
김믿음	192
김병오	119
김병주	69, 72, 90
김보경	16, 17, 31, 34, 53, 62, 66, 67, 72, 74, 76, 78, 79, 121, 127, 133, 138, 141, 151
김보슬	93
김상규	86, 94, 150, 162
김상미	176
김상수	108
김상열	56
김선림	42, 129
김성철	128, 144, 251
김세종	135, 145
김송림	289, 292, 297
김양길	29, 67, 76, 82, 83, 141
김양지	232
김연복	144, 251
김영미	288
김영진	55
김옥례	110
김용경	148
김용철	155
김용호	184
김우재	17, 31, 34, 53, 62, 138, 151
김욱	148
김원호	55
김은경	128
김은석	128
김은실	15
김재명	89, 156
김정구	235
김정인	134
김정주	17, 61, 62, 66, 72, 133, 138
김정호	97
김지은	49, 95, 96, 176, 321
김진중	112
김진희	97
김학신	16
김해인	107
김현명	115
김현순	34, 53, 103, 151
김현태	84, 85, 148
김현호	77
김호방	144, 288
김홍식	115, 192
김회택	88
ㄴ	
나성준	112
남민희	56, 57
남상식	89, 156
남정권	17, 62, 74, 79, 121, 127, 133, 138
노미영	110
노설아	295
노일섭	88, 279, 302
노재환	78
노태환	17
ㄹ	
류경열	86, 94, 150, 162
류수노	139
류시환	70, 75, 127
ㅁ	
문기범	103
문준경	15
문중경	42, 134
문지혜	110
ㅂ	
박기웅	180
박기진	70, 75, 127
박노봉	56, 57
박동수	56, 57, 58, 107, 136, 143
박두상	128
박명렬	69
박미소	286
박민영	87
박병덕	115
박병명	57
박상렬	235
박상언	103
박석만	102
박세준	148
박소연	154, 155
박소현	251
박수권	42, 129
박수민	15
박수형	87
박순기	312
박슬기	62
박영준	148
박영춘	77
박용진	130
박은준	110
박응준	295

Name	Page
박장환	69
박재호	102
박종열	70, 75, 127
박종인	88, 302
박종철	16, 29, 67, 76, 82, 83, 141
박종택	104
박종호	29, 67, 76, 82, 83, 141
박지선	103
박진선	229
박철수	16, 49, 95, 96
박철우	26
박태성	110
박태일	29, 67, 76, 82, 83, 141
박해림	137
박향미	78
박현수	17, 53, 62, 74, 79, 121, 127, 133, 138
박형호	67, 68, 76, 140
배상수	327
배신철	235
배은경	295
배정숙	67, 135, 141, 145
백남현	61, 63
백만기	17, 62, 74, 79, 121 127, 133, 138
백인열	84, 85
백형진	86, 94, 150, 162

ㅅ

Name	Page
서민정	69, 84
서영호	70, 75, 127
서우덕	136
서정필	63, 66, 72, 78
서정현	84, 85
성낙식	66
성열규	78, 90
성정숙	86, 94, 150, 162
소윤섭	145
손범영	129
손수인	180
손영보	56, 57, 58, 107, 136, 143
손재한	16
송석보	66, 134
송수향	154
송연상	89, 156
송유천	56, 57, 58, 107, 136, 143
송재기	67
송종태	26
송태화	29
송필순	232
신동진	136, 143
신상욱	84, 85
신운철	17, 53, 61, 62, 74 121, 127, 133, 138
신유승	288
신정호	54
신주희	295
신지언	286
신학기	104
심규찬	298
심동환	112

ㅇ

Name	Page
안광환	128
안동춘	106
안상낙	17, 298
안승현	89, 156
안억근	63, 66, 72, 78, 90
안영은	86, 94
안율균	97
안일평	235
안종성	148
안종웅	61
안호근	235
양기웅	302
양대화	232
양은영	110
양정욱	89, 156
양창인	61, 63, 66, 72, 78
양현천	150, 162
엄유리	144, 251
여운상	56, 57, 134
오명곤	61
오성환	57, 58, 107, 136, 143
오세관	66
오영진	16, 29, 67, 76, 82, 83, 141
오은영	85
오인석	66, 84, 85, 134
오인여	57
오재은	321
오태영	145
옥선	93
옥현충	42, 129
왕정은	115
왕형	154
용우식	70, 75, 127
우관수	112
우관식	134
원용재	63, 66, 72, 78, 90
유봉식	104
유의수	286
육민정	75, 137
윤건식	67, 115, 141
윤광섭	63
윤덕상	77
윤문섭	86, 94, 150, 162
윤미라	31, 78
윤서경	295
윤수영	93
윤수현	102
윤여진	229
윤영미	49, 95, 96
윤영환	63
윤혜진	289, 292, 297
윤홍태	84, 85
이가영	192
이건미	121
이경보	54, 89, 156
이광원	16, 29, 67, 76, 82, 83, 141
이규성	72
이기원	55
이나리	68, 140
이동호	119
이미자	82, 141
이민휘	148
이범규	180
이병원	85
이병정	98, 106
이보희	77
이봉우	176, 321
이상대	98, 106
이상복	63, 66, 72, 78, 90
이상학	55, 68, 140
이상훈	55
이선이	97
이승욱	286
이승인	331
이시명	180
이아림	154

Name	Page
이영화	54
이영희	57
이예린	107
이원도	130
이은경	289, 292, 297
이은수	97
이은자	135, 145
이이	144, 251
이인성	110
이장용	70
이점식	31
이점호	63, 66, 72, 78
이정동	26, 119, 135
이정훈	70, 75, 127
이정희	31, 66, 72, 78, 90, 176, 321
이종열	49, 95, 96
이종희	17, 56, 57, 58 107, 136, 143
이주경	145
이주석	15
이주영	184
이주희	86, 94, 150, 162
이준구	150, 162
이준대	86, 94, 107
이준설	89, 156
이지우	108
이지윤	56, 57, 58, 107, 136, 143
이진호	148
이춘석	42
이현숙	298
이현오	286
이형운	89, 156
이홍석	289, 292, 297
이효신	295
이효연	232
인민식	77
임다은	154
임명호	312
임수현	75, 137
임철희	292, 297

ㅈ

Name	Page
장석우	87
장성규	154
장영석	54
장은규	192
장은하	75
장재기	56, 66, 72, 78
장지영	103
장하영	87
전용희	63, 66, 72, 78
전재범	31, 34, 53, 151
전푸름	235
정건호	69
정국현	63, 66, 72, 78
정규미	107
정규화	26
정남희	302
정미남	89, 156
정병룡	106
정영근	16, 29, 67, 76, 82, 83, 141
정영수	180
정오영	72
정용모	98, 106
정응기	63, 66, 72, 78
정재아	104
정정수	108
정종민	17, 62, 63, 72, 74, 79 90, 121, 127, 133, 138
정종성	55
정지웅	17, 31, 34, 53, 151
정지윤	302
정지희	288
정진태	144, 251
정찬식	144, 251
정태욱	134, 143
정희정	279
조강희	176
조명철	110
조미정	15
조성우	34, 53, 151
조성환	176, 321
조수현	141
조아르나	288
조영찬	17, 53, 58, 62, 66, 72, 74 78, 79, 121, 127, 133, 138
조유현	130
조윤상	108
조준현	56, 57, 58, 107, 136, 143
조현석	312
조현숙	61
주정일	77
지현소	289, 292, 297
지희정	55
진영돈	98, 106

ㅊ

Name	Page
차선우	144
채수영	110
채원병	87
천아름	31
최경후	148
최규환	54, 76
최기준	55
최만수	84, 85
최명은	66, 134
최범순	286
최성태	128
최아영	286
최영임	295
최용환	66, 72
최유미	134
최인찬	289, 292, 297
최임수	66, 72, 78
최재근	70, 75, 127
최준경	321
최지명	66
최현모	295
최홍집	135, 145

ㅎ

Name	Page
하기용	53
하운구	66, 72, 78
하장호	103
한상억	112
한상익	56, 57
한선경	89, 156
한옥규	61, 67, 141
한정아	115
함진관	108
함태호	139
허목	144, 251
허연재	136, 143
허온숙	86, 94, 150, 162
현웅조	66, 90
현종내	68, 140
형남인	229
홍기흥	67, 76

Name	Page
홍예지	88
홍지화	148
홍하철	42, 72, 129
황기호	78
황덕주	235
황사달	42
황세구	192
황엄지	89, 156
황인덕	279
황주천	98, 106
황태영	55

한국육종학회

Korean Society of Breeding Science

인 쇄 2016년 6월 25일

발 행 2016년 6월 30일

발행자 **사단법인 한국육종학회**

경기도 수원시 권선구 수인로 126 국립식량과학원 중부작물부 내

인쇄처 교보문고 (070-8854-5572)

경기도 파주시 광인사길 226 두성종이빌딩 4층