

2018 한국육종학회-차세대BG21사업-GSP사업 공동심포지엄

전통육종과 분자육종의 통합적 성과, 그리고 비전!!

Synergistic Achievement of Breeding and
New Technologies, and the Vision!!

일시 : 2018년 7월 11일(수)~7월 13일(금), 7월 2째 주

장소 : 제주 라마다 플라자 호텔



주 최

사단법인 한국육종학회

공동주관

차세대BG21사업단

(농생물게놈활용연구사업단, 농업생명공학연구원, 식물분자육종사업단, 시스템합성농생명공학사업단),
GSP사업단 (채소종자사업단, 원예종자사업단, 식량종자사업단)

후 원

농촌진흥청, 국립산림과학원,
경북대학교 농업과학기술연구소, 동아대학교 농업생명과학연구소,
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제주대학교 아열대원예산업연구소, 한국농식품생명과학협회,
한국과학기술단체총연합회, CropLife Korea, 농업기술실용화재단



한국육종학회

2018한국육종학회-차세대BG21사업단-GSP사업단 공동심포지엄 [주요일정]

Ⅰ 2018년 7월 11일 (수) Ⅰ

17:00~18:00	이사회 및 조직위원회의
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Ⅰ 2018년 7월 12일 (목) Ⅰ

09:00~09:40	등록 및 포스터 부착
09:40~10:00	<p>개회식</p> <p>▶ 사회: 이강섭 (사무총장, 국립농업과학원)</p> <p>개회사 - 박수철 교수 (조직위원장, 서울대학교 그린바이오과학기술연구원)</p> <p>환영사 - 박순기 교수 (회장, 경북대학교)</p> <p>축사 - 농촌진흥청 청장</p>

Plenary Session 1부

	▶ 좌장: 정영수 교수 (동아대학교)
10:00~10:40	<p>▶ Crop Conventional Breeding: Achievements and Outlook (작물 전통육종: 성과와 전망)</p> <p>- 고희종 교수 (서울대학교)</p>
10:40~11:20	<p>▶ Using Natural Variation and CRISPR to Understand and Improve the Plant Immune System</p> <p>- Dr. Gregory Martin (Cornell University, USA)</p>
11:20~12:00	<p>▶ Current Research & Development of Biotech Crops (생명공학기술활용 글로벌 종자산업현황 및 전망)</p> <p>- 박희영 박사 (SyngentaKorea Co., Ltd., Korea)</p>
12:00~13:00	중식

Plenary Session 2부

	▶ 좌장: 김주곤 교수 (서울대학교)
13:00~13:50	Food Evolution - Director Scott Hamilton Kennedy (Black Valley Film)

2018한국육종학회-차세대BG21사업단-GSP사업단 공동심포지엄 [분과발표]

2018년 7월 12일 (목)

분과발표-1: Breeding for Productivity

장소 라마다볼룸 A

▸ 좌장: 이정동 교수 (경북대학교), 김보경 박사 (국립식량과학원)

15:00~15:20	▶ Current Status and Its Prospects of Rice Breeding in China - Piao Zhong-Ze (Shanghai Academy of Agricultural Science, China)
15:20~15:40	▶ A Genome-Wide Association Study of Seed Protein and Oil in Soybean - 이성우 교수 (충남대학교)
15:40~16:00	▶ Dynamic Effects of Silicon in Crops under Abiotic Stress Conditions - 김윤하 박사 (경북대학교)
16:00~16:10	휴 식
16:10~16:25	▶ Studies on Anaerobic Germination (AG) of Rice for the Development of Cultivars Adaptable to We-Direct Seeding Conditions (벼 답수 직파 재배 적응 품종 개발을 위한 혐기발아 관련 특성 연구) - 정종민 박사 (국립식량과학원)
16:25~16:40	▶ Development and Characterization of Japonica Rice with Diverse Panicle and Grain Shape (벼 용도 다양화를 위한 이삭과 입형 관련 특성 연구) - 박현수 박사 (국립식량과학원)
16:40~16:55	▶ Soybean Production and Breeding in Vietnam - Le Duc Thao (Agricultural Genetics Institute, Vietnam)

분과발표-2: Breeding for Biotic Stress

장소 라마다볼룸 B

▸ 좌장: 강병철 교수 (서울대학교), 강권규 교수 (한경대학교)

15:00~15:20	▶ Isolation and Validation of a Candidate <i>Rsv3</i> Gene from a Soybean Genotype that Confers Strain-Specific Resistance to Soybean Mosaic Virus - 김국형 교수 (서울대학교)
15:20~15:40	▶ Development of SNP Markers Tightly linked to Two QTLs Responsible for Bacterial Wilt Resistance In Tomato - 오창식 교수 (경희대학교)
15:40~16:00	▶ QTL and GWAS Analysis of Phytophthora Resistance in <i>Capsicum</i> - 강병철 교수 (서울대학교)
16:00~16:10	휴 식



분과발표-2: Breeding for Biotic Stress

장소 라마다볼룸 B

▶ 좌장: 강병철 교수 (서울대학교), 강권규 교수 (한경대학교)

16:10~16:25	▶ Transcriptome Dynamics of Cysteine Protease-mediated Response Against <i>Xantomonas oryzae</i> pv. <i>oryzae</i> Race K3a in Rice - Marjohn Nino (Chungbuk National University)
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분과발표-3: Breeding for Abiotic Stress

장소 라마다볼룸 C

▶ 좌장: 정기홍 교수 (경희대학교)

15:00~15:20	▶ NO News is Good News for Plants-Investigation of Plant Defense System Under Nitrosative Stress and Its Application to Crop - 윤병욱 교수 (경북대학교)
15:20~15:40	▶ Towards Breeding for Multiple Abiotic Stress Resistance in Rice: an example using <i>pup1</i> and the others - 진중현 교수 (세종대학교)
15:40~16:00	▶ Screening and Functional Analysis of Rice Transcription Factors Involved in Abiotic Stress Tolerance - 강기윤 박사 (서울대학교 식물유전체육종연구소)
16:00~16:10	휴 식
16:10~16:25	▶ RNA-Seq Transcriptome Analysis of Rice Root Genes in Response to Water Deficiencies - 유요한 박사 (경희대학교)
16:25~16:40	▶ Analysis of Agronomic Traits using Plant Phenomics in Rice - 김송림 박사 (국립농업과학원)
16:40~16:55	▶ The Rice Peroxisomal Ascorbate Peroxidase Affects Transition from Vegetative to Reproductive Growth and Antioxidant Activity - 전윤아 박사과정 (충남대학교)

분과발표-4: Breeding for Functional Crops

장소 라마다볼룸 D

▶ 좌장: 하선화 교수 (경희대학교)

15:00~15:20	▶ Present State of Functional Rice and Application in Industrial Part (기능성 벼 품종 육성 현황 및 활용) - 조준현 박사 (국립식량과학원 남부작물부)
15:20~15:40	▶ Flower Color Modification Through Reconstruction of Flavonoid Biosynthetic Pathway - 임선형 박사 (국립농업과학원 농업생명자원부)
15:40~16:00	▶ Development of Poplar Superclones - 고재홍 교수 (경희대학교 생명과학대학)
16:00~16:10	휴 식

분과발표-4: Breeding for Functional Crops

장소 라마다볼룸 D

▶ 좌장: 하선화 교수 (경희대학교)

16:10~16:25	▶ Comparative Transcriptome Analysis Identified Candidate Genes Involved in Browning of Mycelium in <i>Lentinula edodes</i> - 홍창표 (테라젠이텍스 바이오연구소)
16:25~16:40	▶ QTL Mapping for Agronomic Traits by Genotyping-By-Sequencing in Rice - Cheryl Adeva (Chungnam National University)
16:40~17:00	▶ Diversity of Chloroplast Genome of <i>Cynanchum wilfordii</i> and Development of Species Unique KASP Markers for Authentication of <i>C. wilfordii</i> and <i>C. auriculatum</i> - 이세현 (서울대학교 농업생명과학대학)

Concurrent session : 생명공학기술 활용, 우리의 선택은?

장소 마라홀

그린바이오포럼 주관

▶ 좌장: 박순기 교수 (경북대학교)

15:00~15:30	제목: 생명공학작물 연구개발 현황과 문제점 (노동력절감 잔디) 연사: 이효연 교수 (제주대학교)
15:30~17:00	패널토론



2018한국육종학회-차세대BG21사업단-GSP사업단 공동심포지엄 [사업단발표]

2018년 7월 13일 (금)

Concurrent session-1: 차세대바이오그린21사업 (1)

장소 라마다볼룸 A

식물분자유종사업단/농업생명공학연구원

▸ 좌장: 사업단장 고희중/박순기 (서울대/경북대)

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|-------------|--|
| 09:00~09:25 | ▸ Deciphering the Complex Wheat Gliadin Proteins: Basic Study to Application for Development of Allergen-reduced Wheat
- 이종렬 박사 (국립농업과학원) |
| 09:25~09:50 | ▸ Databases for Metabolomics-assisted Life Science
- Dr. Nozomu Sakurai (National Institute of Genetics, Japan) |

시스템합성농생명공학사업단

▸ 좌장: 사업단장 이상열 (경상대학교)

- | | |
|-------------|--|
| 09:50~10:15 | ▸ The Comparison of Two Base-editors for Precise Nucleotide Substitution in Plants
- 김상규 교수 (KAIST) |
| 10:15~10:40 | ▸ Manipulation of Inflorescence Architecture for Tomato Productivity
- 박순주 교수 (원광대학교) |

Concurrent session-2: 차세대바이오그린21사업 (2)

장소 라마다볼룸 B

농생물게놈활용연구사업단

▸ 좌장: 사업단장 문중경 (국립농업과학원)

- 유전체육종 활성화를 위한 빅데이터 플랫폼 소개 -

- | | |
|-------------|--|
| 09:00~09:25 | ▸ Development of Molecular Marker Tools for Genomics Based Crop Improvement (식량작물(벼,콩) 유전체 정보 이용 분자표지 포털소개)
- 유의수 박사 (DNAcare) |
| 09:25~09:50 | ▸ A Comparative Synteny Analysis Tool for Target-gene SNP Marker Discovery: Connecting Genomics Data to Breeding in Solanaceae (원예작물(가지과) 유전체육종 지원 포털 소개)
- 조성환 대표이사 ((주)씨더스) |
| 09:50~10:15 | ▸ TGIL: An Integrative Bioinformatic Platform for Genomics-Assisted Breeding (두과작물 다중오믹스 분석 플랫폼 소개)
- 최홍규 교수 (동아대학교) |
| 10:15~10:40 | ▸ Genomic Prediction and Development of Omics Open Source Platform in Legume (유전체기반 오픈소스플랫폼 개발 및 공유)
- 김남신 박사 (한국생명공학연구원) |

Concurrent session-3: Golden Seed Project (1)

장소 라마다볼룸 C

채소종자사업단

▶ 좌장: 사업단장 임용표 (충남대학교)

09:00~09:25 ▶ 최근 농업연구 동향 및 엘지화학의 ag-biotechnology에 대한 비전
- 성동렬 박사 (LG화학 중앙연구소)

09:25~09:50 ▶ Surfing the Web of Plant Innate Immunity: from Recognition to Engineering
- 김상희 박사 (경상대학교)

원예종자사업단

▶ 좌장: 사업단장 노일섭 (순천대학교)

09:50~10:15 ▶ Enrichment of Brassica Vegetables' Genepool for Secondary Metabolites and Disease Resistance through Wide-hybridization
- Dr. Ujjal Kumar Nath (Sunchon National University, Bangladesh)

10:15~10:40 ▶ Bioinformatics Applications in Horticultural Crops using Conventional Tools and Methodologies for Crop Improvement
- Dr. Sathishkumar Natarajan (Sunchon National University, India)

Concurrent session-4: Golden Seed Project (2)

장소 라마다볼룸 D

▶ 좌장: 사업단장 정진철 (국립식량과학원)

09:00~09:25 ▶ Seed Potato Business in Central Asia: Achievements and Expectation
(중앙아시아 씨감자시장 진출을 위한 기반조성 성과)
- 서상기 대표 (홍익바이오)

09:25~09:50 ▶ Change of Maize Breeding System in Korea by Doubled Haploid Technology
(배가반수체(Doubled Haploid) 기술에 의한 국내 옥수수 육종체계 변화)
- 류시환 박사 (강원도농업기술원 옥수수연구소)

Concurrent session-5: 산림육종

장소 라마다볼룸 D

▶ 좌장: 이석우 (국립산림과학원)

09:50~10:15 ▶ Progress and Challenges of Tree Breeding in Korea
- 강규석 교수 (서울대학교)

10:15~10:40 ▶ Discovery of Trait-associated Omic-Markers in Korean Chestnut Species
- 박응준 박사 (국립산림과학원)



2018 KSBS-BG21-GSP Joint Symposium

1st day [July 11, 2018]

17:00~19:00	General Meeting of Organizing Committee
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2nd day [July 12, 2018]

09:00~09:40	Registration
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	Opening Ceremony
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09:40~10:00	Opening Address – Dr. Soo-Chul Park (Organizer, (Seoul National Univ.))
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	Welcome Address – Dr. Soon-Ki Park (President of KSBS, Kyungpook National Univ.)
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	Congratulatory Address
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<< Plenary Session 1 >>

▶ Chair: Prof. Young-Soo Chung (Dong-A Univ. Korea)

10:00~10:40	Crop Conventional Breeding: Achievements and Outlook – Prof. Hee-Jong Koh (Seoul National University, Korea)
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10:40~11:20	Using Natural Variation and CRISPR to Understand and Improve the Plant Immune System – Dr. Gregory B. Martin (Cornell University, USA)
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11:20~12:00	Current Research & Development of Biotech Crops – Dr. Hee Young Park (SyngentaKorea Co., Ltd., Korea)
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12:00~13:00	Lunch
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<< Plenary Session 2 >>

▶ Chair: Prof. Ju-Kon Kim (Seoul National Univ. Korea)

13:00~13:50	Food Evolution – Director Scott Hamilton Kennedy (Black Valley Film)
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13:50~14:30	A Genomics Approach to Understand the Genetic Complexity of Genomic Regions Harboring the Prolamin Gene Loci in Hexaploid Wheat – Dr. Yong Qiang Gu (Agricultural Research Service, USA)
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15:00~17:00	Oral Presentation
	(1) Breeding for Productivity (2) Breeding for Biotic Stress (3) Breeding for Abiotic Stress (4) Breeding for Functional Crops

<< Plenary Session 2 >>

▶ Chair: Prof. Ju-Kon Kim (Seoul National Univ. Korea)

17:10~17:30	General Meeting
17:30~18:00	Poster Presentation
18:00~20:00	Banquet

3rd day [July 13, 2018]

09:00~10:40	Concurrent Session <ul style="list-style-type: none">- Plant Molecular Breeding Center- Agriculture and Life Research Center- System & Synthetic Agrobiotech Center- The Agricultural Genome Center- Golden Seed Project (Vegetable, Horticulture, Cereal)- Tree Breeding
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<< Plenary Session 3 >>

▶ Chair: Prof. Yong-Gu Cho (Chungbuk National Univ.)

11:00~11:40	▶ Development and Prevalence of Molecular Markers for The Improvement of Horticultural Crops <ul style="list-style-type: none">- Prof. Ill-Sup Nou (Suncheon National University, Korea)
11:40~12:20	▶ Big Data Based Systems and Synthetic Agrobiotechnology Toward Crop Improvement <ul style="list-style-type: none">- Prof. Dong-Yup Lee (National University of Singapore)
12:20~13:30	Awards Ceremony & Closing Remark

4th day [July 14, 2018]

Field Trip



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공동심포지엄 분과발표 및 구두발표

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Plenary Session



Crop conventional breeding: Achievements and outlook

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Seoul National University

Plant breeding initiated by farmers who selected desirable traits for agricultural purposes. Following the rediscovery of Mendel's principles of heredity in 1900, plant breeding has made tremendous progress in developing diverse methodologies to create genetic variability and to genetically fix the promising lines. Recently, crop breeding has been systematized with state-of-the-art technologies aided by transgenic and genomics approaches. Conventional or traditional breeding refers to the development or improvement of cultivars using conservative tools for manipulating crop genomes within the natural genetic boundaries of the species, which has contributed to the human society by fulfilling our needs on food, feed, medicine, and basic materials for industrial purposes. Green revolution, the spectacular increase in cereal crop yields through new plant varieties during the 1960~70s, has been regarded as the most influential achievement in the history of plant breeding. With the rapid growth of seed industry for recent five decades, plant variety has been regarded as an item for financial profit. This has promoted the activities related to plant breeding in both private and public sectors. More than 15,000 varieties per year have been registered worldwide. Recent concerns about global warming, abnormal weather patterns, and unfavorable environments have pushed breeders to speed up the breeding process. However, conventional breeding has been facing difficulties to meet all the human needs due to the limited genetic variability and genomics information. Concerted approaches among all the breeding technologies are required. Overall achievements, challenges and perspectives of crop conventional breeding will be discussed.

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Using natural variation and CRISPR to understand and improve the plant immune system

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Pseudomonas syringae pv. tomato (*Pst*) causes bacterial speck disease of tomato. The only genetic resistance to *Pst* is conferred by the resistance genes *Pto/Prf*, which recognize the *Pst* effectors AvrPto and AvrPtoB. However, recently *Pst* strains have emerged that lack these effectors, rendering *Pto/Prf*-mediated resistance ineffective. In current work we are seeking new sources of genetic resistance against *Pst* that can be introgressed into tomato breeding lines. Using available whole-genome resequencing data, we identified a set of 216 genetically diverse accessions. Plants of each accession were inoculated by spraying *Pst* mutant strains that lack different effectors and/or flagellin to help elucidate whether the observed host responses involved effector-triggered or pattern-triggered immunity. The screen also uncovered unusual *Pst* disease symptoms beyond the typical specks, and subsequent analyses indicate some of these phenotypes are simply inherited. Using an assay that measures the production of reactive oxygen species, we discovered accessions that have increased, or conversely, no response to the flagellin peptides flg22 or flgII-28, which are recognized by the pattern recognition receptors FLS2 or FLS3, respectively. In a related project, we are using CRISPR/Cas9 to create mutations in over 100 immunity-associated genes in tomato and assessing the effect on the host response to *Pst*. Together, these projects open up new avenues for investigating the molecular mechanisms underlying the plant immune system and augment plant breeding efforts to develop disease-resistant tomato varieties.

생명공학기술활용 글로벌 종자산업현황 및 전망

박희영

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인류는 2030년대 인구 80억 시대를 눈앞에 두고 안정적인 식량공급과 지속가능한 농업이라는 두 가지 화두를 해결하고자 노력하고 있다. 식물 육종은 1996년 GM콩의 상업화이후 생산량 증가와 생산성 향상을 통해 새로운 전기를 마련하였다. 지난 20년간 GM작물의 연구개발 상업화는 비약적인 발전을 거듭하여 전체 종자공급량의 50%이상을 GM종자들이 담당하고 있다. 빅 6 종자회사들은 이러한 성공을 바탕으로 새로운 GM작물 도입과 생산성 향상을 이루었고, 현재 진행중인 인수합병이 완료되면 글로벌 종자업계에 기대와 우려가 섞인 새로운 바람이 불게 될 것이다.

GM작물은 종자시장 점유율이 높고 저장성 및 환금성이 높은 작물들인 옥수수, 콩, 면화, 카놀라 등 대해 Input trait (제초제 저항성 및 해충저항성 형질) 위주로 개발되어져 왔으며, 새로운 제초제 저항성 형질도입 및 Output trait (영양성개선 형질, 내재해성 형질) 들이 도입되고 있다.

GM작물 육종기술의 성공을 바탕으로 유전체정보의 확보, 작물에 따른 형질전환기술 및 재분화기술을 확보하게 되었고 작물 자체 유전자의 원하는 부위를 바꿀 수 있는 유전자 가위법(gene editing)이 실용화되고 있어 향후 식물육종분야에서 이러한 기술들의 상호보완적 협력으로 새로운 형질의 작물들을 시장에 선보이게 될 것으로 본다. 그러나 유전자 가위법(gene editing)의 실용화에도 규제라는 큰 장벽이 기다리고 있다. 미국 뿐만 아니라 EU 등에서도 유전자가 도입되지 않은 경우 GM으로 규제하지 않는 방향으로 규제개선을 시도하고 있어 막대한 등록비용을 줄일 수 있는 길을 열어가고 있다. 향후, 전통육종, 분자육종, GM, gene editing 등 모든 육종기술이 각자의 역할을 담당하여 인류의 식량문제를 해결해나가는 통합적 solution을 제공해줄 수 있을 것으로 기대한다.

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A genomics approach to understand the genetic complexity of genomic regions harboring the prolamin gene loci in hexaploid wheat

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Wheat is one of the food crops most consumed by humans worldwide. However, the molecular basis of wheat flour end-use quality is still only partially understood. A single wheat cultivar contains about 70 to 100 similar but distinct gluten proteins (prolamins) that determine its end-use quality. Wheat flour proteins also trigger human health problems, including food allergies (FA), celiac disease (CD) and non-celiac wheat sensitivities (NCWS). Previous studies indicated that the wheat prolamins are encoded by complex multiple gene families that are mapped to three major genomic regions. To better understand the evolution, expression, and function of prolamins in relation to end-use quality and immunogenic potential, genomic regions harboring the prolamin gene loci were sequenced, annotated, and compared with the orthologous regions from different species (rice, Brachypodium, and sorghum) and from different homeologous wheat genomes (A, B, and D). Our results indicated that rapid evolutionary dynamics are present only in the wheat genomes. The high frequency of sequence rearrangements including deletion, duplication and translocation events have resulted in considerable synteny erosion in the prolamin genomic regions. We propose that the HMW-glutenin genes originate from a tandem duplication of an ancestral globulin gene, while other prolamin genes (LMW-glutenin, α -, ω -, and γ -gliadins) are likely derived from gene translocations followed by multiple rounds of gene duplications. A complete set of wheat prolamin genes including both intact genes and pseudogenes were identified from a single wheat cultivar cv Chinese Spring, allowing for more accurate and robust characterization of individual prolamin gene expression using transcriptomics analyses. We found that the A genome contributes the least to prolamin expression in cv Chinese Spring because of its smaller number of expressed intact genes and their low expression levels, while the B and D genome contribute similarly. Our study also provided insights into the evolution of CD epitopes and identified that a single indel event in the hexaploid wheat D genome likely resulted in the generation of the highly toxic 33-mer CD epitope. A DNA sequence capture array was designed for studying the genetic diversity of prolamin genes in other wheat cultivars, with an aim to facilitate breeding wheat varieties with improved end-use traits and reduced immunogenic potential.

Development and prevalence of molecular markers for the improvement of horticultural crops

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With the advent of genome sequencing technologies, the scientific era has crossed the borders of utilizing model plant in genomic research. The basic research in the Department of Horticulture in Suncheon National University mainly emphasizes in the program (The Golden Seed Project) to develop horticultural crops in the families Brassicaceae (Cabbage, Chinese cabbage), Cucurbitaceae (Melon, Watermelon), Solanaceae (Tomato, Hot pepper) and Strawberry with high quality traits. The research program mainly focused to identify the genes essential for economically important traits in horticultural crops through physiology and phenomics-guided omics (genomics, transcriptomics, proteomics and metabolomics) investigations. The next-generation sequencing approaches viz genome sequencing, transcriptome sequencing, whole genome resequencing, deep sequencing, restriction site associated DNA sequencing (RAD-seq) and genotype-by-sequencing (GBS) are in practice under this program for the development of the trait-specific molecular markers and to address appropriate solution in population genomics. Those molecular markers including small sequence repeats (SSR), single nucleotide polymorphisms (SNPs), sequence characterized amplified regions (SCAR), small insertions and deletions (INDELs) and cleaved amplified polymorphic sequences (CAPS) associated with particular quality traits have been developed. Such developed molecular markers were capable to alter the fate of the plant through molecular breeding strategies like marker-assisted selection (MAS), marker-assisted backcrossing (MABC), marker-assisted recurrent selection (MARS), and genome-wide selection (GWS) or genomic selection (GS). For instance, shortening the breeding cycle and the increasing the breeding efficiency of the breeders. We have also developed SNP and SSR chips to test the purity in these horticultural crops. In addition, web-database and web-server based research information system have been developed with user-friendly interface. The efforts in the development of molecular markers have enabled us to render quality service to companies or breeders, commercially and privately. Therefore, this project would be a great asset for the global research community and the industrialists for the development of novel horticultural crops with high quality traits through peer-reviewed publications and communication.

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Big data based systems and synthetic agrobiotechnology toward crop improvement

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Big Data have been rapidly generated in the modern biological science and biotechnology fields, including plant science and agrobiotechnology, due to the recent advances in high-throughput omics technology. Now, one of major challenges is to analyze and integrate these large and heterogeneous datasets in order to enhance the crop productivity and quality which are severely hampered by various biotic and abiotic stresses as well as inherent genetic limitation. Thus, it is required to develop and understand various systems and data mining approaches for systematic applications. To this end, we have established the integrative framework for characterizing model plant such as rice by resorting to systems biology techniques which include in silico modeling and machine learning. The information derived from the current in silico analysis of virtual plant cells in conjunction with multi-omics profiling and synthetic biology tools can potentially guide for developing new breeding and/or engineering targets for next generation crop development. In this talk, modeling of various plant systems will be introduced, and current challenges and future direction in the field, e.g., smart farming, will be discussed. [This work was supported by Next-Generation BioGreen 21 Program (SSAC, No. PJ01334605), the Rural Development Administration, Republic of Korea]

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공동심포지엄 분과발표 및 구두발표



Current status and its prospects of rice breeding in China

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Rice production in China has more than tripled in the past five decades mainly due to increased grain yield rather than increased planting area. This increase has come from the development of high-yielding varieties and improved crop management practices such as nitrogen fertilization and irrigation. However, yield stagnation of rice has been observed in the past ten years in China. As its population rises, China will need to produce about 20% more rice by 2030 in order to meet its domestic needs if rice consumption per capita stays at the current level.

By using a large amount of data, China's rice production, market supply and demand, and trade changes is analysed in recent years. At the same time, many constraints that China's current rice production is facing on is pointed out. What's more, based on the new situation of rice production and consumption in China, the development direction of rice genetics and breeding in China is proposed.

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A genome wide association study of seed protein and oil in soybean

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Soybean [*Glycine max* (L.) Merr.] protein and oil are widely used in feed, food, and industrial raw materials. Soybean seed protein is negatively correlated with seed oil and yield. A genome-wide association study (GWAS) was conducted using phenotypic data collected from five environments for 621 soybean accessions in maturity groups I–IV and 34,014 single nucleotide polymorphism (SNP) markers to identify QTL for protein and oil. Compressed Mixed Linear Model (CMLM) identified three and five quantitative trait loci (QTL) significantly associated with seed protein and oil contents, respectively. Of them, QTL on chromosomes (Chrs) 15 and 20 were the two most significant QTL for protein and oil contents, which exhibited a strong negative correlation between the two traits. Multi-trait mixed model (MTMM), also allowed identification of common effect QTL on Chr 5 that increased oil with no effect on protein, and on Chr 10 that increased protein with little effect on oil. Haplotype analysis revealed that the positive-effect haplotypes for the 4 loci varied in frequency across geographic regions where the soybean accessions originated. This finding informs which alleles will potentially better contribute to marker-assisted region-specific improvement of soybean.

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Dynamic effects of silicon in crops under abiotic stress conditions

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Regardless of silicon (Si) is the second most abundant element in soil, various plant species shows significantly different Si uptake ratio. Therefore, many scientists believed that Si could induce physiological responses in restricted plant species such as rice, barley, and wheat. In 2006 and 2007, Japanese research team reported Si transport genes (low silicon gene; *Lsi1* and *Lsi2*) in rice plant. These two genes are antithetically located in the exodermis and endodermis of rice root thus, Si regulates influx and efflux by *Lsi1* and *Lsi2* respectively. Since identification of Si transport gene, we can figure it out how Si can transfer from soil to plant. Moreover, recently developed Si-mutant plant can facilitate evaluation of Si effect on endogenous phytohormones regulation, scavenging of reactive oxygen species (ROS) and reactive nitrogen species (RNS). In this presentation, I focused on how Si can mitigate various abiotic stress conditions such as mechanical wounding, salinity and heavy metal stresses. When we applied Si to rice plant under normal condition, increased bioactive GA₁ and suppressed Ca uptake in comparison with control was measured. Moreover, Si application was found to mitigate various abiotic stresses such as mechanical wounding, salinity, and heavy metal stress by different physiological strategies. In the mechanical wounding stress, Si supplementation reinforce the cell membrane thus, down-regulated jasmonic acid (JA) was detected in rice plant to enhance the resistance against mechanical wounding stress. While during salinity stress, Si treatment to rice plant increased endogenous abscisic acid (ABA) content meanwhile, decreased transpiration and reduced Na uptake from root. Whereas, when rice plants were grown under heavy metal (high concentration of Cu and Cd) stress condition, Si application down-regulated heavy metal transport genes such as *OsHMA2* and *OsHMA3* (P1-type heavy metal ATPase) thus, decreased heavy metal contents were detected in rice plants (shoot and root). Therefore, Si treated rice plants showed resistance against heavy metal stress through decreased heavy metals uptake. Furthermore, exogenous application of Si has been found to induce stress tolerance by scavenging of reactive oxygen species (ROS) such as ascorbate peroxidase (APX), catalase (CAT) under overall stress conditions. Because, under natural condition, plants continuously produce several ROS during photosynthesis and respiration processes in cell organelles such as mitochondria, chloroplast, and peroxisomes. Particularly, the ROS production significantly increases under stress condition. Therefore, ROS scavenging is one of the most important strategy to mitigate stress condition.

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벼 답수 직파 재배 적응 품종 개발을 위한 혐기발아 관련 특성 연구

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직파 재배는 육묘와 이앙 과정이 없어, 이앙재배보다 노동력 및 생산비가 적게 드는 장점이 있으나 초기 입모불량, 잡초 발생 및 도복에 따른 재배 안정성 문제로 인해 재배면적 확대에 어려움이 있다. 답수 직파 재배법은 답수 상태에 직접 볍씨를 파종하므로 다른 직파재배법에 비해 답수로 인해 초기 잡초 발생이 억제되어 잡초방제 효과가 우수한 장점이 있으나 답수로 인한 혐기 상태로 인해 종자의 발아 및 입모가 불량해지는 단점이 있다. 현재 개발된 직파 품종은 저온 발아성 및 도복 관련 형질은 우수한 편이나 혐기발아 답수 중 발아율은 다소 부족한 편이다. 따라서 답수중 입모율이 우수한 직파 전용 품종 개발을 위해서는 혐기 발아성이 우수한 유전자원 탐색 및 관련 유전자 분석 및 도입이 필요하다. 본 연구는 답수중 혐기 발아성이 개선된 답수직파용 품종 개발을 위하여 혐기발아 연관 유전자 탐색 및 혐기 발아 연관 유전자를 국내 자포니카형 벼에 도입하는 것을 목적으로 수행되었다. 국내 벼 품종의 답수중 혐기발아성 향상을 위하여 혐기 발아(anaerobic germination, AG)성이 우수한 미얀마 landrace 'Khao HlanOn'(KHO)과 국내 벼 품종 ('동안', '수안', '보람찬')과 교잡을 통하여 혐기발아 내성 유전자 AG1과 AG2가 이전된 근동질 계통 (BC₂F₅와 BC₃F₅)을 육성하였다. AG1과 AG2 연관 marker를 이용하여 MAB를 수행하고 초형선발 및 유전자형 분석을 거쳐 3조합에서 혐기발아 내성이 반복된 보다 향상되고 농업 형질이 양호한 3계통을 선발하였다. 한편 새로운 AG 유전자 탐색을 위하여 혐기발아 내성이 우수한 광발성 잡초벼 유전자원 'PBR'와 국내 고품질 품종 '남평' 이 교배 된 Mapping 집단을 육성하였다. Illumina 7K SNP chip을 이용한 mapping 결과 총 942개의 SNP 마커가 1496.5Mbp의 벼 염색체 상에 anchor 되었다. 온실 조건과 포장 조건을 이용한 AG 내성에 관한 QTL 분석결과 염색체 1번, 3번 그리고 11번에서 AG관련 형질을 표현형 대비 6.7%~14.5%로 설명하는 3개의 QTLs (qAG1, qAG3, qAG11)이 각각 탐색 되었다. 향후 이들 결과를 활용하여 답수 직파 초기입모 관련 유전자 집적을 통해 직파 적성 개선을 위한 직파적응 우량 계통/품종 육성에 활용할 계획이다.

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Development and Characterization of *japonica* Rice with Diverse Panicle and Grain Shape

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Rice panicle and grain-related traits have important roles in rice yield and quality. Korean *japonica* rice cultivars showed narrow genetic background on panicle and grain. To overcome the limit and pioneer new uses, we developed *japonica* rice with diverse panicle and grain shape, New Panicle Architecture (NPA) and Diverse Grain Size and Shape (DGS), and characterized those agronomic traits. For enhancing yield potential by increasing number of spikelets per panicle (NS), we developed dense panicle rice with clustered spikelets. Dense panicle rice with clustered spikelets have many spikelets clustered two to five together on more increased panicle branches. Rice with NPA was derived from a cross between Binhae Col.#1, lodging resistance rice germplasm with dense panicle, and ARC10319, tall rice germplasm with clustered spikelets. It showed dramatically increased spikelets (average NS 255-277) compared to Nampyeong (93), Boramchan (96), Hanareum2 (114), Binhae Col.#1 (144), and ARC10319 (161). The other rice with NPA derived from same combination is very tall and high biomass rice with clustered spikelets, Jeonju626. It is the tallest among Korean rice cultivars with lodging resistance and fast-elongation. The plant height of Jeonju626 was 183 cm (culm length 155 cm, panicle length 28 cm), while those of Korean rice cultivars were 73-151 cm (n=390). Jeonju626 is expected to contribute the transition from semi-dwarf to tall plant architecture in Korean rice cultivars. To diversify the grain size and shape of *japonica* rice, we developed 91 Breeding Materials with DGS (BM_DGS, DGS6-96) derived from four cross combinations between donor parents, extremely large grain germplasm Jizi 1560 (1,000 grain weight 48.1 g) and Jizi1581 (38.0 g), and Korean high-yielding rice cultivars, Deuraechan(24.7 g) and Boramchan (22.9 g), by anther culture. The grain size and shape of BM_DGS exhibited beyond the characteristics of previously developed Korean rice cultivars; most of Korean *japonica* rice cultivars have medium-short and semi-round shaped grain. BM_DGS are being practically utilized in the breeding programs to diversify the grain size and shape. Using DGS79, the breeding material with extra-long and spindle-shaped grain, we developed elite *japonica* rice line with long and spindle-shaped grain, Jeonju625. It showed good characteristics for rice yield and grain quality. Jeonju625 is expected to be used as cultivar aimed at exporting rice and the breeding programs for enhancing the resistance to biotic stress and diversifying the heading date of Jeonju625 are in progress. Developed rice with NPA and DGS could be contribute to diversify the genetic background and pioneer new uses of Korean *japonica* rice.

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Soybean production and breeding in Vietnam

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In Vietnam, soybean is one of the oldest and important food crops that provide human food and animal feed. However, in recent years, soybean production in Vietnam tends to decrease, while soybean demand is increasing. From 2010 to 2016, the area decreased from 197.8 thousand hectares to 94.0 thousand hectares, output decreased from 296.9 thousand tons to 147.6 thousand tons. By 2016, the yield is 1.57 tons/ha, equal to 56.5% of the world average (2.78 tons/ha). Currently, soybean production only meets about 8% of domestic demand, while demand for soybean oil industry and animal feed is on the rise. In 2011, Vietnam imported 0.90 million tons of soybeans and by 2016 it increased to 1.56 million tons, mainly from the United States, Argentina and Brazil. In addition, Vietnam has to import millions of tons of soybean products. There have been more than 50 varieties released and applied in production through main methods are imported selection, hybridization and mutation. Soybean varieties commonly used in production now include: local varieties (Ha Giang Green, Muong Khuong Vang, Bac Ha Green ...), imported varieties (ĐT12, AK03, VX92, DT 2000, DH4, ...), hybrids (DT80, Đ92, Đ93, Đ96-02, DT42, TL57, 98-04, DT26, Đ2102, Đ2501, DT96, DT2001, ĐVN5,...) and mutant varieties (DT84, DT90, DT99, DT95, DT83 ...). Due to the features diverse ecologicals, soybean varieties were classified into groups:

- The group of varieties suitable for cold crop: V74, AK02, AK03, AK04, AK05, VX92, VX93, ĐT2000, ĐN42, ĐT92, DT90, TLA57, 98-04, ĐT26, Đ2101...

- The group of varieties suitable for hot crop (summer in Northern Delta): ĐH4 (ĐT76), M103, ĐT80 and local varieties.

- The group of varieties suitable growing 3 crops/year: DT84, DT94, DT95, DT96, DT99, DT2001, ĐVN6, ĐVN10, AK06, ĐT93...

The orientation of soybean breeding is focused on improving productivity, pest and disease tolerance and adaptation to different regions and seasons. Solutions of developing soybean production in Vietnam are: 1) Improving the yield; 2) Increasing the area by taking advantage of the land cultivating other crops and intercrops; 3) Using new varieties with high tolerance to diseases and unfavorable conditions (drought, flood, cold...) and good quality; 4) Extention agriculture and transferring advanced techniques; 5) Policies of supporting seeds, capital, supplies, market solutions.

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Isolation and validation of a candidate *Rsv3* gene from a soybean genotype that confers strain-specific resistance to soybean mosaic virus

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Soybean mosaic virus (SMV), a member of the genus *Potyvirus*, significantly reduces soybean production worldwide. *Rsv3*, which confers strain-specific resistance to SMV, was previously mapped between the markers A519F/R and M3Satt in chromosome 14 of the soybean [*Glycine max* (L.) Merr.] genotype L29. Analysis of the soybean genome database revealed that five different NBS-LRR sequences exist between the flanking markers. Among these candidate *Rsv3* genes, the full-length cDNA of the *Glyma.14g204700* was successfully cloned from L29. Over-expression of *Glyma.14g204700* in leaves inoculated with SMV inhibited viral infection in a soybean genotype lacking *Rsv3*. In addition, the transient silencing of the candidate gene caused a high accumulation of an avirulent strain in L29 carrying *Rsv3*. Our results therefore provide additional line of evidence to support that *Glyma.14g204700* is likely *Rsv3* gene that confers strain-specific resistance to SMV.

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Development of SNP markers tightly linked to two QTLs responsible for bacterial wilt resistance in tomato

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Bacterial wilt caused by *Ralstonia pseudosolanacearum* (previously known as *R. solanacearum*) is a very devastating disease in tomato. Previous studies have identified two major quantitative trait loci (QTLs), *Bwr-6* at the chromosome 6 and *Bwr-12* at the chromosome 12, responsible for disease resistance against bacterial wilt in tomato cultivar ‘Hawaii7996’. However, the genetic identities of two QTLs have not been uncovered yet. In this study, using whole-genome resequencing, we analyzed genome-wide single-nucleotide polymorphisms (SNPs) that can distinguish a resistant group, including seven tomato varieties resistant to bacterial wilt, from a susceptible group, including two susceptible to the same disease. In total, 5,259 non-synonymous polymorphic SNPs (about 0.13% of the total homozygous SNPs) were found between the two groups. Among them, only 265 SNPs are located in the coding DNA sequences, and 53 and 168 out of these SNPs were located on chromosomes 6 and 12, respectively. The genes that both carry SNP(s) and are near *Bwr-6* and *Bwr-12* were selected for development of SNP markers. First, 13 SNPs in four genes encoding putative leucine-rich repeat (LRR) receptor-like proteins out of 26 genes near *Bwr-12* in chromosome 12 were analyzed. Each SNP marker was validated by a high resolution melting method with 42 tomato cultivars and one segregation population. Consequently, one SNP marker, including a functional SNP in a gene, *Solyc12g009690.1*, could efficiently distinguish tomato varieties resistant to bacterial wilt from susceptible varieties. These results indicate that *Solyc12g009690.1*, the gene encoding a putative LRR receptor-like protein, might be tightly linked to *Bwr-12*. Next, analysis of SNPs in 15 genes near *Bwr-6* is in progress. Overall, the SNP markers developed in this study will be useful for selection of tomato cultivars resistant to bacterial wilt.

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QTL and GWAS Analysis of Phytophthora Resistance in *Capsicum*

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Phytophthora capsici is a globally prevalent devastating Oomycetes pathogen causing root rot in pepper. *Capsicum annuum* CM334 is widely used as a source of resistance. We constructed a high-resolution linkage map using 188 recombinant inbred lines (RILs) derived from a cross between resistant CM334 and susceptible ECW30R. A total of 8,979 high quality genotyping-by-sequencing derived single nucleotide polymorphism (SNP) markers were used to map resistance against low, medium and high virulent isolates of *P. capsici*. Quantitative trait loci (QTL) analysis for *P. capsici* root rot (PcRR) mapped two major effect QTLs, *qtl5.1*, and *qtl5.2* on chromosome P5 conferring broad-spectrum resistance to *P. capsici* isolates. In addition, QTLs with minor effects and isolate specificity were detected on P2, P4, P8, and P11. QTL analysis was complemented with a genome-wide association study (GWAS) of root rot resistance in a pepper core collection consisting of 352 diverse accessions. A total of 168,714 SNPs derived from two GBS libraries were used for GWAS. GWAS detected 98 significant SNPs associated with resistant to highly virulent isolate, and the regions on P2, P5, and P11 were co-located with QTLs identified in the present study. By leveraging combined use of QTL mapping and GWAS, clusters of nucleotide-binding site leucine-rich repeat (NBS-LRR) and receptor like kinases (RLKs), and *Mildew resistance locus O*(MLO) like protein candidate genes involved in plant disease resistance mechanisms were predicted within the QTL regions. Highly significant SNP markers identified through QTL mapping and GWAS for PcRR resistance herein could accelerate the marker-assisted breeding for durable resistance in pepper by combining alleles of race specific and non-race specific resistance in pepper.

Transcriptome dynamics of cysteine protease-mediated response against *Xanthomonas oryzae* pv. *oryzae* race K3a in rice

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Pathogen infection modulates defense reactions in the host cells. Numerous findings proved that papain-like cysteine proteases (PLCPs) function as a central hub in plant defense. While diverse roles of PLCPs in different pathosystems have become more evident, information on which gene networks and signaling pathways are activated to orchestrate downstream responses remains limited. To understand the biological significance of cysteine protease against *Xanthomonas oryzae* pv. *oryzae*, RNAi-mediated knockout and overexpression of xylem cysteine protease gene were constructed in rice. Pathogenicity test showed that transgenic rice attenuated the virulence of *X. oryzae* pv. *oryzae* race K3a which could be attributed to a high accumulation of hydrogen peroxide and free salicylic acid. To provide useful insights into genome-wide transcriptome profile during early interaction with the pathogen, next-generation sequencing of RNA from transgenic and wild type plants infected for 30 minutes was carried out. A total of 2,086 combined differentially expressed genes were identified, 471 of which were exclusively regulated in the transgenic library. The resistance observed in transgenic rice is ascribed to an extensive participation of genes with predicted functions in intracellular signal transduction, transcription activity, secondary metabolic process including phenylpropanoid and lignin biosynthesis, and defense response. Moreover, protein-protein interaction network revealed the indispensable network of defense layer in transgenic rice.

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NO news is good news for plants – investigation of plant defense system under nitrosative stress and its application to crop

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Reactive oxygen and nitrogen intermediates (ROIs and RNIs) are central features of the plant immune responses and abiotic stress tolerance. The latter is one of the major challenges that restricts plant growth and yield thereby affecting human race directly. Understanding the molecular mechanism of how these adversities effects plant life and how green producers cope with these insults, is of paramount importance. One of the relatively less-known feature of abiotic stress is the production of nitric oxide (NO), an important redox based signaling molecule. Among various others, chief of the mechanisms through which NO transfer its bioactivity is *S*-nitrosylation, the covalent attachment of a nitric oxide (NO) moiety to a protein cysteine thiol to form an *S*-nitrosothiol (SNO). This rapidly emerging prototypic, redox-based post-translational modification may act as a key switch in regulating biotic and abiotic stress responses. For instance, *S*-nitrosylation of NADPH oxidase regulates hypersensitive response during plant immunity. Similarly, an Arabidopsis homologous AtRBOHD at Cys 890, abolishing its ability to synthesize ROIs. Accordingly, mutation of Cys 890 compromised *S*-nitrosothiol-mediated control of AtRBOHD activity, perturbing the magnitude of cell death development. On the other side NO is required for ABA-induced stomatal closure, thereby enhancing plant resistance towards drought stress. NADPH oxidase is thought to have a role in the process hence playing vital role in both type of stresses. Recently, we found that mutation in one of the ABA biosynthetic pathway gene *AAO3* resulted in reduced level of ABA and were unable to close stomata upon induction of drought stress. In addition, our current study to isolate novel nitrosative stress-responsive immune and abiotic stress regulators such as WRKY and MYB transcription factors by transcriptomic approach in both Arabidopsis and rice will be introduced, exemplifying with an agriculturally important trait of seed shattering involved in NO signaling and plant immunity.

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Towards breeding for multiple abiotic stress resistance in rice: an example using *Pup1* and the others

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Pup1 (Phosphorus uptake 1) is a major QTL for phosphorus-deficiency tolerance in rice. *PSTOL1*, the major gene of *Pup1* was firstly identified from a Bangladesh landrace, Kasalath. However, *Pup1* is present in almost all the upland and/or drought tolerant varieties. Due to its contribution to early root vigor and water-P interaction mechanism, *Pup1* might contribute to the drought tolerance in early rice growing stage. Vigorous shoot growth of the *Pup1* introgression lines was observed in different varietal background in upland condition. In reality, the genetic interactions among multiple abiotic stresses should be considered. As one example, by combination of several abiotic-stress tolerant QTL near isogenic lines, two and three QTL pyramiding lines including *Pup1*, *Sub1* for submergence, and *AG1* for anaerobic germination were developed. Primary result showed that the pyramiding approach of *Pup1* and *Sub1* is not successful under low phosphate rainfed condition, implying the presence of genetic interactions between the QTLs. Here in this presentation, a progress of the multiple trait pyramiding for multi-abiotic stress tolerant breeding line development will be introduced and its implication for rice breeding will be discussed.

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Screening and functional analysis of rice transcription factors involved in abiotic stress tolerance

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

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RNA-Seq transcriptome analysis of rice root genes in response to water deficiencies

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Water deficiencies are one of the most serious challenges to crop productivity. To improve our understanding of soil moisture stress, we performed RNA-Seq analysis using roots from four-week-old rice seedlings grown in soil that had been subjected to drought conditions for 2 to 3 d. In all, 1098 genes were up-regulated in response to soil moisture stress for 3 d, which causes severe damage in root development after recovery, unlikely that of 2 d. We then validated the expression patterns of two candidate genes using a promoter-GUS reporter system in *planta* and monitored the stress response with novel molecular markers. An integrating omics tool, MapMan analysis, indicated that transcription factor, kinase and RING box E3 ligases are significantly stimulated by induced drought. We also analyzed the functions of 66 candidate genes that have been functionally investigated previously. Of these, we used a T-DNA insertional mutant of *rice phytochrome B* (*OsPhyB*) that negatively regulates a plant's degree of tolerance to water deficiencies through the control of total leaf area and stomatal density based on previous finding. Unlike previous result, we found that *OsPhyB* represses the activity of ascorbate peroxidase and catalase mediating ROS processing machinery required for drought tolerance of roots in soil condition, suggesting the potential significance of remaining uncharacterized candidate genes for manipulating drought tolerance in rice.

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Analysis of agronomic traits using plant phenomics in rice

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Plant phenomics is a nondestructive analyzing methodology using image information of various phenotypes. In this study, rice was used as a model plant for application of phenomics approaches. Agronomic traits of rice were measured using parameters such as leaf area (LA), leaf width (LW), leaf color, projected plant height (PPH), convex hull (CVH), center of mass Y (COMY), compactness (COMP), and eccentricity (ECC) with a recombinant inbred lines (RILs) population derived from a cross between 'Milyang23' and 'Gihobyeo'. In seedling stage (2 and 4 weeks after sowing), two major growth related QTLs were discovered at *semidwarf-1* (*sd-1*) region of chromosome 1 and loci of chromosome 12. In vegetative stage (6 and 8 weeks after sowing), growth related QTLs were detected at chromosomes 1, 2, 3, 7, 9, 11, and 12. *Phytochrome B* mutants (*osphyb*) was also investigated to analyze agronomic traits for drought stress. In recovery stage after drought stress, *osphyb* was more increased than WT in the leaf area (LA) and leaf width (LW) of RGB and water contents of Near infrared (NIR). It definitely well reflected drought resistance of *osphyb*. Besides, we are also trying to minutely detect nitrogen deficient traits through color classification of green color in leaf. We are gradually optimizing various traits analysis, and it will be widely applied for improving accuracy for crop breeding and phenotyping.

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Probable L-ascorbate peroxidase 4 (APX4-P) controls flowering time and antioxidant activity in rice

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Flowering time (heading date) is an important agronomic trait that determines yield in rice (*Oryza sativa* L.). In this study, we characterized probable L-ascorbate peroxidase (*APX4-P*) gene in near isogenic line (NIL) derived from a interspecific cross between Hwaseong and *Oryza rufipogon*. The NIL plants showed delayed flowering about 6 days compared to Hwaseong under the natural long-day condition. To study how *APX4-P* is involved in the mechanism of flowering, we examined expression levels for flowering time regulators under short-day (12h light/12h dark) and long-day conditions (14h light/10h dark). No difference in days to heading was observed between Hwaseong and NIL in short-day condition whereas NIL plant showed delayed flowering in long-day condition. Also, to investigate the antioxidant activity in Hwaseong and NIL, the 3,3-diaminobenzidine (DAB) staining and 2,2-diphenyl-1-picrylhydrazyl (DPPH) assay were both conducted. The DAB staining was performed to understand whether *APX4-P* gene plays role in scavenging H₂O₂ in rice. Based on DAB staining, dark-brown color was barely detected in NIL than Hwaseong. The DPPH scavenging ability of NIL plants showed higher value than Hwaseong. Hence, these results suggested that flowering time and antioxidant activity might be controlled by *APX4-P* gene.

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기능성 벼 품종 육성 현황 및 활용

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최근의 급격한 고령화 가속화로 건강기능식품에 대한 관심증가 및 연이은 풍작이 지속되고 있는 반면 소비가 크게 줄면서 쌀 소비를 촉진시키기 위한 방안으로 고기능성 식품 개발을 통한 부가가치 향상 대책의 필요성이 크게 대두되었다. 2000년 이후 기능성 쌀 소비시장 변화와 다양한 쌀 가공품의 시장 진출에도 불구하고 쌀 가공 산업은 아직 시작단계이다. 이러한 배경에는 흑미 중심의 제한된 기능성 쌀의 소비자 인식부족과 함께, 특히 밀가루 등 타 전분에 비해 낮은 가공특성 및 고미나 수입쌀 사용에 의한 쌀 가공품의 신뢰성 부족으로 평가될 수 있다. 국내의 경우 기능성 원료곡 시장은 흑미 등 일부 유색미 품종들을 제외하면 아직 초기 단계이다. 따라서 기능성을 이용한 가공시장으로 도약·발전하기 위해서는 다양한 기능성 품종개발에 따른 고부가가치 상품의 개발이 요구되고 있다. 향미의 향기성분은 심리안정 등 일부 기능성 관련 보고도 되어 있으나 기능성 성분 보다는 기호성에 따른 소비 형태로 분류되고 있다. 따라서 향미는 최근 까지도 일부 소비층에서 소비되는 매우 제한적인 소비 형태를 유지하고 있었으나, 해외 근로자와 다문화 가족을 중심으로 향미벼의 소비가 크게 늘고 있는 추세에 있다. 국내의 경우 주로 찰벼 및 기능성이 복합화된 흑미 형태의 향미품종들이 개발 보급되어 있으나, 향의 구분이 불분명하고 향기 정도가 약한 품종이 대부분이다. 쌀 소비측면에서는 기능성 보다 가공용 품종의 활용성이 매우 크다. 현재 쌀 가공용으로 육성 보급되고 있는 품종들의 경우 수입쌀 등에 비해 가격이 높아 경쟁력이 낮고, 특히 다양한 쌀 가공품을 위한 가공적성이 낮아 활용이 매우 낮은 실정이다. 따라서 쌀 소비 촉진을 위해서는 기존의 정제된 유색미 및 양조·떡 등 전통식품을 벗어난 새로운 쌀 소비 시장창출을 위한 다양한 기능성 품종개발과 함께 원료곡의 가격 경쟁력이 높은 초다수성 품종의 개발이 절실한 상황이다. 또한 코팅기술을 이용한 고부가가치 기능성 쌀과 함께 다양한 형태의 전분을 이용한 산업용 소재로의 활용 등 특수미의 활용성을 높이기 위한 연구를 통하여 밥쌀 중심구조에서 벗어나 시장창출이 필요하다.

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Flower color modification through reconstruction of flavonoid biosynthetic pathway

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Flavonoids belong to polyphenolic secondary metabolic compounds ubiquitously found in the plant kingdom. They play important roles not only in plant biological processes including accumulation of pigments in flowers, fruits and seeds for pollination and seed dispersal and protection of UV light, but also in human health including inhibition of cell proliferation and antioxidant properties. For these reasons, flavonoids metabolism have received increasing attention for breeders and researchers. For the past decades, many researchers tried to modify the flower colors through the modification of flavonoid biosynthesis. It has been reported the various strategies and approaches for successful metabolic engineering of flavonoids in plants. It requires an elucidation of structural and regulatory genes for the biosynthetic pathway and a detailed understanding of metabolic flux through competitive pathways. From this point of view, I will present our recent results divided into three parts; (I) modification of flower color by metabolic engineering; (II) elucidation of the regulatory mechanism controlling the onset of the pathways; and (III) identification of genes involved in the desired metabolites.

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Development of poplar super clones

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Research of woody biomass production has increased as a potential renewable resource for biofuel. During past five years, we performed a project called “development of poplar super clones” supported by Korea Forest Service. Here, research products of the project will be shared and discussed. Firstly, a functional genomics study on the entire family of poplar MYB transcription factor will be introduced. Poplar, a model woody plant, has a total of 212 R2R3-MYBs, which is much larger than that of Arabidopsis (159 members). Expansion of poplar MYB family suggests specific components of poplar life history, such as secondary growth (e.g., wood formation), perennial growth, and reproductive development. As a first step towards understanding of functional role of MYB family in woody perennials, the entire MYB family members of *P. trichocarpa* were cloned in overexpression and suppression constructs. Through the phenotype-based screening of both transgenic poplar and Arabidopsis populations, we could identify many of plants having altered secondary growth or secondary cell wall formation. Secondly for the targeted approach, we utilized plant hormone Gibberellin (GA) and secondary wall forming MYB regulators as well. We produced transgenic Arabidopsis plants and Poplar expressing GA20-oxidase isolated from *Pinus densiflora* (PdGA20ox) under the control of either 35S or developing xylem-specific promoter, respectively. Both transgenic Arabidopsis plants and Poplar exhibit an accelerated stem growth and results in a massive increase of biomass compared to control plants. Finally, a novel approach for biotechnological improvement of the quantity and quality of woody biomass with minimizing undesirable growth penalties will be discussed. Our results demonstrate that the controlled production of GAs and secondary wall regulating MYB TF through a DX promoter can be utilized as an efficient biotechnological tool for producing enhanced plant biomass without undesirable side effects. This work was funded by the Korea Forest Service (S111213L080110).

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Comparative transcriptome analysis identified candidate genes involved in browning of mycelium in *Lentinula edodes*

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Lentinula edodes is one of the most popular edible mushrooms in the world and contains useful medicinal components such as lentinan, beta-glucans and many metabolites. Light-induced brown film formation on vegetative mycelial tissues in *L. edodes* is one of the most important processes for ensuring the quantity and quality of this edible mushroom. However, the molecular mechanisms underlying this critical developmental process is still unclear especially at the level of transcriptome. In this study, we newly identified a proper *L. edodes* mutant, chamaram cultivar, showing abnormal functional brown film formation. We performed global genome wide transcriptomic analysis in the three different types of brown film mycelial tissues including white, brown and abnormal dark yellow partial brown film states. Comparative transcriptome analysis between normal browning and whitening status, that consisting of 1490 differentially expressed genes, revealed the significant changes of genes associated with hydrolase activity and carbohydrate metabolic process for browning, and proteolysis for whitening. Changes of transcription factors were also identified. Interestingly, genes encoding glucans, especially *exg* family, belonging to glycoside hydrolases were significantly changed, suggesting the involvement in lentinan biosynthesis. Partially browning strain showed expression pattern distinct from browning and whitening strains, with significant association with flavin adenine dinucleotide binding, indicating lack of catalysis difficult redox reactions. Our data will provide the understanding for browning formation in *L. edodes* and a foundation for future breeding.

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QTL mapping for agronomic traits by genotyping-by-sequencing in rice

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Genotyping-by-sequencing (GBS) is the latest approach that facilitates and allows efficient and high-density SNP discovery and genotyping; thereby, can be used in several genetic studies like QTL mapping in a variety of crop species. Starch, the primary component of food crops for human diet, is normally digested in the small intestine. However, a proportion of starch in cereals is resistant to digestion and escapes degradation in the stomach and small intestine. This starch is known as “resistant starch” (RS). A cereal grain higher in amylose content (AC) is considered a good source of RS. Hence, cereal grains higher in RS are said to be an important contributor to improve gastro-intestinal health. In this study, 92 recombinant inbred lines (RILs) derived from a cross between two japonica rice cultivars, Dodam (high in RS) and Hwayeong (a non-waxy cultivar) were evaluated for mapping QTL for agronomic traits using GBS approach. One major QTL was identified and mapped on chromosome 2 resulting to an increased AC and RS which was similar to previous report. QTLs were also identified that are associated with the early heading trait and micronutrients. Thus, these results implied that using a high-density of SNP markers for QTL mapping for agronomic traits through GBS offers substantiation for various applications in rice research and breeding.

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Diversity of chloroplast genome of *Cynanchum wilfordii* and development of species unique KASP markers for authentication of *C. wilfordii* and *C. auriculatum*

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Cynanchum wilfordii has long been regarded as a medicinal plant in Korea. The cultivation area and annual production have increased due to its various pharmacological effects, especially for menopause. However, *C. wilfordii* is morphologically similar with *C. auriculatum*, which may cause misidentification or mal-utilization in the market. Therefore it is necessary to develop discrimination methods between two species. Most of the markers are designed from chloroplast genome sequences for the identification of plant species. For *Cynanchum* species, several markers have been developed for species identification but they often showed confusable result which might be caused from intra-specific variations due to the natural diversity. Therefore, to develop more stable authentication markers, we assembled complete chloroplast genome and 45s rDNA of four *C. wilfordii* using NGS data with dnaLCW method (de novo assembly of low coverage WGS sequence). By comparative analysis, we identified six SNPs and six InDels in the chloroplast genome of four *C. wilfordii* accessions. Five SNPs were identified in the intergenic region and one SNP was found in the exon region. We also identified six InDels, two in the intergenic region and four in the exon region. Additionally, we filtered out the areas where the NGS reads were mapped heterogeneously. We also identified approximately 34.3% of chloroplast genome sequences were shared in the mitochondrial genome which show higher sequence homology. After excluding these chloroplast-mitochondrial flux genome regions, and ambiguous intra-species polymorphic regions, we identified 818 SNPs between two species. Among them, we developed seven KASP markers for the identification of *C. wilfordii* and *C. auriculatum*. The intra-specific variation of the chloroplast genome of *C. wilfordii* could be used for understanding of natural diversity of this species and developed KASP marker contribute to more accurate and clear authentication of *C. wilfordii* and *C. auriculatum*. This research was supported by “Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ013238)”, Rural Development Administration, Republic of Korea.

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공동심포지엄 포스터 발표



Chromosomal karyotype with simple sequence repeats by fluorescence in situ hybridization in Korean wheat

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Chromosomal karyotype of 26 Korean wheat cultivars were observed to identify diversity of B genome using (AAC)₅ and (AAG)₅ as simple sequence repeats (SSRs) by fluorescence in situ hybridization (FISH). Two SSR markers as a chromosomal marker are useful to identify B genome with a higher divergence rather than A- and D-genomes. Several chromosomes of A and D genomes were identified by the two SSR markers, and each chromosome of B genome was discriminated by those markers. Also, FISH revealed the same signal pattern(s) of the SSRs on satellite of chromosome 1B of B genome. However, in euchromatic region on the short arm of chromosome 1B, the signal patterns of the SSRs were different among the Korean wheat cultivars. Especially, Olgeuru had low density of (AAG)₅ signal of chromosome 1B rather than the other Korean wheat cultivars, while Joeun showed wide distribution of (AAG)₅ signal on the near centromeric region of chromosome 1B rather than the others. Johan showed low density of (AAC)₅ signal of chromosome 1B rather than Keumkang as a control. Based on this study, it can be expected that other SSR markers such as (AC)₈, (AG)₁₂, and (CAG)₅ are useful to identify other chromosomes of A and D genomes. Hence, we suggest that chromosomal markers using SSRs are useful to investigate and compare karyotype of Korean wheat chromosomes for Korean wheat breeding program.

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Marker association analysis to improve tiller number in Korean wheats for wheat breeding

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Twenty-eight Korean wheats were evaluated tiller number according to STS markers for agronomic traits and processing quality genes and SSR markers related to tiller number for improvement of tiller number. For vernalization (*Vrn*), the mean of tiller number per m² (TN) of 23 Korean wheats harboring *vrn-B1* allele was higher than it of the other Korean wheats harboring *Vrn-B1a*, and effective alleles (*Ne*), Shannon's information index (*I*), and Nei's gene diversity (*h*) were 1.41, 0.47, and 0.29, respectively at *VRN-B1*. At *VRN-D1*, TN of 17 Korean wheats carrying *Vrn-D1a* was higher than it of the other Korean wheats carrying *vrn-D1*, and *Ne*, *I*, and *h* were 1.91, 0.67, and 0.48, respectively. For photoperiod (*Ppd*), TN of 24 Korean wheats carrying *Ppd-B1b* was lower than the other Korean wheats carrying *Ppd-B1a*, and *Ne*, *I*, and *h* were 1.32, 0.41, and 0.25, respectively at *Ppd-B1*. For puroindoline (*Pin*), TN of 25 Korean wheats carrying *Pina-D1a* was similar to it of the other Korean wheat carrying *Pina-D1b*, and *Ne*, *I*, and *h* were 1.24, 0.34, and 0.19, respectively at *Pina-D1*. At *Pinb-D1*, TN of 15 Korean wheats carrying *Pinb-D1a* was lower than it of the other Korean wheats carrying *Pinb-D1b*, and *Ne*, *I*, and *h* were 1.99, 0.69, and 0.50, respectively. Among Korean wheats, markers related to tiller and fertile tiller inhibition were not contributed to evaluate tiller number. Also, it is possible to evaluate tiller number by six markers. Based on those results, Korean wheats were classified into three groups by unrooted dendrogram.

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Marker association analysis to improve tiller number in double haploid population for wheat breeding

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Double haploid population with 104 lines were evaluated tiller number according to STS markers for agronomic traits and processing quality genes and SSR markers related to tiller number for improvement of tiller number. For vernalization (*Vrn*), the mean of tiller number per m² (TN) of 50 double haploid lines harboring *vrn-B1* allele was similar to it of the other double haploid lines harboring *Vrn-B1a* allele, and effective alleles (*Ne*), Shannon's information index (*I*), and Nei's gene diversity (*h*) were 1.41, 0.47, and 0.29, respectively at *VRN-B1* locus. At *Pinb-D1* locus, TN of the double haploid lines carrying *Pinb-D1a* allele was similar to it of the other double haploid lines carrying *Pinb-D1b* allele, and *Ne*, *I*, and *h* were 1.97, 0.69, and 0.49, respectively. All lines of the double haploid population were harboring *vrn-A1*, *vrn-D1*, *vrn-B3*, *Ppd-A1b*, *Ppd-B1a*, *Ppd-D1a*, and *Pina-D1a* alleles. Most markers related to tiller number divided the double haploid population as two groups. TN of each group was not significantly different. Based on those results, the double haploid population was classified into two types.

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Marker association analysis to improve tiller number in F₈ population for wheat breeding

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Genetic F₈ population with 157 lines were evaluated tiller number according to STS markers for agronomic traits and processing quality genes and SSR markers related to tiller number for improvement of tiller number. For vernalization (*Vrn*), the mean of tiller number per m² (TN) of 149 F₈ lines harboring *vrn-A1* allele was similar to it of the other F₈ lines harboring *vrn-A1a* allele, and effective alleles (*Ne*), Shannon's information index (*I*), and Nei's gene diversity (*h*) were 1.11, 0.20, and 0.10, respectively at *VRN-A1*. At *VRN-D1* locus, TN of 150 F₈ lines were harboring *vrn-D1a* allele was similar to it of the other F₈ lines harboring *vrn-D1* allele, and *Ne*, *I*, and *h* were 1.09, 0.18, and 0.09, respectively. For photoperiod (*Ppd*), TN of 125 F₈ lines were harboring *Ppd-D1a* allele was not significantly different from it of the other F₈ lines harboring *Ppd-D1b* allele, and *Ne*, *I*, and *h* were 1.48, 0.51, and 0.32, respectively. For puroindolines (*Pin*), TN of 98 F₈ lines were harboring *Pinb-D1b* allele was similar to it of the other F₈ lines harboring *Pinb-D1a* allele, and *Ne*, *I*, and *h* were 1.88, 0.66, and 0.47, respectively. Among SSR markers related to tiller number, 5 SSR markers divided the F₈ population as two types. TN of each type according to the 5 markers was not significantly different. Unrooted dendrogram revealed many branches with many subclasses.

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Dynamics of small RNAome in *Arabidopsis thaliana* during breaking seed dormancy

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Pre-harvest sprouting (PHS) is one of the economic problems associated with seed dormancy. It seriously affects crop production in the regions under humid climate and causes a sharp reduction in grain quality. Therefore, understanding the processes controlling dormancy is crucial to overcome PHS problem. To unveil how seed dormancy is regulated in *Arabidopsis*, we compared two different ecotypes of *Arabidopsis*, Col-0 (low dormancy) and Cvi-0 (high dormancy) under three different stages of seed development. We investigated transcriptome-wide responses of small RNAs during breaking seed dormancy. We found that differential expression of well-known marker genes associated with processes of dormancy and germination between Col-0 and Cvi-0 (*dog1*, *abi3*, *fus3*, *cyp707a2*, *ga3ox1*). Also, we identified approximately 1,500 small RNAs and some of them located near genes which are related to dormancy. This study might provide a foundation for understanding dynamics of transcriptome during breaking seed dormancy.

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Capillary electrophoresis-mass spectrometry-based on metabolome analysis in tomato germplasms

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Capillary electrophoresis-mass spectrometry (CE-MS) can be considered a useful analytical technique for the global profiling of polar and charged metabolites in biological samples. In this study, we have established and evaluated for the separation and relative quantitative analysis of cationic polar metabolites in the 46 tomato germplasms. Experimental setting (the CE-MS interface, BGE (background electrolyte) and mass spectrometer) was optimized to afford a good separation of 20 polar metabolites among the 46 tomato germplasms in less than 40 mins. The sheath-liquid of 50% (v, v) methanol was delivered through a syringe pump at a flow rate of 4 μ L/min. The BGE was consisted of 0.25 mol/L formic acid. The identification of each compound to be present in the extracts of 46 tomato germplasms was identified using available information of standard compounds (retention time, accurate mass and enhanced product ions). In this way, totally 20 targeted metabolites were identified with our available standard library as follows: Spermidine, 1,4-Butanediamine, L-2,4-Diaminobutyric acid monohydrochloride, N,N-Dimethylglycine, 4-Aminobutyric acid, Cytidine, Adenosine, 5'-Deoxy-5'-(methylthio) adenosine, L(+)- Isoleucine, L(+)-Lysine, L-Glutamic acid, L-Aspartic Acid, Glutathione reduced, L-pyroglutamic acid, L(-)-Phenylalanine, Tyramine, L-Citrulline, L-Threonine, L(-)- Proline, L-Histidine and L-Pipecolic acid. Principal component analysis results showed the sum of two components amounted to 66%. In this case, the diversity of metabolites was found L-Histidine, L-Citrulline and Tyramine in the tomato germplasm. Moreover, we proposed CE-MS methods and a successful relative quantification of polar metabolites to understand metabolite diversity within tomato germplasm. Therefore, this approach help us understand a broad range of fields for identifying ionic components in plant germplasm.

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Construction of a Linkage map and mapping of QTLs related to agronomic traits in DH population of maize using simple sequence repeat markers

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The double haploid (DH) technology offers an array of advantages in maize genetics and breeding. In our study, we constructed a maize genetic linkage map using SSR markers and DH population derived from a cross of normal corn (HF1) and normal corn (11S6169). Total of 200 SSR markers were assigned to 10 linkage groups which spanned 1,145.4 cM with an average genetic distance between markers of 5.7 cM. The 68 SSR markers showed Mendelian segregation ratios in the DH population at a 5% significance threshold. A total of 15 quantitative trait loci (QTLs) for plant height (PH), ear height (EH), ear height ratio (ER), leaf length (LL), ear length (EL), setted ear length (SEL), setted ear ratio (SER), ear width (EW), 100 kernel weight (100KW), and cob color (CC) were found in the 121 DH population. These QTLs were mapped to chromosomes (ch.) 1, 2, 3, 4, 5, 7, and 10. Among these QTLs, two QTLs was associated with PH on ch. 4 and 10, one with EH on ch. 10, one with ER on ch. 5, two with LL on ch. 2 and 7, two with EL on ch. 2 and 5, two with SEL on ch. 7 and 10, two with SER on ch. 2 and 4, one with EW on ch. 3, one with 100KW on ch. 7, and one QTL was related to CC on ch. 1. We found that four QTLs (qEL5, qEH10, qEW3, qCC1) were major QTLs based on over 15% for phenotypic variation. These new QTLs identified by the present study could provide as molecular markers as possible for selecting important agronomic traits in maize. The results of this study may help to improve the detection and characterization of agronomic traits and provide great opportunities for maize breeder and researchers using DH population in maize breeding program.

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Genetic diversity analysis among accessions of *Perilla* crop using new development microsatellite markers

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In this study, 40 new simple sequence repeat (SSR) primer sets were developed from RNA sequences using transcriptome analysis. These new SSR markers were applied to analyze the diversity, relationships, and population structure among 35 accessions of the two cultivated types of *Perilla* crop and their weedy types. A total of 220 alleles were identified at all loci, with an average of 5.5 and a range between 2 and 10 alleles per locus. The MAF (major allele frequency) per locus varied from 0.229 to 0.943, with an average of 0.466. The average polymorphic information content (PIC) value was 0.603, ranging from 0.102 to 0.837. Based on population structure analysis, all accessions were divided into three groups: Group I, Group II and the admixed group. The GD of each locus for accessions of cultivated var. *frutescens*, weedy var. *frutescens*, cultivated var. *crispa*, and weedy var. *crispa* were 0.415, 0.606, 0.308, and 0.480, respectively. Both weedy accessions exhibited higher GD and PIC values than their cultivated types in East Asia. In conclusion, the new SSR primers of *Perilla* species reported in this study may provide potential genetic markers for population genetics to enhance our understanding of the genetic diversity, genetic relationship and population structure of *Perilla* crop in East Asia. In addition, new *Perilla* SSR primers developed from RNA-seq can be used in the future for cultivar identification, conservation of *Perilla* germplasm resources, genome mapping and tagging of important genes/QTLs for *Perilla* breeding programs.

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사료가치가 우수한 중만생 고바이오매스 복합내병충성 보유 내도복 사료용 벼 ‘미우’

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2017년 국내 쌀 생산량은 397만톤, 일인당 쌀 소비량이 61.8kg로 생산과 소비의 구조적 수급 불균형 현상이 지속되고 있다. 이에 정부는 쌀 수급조절을 위해 2018년부터 2년간 한시적으로 「논 타작물 재배 지원사업」을 추진하고 있다. 사료용 벼는 논외의 형상과 기능을 유지하면서 이러한 수급불균형을 해결할 수 있는 좋은 수단임에도 불구하고 현 시점에서는 밥쌀용과 비교하여 소득이 낮아 정부보조금 없이는 농가현장에서 재배를 기피하는 경향이 있다. 이에 수량성, 내병충성 향상 등을 통한 경제적 가치 및 재배안정성을 올릴 필요가 있다. 이번에 육성한 사료용 벼 ‘미우’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. ‘미우’의 지상부 건물수량은 중부평야, 영남평야 및 호남평야지 4개소에서 3년간 시험한 결과 평균 19.9톤/ha으로 ‘녹양’ 대비 높은 수량을 나타내 경제적 가치도 높일 수 있을 것으로 기대된다. 더구나 가축이 소화 흡수할 수 있는 사료의 영양가 지표인 가소화양분총량(Total Digestible Nutrients, TDN)도 70.7%로 일반 사료작물과 비교하여 떨어지지 않아 사료적 가치가 높다고 판단된다. 이처럼 복합내병충성, 높은 지상부 건물수량 및 가소화양분을 보유한 ‘미우’는 밥쌀용과 비교해 거의 동등한 수준까지 경제적 가치를 올릴 수 있을 것으로 기대되어 정부정책 과제인 쌀 생산조정을 통한 수급조절에 일익을 담당할 것이다.

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Overexpression of *Brassica rapa* GROWTH-REGULATING FACTOR genes in *B. napus* increases organ size by enhancing cell proliferation

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GROWTH-REGULATING FACTOR (GRF) genes encode plant-specific transcription factors, and play critical roles in regulating the growth and development of lateral organs. In order to explore the agricultural potential of *Brassica rapa* GRF genes (*BrGRFs*), we constructed two *BrGRF*-overexpressing *B. napus* plants (*BrGRF3-10X* and *-90X*). *BrGRF3-10X* and *90X* developed larger cotyledons, leaves, and seeds than the wild type. The increases in size of these organs were due to increases in cell number, but not due to cell size. RT-PCR analysis revealed that *BrGRFs* regulated expression of a wide range of genes that are involved in gibberellin-, auxin-, cell division-related growth processes. Taken together, our data indicate that *BrGRFs* act as positive regulators of *B. napus* growth, thus raising the possibility that they may serve as a useful genetic source for crop improvement with respect to organ size and seed production.

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QTL analysis of yield-related traits using high-resolution genetic map in rice (*Oryza sativa* L.)

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Rice (*Oryza sativa* L.) is one of staple food in the world, especially in Asia. As the population of world increase, food security is important because consumption is gradually increasing. Therefore, the development of new varieties with high productivity is a major goal in rice breeding. In this study, yield-related phenotypes and quantitative trait loci (QTLs) were analyzed using the recombinant inbred lines derived from 'Milyang23' and 'Gihobyeo' (MGRILs). In phenotype investigation, normal distributions were shown in all 11 traits; flag leaf length (FL), culm length (CL), plant height (PH), 100 grain weight (100GW), panicle length (PL), panicle number (PN), spikelet number per panicle (SNPP), spikelet density (SD), grain numbers per plant (GNP), grain weight per panicle (GWP) and grain density (GD). Also, significant difference was mostly shown between 10 traits excepted 100GW. For QTL analysis, newly developed 48 CAPS markers and previous 3,202 SNP and PCR-based markers were integrated to construct high-resolution genetic map. Total genetic distance and an average of marker density were 2,628cM and 0.82cM/marker, respectively. When the genetic map was applied to detect QTLs on yield-related traits, a total of 56 QTLs were identified. Among these QTLs, 7 QTLs were detected from both SNPP and FL, and 16 QTLs were detected from chromosome 1, which mostly included the high LOD value (≥ 10). In the future, it will be possible to narrow down QTL region and identify genes related to yield by map-based cloning. Furthermore, QTLs information of agriculturally various traits in this study will be used for rice breeding.

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In vitro clonal propagation and cryopreservation of Korean Arbor-vitae (*Thuja koraiensis* Nakai) via somatic embryogenesis

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The genus *Thuja*, a member of the Cupressaceae family, comprises five species in the world. Among them, Korean Arbor-vitae (KAV; *Thuja koraiensis* Nakai) only occurs in the northeast China and in high mountains over the Korea. As the warming due to climate change has progressed in recent years, natural populations of KAV have been declined. Thus, KAV is designated as a rare and endangered tree species in Korea. Cryopreservation is one of the promising conservation technology for long-term storage of plant cells and tissues. There has not been any study on somatic embryogenesis and cryopreservation system in the genus *Thuja* until now. Here, we established an *in vitro* propagation and cryopreservation system for KAV via somatic embryogenesis. Whole megagametophytes with zygotic embryos from immature cones were used as initial explants and cultured on initiation medium. The initiation frequency was about 23.7% although we could not observe the stages of zygotic embryo development due to limited seed resources. The frequency of somatic embryo formation from both non-cryopreserved and cryopreserved cell lines was also tested. There were no statistical differences on the production of somatic embryos between non-cryopreserved and cryopreserved cells ($P = 0.1896$). We also investigated the effect of cryopreservation on genetic fidelity of the plantlets regenerated from non-cryopreserved and cryopreserved embryogenic cell lines. From ISSR analysis, there was no genetic instability in the regenerated plantlets from cryopreserved embryogenic cell lines. The embryogenesis and cryopreservation systems described here have the potential to contribute the conservation and clonal propagation of KAV germplasm.

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더뎡이병 저항성 신품종 감자 ‘탐나’ 육성

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제주지역의 감자재배 역사는 1950~60년대 200~300ha 수준에서 1980년대부터 급격히 증가하였고 1990년대 말 7,000ha를 상회하여 전국 재배면적의 30%를 점유하고, 생산액이 1,000억 원에 이르는 중요한 소득 작목이었다. 그러나 제주 주 재배품종 ‘대지’가 90%이상 계속적인 연작재배로 더뎡이병 발생 등 문제점이 발생하면서 재배면적이 2005년 6,174ha에서 계속 감소되어 2016년 1,636ha까지 감소하였다. 이러한 ‘대지’ 품종을 대체하기 위하여 제주특별자치도 농업기술원에서는 더뎡이병 저항성 등 다양한 품종육성을 추진한 결과 맛이 있고 더뎡이병에 강한 신품종 ‘탐나’를 육성하였다. ‘탐나’의 지상부 형태는 반직립형이며, 경장은 ‘대지’에 비하여 크고, 화색은 흰색으로 꽃이 많이 피고, 속기는 만생종으로 ‘대지’에 비하여 늦은 편이다. 괴경 모양은 원형이고, 표피는 매끄러우며, 엷은 담황색을 갖고 있으며 육색은 흰색이다. 눈 깊이가 얇아 소비자들이 선호하는 품종으로 재배기간이 충분하면 상품수량이 많은 편이다. ‘탐나’의 휴면기간은 20℃ 저장 시 50~60일에 90% 이상이 타파되어 2기작 재배를 하는 제주지역 및 남부지방에 적당하다. 또한 ‘탐나’는 감자 더뎡이병 발생이 제주 주 품종 ‘대지’에 비하여 저항성을 가지고 있어 재배농가들이 선호하는 품종이다. ‘탐나’의 수량은 지역적응시험 결과 대비품종 ‘대지’와 비슷한 경향을 보였다.

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밥맛이 매우 우수한 중만생종 벼 ‘새칠보’ 육성

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밥맛에 따른 소비자 기호성 변화에 대응하기 위해 국립식량과학원 영덕출장소에서는 밥맛이 우수한 최고품질 벼 품종을 육성하고자 노력한 결과, 우리나라 영남 평야지와 동해안 냉조풍지에 알맞은 밥맛이 매우 우수한 벼 ‘새칠보’를 개발 하였다. 모본으로 재배 안전성이 뛰어난 ‘계화26호’를, 부분으로는 최고품질 ‘영덕44호(칠보)’를 2005년 하계에 인공교배 하여 2005/2006년 동계 온실에서 17개체의 F₁ 식물체를 양성, YR25952의 교배번호를 부여하였다. 2006년 하계포장에 전개한 F₂ 집단을 포장과 실내 선발하여 2007년 하계에 F₃ 세대 28계통을 육성하였다. 이후 F₄~F₆ 세대를 계통육종법으로 전개하면서 2011년 예비선발 시험을 실시하여 미질특성이 우수하고 병해와 재해에도 안정적인 계통을 선발하였다. 2012년 생산력검정 예비시험, 2013~2014년 생산력검정 본시험을 실시한 후 중생이면서 우량계통인 YR25952-21-2-2-1을 선발하여 ‘영덕61호’로 명명하였다. 2014년부터 3년간 지역적응시험을 실시한 결과, 특히 밥맛이 매우 우수한 것으로 평가되어 2016년 12월 농작물직무육성신품종선정위원회에서 ‘새칠보’로 명명하게 되었다. ‘새칠보’는 보통기 재배 시 출수기는 8월 14일로 중만생종이며, 간장은 65cm로 단간이면서 반직립 초형이다. 탈립은 잘되지 않고 이삭추출은 양호하며 까락이 거의 없다. ‘화성벼’ 보다 주당수수는 2개, 수당립수는 14개 더 많으며, 현미천립중은 22.4g으로 다소 가볍다. 쌀알이 맑고 투명하며, 밥맛은 ‘화성벼’ 보다 매우 좋다. 또한 불시출수는 안되는 편이고, 위조현상에 강하고 성숙기 엽노화가 느린 편이며, 내냉성은 ‘화성벼’ 보다 약한 중약 정도이다. 잎도열병과 이삭도열병에는 약한 저항성을 보였고, 줄무늬잎마름병, 흰잎마름병(K₁)에는 강하나 오갈병, 검은줄오갈병에는 약하고, 벼멸구 등 충해에는 감수성이다. 쌀 수량은 지역적응시험 보통기 재배 7개소에서 6.13T/ha로 ‘화성벼’ 보다 9% 증수 되었으며 적응지역인 영남평야지, 남부중산간지, 동남부해안지에 보급하게 되었다.

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반응표면분석을 이용한 낙엽송 종자의 저장기간별 최적 저장조건 구명

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낙엽송은 결실주기가 긴 특성을 가지므로 조림수요를 충족하기 위해서는 종자의 활력 저하를 최소화 하는 저장조건을 갖추는 것이 중요하다. 낙엽송 종자는 저장성이 좋은 종자로 알려져 있으나 조림수요가 꾸준히 높은 데 비해 결실 예측이 어려워 종자 공급에 차질을 빚고 있으며, 구체적인 저장조건과 수명에 대한 자료는 부족한 실정이다. 따라서 본 연구는 낙엽송 종자의 장기 저장 및 안정적 공급을 위해 저장기간별 최적 저장조건을 찾아 저장종자 관리에 이용하고자 수행되었다. 이를 위하여 낙엽송 종자를 저장온도 5조건(-18℃, -4℃, 4℃, 15℃, 25℃), 종자함수율 3조건(5%, 10%, 15%)을 조합하여 총 15가지 처리를 하였으며, 이를 각각 6개월, 18개월, 30개월 후에 발아실험하였다. 발아실험 결과를 바탕으로 저장기간별 가장 적합한 저장조건을 탐색하기 위해 데이터에 이차회귀모형을 적합하여 최적 반응값과 요인수준을 예측하는 통계 분석법인 반응표면분석법(RSM)을 이용하여 저장기간별로 최고 발아율을 보이는 저장조건(저장온도, 종자함수율)을 예측하였다. 분석 결과 최고 발아율을 보이는 저장온도, 종자함수율은 각각 6개월 저장 종자에서 6.43℃, 9.83%, 18개월 저장 종자에서 8.01℃, 7.36%, 30개월 저장 종자에서 -13.95℃, 9.76%로 나타났다. 본 결과로 미루어볼 때 낙엽송 종자의 2년 이하 단기 저장의 경우 일반적인 종자 저장 온도인 4℃ 이상의 온도 조건에서도 종자의 활력이 크게 떨어지지 않고, 저장기간이 2년 이상일 경우 약 -14℃의 저온 조건에서 종자함수율 10% 내외로 저장하는 것이 종자의 활력 유지에 유리한 것으로 보인다.

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초분광영상 분석을 통한 편백 종자의 비파괴선별 검증

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본 실험은 초분광영상 분석을 수목종자에 적용하기 위해 시험적으로 선별된 편백 종자의 선별 결과를 검증하고자 수행되었다. 초분광영상은 물체가 광에 반응하여 방출하는 파장을 slit과 분광장치를 이용해 수백개의 구역(밴드)로 세분하여 촬영한 영상으로, 초분광영상 분석을 통한 종자의 비파괴선별은 개별 종자의 광스펙트럼을 분석하여 활력종자와 퇴화종자를 구분하는 원리이다. 채종원 생산단지별(상호 69, 동흥 80)로 각각 약 500립의 편백종자를 충남대학교 비파괴바이오센싱 실험실에서 초분광영상 분석을 이용하여 선별한 결과, 상호69에서 생산된 종자 37립, 동흥80에서 생산된 종자 30립이 충실한 것으로 선별되었다. 선별 결과를 검증하기 위한 발아실험 결과, 상호69의 종자에서 총 437립의 샘플 중 선별 결과와 발아실험 결과가 일치하는 경우는 434립으로 99.31%의 정확도를 보였고, 동흥80의 종자에서는 총 430립의 샘플 중 426립의 결과가 일치하여 99.07%의 정확도를 보였다. 검증실험 결과 초분광영상 분석을 통한 선별이 99% 이상 정확하게 이루어졌으며, 조사 기간 중 7-9일차에 발아가 집중되어 선별된 발아종자의 종자세가 좋은 것으로 나타났다.

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건식 쌀가루 전용 연질·등근형 전분 ‘미시루’의 농업적 특성

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쌀의 굳기가 약한 연질이고 쌀 배유에 밀과 같은 형태의 등근 전분을 가지고 있으면서 건식쌀가루 품질 특성이 개선된 신품종 ‘미시루’를 개발하였다. 건식 쌀가루 전용 벼 ‘미시루’는 2007년 하계에 중만생종이면서 현미천립중이 34.8g인 대립으로 쌀 튀김성과 현미 튀김 정립률이 좋은 ‘대립벼1호’를 모본으로, 밥맛이 우수한 ‘일품’의 돌연변이로 뽀얀 멍쌀 특성을 가져 양조용으로 산업화에 성공한 ‘설갱’을 부분으로 교배하여 대립이면서 뽀얀 멍쌀의 특성을 조합하여 개발된 건식 쌀가루 전용 품종이다. ‘미시루’의 이삭 패는 시기는 8월17일로 중만생종이다. 벼키는 85cm로 ‘화성’보다 작고, 현미천립중은 30.8g으로 ‘화성’보다 1.5배 정도 무거우며, 쌀 수량은 566kg/10a 이다. 쓰러짐에 강하지만 병해충에 약하고, 수발아에 중정도의 반응을 보여 재배적용지역은 중부평야이다. ‘미시루’는 쌀알의 굳기가 2,239g으로 대립벼1호 4,280g의 52%에 불과하다. 배유내 전분구조가 밀과 같이 등글어 건식 쌀가루의 입자는 평균 65μm 로 작고, 손상전분이 5.1%로 낮아 쌀가루용 쌀로 적합하다. 향후 ‘미시루’의 내병성, 내재해성을 개선하고 원료곡의 경제성을 높일 수 있도록 수향성을 향상시킬 계획이다. 본 연구는 농촌진흥청 연구사업(세부과제명: 중부지역 적응 초다수성 쌀가루 전용품종 육성, 세부과제번호: PJ012890012018)의 지원에 의해 이루어진 결과임.

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가공용 초다수성 복합내병성 벼 신품종 “금강1호”

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“금강1호”는 가공용 원료곡의 가격 경쟁력 향상을 위해 개발된 초다수성 벼 품종이다. 2007년 하계에 복합내병성을 가지며 수량성이 높은 다산1호와 초형이 직립하여 수광태세가 좋은 금강을 각각 모본과 부분으로 인공교배를 실시하였다. 2008년 하계에 F₁ 양성, 2009년 F₂ 집단에서 선발된 80개체를 2010년 하계에 F₃ 계통으로 전개하였다. 이 후 2011년부터 2012년까지 2년간 계통육종법에 따라 세대를 진전시켰으며, 2013년 예비선발시험과 2년간의 생산력검정시험을 거쳐 밀양307호의 계통명이 부여되었다. 2015년부터 2017년까지 3년간의 지역적응시험 결과, 수량성이 높고 흰잎마름병(K1~K3a), 줄무늬잎마름병, 도열병 저항성 등의 우수성이 인정되어 2017년 농작물 직무육성 신품종선정위원회에서 “금강1호”로 명명되었다. “금강1호”는 출수기가 8월 14일인 중만생종이며, 간장은 74cm 로 “다산”과 비슷하다. 수장과 주당수수는 각각 은 26cm와 13개이며, 수당립수가 142개로 다산보다 25% 많다. “금강1호”는 도복에 강하고 수발아가 거의 되지 않는다. “금강1호”는 쌀수량이 817kg/10a로 우리나라에서 개발된 벼 품종 중에서 수량성이 가장 높다. 향후 “금강1호”에 대한 다양한 가공적성이 구명된다면 우리나라 쌀 가공용 원료곡의 가격 경쟁력 향상에 일조할 것으로 전망된다.

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A study of the role of *INFLORESCENCE DEFICIENT IN ABSCISSION* gene expression in tomato

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Abscission, organ separation, plays a crucial role in the life cycle of a plant. Precise and timely regulation of abscission is fundamental to improvement of crop productivity as it influences fruit quality and the timing of harvest. To gain insights into commonalities of abscission processes conserved across the plant kingdom, we examined the transcriptomes for abscission in tomato (flower pedicels), soybean (leaf petioles), and Arabidopsis (floral organs). Comparative analyses of the transcriptome data in three different systems allowed us to acquire unprecedented perspectives that assist in successful separation from the parent plant. We uncovered an early increase in the expression of genes that underlies the synthesis of a waxy-like cuticle, which mirrored the expression pattern for cell wall disassembly genes. Similarly, an abundance of expression for small pathogenesis-related (PR) genes also indicated that these genes are more closely related to the structural changes in the abscission-zone (AZ) than an enzymatic role in pathogen resistance. In addition, sequences and the expression of *INFLORESCENCE DEFICIENT IN ABSCISSION* (*IDA*) and *IDA*-like genes in three different systems were conserved and associated with the abscission processes. To functionally validate the *IDA*-like gene in tomato, we generated tomato (*Solanum lycopersicum*, VF36) RNAi lines that target AZ-specific expression of *SIIDA1* (*SIIDA1* RNAi) and examined the effects of suppression of *SIIDA1*. Alternatively, we investigated expression for *SIIDA*-like genes (*SIIDA1* to *SIIDA5*) in pedicel AZ from a variety of natural abscission variants in tomato (i.e., *jointless*, *functionally impaired jointless* (knuckle-like AZ), normal joint). Whereas the suppression of *SIIDA1* expression did not correlate with the expected delay in pedicel abscission of *SIIDA1* RNAi, transcript profiles of *SIIDA*-like genes in the natural tomato variants indicated that expression of *SIIDAs*, to some extent, is associated with the formation of AZ. Treatment of ethylene action inhibitor, 1-MCP, in detached fruits and leaves of *SIIDA1* RNAi that blocked dark-induced senescence processes further substantiated the previous finding that ethylene is essential in tomato abscission, and the function of *SIIDA1* expression is ethylene-dependent in tomato. Functional redundancy and possible divergence of *SIIDA*-like genes in relationship with ethylene will be discussed.

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Genome-wide SNP selection associated with protein and oil content in core collection of wild soybean using the elastic-net method

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Soybean is a major crop that provides a crucial source of edible protein and oil. Wild soybean (*Glycine soja*) contains an important genetic variation for improving agronomic traits in cultivated soybeans. In this study, SNPs associated with protein and oil contents were identified using a core collection of wild soybeans genotyped with Affymetrix Axiom 180k SoyaSNP genotyping array by RDA (Rural Development Administration), Korea. Seed compositions of 445 wild soybean accessions were evaluated at Gwangju in 2016 and 2017. The content of the protein ranged from 40.53 to 55.83% with the mean of 48.97% and the content of the oil ranged from 4.03 to 12.82% with the mean of 7.35%. The protein content negative correlated with oil content ($P \leq 0.01$). The elastic-net method was used for the multiple-SNP analysis. Based on the selection probability of 0.5, 28 SNP markers associated with protein content were identified across soybean chromosomes, while 64 SNP markers associated with oil content were discovered. This study provides resources for genomics-enabled improvements in soybean breeding.

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Genome-wide SNP selection associated with amino acid content in core collection of wild soybean using the elastic-net method

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Soybeans are one of the most important food crops because they contain all of essential amino acids. In this study, we identified genome-wide SNP markers associated with amino acid content in core collection of wild soybeans genotyped with Affymetrix Axiom 180k SoyaSNP array. A total of 375 wild soybean accessions were used to determine amino acid content with amino acid auto-analyzer. The contents of total amino acids ranged from 33,843 to 50,819 (mg/100g), and all amino acids was positively correlated with each other ($P \leq 0.05$). As a result of SNP estimation using elastic-net method, total of 59 SNPs associated with amino acids content were identified across soybean chromosomes. The identification of SNP markers associated with amino acids contents are expected to be helpful for the development of molecular markers that can be used for soybean breeding.

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다수성 사료용 옥수수 신품종 ‘다청옥’의 생육특성 및 수량성

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국내 조사료 안정생산 기반을 마련하기 위해 사료 품질이 우수하고 수량이 많은 사료용 옥수수 신품종 ‘다청옥’을 육성하였다. ‘다청옥’은 2016년에 농촌진흥청 국립식량과학원에서 자식계통 KS197와 KS202를 교잡하여 육성한 다수성 단교잡종이다. ‘다청옥’의 종피색은 황색이며 입질(립형)은 마치종이다. 2013년 1년간 생산력검정시험을 거쳐, 2014년~2016년까지 3년 동안 4지역에서 지역적응시험을 수행하였다. 그 결과 우수성이 인정되어 2016년 농작물 직무육성 신품종으로 결정되었고 ‘다청옥’으로 이름 지어졌다. ‘다청옥’의 생육특성 중 출사일수가 80일, 간장은 267cm, 착수고율은 51%, 도복은 1.5, 100주당 이삭수는 95개, 후기녹체성은 2.9로 대비품종인 ‘광평옥’과 비슷한 특성을 가졌다. 이삭길이(18.6cm)는 ‘광평옥’보다 길었지만 통계적 유의성은 인정되지 않았다. 깨씨무늬병(5.7)에는 중간정도의 저항성이며, 그늘음무늬병(1.0)에는 강한 편이다. 조명나방(6.7)에는 중간정도의 저항성을 보인다. ‘다청옥’의 잎과 줄기의 조단백질 함량(7.3%)은 ‘광평옥’과 비슷하나 수입종인 ‘P3394’보다 많았다. ‘다청옥’의 잎과 줄기의 사료가치인 NDF(64.2%)와 ADF(36.3%)는 ‘광평옥’ 및 P3394와 유의한 차이는 없었다. ‘다청옥’의 건물수량은 23.69톤/ha, TDN수량은 16.11톤/ha로 각각 10%, 7% ‘광평옥’보다 많았으나 통계적 유의한 차이는 없었다. 채종 특성 및 수량을 검토하기 위해 모본(종자친)과 부분(화분친)의 재식비율(모본 : 부분)을 4 : 1로 동시 파종하여 시험한 결과 ‘다청옥’은 모본(KS197)의 출사기와 부분(KS202)의 화분비산시기가 잘 일치하는 품종이며 채종수량(2.46톤/ha)이 많았다. ‘다청옥’은 전국적으로 재배가 가능한 품종이다.

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Genetic relationship of tropical region-bred temperate *japonica* rice plants and their grain yield variations in three different tropical environments

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Temperate *japonica* rice (*Oryza sativa* L.) is usually grown in temperate regions. When grown in tropical areas, most temperate *japonica* rice plants flower prematurely and do not show sufficient vegetative growth. Fourteen *japonica* rice varieties and lines adapting to tropical environments were developed in the Philippines (tropical Asia) between 2008 and 2014. Their genomes were characterized by genome-wide single nucleotide polymorphism genotyping and their grain yields were examined in the Philippines during the wet and dry seasons and in a high-altitude area of Burundi (tropical Africa). Based on the genotyping, all 14 materials were found to belong to the temperate *japonica* rice group. Grain yields were more affected by the environment than by the genotypes. Two of the 14 rice materials showed more stable and higher yields than the check varieties across the three environments and one of the two has been released as a commercial variety in the Philippines. Collectively, these results demonstrate that rice plants genetically belonging to the temperate *japonica* group can be bred to adapt to tropical areas.

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De novo assembly of complete chloroplast genome from *Pinus densiflora* using oxford nanopore and illumina MiSeq

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The chloroplast (cp) genome is useful in the study of phylogenomics, molecular dating, and molecular evolution. Red pine is an evergreen conifer in the genus *Pinus* and widely distributed worldwide. It is very important for its economic, scientific, and ecological niches in Korea. Here, we report the complete chloroplast genome sequence of Korean red pine (*Pinus densiflora*). Genome sequencing was achieved by a combination of Oxford Nanopore MinION and Illumina MiSeq technologies. With the rapid development of sequencing technology and the plummeting cost, assembling whole genomes from non-model plants will soon become routine for plant systematists and evolutionary biologists. In the present study, Korean red pine chloroplast genome size was 119,875 base pairs (bp) (LSC 65,654 bp and SSC 53,231 bp). Compared to the chloroplast of other congeneric species (*P. sylvestris*, *P. thunbergii*, *P. taivanensis* and *P. tabuliformis*), six highly variable intergenic regions (*ndhC/psaC*, *rps16/trnQ*, *trnK/rps16*, *trnL/trnF*, *trnM/atpE*, and *trnQ/psbK*) were also identified. The chloroplast resources generated by the present study will help to elucidate chloroplast evolution within the genus and to resolve phylogenetic relationships within highly complex and reticulated lineages.

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Comparative transcriptome analysis of dwarf and normal soybean obtained from crossing of *G. max* and *G. soja*

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Plant height is an important component of plant architecture, and significantly affects crop breeding practices and yield. We obtained few segregated dwarf soybeans in the populations derived from crossing of *G. max* var. Peking and *G. soja* var. IT182936 in F5 RIL population. These could be useful genetic resource for plant breeders, geneticists and biologists. We tried to find differently expressed genes to classify and understand the regulation of genes related to plant growth in a mutant dwarf soybean, which occurred in F5 generation. With the help of Illumina high-throughput platform transcriptomes were generated and compared among normal and dwarf in triplicates. We found that the expressed genes relationship are complexed to the plant growth. There are highly significantly up-/down-regulated genes in the comparing of gene expression in normal and dwarf soybeans. The genes related to disease and stress responsive were found to be up-regulated in dwarf soybean. Such over-expression of disease resistance and other immune responsive genes could be targeted to understand the gene regulation of how the immune genes regulate the response of plant growth. In addition, photosynthesis related genes showed very low expression in dwarf lines. The transcriptome expression and genes classified related plant growth could be useful resource to researchers studying plant growth.

Keywords: soybean, growth, dwarf, transcriptome, DEG

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Effects of different seeding methods on growth and yield of wheat

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At present, domestic wheat has been developed various harvesting methods for labour-saving and high yielding in order to strengthen price competitiveness with imported wheat, but no cultivation method suitable for regional characteristics of the soil has been established. This study was carried out to determine the effect of different seeding methods on wheat yield. Wheat varieties, Keumkang and Jokyung were used, and sown in Nov. 2nd 2017 at a paddy field in Haman region. Standard fertilizer level was 91-74-39 kg (N-P₂O₅-K₂O)/ha. The seeding methods consisted of 4 plots. According to the sowing method, When drill seeding with Jokyung, the heading was delayed by one day. When no-tillage broad ridge seeding and broad ridge seeding after rotary with Keumkang, the heading was two days earlier. The maturity was almost the same. Broadcast seeding-rotary showed the highest number of spikes per m² in Jokyung (888) and Keumkang (851). The tendency was similar to that of the 1,000-seed weight and grain weight (g/L), but they were heaviest in the broad ridge seeding after rotary and lowest in the broadcast seeding-rotary. Dry matter yield of Jokyung by seeding methods of wheat revealed that there was an increase in orders; broadcast seeding-rotary (502kg/10a) > no-tillage broad ridge seeding (394kg/10a) > broad ridge seeding after rotary (358kg/10a) > drill seeding (336kg/10a). The yields of Keumkang were higher in the order of broadcast seeding-rotary (517kg/10a), followed by broad ridge seeding after rotary (429kg/10a), no-tillage broad ridge seeding (367kg/10a) and drill seeding (332kg/10a). The highest yield was observed in broadcast seeding-rotary, which were sown more than the other sowing methods at 20kg/10a, because they were well grown without suffering from the harmful effects due to severe drought in the fall of 2017 and cold conditions during winter.

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Map-based cloning of SPLIT-HULL (SPH) gene related to hull splitting in rice (*Oryza sativa* L.)

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Rice hull consist of two bract-like structures, lemma and palea. This is an important organ protecting the seeds from environment, and determining shape and filling of kernel. An optimal size and morphology will be beneficial for seed development, affecting yield and quality. A split-hull (sph) mutant was induced by treating with a chemical mutagen, N-methyl-N-nitrosourea (MNU), on the fertilized egg cells of a japonica rice cultivar "Hwaseonchal". The sph mutant showed split hull phenotype, a chasm between lemma and palea, during grain filling period and reduced seed setting rate. Hull splitting initiated 15 days after flowering (DAF), and about 40 percentage of grains showed split-hull phenotype after seed maturation. Genetic segregation analysis indicated that sph mutant phenotype is controlled by single recessive gene. To identify the SPH gene, BSA and fine-mapping was conducted using F2 and F3 population derived from the cross between sph mutant and Milyang 23 ('Tongil'-type variety). SPH gene mapped to 113 kb region containing 27 annotated ORFs in chromosome 4. Through sequence analysis of the candidate ORFs, candidate gene for the mutant phenotype was identified. The SPH gene might be involved in the spikelet development.

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Development of late flowering chinese cabbage using CRISPR system

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Controlling flowering time is essentially important in crop plants for high agricultural productivity and adaptation to environmental changes. Currently, a growing number of genes related to flowering time have been studied in crop plants. This study was conducted to produce the plants with late-flowering time using *A. tumefaciens* - mediated CRISPR-Cas9 system in chinese cabbage. *A. tumefaciens* harboring pHATC containing genes encoding Cas9, guide RNA of target gene, and hygromycin phosphotransferase was used to infect hypocotyl explants. After 3 weeks, the calli and roots were observed from the explants. The shoots were developed from the calli after 7 weeks. The insertion of transgenes in plantlets was confirmed using PCR analysis. Targeted deep sequencing of transgenic plants revealed the indel at the target site. To obtain seeds, transgenic plants are being cultivated. These results showed that gene editing with CRISPR-Cas9 system in chinese cabbage could be useful for the development of the new valuable varieties.

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밀 핵심집단 구축을 위한 유전자원 특성조사

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국내에서 밀은 높은 활용도와 소비율에 비해 자급률이 낮기 때문에 자급률을 높이기 위한 고품질 품종 육성이 시급함에도 불구하고, 밀이 가지고 있는 유전체 구조는 크고 복잡하여 유전체 분석의 어려움이 크다. 본 연구에서는 다양한 소비자 욕구에 맞는 고품질 밀 개발을 위한 기반을 조성하기 위해, 국내 기상환경에 적합하면서 유전적 다양성을 가진 밀 핵심집단의 구축을 위하여, 본 연구팀은 전세계 60여개 국가로부터 수집한 1,969점 (국내 350여 점, 중국 160여점, 아프가니스탄 75점, 미국 155점, 멕시코 367점 등)의 밀 유전자원을 확보하여 생육 특성조사를 수행하였다. 입모율, 엽색, 초형, 수형, 출수기, 성숙기 등의 표현형질을 조사하였으며, 그 외에 도복율 및 이병율 (붉은곰팡이병, 녹병, 흰가루병 등) 등을 조사하였다. 현재 전체 유전자원으로부터 국내 기상환경에 적합한 600여 점을 선발하고, 밀 품질특성 및 농업형질 관련 functional marker (FM)를 이용하여 genotype을 분석하고 있으며, 표현형과 genotype 간의 연관관계를 분석할 예정이다. 아울러 대부분의 계통으로부터 종자를 수확하였으며, 앞으로 NIR 및 Seed counter 분석을 통해 밀 가공적성 등 종자특성을 조사할 예정이다.

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적립계 조숙 다수성 국수용 밀 ‘조중’

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국내 밀 재배는 주로 벼 수확 후 10월 중순부터 파종하여 이듬해 6월 모내기 전에 수확하는 답리작 재배방식으로 진행되어 왔다. 답리작 재배에 적합한 숙기가 빠른 밀 품종 개발을 목표로 2002년도에 조숙 단간인 수원272호/올그루의 교잡종을 모본으로 하고, 조숙 고품질인 금강/수원252호의 교잡종을 부분으로 인공교배하여 SW02059 조합을 육성하였다. 경기도 연천에서 집단재배 후 계통을 전개하여 초형과 수형이 양호하며 내한성이 강한 계통인 SW02059-B-B-B-5-8-8-5는 조숙계통으로 2010년부터 2개년간 생산력 검정을 거쳐 ‘익산360호’로 계통명을 부여하였다. 그 후 2012년부터 3개년 동안 지역적응시험을 실시한 결과 숙기가 빠르면서 답리작 적응다수성이고, 수발아와 도복에 대한 저항성이 강하여 생산안정성이 우수하였다. 밀가루 품질에 있어서도 중력분에 적합한 단백질과 글루텐을 함유하고 있으며, 밀가루 색과 국수 색택이 좋고, 삶은 국수의 점성과 탄성이 우수하여 2014년 직무육성 신품종선정심의회에서 “조중”으로 명명하였다. 그 후 국립종자원의 재배심사를 거쳐 2018년 종자산업법에 따라 품종보호 등록원부에 등록(품종보호 제6970호)되었다.

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백립계 답리작 적응 빵용 밀 ‘백강’

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국내 밀 품종개발은 1970년 이후 금강밀 등 35개 품종이 개발되었으나 국수용이 대부분이며, 과자용 3품종, 빵용으로는 조경밀 1품종이 개발 보급되고 있다. 이에 농촌진흥청에서는 국산밀 용도의 다양화를 위해 빵용 밀 품종개발을 목표로 2005년도에 내한성이 강하고 밀 단백질 글루텐 중 HMW-GS 조성이 5+10을 지니고 있는 탐동을 모본으로 하고, 빵용 특성이 우수한 Klasic을 부분으로 인공교배를 실시하여 IW200502001 조합을 육성하였다. 전라북도 남원에서 집단재배 후에 계통을 전개하여 초형과 수형이 양호하고 내한성이 강한 계통인 IW200502001-B-B-B-6-10는 조숙계통으로 2011년과 2012년에 2년간 생산력검정시험에 공시한 결과 생육특성, 생리장해, 내병성 및 수량성이 우수하여 “익산366호”로 계통명을 부여하였다. 2013년도부터 3개년 동안 전작 4개소와 답리작 4개소에서 지역적응시험을 수행한 결과, 숙기가 빠르면서 답리작 적응 다수성이고, 백립계이면서 대립이고, 붉은곰팡이병에 중도저항성이었다. 밀가루 품질에 있어서도 제빵용에 적합한 단백질과 글루텐을 함유하고 있으며 밀가루 색택이 밝고, 식빵의 부피가 크고 부드러워 빵 가공적성이 우수하여 2015년 직무육성 신품종선정심의회에서 “백강”으로 명명하였다. 그 후 국립종자원의 재배심사를 거쳐 2018년 종자산업법에 따라 품종보호 등록원부에 등록(품종보호 제6966호)되었다.

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백립계 찰밀 취반용 밀 ‘백찰’

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최근 비만, 당뇨와 같은 성인병을 예방하기 위하여 흑미, 보리, 콩과 같은 잡곡류를 취반시 혼합하고 있으며 밀도 통밀을 취반용으로 사용하고 있다. 현재 취반용으로 이용되고 있는 “신미찰1호”는 아밀로스함량이 매우 낮은 찰밀이지만, 종피색이 붉어 일부 소비자들이 기피하기 때문에 도정을 실시하여 판매되는 단점을 가지고 있다. 농촌진흥청에서는 이러한 단점을 개선하고 취반적성을 향상시키기 위하여 2006년도에 적립계 찰밀인 “신미찰”을 모본으로 하고, 백립계인 금강밀을 부분으로 인공교배를 실시하여 IW20060336 조합을 육성하였다. 이후 F1 세대를 멕시코 CIMMYT 연구소에서 반수체 배양을 실시하여 DH10326 계통을 육성하였다. 전북 익산에서 내한성이 강하고 초형과 수형이 양호한 DH10326은 백립계 찰밀이면서 수량성이 우수하여 2008~2009년도 2년간 생산력 검정에 공시하였다. 생산력 검정에서 생육특성, 생리장해, 내병성, 내도복성, 수발아성 및 수량구성요소를 조사한 결과 그 특성이 우수하여 “익산345호”로 계통명을 부여하였다. 2010년도부터 3개년 동안 전작 3개소와 답리작 3개소에서 지역적응시험을 수행한 결과 도복에 대한 저항성이 강하고 백립계이면서 수발아중도저항성으로 생산안정성이 우수하였다. 품질에 있어서도 취반시 흡수성, 퍼짐성 및 백도가 높으며 밥알이 부드럽고 점탄성이 높아 혼반용으로 적합하여 2012년 직무육성 신품종선정심의회에서 “백찰”로 명명하였다. 이후 국립종자원의 재배심사를 거쳐 2018년 종자산업법에 따라 품종보호 등록원부에 등록(품종보호 제6972호)되었다.

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반매끈망, 사일리지 품질이 우수한 청보리 신품종 ‘연호’

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⁶경상남도 진주시 대신로 570 경상남도농업기술원

청보리는 곡류를 포함한 사료맥류로 남부지역을 중심으로 대부분 벼+보리 작부체계로 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 2005년에 매끈망, 장간, 다열성이면서 내도복성이 양호한 ‘우호’를 모본으로 하고, 장간, 총체적성이 높은 ‘영양’을 부분으로 인공교배하여 반매끈망, 다수성이면서, 사일리지 품질이 우수한 ‘연호’를 개발하였다. ‘연호’는 직립초형으로 초장은 100cm로 ‘영양’보다 크며, 파성은 IV이다. 답리작 재배시 출수기는 4월23일, 황숙기는 5월22일로 ‘영양’보다 하루 빠르다. 줄기수는 m²당 713개로 다열성이며, 내한성은 고희에서 고사주율이 72.0% ‘영양’보다 강하고, 호위축병은 나주(I형), 진주(IV)에서 저항성, 익산(III형)에서 중도저항으로 ‘영양’과 비슷한 내재해성 품종이다. 조사료 건물수량은 전작에서 17.3톤/ha로 ‘영양’에 비해 7%, 답리작에서 평균 11.4톤/ha로 ‘영양’에 비해 5% 높다. 조사료 품질은 조단백질 함량이 9.3%로 영양보다 높았다. 총가소화영양분(TDN)은 68.8%로 ‘영양’에 비하여 낮았으나, TDN수량은 883kg/10a로 ‘영양’보다 높았다. 사일리지 품질은 pH4.4로 ‘영양’의 pH4.6보다 낮았다. 젖산함량은 68.2%로 높고 초산 및 낙산함량이 낮아 사일리지 품질이 I등급으로 ‘영양’보다 양호한 품종이다. ‘연호’의 적응지역은 1월 최저평균기온 -8°C 이상으로 북부 산간내륙지방을 제외한 전국에서 재배가 가능하다. ‘연호’는 반매끈망으로, 총체 다수성을 가지면서, 사일리지 품질이 우수하여 금후 축산 농가들로부터 큰 호응을 얻을 것으로 기대되며, 금후 신품종이용촉진사업을 통한 종자 생산단계를 거쳐 2020년부터 농가에 보급될 예정이다.

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적립계 답리작 적응 수밭아와 붉은곰팡이병 저항성 국수용 밀 ‘새금강’

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현재 국내 밀 보급종 품종은 금강, 조정, 백중이 보급되고 있으며, 금강밀이 전체 재배면적이 70%이상을 차지하였으나 붉은곰팡이병에 약하고, 다른 품종에 비해 수량이 적어 농가에서 재배를 점차 기피를 하고 있다. 이에 농촌진흥청에서는 금강밀의 단점인 붉은곰팡이병과 수밭아 저항성을 증진시키고, 다수확 품종 개발을 목표로 2007년도에 금강밀을 모본으로 하고, 내재해성이 강하고 분얼이 많아 수량구성요소 특성이 우수한 올그루밀을 부분으로 인공교배를 실시하여 IW2007097 조합을 육성하였다. 그후 F1 세대를 멕시코 CIMMYT 연구소에서 반수체 배양을 실시하여 DH2010036 계통을 육성하였다. 전북 익산에서 내한성이 강하고 초형과 수형이 양호한 DH2010036은 수량성이 우수하여 2011~2012년도 2년간 생산력 검정에 공시하였다. 생산력검정시험에 공시한 결과 생육특성, 생리장해, 내병성 및 수량성이 우수하여 “익산367호”로 계통명을 부여하였다. 2013년도부터 3개년 동안 전작 4개소와 답리작 4개소에서 지역적응시험을 수행한 결과, 숙기가 빠르면서 답리작 적응 다수성이고, 수밭아와 붉은곰팡이병에 저항성이 강하였다. 밀가루 품질에 있어서도 국수용에 적합한 단백질과 글루텐을 함유하고 있으며, 밀가루와 국수 면대색이 밝고, 면발이 부드럽고 쫄깃하여 국수 가공적성이 우수하기 때문에 2015년 직무육성 신품종선정심의회에서 “새금강”으로 명명하였다. 그 후 국립종자원의 재배심사를 거쳐 2018년 종자산업법에 따라 품종보호 등록원부에 등록(품종보호 제6967호)되었다.

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더뎡이병에 강한 2기작감자 ‘수선’ 육성

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우리나라 가을감자는 남부지방과 제주도를 중심으로 재배되고 있으며, 주품종은 일본에서 도입된 대지와 국내에서 육성한 추백이다. 대지는 수량성이 높고 큰감자가 많은 좋은 품종이지만 더뎡이병에 약하고 전분함량과 식미가 낮은 것이 문제이다. 추백은 숙기가 빠른 조생종이지만 바이러스에 약하고 전분함량이 낮다. 따라서 더뎡이병에 강하고 식미도 우수한 2기작 가을감자 품종을 육성하기 위하여 2010년 고운과 대관1-109호를 교배하여 ‘수선’을 육성하였다. ‘수선’은 중생종으로 지상부는 반직립성으로 자라고 꽃은 흰색이며 장과는 거의 달리지 않는다. 감자 괴경은 원형으로 표피는 완숙시 거칠거칠한 러셋 형태를 보이며 육색은 흰색이다. 일반 포장과 다발 포장에서 시험하였을 때 더뎡이병 발생이 매우 적었으며, 잎말림바이러스에도 강한 특성을 보였다. 모자이크바이러스에는 중도저항성이며, 감자역병과 겹등근무늬병에 대해서도 중도저항성을 보였다. 수량성은 봄재배시 3지역 평균 31.4ton/ha, 가을재배시 28.2ton/ha로 대지와 비슷하였다. 그러나 생리장해 발생이 적어 상품성 있는 감자 수량은 더 높았으며, 건물률도 봄재배시 21.74%, 가을재배시 19.80%로 높게 나타났다. 괴경의 휴면기간은 대지와 비슷한 수확후 50~60일이다. ‘수선’의 적응지역은 전라남북도와 경상남도의 해안지방과 제주도 지역이다. ‘수선’은 괴경형태가 국내 소비자 기호에 맞고 더뎡이병에 강하여 남부지방 2기작용으로 재배면적이 확대될 것으로 기대된다.

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안토시아닌 함량이 많은 유색 쌀보리 ‘흑보찰’

김양길¹, 이미지¹, 김경호¹, 강천식¹, 박종호¹, 박태일¹, 윤영미¹, 한옥규¹, 최진경², 배정숙³, 송재기⁴, 손재한¹, 최창현¹, 이점호¹

- ¹전북 완주군 이서면 혁신로 181 농촌진흥청 국립식량과학원
- ²전라남도 나주시 산포면 세남로 1508 전라남도농업기술원
- ³대구광역시 북구 칠곡중앙대로 136길 47 경상북도농업기술원,
- ⁴경상남도 진주시 대신로 570 경상남도농업기술원

최근 건강한 삶을 즐기려는 소비자층이 늘고 이를 겨냥한 기능성 곡물을 이용한 식품 등이 인기를 얻고 있다. 그로 인하여 기능성분이 풍부하고 다양한 용도의 차별화된 품종 개발이 요구되고 있다. 따라서 이에 적합한 품종을 육성하기 위해 1998년에 쓰러짐에 잘 견디고, 유색, 다수형 등 특성을 가진 ‘긴쌀보리/창녕재배’ 계통을 모본으로, 이삭이 긴 다수형 ‘긴쌀보리’를 부분으로 여교배하여 국내 최초로 흑색 찰성 쌀보리 ‘흑보찰’을 개발하였다. ‘흑보찰’은 6조이며 파성이 IV인 불시출수가 안정적인 병성 쌀보리로 이삭의 형태는 소수형이고, 까락이 길며 탈부성이 좋다. 간장이 79cm로 쓰러짐에 잘 견디고, 토양전염 바이러스병인 보리호위축병에 대한 저항성인 품종이다. 성숙기는 새찰쌀보리와 비슷한 5월 25일이며, 천립중은 30.4g인 대립종으로 수량성(조곡)은 ha당 4.02톤으로 새찰쌀보리의 95% 수준이다. 이 품종은 아밀로스 함량이 낮은 찰성 품종으로 흡수율, 퍼짐성이 좋으며, 출수 후 25일 전후 자색발현이 되고 출수 후 30일 전·후에서 흑색이 발현되는 특징을 가진 품종으로 안토시아닌 함량이 0.116±0.005 mg/brain g으로 기존품종 보다 많이 함유되어 혼반 및 가공용 이용될 것으로 기대되며, 보급될 재배적응지역은 1월 최저평균기온이 -6℃ 이상인 보리 재배지역이다.

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수량 많고 꼬투리 터짐에 강한 녹자엽 검정콩 ‘청자5호’

서정현¹, 한원영¹, 김현태¹, 강범규¹, 신상욱¹, 박장환¹, 김홍식¹, 오은영¹, 이병원², 윤홍태², 최만수³, 이영훈³, 곽도연¹

- ¹경남 밀양시 점필재로20 국립식량과학원 남부작물부
- ²경기 수원시 수인로126 국립식량과학원 중부작물부
- ³전북 완주군 이서면 혁신로181 국립식량과학원

검정콩은 우리나라에서 주로 주식인 쌀과 함께 밥을 지어 먹는 용도로 사용되어 왔다. 소비자들은 검정콩 껍질안의 자엽색이 녹색인 것을 선호하며 알이 굵어 무름성이 좋은 콩을 선호한다. 이러한 검정콩은 일반콩 보다 높은 시장가격을 형성하고 있어 농가의 선호도가 높다. ‘청자5호’는 대립, 녹자엽인 검정콩 품종 개발을 목표로 하여 ‘밀양181호’와 ‘YS1886(청두1호×Tanbaguro)’을 2007년 인공교배 하였으며, 계통육종법을 통하여 ‘YS2000-2B- 11-5-1-2-1’을 선발하였다. ‘13~’14년도에 실시한 생산력검정시험에서는 만숙, 대립, 녹자엽 계통으로 유망하여 ‘밀양294호’의 계통명을 부여하고 ‘15~’17년 3년 간 전국 7개소에서 지역적응시험을 실시하였다. ‘청자5호’는 유한신육형, 엽형이 난형, 꽃색이 백색, 모용색이 갈색, 종실은 편구형이며 검은색 종피에 자엽색이 녹색인 고유 특성을 가지고 있다. 성숙기는 10월 24일로 표준품종인 ‘청자3호’에 비해 6일 늦은 만숙종이며 100립중이 37.0g인 대립종이다. 지역적응시험에서 ‘청자5호’는 ‘청자3호’ 보다 불마름병 및 콩모자이크바이러스에 강하였고, 밀식재배시 도복에 다소 약하였으나 시험포장과 건조기를 이용한 실내검정에서 ‘청자3호’ 보다 꼬투리 터짐에 매우 강한 특성을 나타냈다. ‘청자5호’의 수량성은 지역적응시험 7개소 평균 343kg/10a로 ‘청자3호(265kg/10a)’ 보다 30% 증수되었다. ‘청자5호’는 ‘청자3호’의 환경에 따른 종피의 열피(裂皮)현상을 없게 하고 ‘청자4호’의 종실크기를 크게 개량한 품종으로서 높은 수량성과 소비자의 기호도에 적합한 종실 품위를 가지고 있어 농가 소득 향상과 동시에 소비자의 기호를 만족시킬 수 있는 밥밑용 콩으로서 널리 소비될 것으로 기대된다.

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부분용 완전단감 ‘단연 09-12-1’ 육성

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경상남도농업기술원 단감연구소

단감의 주요 육종 목표는 만생종 ‘부유’에 비하여 수확이 빠르거나, 씨가 없거나, 고품질의 특성을 지니며 떫은맛의 우려가 없는 완전단감 품종의 육성이다. 완전단감은 열성 형질로 완전단감과 교배조합에 의해 출현될 확률이 월등히 높다. 고품질의 완전단감을 육성하기 위해서는 요구 형질을 지닌 고품질의 완전단감의 종류가 많아야 하지만 완전단감 품종의 수는 제한적이고, 그 중 부분으로 쓰일 수 있는 수꽃이 피는 완전단감 품종 수는 극히 일부이다. 그러므로 교배부분으로 쓰일 고품질의 완전단감 육성은 꼭 필요하다. 완전단감이면서 수확기가 빠르고 고품질의 특성을 지니는 수꽃이 피는 품종을 육성하고자 본 시험을 수행하였다. ‘단연09-12-1’는 2009년 완전단감 ‘양풍’과 ‘태추’를 각각 모본과 부분으로 교배하여 얻은 수꽃이 착생하는 완전단감 계통이다. 숙기가 10월 6일로 빠르고, 과중이 147g으로 중·소과에 속하지만 당도는 17 °Brix로 높고, 경도는 40 N 이상으로 ‘태추’ 18.3 N에 비해 육질이 단단하고 과피가 깨끗한 특징을 지닌다. ‘태추’를 부분으로 사용하여 육성된 계통에서 흔히 나타나는 과피오염이 거의 없다. 따라서 숙기가 빠른 고품질 완전단감 육종의 중간모본 및 부분용으로 사용 가치가 높고, 과육이 단단하므로 중·소과를 선호하는 수출용단감으로서의 효용 가능성도 있어 이 계통을 선발하였으며, 추후 세부특성조사 수행 후 품종보호출원 예정이다.

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칼라 찰옥수수 개발을 위한 다양한 색 여교잡 계통 육성

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찰옥수수 육종은 80년대 중반 이후 국내 재래종의 수집을 시작으로 분리, 교배 등의 과정을 거쳐 약 40년 정도 개량을 지속하였다. 품질과 도복 등 주요 형질에서 많은 성과를 거두었고 간식 또는 여름철 별미로 인기가 있어 옥수수 전체 재배면적의 약 60%정도를 점유하고 있다. 하지만 대부분 흰색 또는 검정색 품종개발에 집중되어 다양성이 부족한 실정이다. 찰옥수수 시장을 주도하는 미백2호 품종을 활용하여 보는 맛과 기능성을 높인 다양한 색의 미백2호를 개발하기 위하여 품종의 양친을 각각 반복친으로 3~4회 여교잡 하였고 최종적으로 고정된 다양한 색의 8계통을 선발하였다. 이들 여교잡 계통과 미백2호의 양친을 활용한다면 총 10계통(HW9 계열 4계통, HW3 계열 6계통)으로 미백2호와 유사한 다양한 색의 안토시아닌 품종을 개발할 수 있게 되었다. 기존의 품종은 대부분 종피 아래의 호분층에서 색깔이 발현되고 이 색깔은 수정 당시 화분 유전자의 영향으로 색이 변할 수 있는 특징이 있으나 새롭게 개발한 다양한 색의 계통은 안토시아닌 함량에 따른 색의 차이가 분명하게 나타나지만 수정 당시 화분 유전자의 영향을 받지 않는 종피에서 발현되는 특성을 가지고 있다. 따라서 호분층의 색에 영향을 줄 수 있는 화분유전자의 색유전자가 종피색보다 진하지 않다면 재배상의 품종간 격리가 필요 없게 된다. 그러나 종피에 발현된 안토시아닌 계열의 색은 손에 묻어나거나 증숙으로 쉽게 물로 용출되어 가공 또는 취식과정에서 다른 색과 분리해야 하는 특성이 있지만 진한 보라색의 경우 기존의 호분층에 침착하는 검정색 찰옥수수보다 10~25배 이상 함량이 높아 기능성으로 활용 가치가 높다.

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Development of *Tos17* insertion mutants from Korean domestic rice cultivars

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With the release of complete genome sequences in 2005, rice has become one of model systems for genomic studies of monocotyledonous plants. Aiming to improve agronomic traits through functional analysis of genes, we generated mutants via the insertion of *Tos17*, a mobile retrotransposon that is active during tissue culture. We used two Korean cultivars, *Oryza sativa* L. ssp. *japonica* cv. Ilmibyeo (IM) and Baegjinjuho (BJJ1), representing white and brown rice in the domestic market, respectively. We analyzed 7,608 flanking sequences of newly transposed *Tos17* insertions by the flanking adaptor-ligation PCR method. By applying this strategy, 1,672 and 843 mutants (M₂ generation) were produced in IM and BJJ1, respectively. The *Tos17* element was preferentially inserted into the genic regions (approximately 70%) of rice chromosomes. Among the 1,533 genes representing 2,515 domestic mutants, 830 genes harbored new mutations but not Nipponbare *Tos17* mutants. The phenotypes of the *Tos17* insertion lines showed three semi-dwarf mutants and various leaf type mutants, including those with narrow, pale green, and striped leaves at the vegetative stage. At the reproductive stage, 10 lines showed a 117~156% (2.9~3.9 g) increase in the 100-grain weight compared with that of the wild type. This study demonstrates the potential utility of *Tos17* mutants for the improvement of agronomic traits using domestic rice cultivars via an efficient tissue culture method with relatively little time and cost.

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최고품질 중만생 복합내병성 벼 ‘예찬’

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‘예찬’은 쌀 밥맛이 좋고 외관미질이 깨끗하고 병에 강하며 재배안정성이 높은 남부지역 적응 중만생 고품질 품종개발을 목적으로 국립식량과학원에서 2010/2011년 동계에 밥맛이 좋고 수량성이 높으며 내도복성이며 복합내병성인 호품을 모본으로 하고 중생종으로 밥맛이 좋고 쌀이 깨끗하며 흰잎마름병 K1, K2, K3, K3a에 강한 익산537호(해품)를 부분으로 교배하였다. 인공교배로 교배립 60립을 수확하였고 이 교배립은 세대진전을 위하여 2011년 하계에 국립식량과학원 벼육종포장에서 F1 30개체를 재배하였다. 우량품종을 조기 육성하기 위하여 F1개체에 대하여 약배양을 실시하여 2011/2012 동계에 분화된 식물체를 온실에 재배하여 임성이 정상인 124개체를 수확하였다. 2012년 하계에 포장에 AC1 세대 124계통 중 초형과 수량성, 미질, 잎도열병, 흰잎마름병검정을 실시하여 우수한 93계통을 선발하였다. 이 중 HR29177-AC73-2에 대하여 2013년과 2014년에 계통육성과 동시에 생산력검정을 실시하였고 생육특성, 수량성, 내병성(도열병, 흰잎마름병, 줄무늬잎마름병), 미질, 밥맛 등을 조사하여 내도복성이며 흰잎마름병 및 줄무늬잎마름병에 저항성이고 쌀 외관 품위가 우수한 HR29177-AC73-2-1 계통을 선발 ‘익산583호’로 계통명을 부여하였다. ‘익산583호’는 2015~2017년 보통기재배 전국11개소, 이모작재배 2개소에서 지역적응시험을 실시한 결과 수량성, 내병성(흰잎마름병, 줄무늬잎마름병)이 강하고 쌀 외관품위와 밥맛이 좋은 계통으로 2017년 12월 농촌진흥청 농작물직무육성 신품종선정심의회에서 그 우수성이 인정되어 품종명을 ‘예찬’으로 명명하였고 충남이남평야지 및 서남부해안지(충남, 전남북, 경남북)에 적응하는 품종으로 보급하게 되었다.

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An ERF family gene, *OsTF1*, plays functional roles in the control of plant growth and grain size in rice

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The ethylene response factor (ERF) genes that belong to APETALA2/ethylene-responsive element-binding factor (AP2/ERF) superfamily have a variety of functions in the transcriptional regulation of plant growth and development, and responses to biotic and abiotic stresses. We identified an ERF family gene, *OsTF1*, from rice. Sequence comparison conducted with two sequences of Arabidopsis ERFs classified as IXc subgroup revealed that *OsTF1* protein has 'EDLL' activation domain as well as highly conserved AP2 domain. Transgenic rice plants overexpressing *OsTF1* (*OsTF1-ox*) and *OsTF1* fused to EAR-repression domain (*OsTF1-SRDX*) were generated to demonstrate the functional role of *OsTF1*. The *OsTF1-ox* lines exhibited reduced height of plant, and this was recovered in the *OsTF1-SRDX* lines. This suggests that *OsTF1* may negatively affect plant growth. However, the grain size of *OsTF1-ox* lines was found to be enlarged compared to non-transgenic rice. The length and width of the grains of *OsTF1-ox* lines increased approximately 15% and 5%, respectively, resulting in a significant increase in grain weight. Scanning electron microscope (SEM) analysis revealed that the number of cells increased in lemma across the longitudinal axis, suggesting that *OsTF1* may play a role in the control of grain size in rice by regulating cell proliferation.

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자근 발생 감귤류의 조기 판별을 위한 SCAR마커의 개발

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제주도내 부지화[(*C. unshiu* × *C. sinensis*) × *C. reticulata*]를 포함한 감귤류(세포까, 탐나는봉, 청견)들을 재배하고 있는 대부분의 농가들은 감귤 대목으로써 탕자(*Poncirus trifoliata*)를 주로 사용하고 있다. 그러나 최근 이러한 탕자 대목에 접목된 부지화와 같은 감귤류의 접목부위에서 자근이 발생하여 착화 및 착과량이 감소하고 품질이 저하되는 문제가 발생하고 있으나, 정확한 자근 발생여부를 판별하는 것은 쉽지 않다. 따라서, 본 연구는 이 발생된 뿌리가 탕자인지 자근 인지를 단시간 내에 정확하게 판별 할 수 있는 SCAR 마커를 개발하기 위하여, SRAP F4/R15 프라이머를 가지고 착과량이 감소한 부지화의 자근 뿌리와 정상적인 탕자 뿌리로부터 추출한 DNA에 대하여 PCR를 수행하여 자근 뿌리에서만 특이적으로 증폭된 산물에 대하여 염기서열을 분석하였다. 또한, SCAR 프라이머의 조합은 분석한 염기서열을 기초로 하여 자근 품종에서만 특이적으로 증폭되도록 9조합으로 제작하였으며 이들 9조합 중 자근의 발생으로 문제가 되는 품종(세포까, 탐나는봉, 청견)에서만 특이적으로 증폭되는 5개(P1, P2, P3, P4 그리고 P6)의 SCAR 마커를 얻었다. 그리고 이 선발된 SCAR 마커는 제주도내 농가에서 널리 재배되고 있으며 자근발생으로 심각한 문제가 대두되고 있는 부지화 나무 12주에 대하여 정확한 판별이 가능하였다. 따라서, 이 선발된 SCAR 마커의 개발은 자근 발생으로 인하여 문제화 되고 있는 감귤류들을 단시간 내에 정확하게 판별 할 수 있으며 이를 기초로 하여 개선된 재배기술 방법을 적용함으로써 정상적인 착과량을 갖도록 관리체계를 개선할 수 있을 것으로 기대된다.

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Antioxidant activity of Korean black soybean (*Glycine max.* L.) landraces

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Black soybean has been used as a food source in traditional medicines because their seed coats contain natural phenolic compounds. The objective of this study is to reveal the genetic variation on the antioxidant activity present in the 203 Korean black soybean landraces. Antioxidant activity of 203 Korean black soybean landraces was evaluated with DPPH, ABTS, ferric reducing antioxidant power (FRAP), and total phenolic contents (TPC) in 2012 and 2015, respectively. The antioxidant activities assessed by DPPH, ABTS, FRAP, and TPC assays showed wide variation among accessions and years, respectively. Using the relative antioxidant capacity index, we found that the IT178047 had the highest antioxidant activity. In correlation analysis, days to 50% flowering (DF) and 100-seed weight (SW) showed the positive and negative correlations with antioxidant activity, respectively. In clustering analysis, 203 Korean black soybean landraces were classified into five clusters. Among them, cluster I contained 10 accessions with higher antioxidant activities, smaller SW, longer DF and days to maturity than other accessions. It is anticipated that our results will expand the antioxidant activity database and provide information on Korean black soybean landraces which could be valuable for development of new soybean varieties.

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Classification of *Aegilops* genus based on pollen morphology

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Aegilops is closely related to *Triticum*. It is rich in genetic diversity which can be used as a donor material for wheat breeding. There is high ambiguity in the classification of *Aegilops*. Thus, it is crucial to conduct further investigation on classification of *Aegilops*. The pollen morphology based on LM quantitative pollen characteristics among 12 species of *Aegilops* was observed. The pollen parameters in the *A. bicornis*, *A. columnaris* and *A. juvenalis* species showed taxonomic value in discriminant analysis. However, significant difference was not found between and other types of *Aegilops*. Clustering analysis based on quantitative pollen characteristics showed a correlation with classification based on morphological data. This study provided the basis for interspecific classification among the species in the genus *Aegilops*. The basis for the interspecific classification of the genus *Aegilops* was provided.

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Distribution of α -tocopherol content in the Korean landrace black soybean

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Korean landrace black soybeans (*Glycine Max L.*) are rich in antioxidants, minerals, proteins and fats. The fatty components of black soybean include fatty acids and vitamin E, a fat-soluble vitamin. Vitamin E refers to α -tocopherol. Among the eight tocopherol isomers, it has the highest antioxidant activity in the body. α -tocopherols, like other antioxidants, prevent cancer and cardiovascular disease. We cultivated 225 Korean landrace black soybeans, which were collected in 2015 at the National Agrobiodiversity Center. The harvested seeds were re-cultivated in 2017 to determine the α -tocopherol content. The average amount of α -tocopherol was 211.7 ± 187.3 mg% and 336.2 ± 224.1 mg% in 2015 and 2017, respectively. In 2015, the highest α -tocopherol content, 1082.2 mg%, was found in IT177459 and the lowest amount, 7.8 mg%, was in IT177220. However, IT178011 showed the highest α -tocopherol content, 1281.8 mg%, while IT177390 showed the lowest, 115.3 mg% in 2017. In comparison to the three standard soybean cultivars, Geomjeongkong 1, Cheongjakong 3, Ilpumgeomjeongkong, which contained respective α -tocopherol content of 692.2 mg%, 414.8 mg% and 415.5mg%, 9 accessions showed higher content of alpha tocopherol. The highest content was found in IT177459 (968.5mg%), followed by IT177305 (864.2mg%), IT177467 (831.8mg%), IT177504 (779.9mg%), IT177485 (746.8mg%), IT178011 (746.6mg%), IT 177573 (744.4mg%), IT177573 (742.1mg%) and IT177530 (727.6mg%). The α -tocopherol content data of Korean landrace black soybeans could contribute to the nutritional evaluation of genetic resources.

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ICRISAT의 유전자원 관리 현황 및 핵심집단 구축

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국제반건조열대작물연구소(ICRISAT)는 UN의 국제농업개발연구자문기구(CGIAR) 산하 연구기구로서 조, 수수, 기장, 병아리콩, 땅콩 등 11개 작물에 대한 유전자원을 보존 및 관리하는 기관으로 약 12만여 점의 유전자원을 보유하고 있다. ICRISAT의 자원 분양패턴을 보면 각 작물별 총 보유자원중 80%이상이 분양이 되고 있어서 이상적인 유전자원 보존 및 관리의 방향을 제시하고 있다. ICRISAT에서는 모집단의 10%이하의 자원으로 전체의 80%이상의 변이를 대변 할 수 있는 핵심집단과 핵심집단의 10%이하의 자원으로 구성된 미니핵심집단을 작성, 활용하고 있다. ICRISAT에서는 병아리콩 1,956자원, 땅콩 1,704자원, 비둘기콩 1,290자원, 진주조 2,094자원, 수수 2,247자원, 손가락조 622자원, 조 155자원 수준의 핵심집단을 작성하여 작물 육종 프로그램에 활용 중이다. 또한 병아리콩 211자원, 땅콩 184자원, 비둘기콩 146자원, 진주조 238자원, 수수 242자원으로 미니핵심집단(핵심집단의 10%내외, 전체모집단의 1%내외)을 작성하여 육종 프로그램에 활용 중이다. ICRISAT에서는 핵심 집단 및 미니 핵심 집단을 찾기 위한 평가를 지속적으로 수행중이며 이 중 19세트의 핵심집단과 84세트의 미니 핵심 집단은 20여개국의 연구자들에게 분양되었고 수량 및 품질 향상, 내재해성 도입 등의 육종 프로그램에 활용되었다. ICRISAT는 유전자원의 특성평가에 각 작물별 특이적으로 개발된 특성조사표를 이용하고 있으며 사용자가 필요로 하는 유용한 특성정보를 제공하고 있으며 이는 품종개발 등 이용성이 높을 것으로 판단된다. 또한 ICRISAT에서 개발한 미니핵심집단의 개념은 작물육종프로그램에 있어 유전자원의 이용을 강화시키는 목적으로 연구자들에게 인식되어지고 있어 제한된 종자로 구축한 핵심 집단 및 미니 핵심 집단이 육종가들의 연구와 훈련에 유용할 것이라 생각된다.

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Morphological characteristic of seed traits among the *Vicia* species

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The National Agrobiodiversity Center (NAS, RDA, Republic of Korea) has been collecting the new valuable genetic resources continually. In this study, we collected 44 *Vicia* spp germplasm which includes wild type *Vicia* species in Korea. Genus *Vicia* is most popular as manure crops and cover crops in orchards. However, there are few studies on seed morphological characteristics. Therefore, we investigated the characteristics and diversity of seeds in order to provide basic information for its usage in breeding of agricultural traits. We investigated the morphological characteristics of *Vicia* seeds on the basis of 9 morphological traits (seed shape, seed color, seed surface, seed colour mottling, hilum shape, hilum colour, hilum length, seed length and seed width). Seeds size were spherical (45.5%) cubical (40.9%), and elliptical (13.6%). Seed color was black (47.7%), brown (22.7%), red-brown (11.4%), yellowish (15.9%), and Apricot (2.3%). Hilum shape was linear (79.5%), oblong (6.8%), and oval (13.6%). Principal component analysis (PCA) showed four principle components included PC-I (30.7%), PC-II (17.7%), PC-III (14.1%), and PC-IV (11.3%). Cumulatively, the four components explained 73.8% of total variations. The cluster analysis based on morphological characters detected 5 main clades. This study provides the key insights to the characteristics of *Vicia* seeds and a basis information with *Vicia* spp. which could be useful for bio-industry.

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Application of AFLP and CAPS Markers to Screen Somaclonal Variations among Diploid and Autotetraploids of Small Watermelons

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Autotetraploids could be obtained spontaneously from the *in vitro* cultured cotyledon explants of small watermelons. Phenotypic dissimilarities observed in leaf size, reduction of fruit length and seed size and number of autotetraploid regenerants compared to its diploid donor plant suggesting a possibility of genetic alterations led to somaclonal variations or changes in genetic levels. Using AFLP and CAPS markers to analyze somaclonal variations between diploid donor plants and autotetraploids revealed a high polymorphism (64%, AFLP) and genetic alteration in gene control of fruit shape (CAPS). According to AFLP analysis, the highest number of fragments was found in diploid donor plants while all autotetraploid lines reduced approximately 6-27% of fragments in comparison to its diploid donor plant. The losses of fragments and genetic variations among diploid and autotetraploids clearly revealed genetic alterations during *in vitro* culture. UPGMA cluster analysis showed a significant separation between diploid and two groups of autotetraploids, indicating that AFLP is efficient for identifying the somaclonal variants. It may be the first report of using AFLPs and CAPS to identify somaclonal variations causing genetic changes in autotetraploids of small watermelon.

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The complete chloroplast genome of *Panicum sumatrense* Roth ex Roem. & Schult. using illumina sequencing

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Little millet, *Panicum sumatrense* Roth ex Roem. & Schult., is an important cultivated species under the tribe Paniceae, sub-family Panicoideae and family Poaceae. In this study, we sequenced the complete chloroplast (cp) genome of *P. sumatrense* for the first time to investigate their phylogenetic relationship in the family Poaceae. The complete cp genome sequence of *P. sumatrense* is 139,384 bp in length with 38.6% overall GC content and exhibits a typical quadripartite structure comprising one pair of inverted repeats (22, 723 bp) separated by a small single-copy region (12,583 bp) and a large single-copy region (81,355). The *P. sumatrense* cp genome encodes 125 unique genes, which include 91 protein-coding genes, 4 rRNA genes, 30 tRNA genes and 20 genes were duplicated in the inverted repeat region. This newly determined cp genome (*P. sumatrense*) could be valuable information for the breeding programs of this cereal crops in the family Poaceae.

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콩의 성숙조절 관련 유용 유전자 선발 및 발현특성 분석

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콩의 기계화 수확효율을 증진시키기 위해서는 꼬투리와 줄기, 잎이 동시에 성숙하는 품종의 개발이 필요하다. 콩에서 개화조절에 관련된 유용 유전자에 대한 연구는 다양하고 심도있게 진행되어졌지만 성숙조절에 관련된 유전자의 연구는 미흡한 편이다. 본 연구는 콩의 꼬투리 성숙관련 유전체를 분석하여 성숙관련 기능을 갖는 유전자를 선발하고, 콩의 부위별 발현분석을 통해 평가된 유전자를 동시성숙성이 높은 콩 품종개발을 위한 육종소재로 활용하고자 실시하였다. 발현분석용 콩 식물재료로는 대풍콩을 비롯하여 성숙기가 다른 18품종을 선발하였고, 각 품종은 꼬투리, 줄기, 잎으로 분리하여 유전자 발현분석에 이용하였다. 이미 알려진 178개 꼬투리 성숙관련 유전자좌(QTL) 영역내에 2,600여종의 유전자가 존재함을 확인하였고, 유전자들의 ontology를 분석하여 560종의 유전자가 seed development 등 성숙관련 기능을 갖는 것으로 확인되었다. 유전자의 발현분석을 위해 실시간유전자발현분석장치(realtime PCR)와 성숙관련 기능을 갖는 것으로 확인된 560종의 유전자중 염기서열 정보가 확인된 215종 유전자를 이용하였다. 부위별로 발현의 양상이 달라진 유전자는 seed development 기능을 갖는 Glyma.19G212200.1를 비롯하여 102종 이었고, 특히 senescence-associated 기능을 갖는 Glyma.06G272800.1 등 21종의 유전자는 만숙종인 대풍콩 보다 3부위 모두에서 발현이 2배이상 증가하였다. Response to stress 기능을 갖는 Glyma.19G193800.1 등 28종의 유전자는 조숙종에서 만숙종으로 갈수록 유전자의 발현이 증가하였고, oxidation-reduction process 기능을 갖는 Glyma.18G257600.1 등 17종은 그 반대의 발현양상을 보였다. 이런 결과를 통해 3부위 모두 발현이 2배이상 증가하는 유전자 Glyma.06G272800.1 등 21종을 동시성숙성이 높은 콩 품종개발을 위한 육종소재로 선발하였다.

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고추 shed-소포자 배양 시 배지내 pH 및 품종이 배 발생 효율에 미치는 영향

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고추에서 품종육성 연한 단축을 위한 반수체 육종법 중 하나인 약배양 기술은 국가연구기관 및 민간 종자회사에서 실제 품종 육성과정 중 중요한 단계로 자리매김하고 있으며 각 연구기관 및 회사 자체 내에서 고유 프로토콜을 보유하고 있다. 최근에는 약배양보다 배가 반수체 획득 효율이 높은 것으로 알려진 소포자 배양 기술에 대한 연구가 진행되고 있다. shed-소포자 배양기술은 고체배지와 액체배지를 동시에 이용하는 변형된 약배양으로 고추에서 다수의 배를 확보할 수 있는 방법이다. 본 연구에서는 고추의 shed-소포자 배양기술 확립을 위해 배지의 pH 및 품종이 소포자배 발생에 미치는 영향을 조사하였다. 밀양재래와 고색소 품종인 7QF4, 7QF9, 7QF36, 7QF38 등 총 5품종을 재료로 이용하였으며, 각 품종에 적합한 pH를 조사하였다. 밀양재래 품종은 전처리 배지와 배양배지 모두 pH 6.0일 때 소포자배 발생 효율이 가장 높았으며, 발생된 배의 총 수 또한 가장 많았다. 7QF4, 7QF9 품종의 경우에는 소포자배 발생 효율 및 배의 총수 모두 전처리 배지로 pH 8.0을 사용하고, 배양배지의 pH를 4.0으로 조절하여 사용한 경우 높았으나 7QF36, 7QF38 품종의 경우에는 각각 다른 경향을 나타내었다. 5가지 품종을 대상으로 비교한 결과 최적 pH가 각기 달랐으며, 소포자배 발생효율 및 배발생 총 수 모두 품종에 따른 차이가 크게 나타났다. 고추 shed-소포자 배양 시 품종이 소포자배 발생 및 발달에 미치는 영향을 조사하고자 12개의 품종을 대상으로 shed-소포자 배양을 실시한 결과 1개의 꽃봉오리에서 1개 이상의 배가 발생한 효율은 LV2319, ECO-1, 7QF4, 7QF9 순으로 각각 95.8, 92.6, 60.8, 48.0%로 높았으며, 중간교잡 F₁ 품종인 16NHC 품종의 경우 배가 전혀 발생하지 않았다. 반면 발생한 배의 총 수는 LV2319, ECO-1, 밀양재래, 7QF4 순으로 각각 24.8, 7.3, 6.3, 3.2개였다. 본 연구결과 고정종인 LV2319와 밀양재래 품종의 경우 배 발생이 높은 것으로 나타났으며, F₁ 품종들에서는 배 발생 효율이 전반적으로 낮게 나타났다. 향후 계속된 연구를 통해서 형질 고정 정도 및 품종 특성이 소포자배 발생에 미치는 영향에 대한 조사가 필요할 것으로 판단된다. 본 연구결과들은 shed-소포자 배양을 통해 반수체 및 배가 반수체를 생산하기 위한 연구의 기초자료로 이용될 수 있을 것으로 기대한다.

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쌀 도정특성 및 입형과 연관된 양적형질 분석

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우리 쌀의 도정수율 향상을 위하여 쌀 도정특성 및 입형을 분석하고 이와 연관된 분자마커를 발굴하여 분자유종에 적용해 보고자 본 연구를 수행하였다. 연구결과를 요약하면 우선, 이삭특성과 등숙율 및 도정수율과 상관성을 분석한 결과, 등숙율은 2차 지경 등숙율과 정의 상관의 유의성(0.764**) 인정되었고, 도정수율은 주당수수와 정의 상관의 유의성(0.711**) 인정되었다. 따라서 등숙율과 도정수율을 높이기 위해서는 2차 지경 등숙율이 높고, 주당 수수가 많은 것이 좋은 것으로 나타났다. 다음으로, 도정특성 및 종자특성에 대한 QTL 분석결과, LOD 값이 3.0이상으로 설명력이 10% 이상인 형질은 정현비율, 현미 천립중, 길이, 너비, 현미 장폭비 이었다. 특히 현미 너비와 장폭비, 현미천립중과 관련된 QTL은 동일 위치의 RM03328마커로 나타났으며, LOD 값이 15.0과 13.0, 6.55로 설명력이 39%와 35%, 20%로 높아 실용적인 QTL 마커로 활용성이 예상된다. 또한, 정현비율과 관련된 QTL도 LOD 값이 4.54로 설명력이 14.1%로 나타나 등숙률과 도정수율이 높은 우량계통 육성을 위한 분자유종에 적용가능성을 확인하였다. 이런 결과들로 볼 때 설명력 높은 QTLs 연관 분자마커 활용으로 등숙률과 도정수율이 향상된 품종육성이 가능할 것으로 기대된다.

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국내 육성 종실용 옥수수의 밀식적응성 평가

류시환*, 박종열, 최재근, 남궁민, 최승출, 김문종, 용우식, 윤석원, 남경남, 박기진, 최준근

강원도 홍천군 두촌면 장남길 26 강원도농업기술원 옥수수연구소

옥수수는 세계에서 가장 중요한 식량공급원 중의 하나이며, 유전 육종적 방법의 발달과 함께 획기적인 생산성 증대의 본보기이다. 단위면적당 재식밀도의 증가는 옥수수 생산량 증대의 또 다른 중요한 요인이다. 미국 corn belt 지역의 재식밀도와 수량성 변화를 보면, 1930년대에는 ha당 3만주 파종하여 1.6톤을 수확하였으나, 현재는 ha당 8만주 이상 파종하여 9.5톤을 수확하고 있다. 그러나 국내에서는 ha당 5.5 ~ 6.6만주가 일반옥수수 표준 재식밀도이다. 수량성 증대를 위해서는 세계적인 재배양식에 따라 밀식하는 것이 필요하다. 국내 육성 종실 및 사료용 옥수수 품종과 밀식적응성이 우수한 수입 품종을 비교하여 국내 품종의 밀식적응성을 평가하고자 본 연구를 수행하였다. 밀식재배시 수입품종과 국내 육성품종의 수량성을 비교해본 결과, 수입품종(32W86)의 수량성을 100으로 할 때, 국내품종의 수량성은 71 ~ 93의 수준이었다. 시험한 국내 육성품종 중에서 밀식적응성이 가장 우수한 교잡종은 종교128호이며, 수량성은 32W86 대비 93 수준이었다. 밀식과 표준 재배에서 국내육성 품종의 수량성 및 생육특성을 비교해본 결과, 밀식에서 수량성이 28% 증수하여 표준보다는 밀식재배가 수량 증대효과가 있는 것으로 확인되었다. 밀식재배의 경우 도복에 약하였고, 간경, 이삭길이, 이삭폭 및 100립중은 표준 대비 감소하였다. 국내 육성품종은 표준 재식밀도에서 선발되었으므로 밀식적응성이 수입품종에 비해 낮은 것은 당연한 결과로 판단된다. 향후 세계 수준의 옥수수 생산성을 위하여 국내에서도 밀식재배에 관심을 가지고 밀식적응성 품종 육성에 노력해야할 것으로 생각되며, 밀식적응성 품종육성은 유전자원의 개량뿐 아니라 도복 등 환경스트레스 저항성 선발이 선행되어야 할 것으로 판단된다.

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Development of CAPS marker for identification of *Lentinula edodes* cultivars Sanmaru 1ho and Sanmaru 2ho

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Lentinula edodes is one of the most popular edible mushrooms in the world. Recently, the breeding and development of new cultivars of *L. edodes* have been actively facilitated, and thus the development of efficient molecular markers that can distinguish the new cultivars is required for protection of the breeder's rights. In this study, we developed cleaved amplified polymorphic sequence (CAPS) markers for the identification of *L. edodes* cultivars Sanmaru 1ho and Sanmaru 2ho. These markers were developed using whole genome sequence data from monokaryon strain B17 and resequencing data from other strains. A single nucleotide polymorphism (SNP) was identified on the 1630048 position of scaffold 9 in Sanmaru 1ho and on the 1803483 position of scaffold 2 in Sanmaru 2ho. DNA containing each SNP in each strain was amplified, and Sanmaru 1ho and Sanmaru 2ho was not cleaved by restriction enzyme TspR I and HhaI respectively. Therefore, Sanmaru 1ho and Sanmaru 2ho were distinguished from other cultivars.

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국내 잡초벼 유전적 배경의 고양식미 우량계통 육성

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전라북도 완주군 이서면 혁신로 181 농촌진흥청 국립식량과학원

우리나라의 밥쌀용 벼 품종은 유전적 배경이 협소하므로 식미를 다양화하기 위해 고유 유전자원인 재래벼와 잡초벼를 활용한 최고 밥맛의 고품질 벼 품종 개발이 시급하다. 유전적 배경이 다양한 중생의 고양식미 품종 개발을 위해 우리나라 잡초벼와 화영벼를 교배하여 육성한 F₅ 세대 16계통을 생산력검정 예비시험에 공시하였다. 화영/횡성앵미3 조합 7계통과 화영/나주앵미15 조합 5계통, 화영/남제주앵미6 조합 4계통에 대하여 주요 농업적 생육특성, 내병성, 미질 및 식미특성을 대비 품종인 남평, 화영 등과 비교하였다. 공시한 16계통 중 농업적 특성이 우수하고, 특히 미질과 밥맛 및 식미 관련 마커를 통한 기대식미치를 종합적으로 평가한 결과 화영/횡성앵미3 조합 2계통(HR31025-12-2-1, HR31025-18-4-1), 화영/나주앵미15 조합 2계통(HR31027-3-3-1, HR31027-26-1-1), 화영/남제주앵미6 조합 2계통(HR31035-2-3-1, HR31035-13-2-1) 등 6개의 우량계통을 선발하였다. 선발한 우량계통들은 대부분 출수기가 8월 7일부터 8월 11일인 중생종에 속하였으며 수량성은 화영에 비하여 11~20% 높았으나 남평과는 유사하거나 다소 낮은 특성을 보였다. 내병성은 도열병의 경우 중도 저항성을 보였고 흰잎마름병(K1~K3)과 줄무늬잎마름병에는 강하였다. 쌀알은 맑고 투명하며 백미 완전미율과 윤기치는 대비 품종과 유사하였으나, 식미 관련 13개의 마커를 이용하여 회귀식으로 추정된 기대 식미치는 74.3~93.3으로서 대비 품종인 남평의 56.8과 화영의 74.3보다 높았다. 그리고 식미패널에 의한 밥맛은 남평(0.00)과 화영(0.14)에 비하여 월등히 좋은 결과(0.33~0.52)를 보였다. 특히 화영/횡성앵미3 조합의 HR31025-12-2-1과 HR31025-18-4-1 계통은 기대식미치가 각각 83.4, 93.3으로 높으면서 밥맛도 0.45와 0.52로서 가장 우수한 특성을 보인 유망계통이었다. 앞으로 「유전자원 접근·이익 공유법」에 따른 자국 생물자원에 대한 주권을 강화하려는 국제적 추세에 대응하기 위해서는 국내 고유 유전자원을 이용한 밥맛 관련 원천 소재 확보가 매우 중요하기 때문에 본 연구에서 선발한 6개의 우량계통을 2018년 생산력검정 본시험에 공시한 후 지역적응시험을 거쳐 고양식미 품종으로 개발할 예정이다.

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Development and characterization of *japonica* rice line with long and spindle-shaped grain

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To enhance rice yield and diversify grain quality of Korean *japonica* rice, we developed *japonica* rice line with long and spindle-shaped grain. Korean *japonica* rice cultivars have narrow genetic background of grain size and shape. Most of cultivars show medium-short and semi-round grain. To diversify the genetic background for grain, we developed Jeonju625, *japonica* rice line with long and spindle-shaped grain, derived from a cross between DSG79, the breeding material with extra-long and spindle-shaped grain, and Boramchan, *japonica* super high-yielding cultivar with medium-short and semi-round grain. Jeonju625 had *GW2gs3qSW5+qGL3* allele type for grain-related genes, which conferred extra-long and spindle-shaped grain. The grain length and ratio of length to width of brown rice of Jeonju625 was 7.06 mm and 2.72, respectively. Jeonju625 was improved the deteriorated traits of DGS79, very late heading, long culm, long awn, droopy flag leaves, and susceptibility to lodging, by strong selection pressure focused on field breeding. The milled rice yield of Jeonju625 was 559 kg/10a, which was similar level of Boramchan (552 kg/10a) and 29% enhanced yield compared to DSG79. Jeonju625 had suitable characteristics for cooked rice. Jeongju625 showed lower protein contents and better glossiness and palatability of cooked rice than Boramchan and Hanareum2. Elite *japonica* rice line, Jeonju625, with extra-long and spindle-shaped grain showed good characteristics for rice yield and grain quality. Jeonju625 could be utilized practical cultivar and breeding material for enhancing rice yield and diversifying grain quality.

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군집소수를 가진 고착립밀도 이삭형 벼 개발 및 특성분석

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전라북도 완주군 이서면 혁신로 181 농촌진흥청 국립식량과학원

우리나라 자포니카 벼의 잠재 수량성 향상을 위해서 군집소수를 가진 고착립밀도 이삭형 벼를 개발하였다. 교배모본으로 ‘빈해수집 1’(IT251527)과 ‘ARC10319’(IT259789)를 이용하여 단교잡 인공교배하였다. 빈해수집1은 강한 도복저항성에 이삭목이 굵고 이삭 내 착생립수가 많아 착립밀도가 큰 고착립밀도형 이삭형태를 가지고 있으며, ARC10319는 키가 크고 이삭 내 지경의 선단 소수가 2-5개씩 군집되어 있는 군집소수형 이삭형태를 가지고 있다. 빈해수집1/ARC10319와 보람찬/ARC10319 F₂ 집단을 이용한 군집소수형 이삭에 대한 유전분석 결과 군집소수형 이삭은 하나의 우성유전자가 불안정하게 관여하는 1:2:1의 분리비를 나타냈다. 분리세대에서 군집소수 고착립밀도 이삭을 가진 개체를 선발해나가면서 고정계통을 육성하였다. 예비선발시험에서 F₈세대 23개 군집소수 고착립밀도 이삭형 계통을 선발하였고, 이들의 이삭관련 형질에 대해서 모부분 및 우리나라 178품종(자포니카 160품종 및 통일형 18품종)과 비교분석하였다. 군집소수 고착립밀도 이삭형 계통들은 주간의 수당립수가 482개(385-581개)로 빈해수집1(342개), ARC10319(302개), 자포니카(151개, 105-236개) 및 통일형(217개, 179-281개) 품종보다 다립인 이삭형태를 나타냈다. 모부분에 비해 1차 지경수와 평균립수는 비슷하거나 중간 값을 가지나 이삭목이 두껍고 2차 지경수와 평균립수가 많아 수당립수가 증가하였다. 수당립수가 증가한 반면 이삭길이는 줄어들어 착립밀도가 증가하였고, 착생립의 임실률은 육성품종에 비해 크게 떨어지는 특성을 나타냈다. 23개 계통 중 농업형질이 양호하고 수당립수가 증가된 4계통(CD9, CD27, CD34, CD39)을 선발하여 남평, 보람찬, 한아름2호, 모부분과 함께 생산력검정시험을 수행하였다. 이들 계통들의 평균 수당립수는 252-277개로 남평(93개), 보람찬(96개), 한아름2호(114개), 빈해수집1(144개), ARC10319(161개)에 비해서 증가하였으나 수수가 9개로 적고(남평 15개, 보람찬 16개, 한아름2호 16개, 빈해수집1 9개, ARC10319 10개) 등숙률이 61.8-67.6%(남평 89.1%, 보람찬 89.6%, 한아름2호 88.3%, 빈해수집1 80.4%, ARC10319 86.4%)로 낮아 쌀 수량성은 404-515 kg/10a로 모부분인 빈해수집1(429 kg/10a)과 ARC10319(345 kg/10a)에 비해 증가하였으나 남평(502 kg/10a), 보람찬(554 kg/10a), 한아름2호(766 kg/10a)에 비해 적었다. 개발된 군집소수 고착립밀도 이삭형 계통은 수당립수를 증가시킴으로써 잠재수량성을 높인 자원으로 수당립수 증대를 위한 육종소재로 활용될 수 있을 것으로 생각된다.

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곡실사료 및 조사료 겸용 조생 사료용 벼 ‘조농’

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‘조농’은 쌀의 공급과잉에 따른 논 이용 다양화와 사료의 자급률을 높이기 위해 개발되었다. ‘조농’은 지금까지 개발된 사료용 벼 8품종 중 이삭 패는 데 걸리는 기간이 가장 짧은 조생 품종으로 높은 수량성을 가지고 있으며 쓰러짐에 강하여 직파재배를 이용한 맥류의 뒷그루 재배가 가능하다. 2010/2011년 동계에 초기신장성이 좋고 도복에 강한 고바이오매스 준조생 유전자원 ‘빈해수집 1(IT251527)’을 모본으로 하고 자포니카 초다수성 품종으로 소열 수중형 초형에 도복에 강한 중만생 품종인 ‘드래찬’을 부분으로 하여 단교잡 인공교배하였다. 고정계통을 조기에 확보하기 위해서 2011년 하계에 F₁ 식물체의 이삭을 채취하여 약배양을 수행하였다. 2012년 210개 약배양 계통 중 출수가 빠르고 바이오매스가 큰 계통을 선발하여 2013-2014년 생산력검정시험을 수행하였다. 공시 계통 중 조생종이면서 초기신장성이 빠르며 바이오매스가 크고 강한 내도복성을 가지고 있는 HR29675-AC10 계통을 선발하여 ‘익산581호’로 계통명을 부여하였다. ‘익산581호’는 2014-2016년 3년간 실시된 사료용벼 지역적응성 검정시험 결과 출수기가 평균 8월 1일로 기존의 사료용 벼 중 가장 빠른 ‘녹양’의 8월 12일에 비해 10일 이상 빠르면서도 조사료 수량은 1,476kg/10a(녹양 대비 99%)로 비슷하고 정조 수량은 807kg/10a로 ‘녹양’보다 12%가 증수되어 높은 수량성을 나타냈다. 또한 가축이 소화 흡수할 수 있는 사료의 영양가 지표를 나타내는 가소화양분총량(TDN)이 ‘녹양’과 같은 70.2%로 사료가치가 우수하여 2016년 12월 직무육성 신품종 선정위원회에서 사료용 신품종으로 선정되었고 조생종이면서 조사료와 농후사료에 겸용으로 활용될 수 있다는 의미로 ‘조농’으로 품종명을 명명하였다. 사료용 벼 ‘조농’은 밥쌀용 벼 대체 작물로 논 이용 다양화와 사료의 자급률 향상에 기여할 것으로 기대된다.

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국내 육성 벼 품종과 수입쌀 판별을 위한 분자마커 세트 개발

박슬기, 이건미, 이효정, 백만기, 박현수, 남정권, 김춘송, 김보경, 조영찬*

전북 완주군 이서면 혁신로 181 국립식량과학원 작물육종과

쌀 관세화에 의한 쌀시장 개방으로 수입쌀 부정유통 방지를 위해 국내 육성 벼 품종과 수입 예상국가의 쌀에 대한 분자표지를 활용하여 품종판별 체계를 확립하고자 본 연구를 수행하였다. 공시재료는 국내 육성 벼 320 품종과 수입가능 외국 브랜드쌀 40종, 일본 주요 자포니카 16 품종의 시료를 활용하였다. 식미관련 마커, 도열병 저항성 연관 마커와 수입 브랜드 쌀의 re-sequencing 정보를 활용하여 개발한 마커 중 42개를 선발하여 품종판별 DB를 구축할 수 있었다. 이들 마커 중 재현성과 다형성이 높은 SNP_1T, SNP_5T, krif6, krif64, ImMF136, ImMF155, GPA 7개의 마커 세트로 국내 벼재배면적을 많이 차지하는 국내 자포니카 34 품종과 수입가능 외국 브랜드쌀 40종, 일본 자포니카 16품종을 분석한 결과, 국내 육성 품종과 외국 품종을 구분할 수 있었다. 그러나, 오묘벼 등 6개 국내육성품종은 외국품종과 그룹화되었고, 수입 브랜드쌀 B3 등 4 품종은 국내육성품종과 그룹화되었다. 국내육성품종과 외국품종을 명확하게 구분할 수 있는 최적의 분자마커조합을 개발하기 위해서는 추가적인 마커선발이 필요하다.

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고품질 기계화 적응성 수수 신품종 “황금찰수수 2호”

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최근 웰빙 문화의 확산으로 건강과 질병의 예방 및 치료에 대한 소비자의 관심이 증가하면서 건강기능성 식품에 대한 수요도 증가하고 있다. 특히 수수는 곡류 중 탄닌을 함유하는 유일한 작물로서 다양한 생리활성을 갖는 폴리페놀을 함유하고 있어 건강기능성 식품 원료로서의 이용 가능성이 매우 크다. 그러나 원료곡 생산 시 생력재배를 위한 간장, 경태, 성숙기 및 콤팩인 수확 수율 등에서 개선이 필요한 것 또한 사실이다. 따라서 생력재배가 가능하며 소비자들의 기호 및 수요에 알맞은 수수 신품종 “황금찰수수 2호”를 육성하였다. 육성모본으로는 강원지역 수수 주산지의 주재배품종인 “황금찰수수”와 울산지역 수집종(IT028592) 분리계통인 강원 190호를 이용하였다. 육성목표는 콤팩인 수확이 가능한 간장, 출수기 등의 생육특성과 소비자 선호 건강기능성인 항산화성분 및 항산화활성 등이었으며, 육성과정 중 농업현장에서 실증비교시험을 수행하였다. 육성과정은 2004년 인공교배 후 2010년까지 후대를 양성하며 선발과정을 거쳤고 2011년부터 2012년까지 생산력을 검정하였다. 2016년부터 2017년까지 강원지역 춘천 등 3개소에서 지역적응성을 검정하였으며, 2017년 생력재배를 위한 농업현장 비교 시험을 수행하였다. “황금찰수수 2호”는 다수성이며 콤팩인 수확이 가능한 밀수형 이삭으로 찰성배유를 가지며 붉은색 종피의 혼반용 품종이다. 가변특성으로 간장 146cm, 이삭장 24cm, 천립중 26g으로 출수기가 8월5일이다. 생력화를 위한 자탈형 콤팩인 수확 농가실증 시험에서 수량성은 390kg으로 파종부터 수확까지 생력화 재배가 가능하였다. 소비자가 선호하는 특성 중 품질특성은 아밀로펙틴 함량이 90.43%로 찰성배유이며, 무기성분 중 칼슘은 15.58mg/100g, 칼륨은 434mg/100g이었다. 항산화성분에서 폴리페놀은 1256.38mg/100g, 플라보노이드 2864.99mg/100g, 수용성 탄닌 1503.75mg/100g 이었으며, 항산화활성은 DPPH 0.31±0.02, ABTS 2012±0.51로 매우 높은 기능성 수수 품종이다.

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Adaptability and clonal selection of poplar clones to combat desertification in arid area of Mongolia

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The objective of this study was to select poplar clones with high adaptability and potential for advanced growth for combating desertification in Elsen tasarkhai an arid and semi-arid area in Mongolia. After the establishment of the research site in Elsen tasarkhai, the first screening was conducted on 22 types of poplar clones. Based on the survival rate in the second year, DN 002, DN 247, DN 034, DN sim, TN 074, *P. sibirica*, *P. simonii* were selected for further studies. Studies on the morphological factors for clonal selection of the introduced poplar clones included measurement of survival rates, the relative growth rate of heights, collar diameter, characteristics of leaves, dry weights and differences of T/R ratio. As for physiological features, relative moisture content, water potential, photosynthesis and fluorescent reactions were measured. Biochemical analysis measurements included chlorophyll content, proline content, ascorbate and free sugar content. The measured values for adaptation index led to the decision on the adaptation capacity and the final selection of clones included *P. sibirica*, DN 034 and DN sim. DN 247 and TN 074 showed low adaptation capacity value. Selected poplar clone's adaptation index and the correlation analysis of morphological, biological and biochemical factor measurements revealed that the factors include survival rate, RWC, carotenoid, proline, total chlorophyll, glucose, fructose, and mannitol measured with positive correlations whereas the measured values with negative correlations were T/R ratio, Pn, Ci, Sucrose.

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중생종 대립형질벼 “고향찰”의 질소시비량에 따른 생육 및 수량성 평가

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중생종 대립형질벼인 “고향찰”은 2015년 강원도농업기술원에서 육성한 특수미 품종으로 누룽지향과 찰벼 특성을 가지고 있어 떡, 혼반 등 쌀시장 확대를 통한 수급안정에 기여할 것으로 판단된다. 이에 따라 농가에 안정적인 종자 보급을 위한 국가종자생산체계를 구축하였으나 재배 확대에 따른 안정적인 재배법 확립이 필요한 실정이다. 따라서 질소시비량 차이에 따른 수량성을 평가하고자 2016~2017년에 강원도농업기술원 시험포장에서 출수기, 수량구성요소 및 수량성 등을 조사하였다. 기타 재배법은 벼 표준재배법을 준용하였으며 대조품종으로는 “설향찰”을 사용하였다. 질소시비량은 0, 7, 9, 11, 13 kg/10a 등 5 수준으로 설정하였다. 시험 결과, 생육은 질소시비량이 증가할수록 엽면적지수 및 건물중이 증가하였다. 수량구성요소인 단위면적당 수수는 증가하였으나 반면 영화수는 N-9kg/10a 시험구에서 가장 많았고 이후 감소하는 경향을 보였다. 현미천립중은 질소시비량이 증가할수록 무게가 감소하는 경향이였다. 백미수량은 질소시비량이 증가할수록 증가하였으나 11kg/10a 이후 증가폭이 크게 감소하여 무비구를 기준으로 한 수량지수에서 11kg/10a 시험구와 13kg/10a 시험구가 같은 수치를 나타내었다. 따라서, “고향찰”의 수량구성요소와 수량을 고려한 10a당 적정 질소시비량은 11kg 내외로 판단된다.

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“YR29169”, A mid-maturing japonica rice elite line in tropical regions

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Japonica rice is getting popular and it has been able to attract huge number of consumers in Asian countries, particularly in the tropics. The temperate country-bred Japonica cultivars, such as the late-maturing varieties from Korea and Japan, show very low adaptability under tropical conditions as they are photoperiod- and thermosensitive varieties. Most of them are heading too early, the grain quality is also low, and yield is significantly reduced. So, there is urgent to develop temperate Japonica cultivars adapted to tropical conditions. Currently, the leading variety, IR142 (MS11), is lower in yield than the local Indica, and is also vulnerable to pests. Therefore, these traits need to be improved in order to expand seed distribution. “YR29169” is a mid late maturing Japonica rice elite line adapted to tropical areas that was selected on the preliminary yield trial inIRRI. This elite lines was derived from three-way cross among Milyang265, Milyang244 and Suwon526. This elite lines have high-yield, which increased by 32% compared to IR142, and the number of grain per panicle increased by 38% and days to heading was longer by about 10 days. Grain yield exhibited significantly positive correlation with the number of grain per panicle ($r=0.85^{**}$), days to heading ($r=0.89^{**}$). Therefore, the results suggest that these traits can be used for selection of high yielding varieties in tropical areas. Also, this elite line has shown resistance against Brown planthopper (BPH), bacterial leaf blight (BLB) and Rice stripe virus(RSV). The protein content of this elite line is low. Eating quality analyzed by Toyo tastemeter was also higher than IR142. This result is indicating that this palatability of line is better than IR142 in taste. This results support that this elite line will be useful genetic resource developing for the adaptation of temperate japonica rice in the subtropical regions.

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SNP(Single Nucleotide Polymorphism) 마커를 이용한 국내 주요 재배 감자 품종의 유전 집단 분석 및 품종 구분

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감자는 벼, 밀, 옥수수과 함께 세계 4대 식량작물로 국내에서는 매년 약 20,000ha가 재배되고 있다. 2017년 현재 약 70여 품종이 등록되었으나 수미를 포함한 약 10개의 품종이 전체 재배면적의 90%이상을 차지하고 있다. 국내에서는 씨감자 보급의 민영화를 통하여 다양한 민간업체, 지자체 등에서 다양한 품종을 생산하여 보급하고 있으나 괴경형태, 화색 등 외부형태적 특성으로는 품종 구분이 매우 어려운 실정이다. 따라서 본 연구는 국내에서 주로 재배되고 있는 수미, 대서, 대지 등 국내 재배면적의 약 95%를 차지하는 16개의 품종과 8,303개의 SNP chip (Illumina SOLCAP Infinium 8 K chip)을 이용하여 국내 감자 품종의 유전적 다양성을 분석하고 16개의 감자 품종을 구분할 수 있는 5개 SNP 마커를 선발하였다. 전체 8,303 SNP 마커 중 minor allele frequency (<5%)를 제외한 결과 약 4,000개의 SNP가 선발 되었다. 감자 품종의 평균 Observed Heterozygosity가 가장 높은 품종은 ‘대서’로 약 75%였으며 가장 낮은 품종은 ‘홍영’으로 41%로 나타났으며 평균적으로 약 58%로 조사되었다. SNP 마커의 평균 PIC (polymorphism information content) value는 약 0.27581로 나타났다. STRUCTURE를 이용하여 국내 감자 품종의 집단 구조를 분석한 결과 16개의 국내 감자 품종은 3개의 유전적 조성($\Delta K=3$)으로 구분되었다. 16개의 품종을 구분하기 위하여 5개의 SNP 마커를 선발하여 TaqMan probe를 디자인하였다. 각각의 SNP 마커 allele에 FAM 과 VIC 형광염색 프로브를 제작 후 Real-Time PCR을 수행하였다. SNP 마커를 additive coding data set 형태로 allele discrimination을 수행한 결과 16개 품종을 효과적으로 구분할 수 있었다. 또한 시중에서 유통되고 있는 감자칩으로부터 DNA를 추출하여 가공품에 사용된 품종 구분 결과 수미, 대서 등이 사용된 것으로 판별되었다.

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High-throughput SNP discovery by transcriptome sequencing to enhance the genomics-assisted breeding in Radish inbred lines

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Recent advancements in next generation genome sequencing (NGS) platforms provide numerous opportunities for the development of molecular markers. Single-nucleotide polymorphisms are powerful tools for the genomics-assisted selection and breeding in horticultural crops. Radish ($2n=2x=18$) is an important root vegetable in Brassicaceae family which is highly cultivated and consumed in Asian countries. The sequencing of radish genome aids in the better understanding and tailoring of traits associated with economic importance. However, very little research has been progressed on the aspects of NGS assisted molecular marker development in Radish on comparison with *Brassica rapa* in Brassicaceae. In order to accelerate the genomics assisted breeding and genetic selection, transcriptomes of 35 radish inbred lines with diverse traits were sequenced for the development of SNP markers. The sequenced reads ranged from 90,560,400 to 38,048,086 with the GC (%) of 48.54 to 47.80. The phred quality score (Q30) of 97% were obtained in the present sequencing approach. The raw data were trimmed and utilized for the identification of SNPs using several bioinformatics tools. The results suggested the discovery of 64,746 SNPs which have been further filtered to 571 potential SNPs. Moreover the SNPs developed in the current endeavor will be genotyped and utilized for the genetic diversity analysis and molecular marker assisted breeding in radish.

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분질성으로 맛이 좋은 감자 품종 ‘다미’ 육성

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우리나라에서 재배하는 감자 품종의 약 60% 정도는 미국에서 도입하여 국내 적응성 시험을 통하여 1978년에 육성된 ‘수미(Superior)’ 품종이다. 이 품종은 더벡이병에 비교적 강하지만 감자잎말림바이러스(PLRV), 감자역병(*phytophthora infestans*) 등에 약하여 씨감자 채종이 어렵고 산간지대 여름재배 작형에서 방제비용이 많이 든다. 또한, 최근에 기후온난화의 영향으로 기형서 발생이 증가하는 등 재배상 많은 문제점이 발생하고 있어 이 품종을 보완할 신품종 보급이 절실한 실정이다. 2014년 육성된 ‘다미’ 품종은 속기가 중생이고 지상부 식물체는 반직립성으로 성장하여 수광태세가 좋아 광합성에 유리하다. 감자의 모양은 원형이며 눈깊이가 매우 얇아 조리엔 편리하다. 감자 표피색은 황색이지만 고랭지 재배시 약한 Russet 형태를 보이며 육색은 흰색이다. 잎은 녹색이며 꽃은 흰색으로 대체로 개화량이 많은 편이다. 기형서, 열개서, 내부생리장해 등 생리장해 발생은 ‘수미’에 비하여 적다. 감자역병에 대한 포장저항성은 ‘수미’에 비해 다소 강한편이며, 진정저항성은 중도저항성이다. 바이러스에 대한 저항성 검정결과 은 ‘수미’는 감수성, ‘다미’는 중도저항성으로 확인되었다. 평년지 봄재배 및 고랭지 여름재배 시 ‘수미’ 품종에 비해 수량이 많고 건물률은 20.5%로 비교적 높다. 삶은 감자는 분질성으로 맛이 좋아 일반부식용으로 적당하다.

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New genome wide SSR markers using high-throughput sequencing in button mushroom (*Agaricus bisporus*)

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Button mushroom (*Agaricus bisporus*) is one of the most widely cultivated species in edible mushroom. Despite their economic importance, relatively little is known about genetic diversity of this strain due to their narrow genetic base. Illumina paired-end sequencing produced 43,871,558 clean reads and 69,174 contigs were generated from five offsprings. These contigs were subsequently assembled into 57,594 unigenes. These unigenes were annotated with reference genome in which, 6,559 unigenes were associated with Clusters of orthologous genes. GOntology classifications showed large numbers of unigenes were assigned. Based on genome data of five offsprings, 44 polymorphic SSR markers were developed. The major allele frequency ranged from 0.42 to 0.92; the number of genotypes and the number of alleles ranged from 1 to 4, and from 2 to 4; the observed heterozygosity and the expected heterozygosity ranged from 0.00 to 1.00, and from 0.15 to 0.64, respectively; and the polymorphic information content value ranged from 0.14 to 0.57. The genetic distances and UPGMA clustering had showed discriminated offspring strains. The SSR markers developed in this study can be applied in the polymorphism analysis of button mushroom and cultivar discrimination.

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양송이버섯에서 개발된 새로운 SSR 마커

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충청북도 청주시 흥덕구 가경동 충북대학교 농업생명환경대학 특용식물학과

양송이버섯은 전 세계적으로 가장 많이 재배되는 식용 버섯 중 하나로 매년 소비량과 생산량이 늘어나는 추세이다. 그러나 양송이의 경제적 중요성에 비해 분자유전학적 연구는 부족한 실정이다. 나고야 의정서 발표에 따라 자국의 유전자원에 대한 보호 및 주권 강화에 대한 연구가 필요하다. 본 연구는 양송이버섯의 전장 유전체를 기반으로 한국, 네덜란드 등 6개 국가에서 수집된 10개 유전자원을 사용하여 SSR마커를 개발하였다. 213개의 SSR마커 중 PCR이 되지 않은 48개 SSR마커와 단일 대립유전자만 나타나는 8개의 SSR마커를 제외한 157개 SSR마커가 다형성을 나타냈다. 157개 SSR마커는 유전적 다양성을 나타내는 PIC값이 0.090에서 0.827로 평균은 0.457이었으며, 대립유전자의 수는 2개에서 9개로 평균 4개였다. SSR마커의 Repeated type에 따른 분석결과 2bp repeated에서 PIC값과 대립유전자의 수가 각각 0.450과 3.4개 였으며 3bp repeated에서는 각각 0.477과 3.7개였다. 4bp repeated에서는 PIC값과 대립유전자의 수가 각각 0.368과 3개였다. 개발된 SSR마커는 양송이버섯 유전자원에 대한 품종구분 및 집단구조 분석, 다양성분석 등의 연구에 활용될 수 있을 것이다.

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야생감초의 새로운 SSR marker 개발

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감초는 콩과의 다년생 식물로 우리나라뿐만 아니라 세계적으로 사용되는 중요한 약용식물이다. 현재 감초는 전 세계적으로 20종이 분포하고 있으며, 일반적으로 만주감초(*Glycyrrhiza glabra*), 유럽감초(*Glycyrrhiza uralensis*), 창과감초(*Glycyrrhiza inflata*)의 뿌리를 통틀어 감초라고 한다. 감초의 성분 중 glycyrrhizin은 triterpene 계열로 주로 항암, 해독, 항산화와 같은 약리 작용을 한다. 야생감초는 재배종보다 비생물학적, 생물학적 요인들로부터 강한 저항성을 가지고 있으므로 이와 관련된 유전자원을 재배종에 도입함으로써 보다 우수한 자원을 확보할 수 있을 것이다. 본 실험은 감초 야생종 중의 하나인 *Glycyrrhiza lepidota*의 전장 유전체를 기반으로 repeated type 2bp인 AC, AG, GT 등 6종류 60개과 3bp인 AAC, GTT, TTA 등 16종류로 40개, 총 100개의 SSR 마커를 제작하였다. 마커에 대한 다양성을 나타내는 PIC값은 최대 0.730, 최소 0.346, 평균 0.529이고, GD 값은 최대 0.765, 최소 0.444, 평균 0.596이다. 대립유전자의 수는 최대 5, 최소 2이다. Repeated type에 따라 2bp의 PIC 값은 최대 0.730, 최소 0.370이고 3bp의 PIC 값은 최대 0.685, 최소 0.346이다. 본 연구에서 개발된 마커는 감초의 유전적 다형성, 집단 구조 분석 품종 구별 등에 활용될 수 있을 것이다.

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New chloroplast microsatellite markers for identification of *Glycyrrhiza* species

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Licorice (*Glycyrrhiza* sp.) is an important medicinal herb, has long been used in traditional medicine for the treatment of several diseases worldwide. Understanding the genetic diversity within *Glycyrrhiza* species is important for the efficient conservation of these medicinal herbs. In this study, we have developed 20 polymorphic chloroplast microsatellite (cpSSR) markers using the chloroplast genome of *G. lepidota*. The cpSSR markers were tested on a total of 27 *Glycyrrhiza* individuals. The number of alleles per locus ranged from two to eight among the *Glycyrrhiza* accessions. Overall, the Shannon index (I) for each cpSSR ranged from 0.315 to 1.694, the diversity indices (h) were 0.140 to 0.793 and the unbiased diversity indices (uh) were 0.145 to 0.825. In addition, the cpSSR markers were successfully divided the 27 *Glycyrrhiza* individuals into four groups. The cpSSR markers developed in this study could be used in assessment of genetic diversity and rapid identification of *Glycyrrhiza* species.

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New CAPS and HRM markers acquired from the chloroplast genome of wild licorice (*Glycyrrhiza lepidota*)

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Licorice (*Glycyrrhiza* sp) is an important medicinal crop often used as health foods or medicine worldwide. The molecular genetics of licorice is under scarce owing to lack of molecular markers. Here, we have developed cleaved amplified polymorphic sequence (CAPS) and high-resolution melting (HRM) markers based on single nucleotide polymorphisms (SNP) by comparing the chloroplast genomes of two *Glycyrrhiza* species (*G. glabra* and *G. lepidota*). The CAPS and HRM markers were tested for diversity analysis with 24 *Glycyrrhiza* accessions. The restriction profiles generated with CAPS markers classified the accessions (2–4 genotypes) and melting curves (2–3) were obtained from the HRM markers. The number of alleles and major allele frequency were 2–6 and 0.31–0.92, respectively. The genetic distance and polymorphism information content values were 0.16–0.76 and 0.15–0.72, respectively. The phylogenetic relationships among the 24 accessions were estimated using a dendrogram, which classified them into four clades. Except clade III, the remaining three clades included the same species, confirming interspecies genetic correlation. These 18 CAPS and HRM markers might be helpful for genetic diversity assessment and rapid identification of licorice species.

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Solidity와 클러스터링을 이용한 특이형태 콩 종자의 검출

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콩은 식물성 단백질 및 지방산의 주요한 공급원이며 세계적으로 중요한 식량자원으로서 종자의 형태와 색상은 보관, 발아 및 기능과 관련하여 매우 중요한 의미를 가진다. 식량과학원에서 분양받은 핵심집단의 재배종 400계통 콩 종자를 100립씩 상단(Top) 1장과 측면(Side) 4장으로 나누어 촬영하여 약 2000장의 이미지를 획득하였다. 그리고, 분석프로그램(ImageJ)을 활용하여 각각의 39,065립의 이미지 데이터를 분리하였으며 종자 크기, 둘레, 부피 등의 정량적 데이터를 생산하였다. 이미지 데이터에는 유전적인 돌연변이나 환경적인 요인에 의해 형태적으로 특이한 패턴을 보이는 개체들이 확인되었다. 이러한 개체들은 계통 내에서 특정 유전자의 발현, 환경 적응 및 피해에 대한 의미를 갖기도 하지만 전체 집단에서 형질을 분석할 때 왜곡된 결과를 도출하는 요인으로 작용한다. 따라서 종자 표면의 매끄러움 정도를 Convex면적과 Area면적의 비율로 판별하는 Solidity값을 이용해 특이형태 종자의 검출 방법을 고안하였다. 하지만 각 계통마다 다른 형태적인 특성으로 Solidity값의 기준이 달라 거리 차에 의한 클러스터링 방법(Euclidean distance clustering)을 활용하여 400계통에서 165개 전체기준으로 약 0.4%의 특이형태 콩 종자를 개별 검출하였다. 이러한 분석 방법은 병충해 피해 및 환경적 요인에 의한 특이한 형태의 종자를 분류하는 방법으로 이용 될 수 있고 디지털 표현형 정보의 품질을 높여줌으로 유전체 정보를 활용한 유전자 기능검정(GWAS), 딥러닝을 통한 종자 표현형 연구 등에 정확하고 신뢰성 있는 데이터를 제공할 수 있을 것으로 예상된다.

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Protein sequence to vector strategy for ML application on proteins

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Machine learning applications, especially artificial intelligence (AI) prediction models impact the fields from science to industry. AI-based solutions on image recognition, natural language process, and sequential decision making problems were largely improved to have human like behavior that may replace human labors. In biology, researchers are trying to apply AI to solve biological problems, such as prediction of diseases, based on bio-bigdata massively generated by next generation sequencers and high-throughput imaging facility. However, another biological questions with regard to “Proteins” are hard to transit to machine learning problem because the protein sequence is not fixed in length to compare each other while the only way to compare has been sequence alignment among the proteins in same family. Here we benchmarked the natural language processing strategy for vectorization of sentences for our new strategy of changing protein sequences into fixed length of vector. The protein to vector strategy successfully represented protein identity similar with the sequence alignment strategy suggesting that this new strategy would accelerate machine learning based solutions on protein based questions such as protein-protein interaction prediction. Moreover, the precomputed protein matrix on well curated proteins from this strategy can be used for similarity search like BLAST without alignments and also without high computational burdens.

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The chloroplast genomes are variable in *Prunus yedoensis*

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Prunus yedoensis is one of most popular ornamental tree species planting in roadside and parks in Korea. Also, there are many natural population in Jeju-Island that the wild morphological characteristics are not distinguishable to cultivate. We compared the chloroplast genome sequence and made up consensus cp genome sequence using the 6 individuals, in which two cultivates and 4 wild individuals are collected. The 4 complete cp genome sequence are generated by *de novo* assembly of the sequencing data generated by Illumina high-throughput sequencing platform and the other two cp genome sequence were obtained from Genbank. The consensus sequence was aligned as 158,149 bp with containing 86,210 bp of LSC, 19,153bp of SSC, and each 26,393 bp of IRA and IRB. A total AT ratio is 63.28% in consensus sequences. Although these are identified same species with the morphological characteristics, we found highly variable sequence in cp genome. A total of 168 SNPs and 531 INDELS were identified and these take 0.106% and 0.336% respectively. One individual was identified highly different cp genome from the others by neighbor-joining tree analysis. This would be good resource to study of genetic diversity in *Prunus yedoensis*. We identified SSRs from the cp genomes that discriminate the accessions and possibly use for the cultivar specific markers in the further investigation.

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Identification of biomass improved gibberellin biosynthesis related gene in rice

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Dwarfing is one of the most important traits in rice, because regulatory mechanisms for plant growth and development. In rice, more than 60 dwarf mutants are well known and its present different phenotype, such as small grain, more tiller and leaf shapes or plant height. In last decade, manifold GA biosynthesis and signaling genes have been characterized in rice that are regulated cell division, development, hormones and various stress. In this study, a novel gene *OsGASD* (*Oryza sativa* Gibberellin Acid Sensitive Dwarf) was identified that an efficient system to create rice mutant by Ac/Ds transposon insertion mutagenesis, such as selected homozygous mutant in dwarf phenotypes. To research the function of dwarf *OsGASD* gene in GA biosynthesis pathway, we generated transgenic rice plants overexpressing *OsGASD* plants for analysis of GA signaling and uptake. Overexpressing *OsGASD* plants shown that internodes length, height, number of tillers and biomass were increased compared with wild-type plant, whereas *osgasd* mutant through Ac/Ds decreased. *osgasd* mutant includes smaller amount of active GAs than wild-type. *osgasd* mutant plant of GA biosynthesis pathway causes GA deficiency and dwarf plants, and endogenous GA suppliance can restore the wild type phenotype in this mutant. The result indicated that *OsGASD* gene regulated the elongation of shoot, stem, plant height and biomass. The increased expression of *OsGASD* gene dramatically induces expression of the factors associated with GA biosynthesis such as CPS, KO, KAO, GA20ox and GA2ox, whereas *osgasd* mutant suppression of the factors associated with GA biosynthesis, leading to dwarf phenotypes. That applied GA₃ at the plant development stage to survey the response of *OsGASD* gene to GA₃. We suggest that *OsGASD* gene is related to factors of GA biosynthesis pathway regulating rice biomass development.

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영상 분석 기술을 활용한 호접란의 형태적 특성 분류

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작물 표현체 연구는 작물의 형태적 특징을 영상 데이터로 수치화 및 객관화하여 분석하는 기술이다. 아시아 열대지방 등이 원산지인 호접란은 화훼 재배산업에서 가장 인기 있는 난초중의 하나로 교배종 포함 20,000여 품종이 넘으며 최근 소문 다화성 미니 호접란에 대한 관심이 높아지고 있다. 국립원예특작과학원에서 호접란을 분양받아 RGB phenome analyzer를 이용하여 난초의 형태적인 특성을 분석하여 객관적인 수치데이터로 형질들을 분류하고자 하였다. 분석에 사용된 호접란 275개체는 꽃을 1개체 당 최소 6개씩 카메라로 촬영하여 총 1,650장의 이미지를 획득하였고, 영상 처리 프로그램(Image J 와 Lemna Grid)으로 데이터를 분석하였다. 분석된 파라미터 중 국립종자원 신품종 심사를 위한 호접란 특성조사표에 따라 꽃의 크기, 너비, 길이의 데이터를 5단계로 나누어 정량화하였다. 너비/길이의 비율(Aspctratio), 이심률(Eccentricity), 진원도(Roundness)와 같은 파라미터도 새로운 영상 지표로 호접란의 형태적 특성을 분류할 수 있었다. 향후 호접란의 잎이나 꽃대, 꽃차례 등 추가적인 영상 이미지를 분석하고자 하며 기존의 특성조사표를 포함한 새로운 표현형 특성 지표를 개발하여 신품종 육종과 유전자 기능분석, 정밀육종 등에 활용될 수 있을 것으로 기대된다.

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식물표현체 기술을 이용한 벼 생육과정 이미지 및 색상변화 분석

최인찬, 김송림, 이흥석, 이은경, 김년희, 백정호, 지현소, 김경환*

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식물표현형 연구는 대량검정시스템(High-throughput system)을 사용하여 이미지 데이터를 획득하고 분석하여 식물의 생장 특성, 농업형질과의 연관성을 통해 유전자 기능분석, 육종선발 등에 활용한다. 영상을 통한 표현형 분석과정의 신뢰성을 확인하기 위해 벼의 초기 생육과정에서 실측값과 이미지 데이터와의 상관관계를 확인하고 정성적인 지표인 색상변화를 정량적으로 표현하기 위한 연구를 수행하였다. 동진벼 96개체를 파종후 16일부터 65일까지 일주일 단위로 총 7회 벼의 크기, 초장, 잎면적, 생체중과 건물중을 실측하고 RGB phenome analyzer로 식물체의 이미지 데이터를 획득하였다. 실측과 영상분석값의 상관관계는 0.93에서 0.99로 높아져, 초기 생육시 영상분석값이 실측값을 대체할 수 있을 것으로 판단되었다. 또한 동진벼 40개체를 매달 온실에 파종하여 79일까지 재배하고 4회 반복하였으며 매회 2주부터 일주일에 한번씩 총 9회 이미지 데이터를 획득하였다. 생성된 영상데이터를 이용하여 생육특성과 색상을 분석하였으며 색상은 HSI 색차계 Hue 값으로 시작, 종료와 단계값을 지정하여 빨간계열, 노란계열, 연한 녹색계열과 녹색계열로 구분하였다. 보통 작물 재배기간이 증가함에 따라 색차계의 연녹색 비율은 감소하고 녹색비율이 증가하였으며 파종후 65일부터 72일 시기에 녹색 비율이 감소하였다. 화분에 질소비료를 시비한 후 연녹색은 감소하고 녹색이 증가하므로 벼의 색상변화가 질소시비와 연계됨을 알 수 있었다. 향후 이미지에서 얻은 식물의 형태적, 색상적 데이터를 이용한 정량적인 식물 표현형 분석이 가능하며 유전자 기능 분석에도 연계시킬 수 있을 것이다.

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콩 핵심집단 종자 표현형 분석을 위한 데이터 생성 및 전처리 기법

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콩의 종자는 크기가 작고 둥근 외형 때문에 버니어캘리퍼스 같은 장비를 이용해서 종자의 장폭, 단폭 등의 표현형질 측정 시, 많은 개체를 일률적으로 측정하기는 어렵다. 최근 주목받고 있는 영상을 이용한 표현체 기술을 이용하여 콩 종자의 특성을 분석하고자 하였다. 국립식량과학원에서 분양받은 콩 핵심집단 400계통 총 39,065개체 종자의 영상 데이터를 획득 후, 버니어캘리퍼스를 이용한 종자의 실제 측정값과 영상을 이용한 측정값을 비교분석했다. 상관계수는 0.95이상으로 높은 상관관계를 나타냈고, 영상분석을 이용한 표현형 분석의 신뢰도가 높다는 것을 알 수 있었다. 종자 크기 측정 시 수분 함량은 평균 8%였고, 수분함량에 따라 그 크기 및 부피가 변하기 때문에 수분 함량에 따른 종자의 표현형을 분석하였다. 영상 분석의 신뢰성을 높이기 위해 데이터 품질개선 과정(Quality control)을 거쳐 영상분석 시 결과의 오차원인을 제거하였다. 오차원인은 주로 충해, 종피 균열, 외부압력에 의한 종자 외형의 변화 또는 혼입종자나 영상촬영과정에서 그림자에 의한 종자 형태 측정 오차 등이 주된 원인으로 1.96%(767개)를 차지하였다. 데이터 품질개선 과정을 통해서 면적, 둘레, 부피 등 분석 값의 상관계수는 전반적으로 0.95이상이었으며 둘레의 상관계수는 0.86에서 0.92로 최대폭으로 증가하였다. 콩 핵심집단 400계통 종자에 대해 영상을 활용한 표현형 데이터를 획득하였으며 향후 형태적 특성 분석, 표현형질과 유전체 정보와의 연관분석(GWAS)을 통해 유전자 기능을 해석하는데 활용하고자 한다.

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Genetic and MutMap analysis of dense green leaf mutant lines of rice

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Dense green leaf mutants can be utilized in discovery of genes regulating leaf growth and development. We found three dense green leaf mutant rice lines which are Ds061942, Ds073406, and Ds074081 among the Ac/Ds insertion mutant population. For genetic analysis, the mutant lines were crossed to their wild type variety, Dongjin. All of F1 plants showed wild type phenotypes, and F2 segregation ratios were fit to 3:1 (wild type : mutant type), which indicated that single recessive gene controls dense green leaf trait in each mutant line. Resequencing of the three mutant lines were performed using Illumina Hiseq 2000 platform. 13.9-15.2 Gbp sequence data were produced per mutant line. After quality trimming and read-mapping onto rice reference genome sequence (Nipponbare), 9.9-10.7 Gbp were mapped onto the reference sequence resulting in average mapping depth of 26.55-28.75x. By comparison with Dongjin resequencing data, 42,386-56,988 single nucleotide polymorphisms (SNPs) were found between each mutant line and Dongjin. MutMap analysis was performed by pooling mutant type F2 plants and resequencing the pooled DNA. It was found that the causative mutated genes were located on chromosome 3, 4, and 7. Map-based cloning of the genes regulating the dense green leaf trait of the mutant lines is under way.

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영상을 활용한 호접란 형태 및 색상 분석방법 개발

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관상용 난초 중 호접란은 한국, 일본, 유럽 및 미국에서 가장 인기가 많으며, 2014년에 무역량이 2억불 이상의 큰 시장을 형성하고 있다. 이에 국내에서도 많은 호접란의 신품종을 연구하고 있다. 그러나 국립종자원의 분류방법인 신품종 특성조사요령은 대부분 육안에 의한 정성적 분석으로 이루어져 있다. 이에 영상을 이용하여 형태 및 색상을 정량적 수치로 표기할 수 있는 프로그램을 개발하고 이를 이용하여 객체 분류 및 형태 분류 기술을 사용할 수 있는지 연구하였다. 호접란의 꽃을 꽃잎, 윗꽃받침, 측면 꽃받침, 끝열편, 측열편, 캘러스(Callus)로 총 6개 부분으로 세분화하여 자체 개발한 프로그램을 이용하여 분석하였다. 호접란의 분석을 위해서 획득한 영상은 노이즈 및 배경 제거, 색인화 후 형태학적 수치와 색상값을 획득하였다. 영상데이터를 통해 획득된 파라미터는 기본 특성을 확인할 수 있는 면적, 너비, 길이, 색상(HSI-H*)을 객관적 수치로서 나타낼 수 있었다. 또한 형태학적 특징이 잘 나타나는 이심률(Eccentricity), 진원도(Roundness), 컨벡스홀 영역(Convex hull area), 밀집도(Density)를 정량적 수치로 분석할 수 있었다. 개발된 형태학적 특징 중에 이심률과 진원도를 통해 꽃잎 및 꽃의 기관의 원형도와 표면의 굴곡을 확인 할 수 있었다. 본 연구를 통해 기존의 특성조사표와 개발된 분석방법을 통해 특성분류에 사용된다면 더욱 정밀한 분류를 실행 할 수 있을 것이다.

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헛개나무(*Hovenia dulcis* Thunb.) microsatellite 표지 개발 및 유전변이 분석

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헛개나무(*Hovenia dulcis*)는 갈매나무과 헛개나무속에 속하는 낙엽교목으로 우리나라에는 헛개나무 속에 한 종만 자생한다. 헛개나무 과병에서 추출한 활성 화합물이 숙취해소 간경화 방지 등에 효과가 있다는 연구 결과가 알려지면서 한약재 뿐 아니라 건강음료 등으로 널리 활용되어 그 수요가 증가하고 있다. 이에 따라 헛개나무 자생지는 급격히 훼손되고 있는데 반해 관련 유전 육종 연구 및 보존 관련 연구는 거의 전무한 실정이다. 본 연구에서는 헛개나무에 대해 다양한 유전연구에 활용 가능한 microsatellite 표지를 개발하였다. Glenn과 Schable (2005) 방법에 따라 microsatellite enrichment 라이브러리를 작성하였다. 이를 기반으로 microsatellite repeat을 가지는 197개 contig 서열(Genebank Acc. KP246504 - KP246700)을 확보하고 모든 contig 서열정보를 이용하여 후부 프라이머를 제작하였다. 6개 헛개나무 샘플을 이용하여 증폭 양상을 확인하여 최종적으로 변이가 있고 재현성이 있는 21개의 프라이머를 선발하였다. 충주(34), 제주(34), 강릉(28) 세 집단으로부터 수집된 96개 헛개나무 샘플을 이용하여 프라이머별 특성 및 집단 분석을 수행하였다. 최종 선발된 21개 프라이머의 특성을 확인한 결과 각 프라이머에서는 최소 2개 에서 14개의 대립유전자(A , 평균 5개)가 확인되었다. 이형접합도 관측치(H_o)와 기대치(H_e)는 각각 0.115-0.870(평균 0.488)과 0.119-0.845(평균 0.520)의 범위에서 확인되었다. 14개 유전자좌에서 3개 집단의 유전다양성을 분석한 결과 대립유전자수(A)는 집단에 따라 3.77-4.18, 이형접합도 기대치(H_e)는 0.467-0.472로 집단에 따라 큰 차이가 없었다. 집단 내 근친교배 정도를 예측할 수 있는 고정계수(F)는 -0.031에서 0.016으로 0에 가까운 값을 보여 거의 평형상태에 가까운 것으로 확인되었다. 본 연구를 통해 개발된 microsatellite 표지는 헛개나무의 유전다양성 평가와 육종연구에 유용할 것으로 기대된다.

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추위에 강한 사일리지용 귀리 신품종 ‘신한’

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귀리는 다른 맥류보다 단백질 함량과 가소화양분함량(TDN)이 높아 사료가치가 우수하고 가축의 기호성도 뛰어나지만 가을에 파종하여 재배할 때 추위에 약한 단점이 있다. 따라서 추위에 강하면서 건물수량이 많고 사료가치를 높여 수입종자를 대체할 수 있는 걸귀리 품종개발이 요구되었다. 이에 국립식량과학원에서는 추위에 강하면서, 엽신비율이 높고, 건물수량이 많으면서도 사일리지 품질이 좋은 조사료용 걸귀리 신품종 ‘신한’을 육성하였다. ‘신한’의 3년간 지역적응시험 결과, 이삭 패는 시기가 평균 5월 6일로 ‘삼한’보다 1일 정도 늦었으나, 초장은 113cm로 ‘삼한’보다 약간 크며, 엽신비율이 16.0%로 ‘삼한’보다 높다. 추위 견딜성은 ‘삼한’과 대등하며, 경기도 연천의 낮은 이랑 재배에서 내한성검정 결과 100% 생존하였다. ‘신한’은 현재 보급되고 있는 ‘삼한’에 비해 생체수량과 건물수량이 헥타당 각각 40톤, 15.3톤으로 6%, 8% 높다. 조단백질 함량은 6.3%, 가소화양분함량(TDN)이 62.1%로 사일리지 품질도 1등급으로 우수하다. ‘신한’은 1월 평균최저기온이 -6℃ 이상이고 중산간지가 아닌 지역에서 재배가 가능하며, 조사료생산 경종 및 축산농가의 확대재배가 기대된다.

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Basic helix-loop-helix 전사인자에 의한 현사시나무 유전자 발현 및 직경 생장 특성 구명

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Basic helix-loop-helix (bHLH) 도메인을 갖는 전사조절 유전자는 식물의 생장과 발달에 중요한 역할을 하는 것으로 알려져 있다. 본 연구에서는 발달과 관련된 유전자 중에서 bHLH 도메인을 갖는 유전자를 현사시나무에서 분리한 다음 형질전환 현사시나무를 제작하였다. 이 유전자의 발현이 증가된 형질전환 현사시나무는 수고와 직경 생장이 대조구에 비해 약 30% 이상 증가하였다. 광학현미경을 이용하여 줄기의 조직학적 특성을 분석한 결과 이차 목부의 세포 수 및 크기가 증가한 것으로 나타났다. 그리고 식물의 생장과 관련된 브라시노스테로이드 생합성 관련 유전자들의 발현에 차이가 나타났다. 형질전환 현사시나무에서 직경 생장과 발달에 관여하는 유전자들의 발현 변화를 분석하기 위하여 마이크로어레이 분석을 실시하였다. 그 결과 2배 이상 발현이 변화하는 1,276개 유전자를 선별하여 네트워크 분석을 통해 381개 유전자의 상호 관련성을 확인하였다. 이를 통해 MYB, NAC, WRKY, WOX 등 생장과 발달에 관여하는 전사인자들이 bHLH 유전자에 의해 조절될 수 있는 표적 유전자로 추정되었다. 이들 유전자의 프로모터 서열을 분석한 결과, bHLH의 결합 부위로 알려진 G-box 및 E-box 서열을 포함하고 있었다. 그리고 선별된 표적 유전자들을 qRT-PCR로 검증한 결과 bHLH의 발현이 증가된 형질전환 현사시나무에서 이 유전자들의 발현이 증가하였다.

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SAP11 유전자 조절에 따른 현사시나무의 가지분화 특성 구명

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현사시나무에서 건조 처리에 의해 발현이 증가하는 stress-associated protein 11(SAP11) 유전자를 분리하였다. 이 유전자의 발현을 증가 또는 억제시킨 형질전환 현사시나무를 만든 다음 환경 스트레스에 대한 저항성을 조사하였다. 그 결과 SAP11 발현억제 형질전환 현사시나무는 대조구에 비해 높은 내염성과 내건성을 나타내었다. AP11 발현억제 형질전환 현사시나무의 생장 특성을 확인하기 위하여 야외 포지에 식재하였다. AP11 발현억제 형질전환 현사시나무는 대조구에 비하여 수고 생장이 저해된 반면 줄기 생장과 가지의 수는 증가하였다. 식재 후 2년간의 모니터링 결과 뿌리를 제외한 상층부의 생중량이 1.5배 그리고 가지 수는 대조구에 비해 2배 이상 증가하였다. 가지 발달에 관여하는 것으로 알려진 신호전달계 유전자들의 발현을 조사한 결과 옥신 관련 유전자들의 발현은 감소한 반면 시토키닌 관련 유전자들의 발현은 증가하였다. 또한, 가지 분화를 억제하는 것으로 알려진 스트리고락톤 관련 유전자들의 발현이 감소하였다. 따라서 AP11 발현억제 형질전환 현사시나무는 건조지 및 간척지와 같은 척박지에서 목질계 바이오매스 생산에 유용하게 활용될 수 있을 것으로 판단된다.

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A new early maturing and high yielding vegetable peanut variety "Sewon"

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Korean usually like to consume large grain of peanut for the roasted or boiled. One of peanut breeding programs is also focused on developing early maturing and high yielding vegetable peanut eaten after boil. A new peanut variety "Sewon" (*Arachis hypogaea* ssp. *fastigiata*.) with large grain and high yield was developed in the Department of Southern Area Crop Science, NICS, in Milyang 2017. This variety was developed from the crossing line between variety "Charmwon" with red testa Shinpung plant type and variety "Pungsan" (Milyang 27) with large grain Virginia plant type. "Sewon" which is short stem and semi-erect Shinpung plant type has 35cm of main stem length, 51cm of branch length and 13 branch number per plant. Each pod has two grains with ellipse shape of red testa and its yield components are composed of 38 mature pods of per plant, 113g of 100-seed weight, 72% of pod shelling ratio, and 81% of mature pod ratio in the regional yield trials (RYT). Its seed quality show 31.7% of crude protein and 35.2% of crude oil and 52.3% of oleate in fatty acid composition. This also have moderate resistance to early and late leaf spot, and more resistant to stem rot and lodging, compared with check variety "Daekwang". Owing to these superior growth characteristics of more lodging resistance and source ability in late maturing stage, the average yield of "Sewon" was more productive than reference variety by 21% with 11.97 MT/ha for fresh pod and by 16% with 5.23 MT/ha for dried grain in 3 year regional yield trials.

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Using genotyping-by-sequencing for revealing genetic relationship and diversity of sesame genotypes (*Sesamum indicum* L.) with black and white Seed Coat

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Sesame is an important oil crop widely grown in Asian countries, including Korea. The genetic relationship and population structure analysis help to infer the history, gene flow, and domestication time of the crop and its wild ancestors, which is critical for designing breeding methods and for the development of improved cultivars. In the present study, we report the successful application of genotyping-by-sequencing (GBS) in revealing the genetic relationship and diversity in 89 black and white seed coat sesame genotypes, mostly from Korea. The GBS libraries were constructed using restriction enzyme *ApeK1*. More than a half million (575,712) SNPs were identified from the GBS data and filtered with the criteria of minor allele frequency (MAF) > 5%, missing data < 30%, and with less than 3 read depth. The genotypes containing more than 30% missing genotype data were also removed. The final dataset comprising 9041 high-quality SNPs were then used for genetic diversity analysis. The STRUCTURE analysis divided the sesame genotypes into five subgroups, whereas the distance-based phylogenetic analysis formed 8 subgroups. The black-seeded wild sesame accessions and the gray-seeded Indian accessions formed distinct clusters. Similarly, the genotypes with white seed coat were clustered together, whereas, the light brown-, yellow- and brown-seeded genotypes clustered together at the close proximity or admixed with the white- or black-seeded sesame genotypes. The genotypes particularly from Korea were found to cluster together in each of the classified groups and were clearly distinct at both genetic as well as phenotypic levels. These results would be useful in understanding the genetic structure of the rough (black) and smooth seeded (white) sesame genotypes from Korea.

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The SNP-based molecular diversity analysis of sesame genotypes and characterization of susceptible and resistant lines to *Phytophthora nicotianae*

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Recent genetic diversity studies involving sesame genotypes from Korea indicated the narrow genetic pool of sesame cultivars or inbred lines. The genetic diversity analyses utilizing molecular markers provides means to select diverse germplasm for variety development, thereby improving the genetic base. Additionally, such studies help to select the genotypes with a diverse background, which also might show variation for different phenotypes such as biotic or abiotic resistance. In the present study, we determined the genetic diversity and phylogenetic relationship among 86 Korean sesame genotypes, which included 68 (to 2 pathotypes of *Phytophthora nicotianae*; 'KX160004', 'KX160000')-susceptible and 18 ('KX160004', 'KX160000')-resistant genotypes. Over nine thousand genome-wide SNP markers were used to screen the selected set of phytophthora susceptible, and resistant genotypes. A dendrogram based on UPGMA tree showed that all the sesame genotypes could be grouped into distinct clusters. Ten of the 18 resistant genotypes were clustered into the groups having the majority of the resistant genotypes. The remaining 8 resistant genotypes, however, were found to be dispersed across the dendrogram tree and grouped with the susceptible genotypes. The results showed that the eighteen sesame phytophthora resistance genotypes have the distinct genetic background. Such diverse parents will be used for the development of mapping populations for Phytophthora resistance genes from different phylogenetic groups and for wise utilization of the Phytophthora-resistant germplasm in sesame breeding programs.

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Development of infectious clones of *Tomato yellow leaf curl Kanchanaburi virus* (TYLCKaV) and *Pepper yellow leaf curl Thailand virus* (PYLCTHV)

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Yellow leaf curl symptoms are caused by TYLCV (*Tomato yellow leaf curl Kanchanaburi virus*) and PYLCV (*Pepper yellow leaf curl Thailand virus*) viruses belonging to the *Begomovirus* group in the *Geminiviridae* family. *Begomoviruses*, circular single-stranded DNA viruses cause severe crop losses in tropical countries, particularly in tomato and pepper. In this study, TYLCKaV and PYLCThV were isolated from the yellow leaf curl symptomatic leaves of pepper. The viral genome was sequenced and infectious TYLCKaV and PYLCThV clones were developed. Both DNA-A and DNA-B were designed to have partial tandem repeats and were inserted into the pICH86988 binary vector using golden gate and restriction enzyme cloning method. *Agrobacteria* containing each constructed clone were infiltrated into tobacco, tomato, and pepper to test their infectivity. One hundred percent infectivity was observed in the tobacco plants showing typical yellow leaf curl symptoms. Among two infectious clones, only TYLCKaV exhibited viral symptoms in tomato. However, TYLCKaV did not show any viral symptoms and no virus accumulation was observed in pepper. Now, we are testing the infectivity of PYLCThV infectious clones in pepper.

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Identification of gene for gametophytic development in Arabidopsis

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Pollen development, a critical step for successful plant proliferation, is proceeded by an asymmetric pollen mitosis I and a symmetric pollen mitosis II under the elaborate genetic control. In order to identify genes important for the pollen development we morphologically screened DAPI-stained mature pollen grains from an activation tagging pool. As a result we isolated a heterozygous mutant line, AP-29-38, producing high levels of abnormal pollen grains. Detailed phenotypic analyses showed that the mutant microspores divide abnormally at pollen mitosis I. In addition, reciprocal crossing results revealed that genetic transmission of the mutant allele is highly reduced both through the male and the female, suggesting the gene function of the responsible gene is important for both sexes. Since the mutant line contains multiple T-DNA insertions we performed a map-based cloning approach and narrowed down to a handful of candidate genes including At1g50710 as the strongest candidate. At1g50710 encodes AUGMIN4, a member of the augmin complex which consists of eight subunits and plays an essential role for dynamic microtubule organization. Currently, we are carrying out genetic complementation analyses. Moreover, to confirm that AUG4 gene is responsible for the mutant phenotype SALK line independent T-DNA insertion lines analysis is in progress.

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실생 초기세대 육성 방법에 따른 감자 계통 선발 효율 분석

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우리나라 감자 품종 육성은 주로 교배육종을 통해서 육성되고 있으며 실생 세대부터 1년에 1세대가 진전되어 신품종 출원까지 9~10년이 소요되고 있다. 국내 가공용 감자 시장은 연간 20%이상 성장하고 있어 새로운 감자 품종에 대한 요구가 증대하고 있지만 기존의 육종 체계에서는 장시간이 소요된다. 감자 육종 체계에서 세대와 연한을 단축하여 조기 선발 할 수 있는 기술과 체계를 개발할 필요가 있다. 본 연구는 여름에 진정종자를 파종하여 9월에 선발하고 이듬해 여름에 다시 실생 2세대를 진전시키는 기존 육종 방법을 대신하여 겨울 온실에서 진정종자를 파종하여 선발하였다. 그리고 그해 가을과 이듬해 봄에 세대를 진전시켜 세대와 연한을 단축하고 실생 초기세대에서 포트 크기에 따른 생육, 괴경 특성을 비교하고자 한다. 2016년 겨울 온실에 G15D01 조합 등 5개 교배조합의 실생 1세대 포트별 생육 특성은 대포트에서 경장이 79.5~117 cm로 소포트 45.2~89.4 cm보다 경장이 더 길었다. 포트별 괴경 특성 조사에서는 대포트에서 주당 괴경 수, 괴경 중이 13.7~23.3 개/주, 93.3~119.1 g/주로 더 많았다. 5개 교배 조합의 실생 2세대 선발은 열개서, 기형서 등 생리장해가 G15M02, D03 교배조합 계통에서 46 %, 40 % 발생하여 도태되었다. 포트 크기에 따른 괴경 균일성은 교배조합별로 달관지수가 4.7~5.1로 포트의 크기에 상관없이 괴경 크기가 균일하였다. 수량성에서는 조합별로는 G15D01 교배 조합에서 달관지수가 3.3~3.9로 제일 낮았으며 포트 크기에 따른 수량성은 소포트에 비해 대포트에서 선발한 계통에서 수량성이 높았지만 G15D03 교배조합에서는 소포트에서 선발한 계통에서 수량성이 더 높았다. 실생 3세대에서 봄 재배 적응성 검정과 괴경, 가공성 특성 평가를 통해 실생 초기세대 육성방법에 따른 선발 효율을 분석하고 감자육종 연한 단축과 조기 품종화가 기대된다.

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CRISPR/Cas9-mediated mutagenesis in *Petunia × hybrida* protoplast system for Modification of Flower Color

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RNA-guided genome editing using the CRISPR/Cas9 (clustered regularly interspaced short palindromic repeats)/Cas9 (CRISPR-associated protein 9) system has been reported to have target-specific modifying potential in many crops. Plant protoplasts are useful for assessing the efficiency of CRISPR/Cas9-mediated mutagenesis. Here, we report successful targeted mutagenesis of a floral pigmentation gene called *flavanone 3-hydroxylase (F3H)* in *Petunia* protoplast cells. We transiently introduced RNA-guided endonuclease (RGEN) ribonucleoproteins (RNPs) complex with different sgRNAs targeting five *F3H* regions in to isolated protoplast cells of *Petunia* (cv. 'midnight'). High resolution melt (HRM) curve analysis showed that the *F3H* gene was mutated at the targeted sites in the protoplast transfectants. In addition, the mutagenesis of INDEL (deletions and insertion types) at the targeted loci was confirmed by targeted deep DNA sequencing. Mutation rates from those five *F3H*-RGEN target sites was estimated which ranging from 0.8% to 49.3% with an average of 20.8 ± 7.2 %. A further analysis showed that the average ratio of deletion to insertion produced by the five *F3H*-targeting RNPs (F3H1 – 5) was about 45.4:54.6. Our results demonstrated that direct delivery of the RNPs into protoplast cells of *Petunia* can be exploited as an efficient tool for genetic manipulation of flower colors in important ornamental flowering plants without the use of traditional transgenic approaches.

Keywords: *F3H* gene, flower color, RNA-guided endonuclease, protoplast, HRM assay, deep sequencing

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Phylogenetic analysis of 22 *Vigna* species using chloroplast RNA-sequencing data

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Vigna is a genus of flowering plants in the legume family, and about 100 species belong to this genus. Azuki bean, blackgram and mung bean are the representative crops of the species which are cultivated and consumed as human food in Asian country-wide. Unlike other major crops, phylogeny of *Vigna* species has not been classified using chloroplast genome, although the method has been established and generalized in other plant species. With the advancement of sequencing technology, RNA-seq became one of the most powerful tools for analyzing biological characteristics and numerous data have been produced for various purposes. In this study, phylogenetic trees of seven *Vigna* species were constructed using DNA and RNA sequences and compared. Each data was aligned to chloroplast reference genome of *Vigna radiata* to analyze variant among the species, using BWA for DNA and Tophat for RNA under consideration of sequence characteristics. As results, 1,836 nucleotide variations were identified using DNA sequence and distributed mainly along small single copy and long single copy region of chloroplast genome of *V. radiata*. While, only 165 variants were identified when using RNA-seq and distributed only on *rrn23*, *psbC* and *psbD*. Despite the relatively low number of sequence variations in RNA-seq compared to the result from DNA sequence data, the phylogenetic trees constructed using DNA and RNA sequence were consistent to each other, represent divergence of *Vigna* species. Consequently, we constructed phylogenetic tree of 22 *Vigna* species using 59 variants derived from RNA-seq data. In conclusion, phylogenetic analysis using RNA-seq is practically applicable to evolutionary studies in *Vigna* species. Furthermore, based on this phylogenetic study, gene expression patterns of chloroplast is under analysis.

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Elucidation of senescence mechanism with T-DNA insertional mutant *ck40* in rice

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Chlorophyll breakdown is a vital catabolic process of leaf senescence and fruit ripening as it allows for recycling of nitrogen and other nutrients. In this study, we found out that T-DNA insertional line *ck40* maintained greenness with increased chlorophyll retention during senescence, while photosynthetic competence was not normally maintained during dark-induced leaf senescence, indicating *ck40* is a non-functional stay-green mutant. qRT-PCR analysis of the genes related to chlorophyll catabolic pathway showed that transcript level of *NOL* was significantly lower especially in the early stage of senescence. This indicates that CK40, a receptor kinase, may indirectly control *NOL* expression by regulating a transcription factor. Ultrastructural analysis revealed that thylakoid membranes were thick but reduced in size in the chloroplasts of senesced *ck40* mutant. In addition, chlorophyll b was highly accumulated as well as Light-harvesting chlorophyll b-binding proteins and a core protein PsbA remained stable in *ck40* mutant than the wild type after dark-incubation. By hormone treatment test, we further revealed that CK40 function is involved in signaling of MeJA and ethylene-induced senescence but not in ABA. Agronomical traits analysis revealed that loss of CK40 function showed significant decreases in spikelet number and length of panicles, leading to yield reduction. Conclusively, these results indicate that CK40 function is critical for the regulations of spikelet number and yield as well as degradation of chlorophyll b and photosystem II during dark-induced senescence. Further analysis is necessary to identify the target of CK40, possibly a transcription factor, in order to elucidate CK40-mediated senescence mechanism.

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Characterization and cytomorphology of F1 and F2 hybrid between transgenic *Brassica napus* and *B. rapa*

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A number of studies have been conducted on hybridization between transgenic *Brassica napus* and *B.rapa* or backcross of F1 hybrid to their parents. However, trait changes must be analyzed to evaluate hybrid sustainability in nature. In the present study, *B.rapa* and transgenic(*BrAGL20*) *B.napus* were hybridized to verify the early flowering phenomenon of F1 hybrids, and F1 hybrid traits were analyzed to predict their impact on sustainability. Flowering of F1 hybrid has been induced slightly later than that of the transgenic *B.napus*, but flowering was available in the greenhouse without low temperature treatment to young plant, similar to the transgenic *B.napus*. It is because the *BrAGL20* gene has been transferred from transgenic *B.napus* to F1 hybrid. The size of F1 hybrid seeds was intermediate between those of *B.rapa* and transgenic *B.napus*, and ~40% of F1 pollen exhibited abnormal size and morphology. The form of the F1 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 ELONGASE1* alleles. Furthermore, F2 hybrids could not be obtained. However, BC1 progeny were obtained by hand pollination of *B.rapa* with F1 hybrid pollen, withanout crossing rate of 50%.

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Early stage assessment of sesame genotypes from worldwide collection for agro-morphological traits and genetic diversity

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Sesame is an important oilseed crop throughout the world. Phenotypic and genetic traits are crucial elements for crop improvement regarding yield and relative desirable traits. The aim of this study is to investigate phenotypic and genetic diversity of a worldwide collection of sesame. A total of 445 accessions from Africa, Asia, America and Europe continents were tested under field conditions for agronomic traits. The field experiment was designed following the augmented block design. The check genotypes were eight-time replicated. The space between two plants as 0.2 m and the sowing line per accession was 1.4 m. Agro-morphological parameters of early stage were recorded during the plants development. DNA extraction of each genotype will be performed and SSR molecular markers will be used for genetic analysis study. The phenotypic and genetic patterns of sesame accessions will provide preliminary information relative to the best accessions based on their performances. A second year of experiment will be planned following by genome comparison of the selected genotypes for a genomic variation investigation.

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Comparison of the irradiation effects between proton beams and gamma rays on M₁ seeds and seedling growth in rice for mutation breeding

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In mutation breeding, ionizing radiations are widely used as physical mutagens. Proton beams (PBs) are known to have physically intermediate properties between low linear energy transfer (LET) gamma rays (GRs) and high LET ion beams, but their mutational effects have still not been characterized. This study was conducted to estimate the biological effect of proton beam irradiation compared with gamma irradiation and investigate the optimal dose for mutation induction in rice. Rice seeds were irradiated using a 100 MeV Linear Accelerator (TR103) at the Korea Multi-Purpose Accelerator Complex for PBs and a ⁶⁰Co gamma irradiator at the Advanced Radiation Technology Institute for GRs, with doses of 50, 100, 150, 200, 250, 300, 400, 500, 600, and 700 Gy in both cases. The PB irradiated seeds did not germinate from 500 Gy or higher doses, whereas the GR irradiated seeds did not germinate from 600 Gy or higher doses. The dose showing a half germination rate against the control were 200 Gy and 350 Gy for PBs and GRs, respectively. The median lethal dose (LD50) and the median reduction dose (RD50) values estimated by analysing the survival rates and growth of the four-week-old seedlings were 150 Gy and 175 Gy for PBs, and 250 Gy and 300 Gy for GRs, respectively. These results suggest that the biological damage of PBs is more severe than that of GRs at the same dose. To induce mutations using PBs in rice, doses from 100 to 150 Gy seem to be proper. Now we are growing four large scale M₁ populations, with irradiation doses of 100 Gy and 150 Gy for PBs and 170 Gy and 250 Gy for GRs, to make mutagenized lines and subsequent genomic analysis.

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Characteristic analysis of the CaCPR1 gene as a class of key enzyme that promote P450 enzyme reactions which related with productivity

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Plant NADPH-P450 reductase (CPR) is essential protein plays a role in transferring electrons for the catalytic reaction of P450 and is known as a key enzyme that regulates the P450 reactions. We identified several P450 genes involved in productivity through previous studies and isolated the *CaCPR1* gene from hot pepper (*Capsicum annuum* L. cv. Bukang) to regulate the reactions of the these P450 genes. To investigate the enzymatic properties, the *CaCPR1* gene was heterologously expressed and purified in *Escherichia coli*. The enzymatic properties of *CaCPR1* was confirmed by measurement of characteristic absorption spectrum and catalytic activities, which were assessed using protein and chemical substrates including P450, cytochrome c, cytochrome b₅, MTT, and CTC. In particular, *CaCPR1* could support abscisic acid 8'-hydroxylation of purified plant CYP707A70 (ABA 8'-hydroxylase) better than rat CPR and FDX/FDR. These results reveal that the overall enzymatic properties of *CaCPR1* is quite similar to those of typical CPR enzymes from other sources that have proven to be of utility value and indicate that *CaCPR1* is better suited to promote the reactions of plant P450s than other sources of CPRs.

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일경일화 복륜 복색 향 춘란 '색동이'

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춘란(*Cymbidium goeringii*)은 3~4월에 개화하는 반 음지성 식물로서 한국, 중국, 일본, 대만 등의 온대 기후를 갖는 동아시아에 자생하고 있다. 수입되는 동양란을 대체하고 경쟁력 있는 한국 춘란품종을 육성하고자 개발된 '색동이' 품종의 잎 길이는 14.5cm로 형태적으로 소형 심비디움에 속한다. 육성과정은 2004년 중국춘란과 한국춘란을 교배하여 2007년 복륜무늬를 발견하였고, 2008년까지 기내 고정 후 2010년 포장시험에서 무늬와 형질이 고정됨을 확인하였다. 해당 품종은 맑고 은은한 향을 가지고 있고, 신아 때부터 복륜이 형성되어 잎 끝에 백황색의 복륜이 들며, 꽃에 두 가지의 색상이 발현되는 복색화로서 향기와 무늬, 복색을 가지고 있어 수출용으로 경쟁력이 높을 것으로 기대된다. 본 연구는 농림기술기획평가원 기술사업화지원사업(815004-3)의 지원에 의해 수행되었다.

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보람찬과 Pecos 유래 재조합자식계통의 농업형질 특성

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전라북도 완주군 이서면 혁신로 181 농촌진흥청 국립식량과학원

‘Pecos’는 *tropical japonica* 생태형의 미국 벼 품종으로 우리나라 *temperate japonica* 품종과 다른 농업형질 특성을 가지고 있다. Pecos는 중원형 입형 특성에 황갈색 외영, 자색의 주두, 부선, 호영을 가지고 있으며 외영과 잎에 모용이 거의 없는 특성을 나타낸다. 우리나라 육성품종에 없는 새로운 형질 특성을 평가하고 육종사업에 활용하기 위해서 Pecos를 부분으로 하고 우리나라 자포니카 초다수 품종인 ‘보람찬’을 모본으로 인공교배하여 단일종자후대법으로 F₇세대 187개 재조합자식계통을 육성하였다. 모·부분과 재조합자식계통에 대한 출수기, 간장, 수장, 수수 및 입형 관련 형질을 조사하였고, 수수 관련 형질인 외영의 모용성과 색, 주두, 부선, 호영의 색을 조사하여 유전분리비를 분석하였다. 보람찬과 Pecos의 파종 후 출수기까지의 기간은 109일과 99일이었으며, 재조합자식계통 집단은 89~127일에 분포하였고 보람찬 보다 출수가 늦은 계통이 117계통이었다. 간장, 수장, 수수는 대부분 정규분포하는 경향을 나타냈다. 보람찬은 현미장폭비 1.61의 단원형, Pecos는 2.18의 중원형 입형 특성을 나타냈다. 재조합자식계통의 입형 관련 형질은 대부분 정규분포하는 경향이었으며, Pecos와 같이 현미장폭비가 2.0이상인 중원형 계통은 51개로 단원형 입형의 계통이 더 많이 존재하였다. 낱알의 길이는 낱알의 두께, 장폭비, 천립중과 정의 상관을 나타냈고, 낱알의 두께는 장폭비와 부의 상관을, 장폭비는 천립중과 부의 상관을 나타냈다. 수수 관련 형질의 형태학적 특성은 보람찬은 모용성이 있는 황백색 외영에 주두는 백색, 부선과 호영은 짙색이었고, Pecos는 모용성이 거의 없는 황갈색 외영에 주두와 부선, 호영은 자색이었다. 재조합자식계통의 외영색, 주두색, 부선색은 보람찬과 Pecos형으로 3:1의 분리비를 보여 Pecos의 형질 특성은 하나의 열성유전자가 관여하는 것으로 판단되었다. 형질들의 관련성을 보면 외영의 모용성은 외영색, 주두색, 부선색, 호영색과는 연관되었고, 주두색은 부선색 및 호영색과 연관되어 있는 것으로 나타났다. 보람찬과 Pecos 유래 재조합자식계통은 우리나라 자포니카 품종과 다른 형태학적 특성을 가지고 있어 육종적 가치를 평가하기 위해 향후 정밀한 특성조사가 필요할 것으로 생각된다.

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눈과 입이 즐거운 레몬 신품종 ‘미니몬’

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최근 우리나라의 분화(pot-flower) 경매 거래량에 따르면 주로 관상용으로 이용되는 분화 거래량은 꾸준한 증가 추세를 보이고 있으며, 그 중 거래되는 과수 분화류는 감귤과 레몬이 유일하다. 따라서 농촌진흥청에서는 관상용 레몬을 육성하여 관상용 레몬 소비를 촉진코자 관상용 레몬 ‘미니몬’을 육성하였다. ‘미니몬’은 ‘Maiyer’레몬의 자연교잡 우연실생으로 기존 ‘Maiyer’레몬과 비교했을 때 과실 크기가 작고 둥근 모양이기 때문에 관상용으로 적합하고 식용으로도 이용할 수 있다는 것이 가장 큰 특징이다. ‘미니몬’은 2006년 교배가 된 후 2007년에 종자를 채종한 후에 시설에서 종자를 파종하고 육묘를 하였으며 2009년 봄 탕자나무에 고접을 하였다. 이후 2013년도에 첫 결실이 이루어져서 2016년까지 특성조사를 실시한 결과 우수하여 1차 선발하였고, 2017년 최종 선발하여 직무육성신품종 심의회에서 신품종으로 선정되었다. ‘미니몬’은 수세가 중간정도이고 나무자세도 개장성이며, 과실은 동그란 구형이고 열매크기는 40g정도로 매우 작은 편이다. 겉껍질은 2.6mm정도로 기존 레몬에 비해 다소 얇은 편이다. 자가 화합성이고 평균 9개의 종자가 형성되며 형성된 종자의 배는 다배성을 나타낸다. 1차 개화시기의 수확기 과실 당도는 8.7°Brix, 산도 5.00%로 대조품종과 비슷한 수준을 나타낸다. 가지에 작은 가시가 발생되나 유년성이 타파되면서 가시가 없어지는 경향을 나타낸다. ‘미니몬’의 새순은 4월 중순에 발아되고, 꽃은 대부분 5월에 개화되는데 사계성이 있다.

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Detected candidate gene related mesocotyl elongation using GWAS and haplotype analysis

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Direct-seeding cultivation is getting important to solve the problems such as water shortage, labor scarcity and cost down in all over Asia, including Korea. Low temperature germination and mesocotyl elongation are important traits for expanding of direct seeding cultivation. In this study, We evaluated elongation ability of mesocotyl, and performed GWAS analysis on core collection of 137 cultivars. Elongation ability of mesocotyl was appeared that average 3.2mm in Indica type, average 3.4mm in Japonica type and average 23mm in Aus type. In result of GWAS analysis, significant SNP was explored for elongation ability of mesocotyl on the chromosome 1, 3, 4, 8, 11. We performed haplotype analysis of candidate genes. These results will be able to use for development of suitable cultivar in direct-seeding. This study was performed by support of National research foundation of Korea (NRF-2015R1C1A1A01054699).

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병에 강하고 기계수확이 가능한 두부용 콩 ‘평원’

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쌀 생산조정에 따라 논에서의 콩 재배가 증가하고 있으며 콩의 재배가 규모화, 집단화함에 따라 기계화의 필요성이 증가하고 있다. 또한, 논 재배에서 배수불량에 따른 습해와 함께 뿌리썩음병이 발생하기도 한다. 이에 식량과학원에서는 병에 강하고 기계수확이 가능한 콩 ‘평원’을 개발하였다. 병과 재해에 강한 육성계통 ‘SS98205’를 모본으로 하고, 다수성인 ‘대망2호’를 부분으로 2008년에 인공교배하여 F₃ 세대까지 집단 양성한 후 F₄부터 계통으로 전개하여 선발하였다. 2013~2014년도에 실시한 생산력검정시험에서는 다수성으로 유망시되어 ‘밀양288호’의 계통명을 부여한 후 2015~2017년 3개년 간 전국 11개소에서 지역적응성을 검정하였다. ‘평원’은 유한신육형으로 모용은 회색이고, 협색은 갈색이며 종피와 배꼽색은 황색이고 꽃색은 백색이다. 개화기는 대원콩보다 7일 늦으나 성숙기는 비슷하며, 경장이 대원콩 대비 13cm 짧은 반면 지면에서 가장 낮은 꼬투리까지의 높이가 4cm 더 높으며, 100립중이 22.8g으로 대원콩보다 3.6g 가벼운 중립종이다. 불마름병에 중도저항성이며 검은뿌리썩음병에 대한 이병주율이 낮다. 콤팩트 수확적성 관련형질인 도복에 강하고, 협고가 14cm로 비교적 높으며, 건조기를 이용한 협개열성 조사에서 탈립이 되지 않아 기계수확이 용이한 품종으로 생각된다. 매주수율은 낮으나 두부와 청국장 제조수율이 높으며 전국 평균수량은 3.66ton/ha로 ‘대원콩’보다 10% 증수한다.

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An ancient regulatory module for tip growth in land plants

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ROOT HAIR SPECIFIC (RHS) genes, which contain the root hair-specific cis-element (RHE) in their regulatory regions, function in root hair morphogenesis. Here, we demonstrate that an *Arabidopsis thaliana* basic helix-loop-helix transcription factor, ROOT HAIR DEFECTIVE SIX-LIKE 4 (RSL4), directly binds to the RHE *in vitro* and *in vivo*, up-regulates *RHS* genes, and stimulates root hair formation in *Arabidopsis*. Orthologs of RSL4 from a eudicot (poplar, *Populus trichocarpa*), a monocot (rice, *Oryza sativa*), and a lycophyte (*Selaginella moellendorffii*) each restored root hair growth in the *Arabidopsis rsl4* mutant. In addition, the rice and *Selaginella* RSL4 orthologs bound to the RHE in *in vitro* and *in vivo* assays. The *RSL4* orthologous genes contain RHEs in their promoter regions, and RSL4 was able to bind to its own RHEs *in vivo* and amplify its own expression. This process likely provides a positive feedback loop for sustainable root hair growth. When *RSL4* and its orthologs were expressed in cells in non-root hair positions, they induced ectopic root hair growth, indicating that these genes are sufficient to specify root hair formation. Our results suggest that RSL4 mediates root hair formation by regulating *RHS* genes and that this mechanism is conserved throughout the tracheophyte (vascular plant) lineage.

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쓰러짐에 강하고 기능이 우수한 담적색 신품종 팥 ‘홍다’

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‘홍다’는 기계화 적성이 우수하고 기능이 뛰어난 팥 품종을 육성하고자 2008년 하계에 국립식량과학원에서 쓰러짐에 강한 재래종 IT1893914를 모본으로 하고 적색이고 대립인 일본수집종 K265217을 부분으로 인공교배하여 계통육종법으로 선발한 품종이다. 2013~2014년 생산력검정시험에서 쓰러짐에 강하고 수량성이 높아 “밀양30호”로 계통명을 부여하였다. 2015~2017년 지역적응시험을 실시한 결과, 기능이 우수하고 내재해성 품종으로 인정되어 2017년 농작물 직무육성 신품종 선정위원회에서 신규등록품종으로 결정되었다.

‘홍다’의 개화일수는 46일로 충주팥보다 7일 정도 빠르고 생육일수가 99일로 5일 빠른 중만생종이다. 경장은 61cm이며 헵당립수는 7.1개로 충주팥보다 많고 쓰러짐에 강하다. 100립중은 14.1g으로 맑은 적색의 종피색을 가진 품종이다. 통팥 가공적성이 우수하고 양금수율이 높아 팥 가공제품 제조시 품질면에서 유리하다. 수량성은 지역적응시험에서 평균수량이 2.10MT/ha로 다수성 품종이다. 적응지역은 강원도 산간고랭지를 제외한 전국 팥 재배 지역에서 재배가 가능하다. 기계수확이 가능한 ‘홍다’는 노동력과 생산비절감으로 생력화와 농가소득 증대에 기여할 것으로 기대된다.

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기후변화 대응 다수성 고구마 품종 육성을 위한 계통 선발

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전남 무안군 무안로 199 국립식량과학원 바이오에너지작물연구소

고구마는 가뭄 등 불량 환경에 대한 적응성이 뛰어난 작물로 알려져 있으나 최근 고구마 정식시기의 가뭄 지속, 병해충 피해 등으로 인해 단위면적당 생산량이 감소하고 있다. 이러한 고구마 생산량 감소에 대응하기 위해 환경 스트레스에 내성이 강한 다수성 품종 육성이 필요하다. 가뭄 등 환경 스트레스에 내성이 강한 다수성 품종 육성을 위한 교배 모·부분 자원을 확보하기 위하여 페루에 위치한 국제감자연구소(International Potato Center)와 공동으로 본 연구를 수행하였다. 국제감자연구소 보유 유전자원 중에서 고구마 주요 병해충인 덩굴쪼김병, 선충에 저항성 반응을 보이는 5개 자원을 교배 부분으로 선정하였고, 괴근 수량이 양호한 90개 자원을 모본으로 선정하여 인공교배를 하였으며 284조합 7,999립을 채종하였다. 2015년과 2016년에 교배 종자를 발아시켜 국립식량과학원 바이오에너지작물연구소 내 육묘상에서 육묘하였고 실생개체선발시험을 통해 괴근의 비대 정도가 양호한 86개 계통을 선발하였다. 2017년에는 86개 계통으로 계통선발시험을 수행하여 대비품종보다 상품괴근 수량이 많거나 포장에서의 생존율이 높은 18개 계통을 선발하였다. 이중 115116-01 등 3계통은 대비품종보다 상품괴근 수량이 55% 내지 107% 더 많았다. 선발된 계통들은 내재해, 다수성 고구마 계통 육성을 위한 교배 자원으로 활용할 예정이다.

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도복에 강한 다수성 흑향미 ‘드림흑향찰’

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흑미 주산지인 전북지역에 적합한 고품질 유색찰벼 품종육성을 목적으로 2006하계에 전라북도농업기술원에서 JR1-2-7-2-2를 모본으로 하고 흑향벼를 부분으로 인공교배하여 F₃이후부터는 계통육종법에 의하여 육성 선발하면서 내도복성 및 선택검정을 실시하여 초형이 직립이면서 도복에 강하고 품질이 양호한 드림흑향찰을 개발하였다. ‘드림흑향찰’은 출수기가 8월 18일로 ‘조생흑찰’ 보다 17일 늦은 중만생종이며, 벼 키는 67cm로 조생흑찰과 비슷하나 좌절중이 무거워 쓰러짐에 강하고 수발아율은 0.6%로 조생흑찰 11.6%보다 낮다. ‘드림흑향찰’은 벼흰잎마름병과 줄무늬잎마름병에 약하고 해충 및 바이러스에 저항성이 없다. 현미 수량성은 2013~2015년 3년간 실시한 지역적응시험 보통기 보비재배에서 5.05MT/ha로 조생흑찰에 비해 11%정도 많으며, 제현율은 80.5%로 조생흑찰 79.8%보다 높고 향이 있다. 드림흑향찰의 적응지역으로는 전북 평야지 1모작에 적합하다.

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농업유전자원센터 자원기탁 절차 및 현황

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농촌진흥청 국립농업과학원 농업유전자원센터의 주요 업무 중의 하나는 자원 접수 및 임시 번호 부여이다. 특히 최근 강화된 기탁 절차를 숙지하지 못하고 국외에서 우수한 도입 자원을 가지고 오는 경우가 존재한다. 우수한 종자라도 기탁 절차에 필요한 서류를 완벽히 갖추지 못하면 농업유전자원센터에 접수하는 것은 어렵다. 그래서 농업유전자원센터의 기탁 절차를 알리는 것은 물론 2017년부터 2018년까지 농업유전자원센터에 기탁된 자원 현황에 대해서 알리고자 한다. 기탁자원 접수 현황은 다음과 같다. 17년은 93건 4,346자원을 접수했다. 밀, 동부, 병아리콩 등 123작물을 입고 되었고 임시번호는 K261321~K265676를 부여했다. 2018년 1분기 자원접수 현황은 6건 819자원이다. 임시번호는 K266048~K266483이 주어졌으며 벼, 밀 등 54작물이다. 2분기 자원 접수현황은 9건 604자원이다. 임시번호는 K266867~K267470이 주어졌으며 콩 녹두 등 15작물이다. 임시번호를 부여받은 자원들은 등록심의회를 거쳐서 IT번호를 부여받을 수 있다. 학명, 자원명, 원산지, 자원구분 등 기초정보를 충분히 갖추고, 보존되어 있는 등록(IT)자원과 중복되지 아니하며 등록기준량 및 발아율을 만족하는 자원이 IT번호를 부여 받는 조건이다. 기탁받은 작물은 식량작물, 원예작물, 특용작물, 기타작물 순으로 식량작물이 가장 높은 비중을 차지한다. 그러나 최근에는 원예, 특용작물의 활용도도 높아지고 있으므로 원예, 특용작물 유전자원의 확보에 집중할 필요성이 있다. 농업유전자원센터에서 작물의 다양성을 보다 확보하여 농업의 발전에 더욱 이바지 해야 할 것이다.

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Haplotype analyze of the *BADH1* gene and their association with salt tolerance in Rice

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Betaine aldehyde dehydrogenase (BADH) is a key enzyme involved in the synthesis of glycine betaine (GB), a powerful osmoprotectant against salt and drought stress which found in many plant species. Our previous study found that the expression of betaine aldehyde dehydrogenase 1 gene (*BADH1*), encoding a key enzyme for the glycine betaine biosynthesis pathway, showed a close correlation with the salt tolerance of rice. Rice (*Oryza sativa* L.) is thought to be a non-accumulator of GB, but it does express BADH at low levels. In this study, we scanned the *BADH1* sequences of 421 rice cultivars, and 54 wild rice accessions to determine their polymorphisms, gene functions and domestication. A total of 44 alleles for *BADH1* were detected in transcribed regions of cultivars and wild species, while 2 alleles (exon 4 present T/A and exon 11 present A/C) showed high correlation with salt tolerance. These results suggest that the *BADH1* gene could be an excellent candidate for rice functional research and breeding.

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국가 농업유전자원(IT자원)의 활용현황 분석

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농업유전자원센터는 농촌진흥청 산하의 연구기관으로, 미래의 식량전쟁을 위한 보루이자, 육종산업의 발전을 위한 기반 시설이다. 식물자원 중 종자를 중심으로 국가등록이 된 IT 자원을 직접 보존하고 있으며, 총 1,590종 224,926자원의 식물(종자) 유전자원을 보존, 평가 및 분양을 통해 식물 육종학의 발전에 이바지하고 있다.

유전자원센터에서는 유전자원의 관리에 많은 예산과 인력이 소모되기에 보존 안전성에 높은 활용성을 추가하기 위해 분양트렌드를 파악하였다. 2000년~2017년에 자원보존을 위한 증식분양 210,786자원을 제외하고 분양된 390,416자원을 기준으로 하였다. 육종을 포함한 식물소재 산업의 발전을 위한 분양은 총 385,042자원이 분양되었고, 교육·전시 및 기타는 5,374 자원이 분양되었다. 연도별로는 2000년대에 비해 2010년대에 연구목적분양이 급격히 증가하였으며, 5년 전과 비교하였을 때, 식량작물은 116%, 원예작물은 140%, 특용작물은 184% 증가하였다. 이러한 현황을 보았을 때, 식물소재 산업의 발전을 위한 유전자원의 활용은 뚜렷하게 증가하고 있으며, 그 중에서도 특용작물 > 원예작물 > 식량작물 순이다.

분양 트렌드를 통해, 육종을 포함한 식물산업 내의 관심과 앞으로의 발전 방향을 예측 할 수 있으며, 그 결과 특용작물에 대한 관심과 가능성을 알 수 있다. 그러므로 활용이 전제로 된 보존을 위해 특용작물 유전자원의 확보 및 관리에 집중할 필요성이 있으며, 이를 통해 식물소재 산업의 발전에 더욱더 이바지해야 할 것으로 판단된다.

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Evolutionary studies on cultivated and wild rice using chloroplast genome sequencing

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Cultivated rice indica and japonica are the main rice crops of the world. The domestication process of rice is complicated. So far, extensive research on the origin of rice has been carried out, but they have not drawn a unified conclusion on the origins of cultivated rice. Recently, we have found interesting results supporting the independent origin of indica and japonica base on a phylogenetic research of rice chloroplast genome. Here, A total of 475 rice samples were collected from 28 regions of the world's rice-rich areas sequencing with a high average coverage (~15.88X), product ~3.42T raw data. We identified 1286 SNVs and 156 InDels in chloroplast genome among the whole samples. In order to have a more comprehensive understanding of cultivated rice and wild rice, we also classify those rice group in to 29 subgroups. The phylogenomic studies showed that japonica and indica were clearly separated. Phylogenetic analysis identified specific selection markers in different regions of their chloroplast genome. This indicates that different selection characteristics may be processed for indica and japonica during domestication.

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Haplotype diversity of the rice bacterial blight resistance gene in 475 accessions of rice genetic resources

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Bacterial blight (BB) caused by *Xanthomona oryzae* pv. *oryzae* (*Xoo*) is one of the major diseases of rice. It occurs in most areas that cultured rice, such as Africa and Asia. In particular, BB causes serious damage to rice cultured in Southeast Asia. Depending on the growing season, it can cause 20-50% reduction in yield, and it also decreases the quality of the rice. To date, about 39 genes are known to be resistant to blight, nine of which are cloned (*Xa1*, *xa5*, *Xa10*, *xa13*, *Xa21*, *Xa3/Xa26*, *Xa23*, *xa25* and *Xa27*) and six of which are mapped (*Xa2*, *Xa4*, *Xa7*, *Xa30*, *Xa33*, and *Xa38*). Using this knowledge of genetic resistance, we analyzed the haplotype diversity in an effort to develop new BB resistant cultivars. We used the genomic information of 475 key clusters of Korean rice genetic resources including 54 accessions of wild rice. Our analysis of the mutation information of the BB resistance gene found that a large number of SNP and indel mutations exist in the BB resistance gene of the domestic core resource. We extracted alleles of MAF > 0.05 from these mutations and classified them into haplotypes.

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Whole genome sequencing revealed a novel fragrance allele and development functional SNP marker for breeding of fragrant rice

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The traits of fragrant rice (*Oryza sativa* L.) are attractive to consumers. Fragrant rice has a huge economic importance and provides a premium price in global trade. Fragrance in rice results from the loss of function of betaine aldehyde dehydrogenase (*Badh2*) gene on chromosome 8. In this study, whole-genome sequencing data of 475 rice germplasms reveals *Badh2* gene in 49 cultivated and 31 wild rice accession numbers. Thirty-nine alleles in exon region of *badh2* were detected in the sequence data. The novel allele (*badh2*-E2.22) of a single accession in cultivated rice was present one SNP (C/A) in exon 2. In wild rice, five SNPs novel alleles (*badh2*-E2.23, *badh2*-E3.24, *badh2*-E6.25, *badh2*-E10.26, and *badh2*-E13.27) were present C/G in exon 2, exon 3 present G/C, exon 6 present A/G, exon 10 present G/A, and exon 13 found A/T respectively. We developed the new functional SNP marker using primers and TaqMan probes for detection of SNP (C/A) in the *badh2*-E2.22 allele with real-time PCR. Twenty-one fragrant and non-fragrant rice varieties were selected to confirm the presence of the novel allele. The SNP marker reliably distinguished between all fragrant and non-fragrant genotypes and showed perfectly allelic discrimination plot between allele1 (A) and allele2 (C) in 20 rice accessions. Detection of this marker is a rapid and precise way to identify SNP fragrance rice and will be used in a *Badh2* diversity study to improve the breeding of new fragrant rice varieties.

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Haplotype diversity of GBSSI in 475 accessions of rice genetic resources

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Granule-bound starch synthase I (GBSSI) is an enzyme involved in amylose synthesis during starch biosynthesis and is encoded as a waxy gene. This gene which is a starch synthase (SS) isozyme bound to starch particles, is a functionally different gene from the SS involved in amylopectin synthesis. *GBSSI* plays a role in polymerizing sugar molecules produced by photosynthesis into amylose, a form of stored carbohydrate. We performed a mutational analysis of *GBSSI* to provide important background data for improving starch quality based on genome information in rice breeding. To investigate the polymorphisms and genetic distribution of *GBSSI*, we implemented variant calling using a total of 475 resequencing data including 54 wild rice and 421 cultivated rice. As a result, *GBSSI* (*Os06g0133000*) was located on chromosome 6, and a total of 4 mutations were confirmed in 16 Exons. Particularly in Exon 1, a 24bp mutation caused by a frameshift mutation and one non-synonymous SNP was observed. In Exons 5 and 8, many non-synonymous SNPs altering amino acid coding were observed.

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Large-scale vector sequence sampling to develop DNA chips for GMO identification

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We designed array based high-throughput DNA markers with high specificity for GMO detection and identification. The information that could be used for the marker design was not formalized, and different methods were used depending on the type of data. Two main types of information were entered into the GMO-related databases. A pair of PCR primers was converted into the PCR product and its marker was designed. If the sequence of a transgenic plant was provided, the marker was designed after confirming the boundaries between the host sequence region and the vector sequence region. However, direct information for identifying GMO sequences was still limited, so we also designed a wide range of markers for vector sequences to greatly enhance detection coverage. From this more extensive vector sequence database, the sequences in the promoter and terminator regions were sampled. To select highly specific markers, we oversampled a larger number of sequences than the number of required markers, and selected the markers with the highest specificity by performing pairwise sequence alignments.

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Genetic diversity in 3,475 rice accessions of the *Oryza* genus

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We analyzed genetic diversity among 3,475 rice accessions consisting of 58 accessions of wild rice, 417 accessions of the Korean rice core set (KRICE_CORE), and 3,000 accessions of Asian cultivated rice (by CAAS, BGI and IRRI). We performed whole-genome genotyping based on whole genome resequencing from 58 accessions of wild rice and 417 accessions of the KRICE_CORE. We extracted integrated high quality SNP/indel variant sites from 475 and 3,000 rice accessions. We identified linkage distribution, genetic diversity, and haplotype blocks in 3,475 accessions by using the variants, and the allelic and genic differentials between populations such as indica/japonica and wild/cultivated.

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Development of candidate DNA markers for 833K rice integrated DNA array

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We designed a number of candidate DNA markers for the 833K rice genotype DNA array to be used for agricultural researches such as GS, GWAS, map-based cloning, subspecies specific gene analysis, plastid genome analysis, evolutionary study, and GMO identification. The SNP/indel site information to be used for the development of the array markers were collected from an approximate total of 3,500 rice accessions, including Asian cultivated rice, KRICE_CORE, as well as wild rice. We classified the markers into two major groups for genome-wide genotyping and the case study. The markers for the SNP/indels of the entire genome were designed within the genome-wide genotyping group, but the minor variants (alleles) of low frequency were filtered. In the case study group, the markers were divided into 5 subgroups according to research purpose, absent any minor allele filtration. The first group consisted of markers for a genetic diversity study on nucleic and plastid genomes, targeting both cultivated rice and wild rice. The second group consisted of markers for studying the diversity of proven genes shown to be key to major agronomic traits. The third group is for breeders consisting of markers covering genes in a wide range pertinent to traits favorable to breeding, such as eating quality, yield, and disease resistance. The fourth group consisted of markers for metabolic pathway analysis. The fifth consisted of markers for GMO identification.

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춘파밀 육성을 위한 유전자원 및 품종의 춘파재배 적응성 분석

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국내 밀재배 면적은 1만ha 내외로 자급율은 2% 이하다. 자급율 향상을 위한 밀재배면적 확대가 중요하나, 밀 적정 파종시기인 10월 중하순에 잦은 강우로 파종을 하지 못하는 경우가 발생한다. 이를 해결하고자 국내육성 42 품종 등 총 1,117 자원을 추파(10월 24일)와 춘파(2월 9일)로 파종하고 춘파재배 적응성을 비교 검토하였다. 국내육성 품종 42점 중 ‘영광’ 등 6개 품종은 파성이 높아 춘파재배에서는 줄기형성이 지연 되거나 지연되어 춘파용 품종으로는 적당하지 않았다. ‘조경’ 등 36개 품종이 성숙기가 6월 10일 이전으로 수확이 6월 15일 이전에 가능하였다. 특히 ‘조품’과 ‘조농’은 춘파재배시 출수기가 5월 4일과 8일로 다른 품종보다 빨랐으며, ‘조경’과 ‘수안’이 상대적으로 초형이 다른 품종보다 양호하였다. 하지만, 추파재배보다 춘파재배에서 국내육성 품종의 간장은 평균 7.5cm(10%) 감소하였다. 국내육성 품종이외의 유전자원 중에 ‘회계2009’, 중계4899 등 중국도입의 유전자원이 출수기가 5월 10일 이전으로 빠른 편이었다. 도입유전자원 중 ‘CHN’과 ‘BECARD/KACHU’은 직립형이며 간강이 70cm~80cm로 상대적으로 초형이 우수했다. 특히, ‘ICW77-0117-K-1AP-0AP-4AP-2’은 직립형이며 수층이 상대적으로 균일하게 위치하여 품질이 안정적인 품종 육성을 위한 유전자원으로 활용할 수 있을 것이다. 또한 ‘ISENGRAIN’ 등의 유전자원은 파성이 높았으며, 이들 유전자원은 파성이 낮은 유전자원보다 뿌리신장이 약 1.5배 길었다. 이는 파성이 높은 유전자원이 내한발성을 포함한 재배안정성이 우수함을 의미하며, 추후 내한발성 중간모본 개발을 위한 부분으로 활용할 수 있을 것이다.

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Selection of indica rice line of high yield potential adaptable to tropical Southeast Asia

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This study was tried to develop the long grain indica rices adaptable to tropical southeast Asia regions in Cambodian Agriculture Research and Development Institute (CARDI), Cambodia. The final goal is to develop rice varieties and export rice seed which can culture in diverse environmental conditions of tropical regions of southeast Asia under climate change. Using rice germplasm from Cambodia, India, Indonesia, Myanmar, Philippines and Vietnam in CARDI, there were developed 1,450 F1 cross combinations, and selected 1,045 lines in 74 cross combinations in F4 subsequent generation. We could select better lines of clear and translucent long grain from the cross combinations with aromatic varieties of Phka Rumdoul, Senpidao and Senkra Ob in Cambodia varieties, Jasmine85 in Thailand variety, and Basmati370, Pusa Basmati1, Sharbati and Sugandha in India varieties. We developed three promising lines of 96~114 days of the growth duration from sowing to harvesting. These lines were evaluated for adaptability in three regions in Vietnam, and one region in Laos with IR66 as standard check variety. A aromatic line KR52-44-3-1-1-1 was higher 2~7% than that of IR66 except to Longan region in Vietnam. KR55-3-3-3-2 showed higher 16% than that of IR66 in Laos. KR64-27-2-2 was higher 33% than that of IR66 in Dong Nai region, Vietnam. The yields of these lines were higher than those of the leading varieties of OM4900 and OM5451 in Vietnam, and TDK8 in Laos. The percentage of ripened grains was important component traits for yield in dry season of tropical regions in this study. These results mean that heat stress was influenced to increase sterility and decrease the grain filling in dry season. In future, we will try to select the lines of heat tolerance in flowering time and high grain filling in ripening period.

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광안콩 올레산 함량을 조절하는 QTL mapping

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콩의 지방은 일반적으로 5가지 지방산인 palmitic(16:0) 12%, stearic(18:0) 4%, oleic(18:1) 23%, linoleic(18:2) 53%, 및 linolenic acid(18:3) 8%로 구성되어 있다, 그 중 Oleic acid에서 linolenic acid로의 생합성에 관여하는 Fad2-1A와 Fad2-1B 유전자가 기능을 잃을 경우 oleic acid가 높아지는 것으로 보고되었다. 국내에서 육성된 재배콩 광안은 FAD2 유전자에 돌연변이없이 약 40%의 oleic acid 함량을 보이는 것으로 보고되었으나, 이 함량을 조절하는 QTL mapping 연구는 진행되지 않아 본 연구에서 실시하였다.

정상적인 oleic acid 함량을 가진 재배콩 5002T와 oleic acid 함량이 약 40%인 광안을 교배한 뒤 2016년 경북대학교 균위 실험장에서 F_{6,7} 세대 150개의 RILs를 육성하였다. RIL의 유전자형은 각각의 RIL 종자에서 DNA를 추출한 후 Soybean 6K SNP chip을 이용하여 확인하였다. RIL의 지방산 변이를 검정하기 위해 2017년에 4개의 환경에서 2반복씩 파종 하였다. 재배환경별 파종 시기는 경북 균위에서 5월 26일과 6월20일, 전남 광주에서 6월 23일, 충남 천안에서 6월 3일에 파종을 하였다. 지방산 함량은 GC를 이용하여 분석을 하였으며, 염색체 지도와 QTL 분석은 'ICIMapping' 프로그램을 이용하여 실시하였다.

2017년 4개의 환경에서 수확한 150개 RILs과 양친의 지방산 함량을 분석하였다. 양친의 oleic acid의 함량은 광안콩이 평균 39.7% ± 2.7의 결과를 보이고, 5002T이 평균 27.8% ± 6.4의 결과를 보여 기존 연구와 같이 광안콩에서 높은 함량을 확인 할 수 있었다. 150개 RILs에서의 oleic acid 함량은 20.7~40.4%의 범위를 보였으며, 평균 함량은 29.9% ± 3.8로 일반적으로 알려진 23%에 비해 높게 조사되었다. 150개의 RILs는 관찰된 평균과 분산을 기준으로 정규분포를 구성하는 것으로 조사되었다. 조사한 표현형과 유전자형을 토대로 ICIMapping 프로그램을 이용하여 QTL 분석을 한 결과 13번 염색체에서 한 개의 유의적인 QTL을 확인하였고, PVE값은 20.6%인 것으로 나타났다. 이에 새로 발견된 locus를 확인하는 연구를 진행하고 있다.

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The haplotype diversity of pivotal genes across 475 Korean rice core sets in a vitamin E biosynthesis pathway provided in the rice reactome database

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Much research has been done on tocochromanols, also known as vitamin E, which play an important role in human and livestock health. Tocochromanols are metabolites synthesized via the vitamin E biosynthesis pathway and are affected by a number of genes involved in the synthesis pathway. Because of the importance of rice in the diets of many Asian populations, including Korea, studies on the genetic diversity of this crop — related to the biosynthesis of tocochromanols — have been carried out. In 475 accessions of the Korean rice core set, we analyzed the genetic diversity of pivotal genes in the pathway of tocochromanols biosynthesis that are provided in the rice reactome database. This allowed us to gather information on its genetic diversity, enabling a more systematic identification of varieties associated with tocochromanols content.

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Productivity abilities of seed and cone in mating design conditions of *Pinus densiflora* for. *multicaulis*

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This study was carried out to enhance seed productivity and secure genetic resources of *Pinus densiflora* for. *multicaulis*(DM). The characteristics of cone and seed produced by mating design between *Pinus densiflora*(D) and *P. densiflora* for. *multicaulis*(DM) were investigated. The highest number of cone scales (63.0) was obtained from self-pollinated(sp) DM clone B, *P. densiflora* for. *multicaulis* (DM-sp-B), whereas the lowest number of cone scales (44.7) was obtained from two hybrid pines including DM-A×D-075 and DM-A×D-0111. Both the female parents of the hybrids were DM-A. The highest seed production capacity(80.8) was obtained from open-pollinated(op) DM clone B, DM-op-B, and the seed production capacities of DM-op-A, DM-B×DM-B, and DM-B×D-0111 were 67.4, 66.5, 63.1, 55.4, and 53.8, respectively. The highest number of fertile scales (41.5) was obtained from DM-op-B and the lowest number of fertile scales (28.8) was obtained from DM-A×D-075. The DM-B×D-0111 showed high number of developed seeds(43.8) as well as the lowest number of 2nd aborted ovules (5.2) and empty seeds (9). Although the DM-op-B showed the highest number of developed seeds(47.6), the number of empty seeds was, also, the highest(41.2). Therefore, the mating combination of DM-B×D-0111 could be recommended for future breeding program to improve seed yield of DM. In addition, the results showed that there was a strong correlation between the NS and NFS and NS and SP ($R = 0.89$ and $R = 0.83$, respectively; both $P < .01$).

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기상요인이 리기다소나무와 테에다소나무 그리고 이들 수종의 중간 잡종인 리기테다소나무의 춘추재 형성에 미치는 영향

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우리나라에서는 북미와 대서양 연안에 자생하고 있는 리기다소나무와 멕시코만과 대서양 연안이 원산으로 알려져 있는 테에다소나무를 도입하여, 교잡육종으로 중간형질을 나타내면서 우리나라의 기후풍토에 적합한 리기테다소나무를 육성하였다. 본 연구에서는 원산지의 기후대가 서로 다른 이들 3수종을 공시재료로 하였다. 공시수종은 서울대학교 광양연습림 내에서 비교적 우수한 생장을 나타내는 47년생 리기테다소나무와 이것의 육종모수종(育種母樹種)인 테다소나무(49년생)와 리기다소나무(43년생) 5개체씩을 공시하였다. 이를 사용해 흉고단면적의 연간 성장량 및 춘추재 성장량을 분석하였으며, 기상데이터를 활용하여 성장과 기후변화간 상관관계를 분석하였다. 기상변수로는 일별기온(최고/평균/최저)과 일강수량을 사용하였다. 그 결과, 리기다소나무는 상록침엽수의 광합성이 최대에 도달하는 7월의 기온이 낮은 해에는 연간 흉고단면적 성장량이 감소하는 음(-)의 상관관계를 나타냈으며, 흉고 단면적을 구성하는 춘추재의 형성량은 그 보다 앞선 6월의 기온이 낮을수록 감소하는 경향을 나타냈다. 이러한 경향은 테에다소나무에서도 나타났으나, 7월의 강수량이 많은 해에는 연간 흉고단면적 성장량이 증가하는 양(+)의 상관관계를 나타냈다. 한편 리기테다소나무는 3월 기온이 높은 해에 연간 흉고단면적 성장량이 증가하는 양(+)의 상관관계를 나타내고, 8월의 기온이 낮은 해에는 연간 흉고단면적 성장량이 감소하는 음(-)의 상관관계를 나타내서 교잡육종의 모수가 되는 리기다소나무 및 테에다소나무와는 상이한 경향을 나타냈다.

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국내 자포니카 벼 품종의 대용량 자동화 유전자형 분석을 위한 KASP 분자표지 제작 및 검증

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차세대염기서열분석 기술의 발달로 유전체에서 단일염기다형성(single nucleotide polymorphism, SNP)가 대량으로 발굴되고 있다. SNP 분자표지는 빈도수가 높고 공우성인 특성이 있어 그 유용성이 높지만 genotyping이 까다로워 활용성에 제한을 받았지만 최근 다양한 기술이 개발되어 이러한 점이 극복되고 있다. 이 중 대립유전자 특이적인 primer로 SNP genotyping을 수행하는 Kompetitive Allele Specific PCR(KASP) 방법은 분석이 용이하고 high-throughput genotyping이 가능하여 많이 활용되고 있다. 본 연구에서는 국내 자포니카 벼 품종에서 51개 SNP를 선별하고 이를 종자산업진흥센터의 대용량 자동화 분석시스템에서 사용 가능한 KASP 분자표지로 제작하였다. 제작된 KASP 분자표지는 자포니카 벼 품종 20개에 적용하여 그 성능을 검증한 결과 전체 51개중 510개(98.6%)가 증폭이 되었으며 이중 424개(82.0%)가 적어도 한 품종 이상에서 다형성을 보였다. 따라서 이들 KASP 분자표지는 벼의 유전 지도 작성, QTL 탐지, 유전자 동정, 여교배 등에 다양하게 활용될 것으로 판단된다.

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Vernalization-related genes regulate development of wheat spike primordium

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Wheat can be classified into Spring and Winter types based on growth habit. In winter wheat, it requires an induction of a plant's flowering process by exposure to the prolonged cold, known as vernalization. The regulation of various vernalization genes and transcription factors work during vernalization i.e. the time when early development stages of wheat. To clarify an influences of vernalization on the early stage of wheat development, we set experimental groups with different exposure length under low temperature. Two Korean cultivars, Keumgang and Yeongkwang, which have different maturity were incorporated in this study. Plants were exposed different periods under the -4°C . To establish the relationship between spike development and vernalization related genes, we performed qRT-PCR. The expression of *Vrn1* and *VER2* which interacted with *Vrn1* shows a particular trend relative to development of spike primordium. We also figure out genes interacted with *VER2* through yeast two hybridization. The obtained results will provide valuable information to understand the role of vernalization wheat aimed at establishing the mechanism of wheat development.

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인공지능 딥러닝 기반 토마토 과실 생중량 및 부피 예측 모델링

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토마토의 생산성 및 품질에 있어 과실의 생중량 및 부피의 변화는 중요 지표 중에 하나이다. 기존의 방법으로, 과실의 생중량 측정에는 파괴적인 방법을 통한 무게 측정을 통해서, 부피의 경우 버니어 캘리퍼를 통한 측정을 통해서 수행된다. 이러한 방식들은 측정 시 파괴적인 과실의 수확이 요구되거나, 측정과정에서의 많은 시간과 노동력이 소요될 수밖에 없어 과실 비대 과정 중의 연속적인 데이터 획득에 장애요인이 되고 있다.

본 연구에서는 스마트폰의 카메라를 통해 획득된 토마토 과실의 이미지를 딥러닝 기반의 영상처리 및 기계학습 기반의 생중량, 부피 예측 모델을 통한 분석으로 실측 대비 98% 정확도를 갖는 분석 방법을 개발하였다. 개발된 방법은 두 과정으로 구분된다. 첫째, 스마트폰을 통해 획득된 이미지를 통해 과실의 과장 및 과폭을 측정하는 딥러닝 모델 생성 과정, 둘째, 딥러닝을 통해 획득된 과실의 과장 및 과폭 정보를 통해 과실의 생중량 및 부피를 예측하는 기계학습 모델 생성과정. 본 연구는 총 800개 과실 정보를 토대로 540개의 정보는 모델 생성을 위한 학습정보로, 260개의 과실 정보는 생성 모델의 검증을 위해 활용되었다.

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The influence of modifiers genes on the stability of self-incompatibility and genetic architecture of Heterostyly and Homostyly in Buckwheat

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Common buckwheat has the sporophytic self-incompatibility mechanism and that's why it has the ability to cross pollinate between two plants with different styles (the pin type and thrum type). The *S* supergene is thought to govern self-incompatibility, flower morphology and pollen size in buckwheat. Already, we have produced self-compatible buckwheat lines by an interspecific hybridization between *Fagopyrum esculentum* and *F. homotropicum* by embryo culture. The pollen size of F_1 plants produced by a cross between a pin type plant and the self-compatible plant was similar to that of the self-compatible lines and segregated together with flower morphology without exception. The pollen tubes of the self-compatible plants were compatible with styles of the pin plants but incompatible with the styles of thrum plants. But, the pollen tubes of thrum flowers were compatible with the styles of self-compatible plants. Also, the pollen tubes of pin flowers were incompatible with the styles of self-compatible plants. Already, from these results, we have reported a tentative genotype for heterostyle and homostyle flower types. Homomorphism was controlled by a single allele S^h , while the pin/thrum-complex gene was governed by a single genetic locus *S*, with two alleles, *S* and *s*, which control *Ss* (thrum-type) as well as the *ss* (pin-type), respectively. Corresponding represents the case of a single locus *S* with three alleles, S^h , *S* and *s*, and the phenotypes, homomorphic, pin and thrum. It can be characterized by relationship of dominance, $S > S^h > s$. Using the two self-fertile lines, one is considered as the long-homostyle flowers and the other is considered as the short homostyle flowers. If the short-homostyle trait had arisen by recombination in the *S* supergene, its genotype would be considered to be $Gf^p a/Gf^p a$. The pollen tubes of the short-homostylous plant should be compatible with the styles of thrum plants. Also, the pollen tubes of short-homostylous plants should be incompatible with the style of long-homostylous plants, and the reciprocal cross also should be incompatible, because the genotype of long homostyle is $g^s PPA/g^s PPA$. Furthermore, the flower morphology of F_1 plants produced by the cross between cross and short homostyle flowers should be thrum or short homostyle and only short-homostylous plants should be produced by the cross between pin and short homostyle flowers. However, the compatibility or incompatibility of short homostyle flower was not clarified. So, we need to clarify the compatibility or incompatibility of the style of short homostyle flowers for the next step.

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Sequence-based genotyping for marker discovery in Lettuce (*Lactuca sativa* L.) using GBS technology

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The lettuce (*Lactuca sativa* L.) is a major horticultural crop from the family Asteraceae (Compositae). The genus *Lactuca* consists of about 100 species, 3 of which—*Lactuca serriola* L. (prickly lettuce), *Lactuca saligna* L. (willowleaf lettuce), and *Lactuca virosa* L. (bitter lettuce)—are wild species sexually compatible with *L. sativa* (Lebeda et al. 2007, Ivan et al 2008). Lettuce cultivars are classified into horticultural types based on head and leaf shape, size, and texture. All lettuce cultivars are self-fertilizing diploids with $2n = 2x = 18$ chromosomes (Ivan et al 2008). For the development of novel SNP marker, we performed GBS (genotype-by-sequencing) with 96 lettuce cultivars, stored in KSVS (Korea seed variety service), varieties for mining reliable SNP loci. Finally we mined reliable 17,877 SNP loci among total 276,462 SNP's matrix for development of novel SNP marker for lettuce variety identification. The statistic result for transition and transversion ratio showed 1.67. Out of 173,599 transition SNPs, C>T is 87,112 and A>G is 86,487. A transversion SNP revealed 102,744, C>G is 16,367, A>T is 35,764, A>C is 25,430 and G>T is 25,183 respectively. All of SNPs are evenly distributed in each 9 chromosome. The result of genetic relationships analysis in Lettuce (*Lactuca sativa* L.) based on 17,877 SNP loci using MEGA program classified as 3 groups. These sequence-based SNP loci using GBS technology will be useful for develop novel SNP marker and reliable database for variety identification related to seed dispute and distinctness, uniformity and stability (DUS) test for lettuce.

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Isolation and identification of the fungal leaf pathogens of mungbean (*Vigna radiata* (L.) R. Wilczek) leaf spot disease

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Due to their high iron and folate contents, mungbean (*Vigna radiata* (L.) R. Wilczek) is one of the most important crops in South-East Asia. However, considerable amount of the yield is lost due to various diseases. In Korea, limited information is available in public databases regarding the diseases of mungbean. The aim of this study was to isolate and identify the pathogens causing a leaf spot disease in mungbean. In October 2017, there was an outbreak of a leaf spot disease in Seoul National University Suwon Experimental farm. The diseased leaf was surface sterilized and grown in 2% water agar for 5 days. Mycelium from water agar was transferred to potato dextrose agar. The Internal Transcribed Spacer (ITS) sequences indicated that four species *Alternaria alternata*, *Plectosphaerella cucumerina*, *Stagonosporopsis cucurbitacearum* and *Fusarium equiseti* were isolated. Out of the four species, we obtained conidia of *Alternaria alternata* and *Plectosphaerella cucumerina*. The two species were further identified using the sequence of ribosomal large-subunit D1-D2 regions. The sequencing result of confirmed the identification based on ITS region. Using the two strains isolated, *in vivo* and *in vitro* tests on to fulfil Koch's postulate on mungbean is currently ongoing. To the best of our knowledge, this is the first time that either of the species are known to cause diseases in mungbean in Korea. The isolated and identified pathogens can be used to identify qualitative trait loci and candidate pathogen resistance genes which can assist in breeding disease resistant cultivars.

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Development of DNA markers for *Slmlo1.1*, a new mutant allele of the powdery mildew resistance gene *SIMlo1* in tomato (*Solanum lycopersicum*)

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Reductions in growth and quality due to powdery mildew (PM) disease cause significant economic losses in tomato production. *Oidium neolycopersici* was identified as the fungal species responsible for tomato PM disease in South Korea in the present study, based on morphological and internal transcribed spacer DNA sequence analyses of PM samples collected from two remote regions (Muju and Miryang). The genes involved in resistance to this pathogen in the tomato accession 'KNU-12' (*Solanum lycopersicum* var. *cerasiforme*) were evaluated, and the inheritance of PM resistance in 'KNU-12' was found to be conferred via simple Mendelian inheritance of a mutant allele of the PM susceptibility locus *Ol-2* (*SIMlo1*). Full-length cDNA analysis of this newly identified mutant allele (*Slmlo1.1*) showed that a 1-bp deletion in its coding region led to a frameshift mutation possibly resulting in *SIMlo1* loss-of-function. An alternatively-spliced transcript of *Slmlo1.1* was observed in the cDNA sequences of 'KNU-12', but its direct influence on PM resistance is unclear. A derived cleaved amplified polymorphic sequence (dCAPS) and a high-resolution melting (HRM) marker were developed based on the 1-bp deletion in *Slmlo1.1*, and could be used for efficient marker-assisted selection (MAS) using 'KNU-12' as the source for durable and broad-spectrum resistance to PM.

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The *Inquieta* gene encoding a subunit of actin filament regulates trichome development in tomato

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Trichomes are hair-like structures on the aerial surface of many plant species. Trichomes are well characterized for their roles as physical barriers and chemical defense against herbivore attack. Here, we describe the characterization of a monogenic recessive mutant of tomato (*Solanum lycopersicum*) called *inquieta* (*ini*). All trichome types on *ini* plants showed distinct morphological defects (e.g., swelling) that are known to be associated with defects in the actin cytoskeleton. Genetic mapping experiments positioned the *Ini* locus within a 1.5 cM interval on chromosome 11 that contains the tomato homolog of the Arabidopsis *ARPC2A* gene, which encodes a protein involved in nucleating the polymerization of actin filaments. Use of *ARPC2A* as a molecular marker showed that this gene strictly co-segregates with the target locus in a mapping population of 135 F₂ plants. Reverse transcriptase (RT)-PCR and genomic PCR experiments showed that full-length *ARPC2A* is amplified in wild-type but not in the *ini* mutant. Flanking PCR and Southern blot analysis showed that the *ini* mutation corresponds to a complex ~6-kb insertion in the 5th intron of *ARPC2A*. Expression of a wild-type *ARPC2A* in the *ini* mutant background restored normal trichome development. These results provide molecular evidence that altered trichome development in the *ini* mutant is caused by a defect in actin cytoskeleton formation.

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식물생체정보 센서를 활용한 토마토 풋마름병 증상 분석

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토마토 재배 시 가장 문제시 되는 병 중 하나인 풋마름병은 *Ralstonia solanacearum*으로 가지과 작물을 주요 기주로 하며 세계 여러 지역에 분포하는 병이다. 우리나라의 경우도 비닐하우스 재배가 늘어가고 연작하는 작부체계가 일반적으로 점점 풋마름병의 피해가 증가하는 추세에 있다. 현재 풋마름병에 대한 대책으로 대목을 사용하고 있으며, 토마토 접목재배가 점차적으로 늘어나는 추세에 있다. 또한 토마토는 장기재배에 대한 요구도가 커 재배기간 동안 다양한 불량환경 및 병해충을 견디고 재배 후기까지 초세를 유지하는 대목과 기존에 개발된 대목들이 풋마름병에 감수성으로 바뀌고 있어서 저항성 대목 개발이 필요한 실정이다. 본 연구는 식물생체정보 센서를 사용하여 풋마름병 저항성을 조기에 예측하고 대목사용 시 풋마름병의 저항성을 조기에 분석하는 방법을 설정하고자 시험을 수행하였다. 시험재료는 풋마름병 저항성 대목에 접목을 한 것과 접목을 한지 않은 접수를 화분에 파종 후 본엽 5~6매가 되었을 때 풋마름병 균을 접종하였다. 병원균의 접종농도는 1×10^8 /mL CFU로 접종하였으며, 조사는 식물생체정보 센서(Telofarm)를 사용하여 물의 흐름 정도를 측정하였다. 측정결과 균 접종 후 접수로 사용한 토마토 품종의 경우 3일 정도에서 물의 흡수가 줄어들었으며 저항성 대목으로 접목한 재료는 정상적인 물의 흡수를 보였다. 이상의 결과를 볼 때 Micro Sap Flow는 풋마름병의 조기진단에 활용할 수 있을 것으로 보인다.

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Selection of novel source of rice stripe virus resistance

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Rice stripe virus (RSV) is one of the major constraints which is transmitted by the small brown planthopper (SBPH; *Laodelphax striatellus*). Typical symptoms of RSV are chlorosis and weakness of newly emerged leaves, white and yellow spots, stripe and necrotic on leaves, necrotic and wilting leaves, as a consequence, plant growth decline and the contaminated plants are gradually die. (Takahashi et al. 1991). In our previous study, we screened 5 RSV resistant cultivar including 'Padi Adongumarat', 'Tung Ting Wan Hien 1', '02428', 'Erguailai', and 'Daw dam', which harbors different resistance allele with *Stv-b*¹. In this study, RSV resistance Six varieties, which does not harboring *Stv-b*¹, reported by Kwon et al. (2012) were used to identify novel source of resistance on rice stripe virus. Sequence analysis revealed that Daw Dam and Erguailai contain resistant allele of *OsSOT1*. Genotype analysis on *Stv-b* using six Sid markers in the *qSTV11*² region represent that Daw Dam and Erguailai harbors *qSTV11*², which showed Daw Dam and Erguailai expected to have *OsSOT1* gene as well as *Stv-b*. Finally, we expect three varieties, 02428 and Tung Ting Wan Hien 1 as the novel source of Rice Stripe Virus resistance.

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Xanthomonas oryzae pv. *oryzae* triggers transcriptional activation of diverse defense-related genes in rice

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Bacterial blight, caused by *Xanthomonas oryzae* pv. *oryzae*, is a serious disease problem of rice causing damage to rice quality and yield. To understand the transcriptional gene network involved in resistance against *Xoo*, a whole-genome oligonucleotide microarray of two popular *japonica* rice Dongjin and Jinbaek were used to infer transcripts of inducible genes between compatible and incompatible interactions at 48 hour post inoculation. A large number of genes are more evident in the resistant cultivar, which is threefold higher than in susceptible plant. Up-regulation of genes with predicted functions in signaling and transcription signifies orchestration of defense signals and robust cellular reprogramming leading to incompatible interaction. To further identify genes crucial to immunity, 13 *Xoo*-DEGs of different protein class were cloned and overexpressed using CaMV 35S promoter into rice. Most of the overexpression plants displayed improved resistance when screened against *Xoo* Korean race K2. Elevated transcripts levels of several defense-related genes at the downstream of defense signal network also corroborate the phenotype reaction of the transgenic plants. ROS levels continuously magnified after inoculation which indicates robust cellular sensing necessary to initiate cell death. Moreover, expression assays revealed regulation of these genes by cross-communicating signal-transductions pathways mediated by salicylic acid. These collective findings revealed the complexity of key immune signaling conduits critical to mount full defense against *Xoo* in rice.

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Molecular mapping of *Chili veinal mottle virus* resistance genes in pepper using two different approaches

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Chili veinal mottle virus (ChiVMV) is the virus causing severe losses of pepper yield mostly in Asia and Africa. Nevertheless, only one resistance locus (*Cvr1*) with several *Cvr1*-linked markers have been reported up to date. In this study, we precisely mapped the single dominant resistance locus, *Cvr1*, in the pepper accession, 'CV3', and identified the other single recessive resistance locus, *cvr4*, in the pepper accession, 'CV9'. To fine map the *Cvr1* gene, we narrowed down the *Cvr1* locus to 0 cM using two previously reported markers and pepper genome sequence. Due to the highly repetitive nature of this locus containing nucleotide binding leucine rich repeat (NB-LRR) sequences, we are trying to use another approach, Cas9-Assisted Targeting of Chromosome segments (CATCH) cloning, to fine map the *Cvr1* gene. On the other hand, we used bulked segregant analysis RNA sequencing (BSA RNA-seq) approach to map the other ChiVMV resistance gene, *cvr4*. We identified that the *cvr4* was located on the upper region on pepper chromosome 11. Based on RNA-seq data, we could map the *cvr4* gene and developed several *cvr4*-linked markers. We are fine mapping the *cvr4* locus with RNA-seq data combining three published pepper reference genome sets at present. This study could help not only the breeding of ChiVMV resistance cultivar and but also the genetic study of disease resistance in pepper.

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Characterization and Isolation of a spotted leaf sheath Mutant with Early Senescence Involved in Defense Response in Rice

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Lesion mimic mutants (LMMs) commonly exhibit spontaneous cell death similar to the hypersensitive defense response that occurs in plants in response to pathogen infection. Several lesion mimic mutants have been isolated and characterized, but their molecular mechanisms remain largely unknown. Here, a spotted leaf sheath (sles) mutant derived from japonica cultivar Koshihikari is described. The sles phenotype differed from that of other LMMs in that lesion mimic spots were observed on the leaf sheath rather than on leaves. The sles mutant displayed early senescence, as shown, by color loss in the mesophyll cells, a decrease in chlorophyll content, and upregulation of chlorophyll degradation-related and senescence-associated genes. ROS content was also elevated, corresponding to increased expression of genes encoding ROS-generating enzymes. Pathogenesis-related genes were also activated and showed improved resistance to pathogen infection on the leaf sheath. Genetic analysis revealed that the mutant phenotype was controlled by a single recessive nuclear gene. Genetic mapping and sequence analysis showed that a single nucleotide substitution in the sixth exon of LOC_Os07g25680 was responsible for the sles mutant phenotype and this was confirmed by T-DNA insertion line. Taken together, our results revealed that SLES was associated with the formation of lesion mimic spots on the leaf sheath resulting early senescence and defense responses. Further examination of SLES will facilitate a better understanding of the molecular mechanisms involved in ROS homeostasis and may also provide opportunities to improve pathogen resistance in rice.

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Characterization of a new mutant affecting trichome development in tomato

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Trichomes are hair-like structures derived from the epidermis of plants and specialized epidermal structures that function in the plant defense against biotic and abiotic stresses. Trichomes exist in the wide range of plant species and are classified as either glandular or non-glandular types. The glandular trichomes function in a chemical defense against herbivory, and the non-glandular trichomes function as physiological barriers for biotic and environmental stresses. Trichomes of tomato are classified as being four glandular types (type I, IV, VI, VII) and three non-glandular types (type II, III, V). We describe the characterization of a monogenic recessive tomato mutant (*Solanum lycopersicum*) called *no trichome* (*nt*). To analyze the morphology of trichomes on the *nt* mutant in detail, we observed with a dissecting microscope and a cryo-SEM. The results showed that the *nt* mutant has normal types of trichomes in all tissues except on young stems compared with wild-type plants. The *nt* mutant does not have any trichomes in young stems compared to wild-type plants. We are currently doing a map-based cloning to identify *NT* gene.

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QTL analysis of irregular cracking in soybean seed coats

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Soybean seed appearance is a quite important factor for determining commercial value. An irregular cracking in soybean seeds is frequently induced in early mature soybean cultivars and reduce a seed quality. This study was conducted to identified QTL for an irregular cracking in soybean seed coat. 167 F₇ RILs crossed between soybean cultivar 'Uram', late mature and hard to appear crack and 'Chamol', early mature and easy to appear crack was used for QTL analysis. Phenotypes were evaluated in Daegu experiment station in 2016 and 2017. Genetic linkage map was constructed with Axiom 180K SNP array using IciMapping 4.1. The cracked seeds was counted with three replications in randomly collected 100 seeds from bulked harvested lines. The cracked seeds number of 'Uram' and 'Chamol' in combined year was 1.1 and 28.8, respectively. The mean of RILs was 12.9 and the range was from 0.3 to 65.3. In correlation analysis, SCC was negatively correlated with plant height, first pod height, yield, flowering day, growing day, but positively correlated with 100-seed weight. The frequency distribution was analyzed after converting cracked seeds number to score from 1(hard) to 5(easy) and close to bimodal distribution which meant that SCC was controlled by one or two major regions. In two environments, a total of 7 QTLs were identified. Among them, *qSCC2* located on chromosome 2 showed positive additive effects explaining 15.04% of phenotypic variances with 12.9 of LOD score in combined environments. Although the gap of position of *qSCC2* existed depends on experimental years, it was consistently identified in two years and combined year. This results showed that an irregular cracking in soybean seed coats in RIL population used in this study was highly related with QTL on chromosome 2.

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Characterization of mutants related to trichome morphology in tomato

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Trichomes are fine outgrowths derived from epidermal cells on the aerial part of plants. They serve important functions in physical and chemical defense against biotic and abiotic stresses. Trichomes vary in morphology as much as they vary in function. Cultivated tomato (*Solanum lycopersicum*) has seven types of multicellular trichomes that are either non-glandular or glandular. Glandular trichomes synthesize and secrete various metabolites, while non-glandular trichomes act as a physical barrier against herbivores and unfavorable environmental conditions. Despite the important roles of trichomes in plant defense, developmental processes of multicellular trichomes are poorly understood. To identify genes involved in trichome development, Micro-tom mutant population generated by EMS (Ethylmethane sulfonate) mutagenesis was screened. Four mutant lines showing abnormal trichome structure were screened. The mutant lines had distorted and twisted trichomes to a greater or lesser extent compared to wild-type plants. The distorted structure was observed from all the seven types of trichomes on entire plants. To identify genes affecting trichome structure in the mutants, map-based cloning will be performed using a mapping population obtained by crossing the mutant lines with *Solanum pennellii*.

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Nitric oxide increases ginsenosides accumulation by lactic acid bacteria elicitors in adventitious root cultures of *Panax ginseng*

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Nitric oxide (NO) is one of the important signaling molecules that activate defense responses in a plant, and it result in the accumulation of secondary metabolites. In the present study, we investigated the role of NO on ginsenoside biosynthesis from *Panax ginseng* adventitious root cultures after various concentrations and exposure times to three Lactic acid bacteria (LAB) [*Lactobacillus rhamnosus* GG (Lr), *Lactobacillus sanfranciscensis* (Ls), *Leuconostoc citreum* (Lc)] treatments. The changes of NO were analyzed using a nitric oxide colorimetric assay kit, and the individual ginsenosides were identified by HPLC after LAB treatments. NO was generated immediately after LAB treatments and reached the highest level at 24 h in almost treatment (Ls 0.02% and Lr 0.2% were maximum at 48 h). The highest of NO content (0.996 $\mu\text{mol} \cdot \text{mg}^{-1}$ FW) was obtained in Lc 0.2% treatment at 24 h. Correlated with NO generation, total saponin content was enhanced in all treatments compared with the control after 7 days of treatments, especially in Lr 0.2% treatment (35.2 $\text{mg} \cdot \text{g}^{-1}$ DW); whereas, biomass (FW and DW) production has no significant difference among treatments. The total of ginsenosides was increased after LAB treatments, and the highest of total ginsenosides content accumulation was obtained in Ls 0.2% treatment. This study suggested that NO play as a signal molecule after LAB treatment and it lead to ginsenosides accumulation in the adventitious root cultures of *P. ginseng*.

Keywords: Adventitious root, ginsenosides, lactic acid bacteria, nitric oxide, *Panax ginseng*.

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콩 들불병원균의 유전적 다양성 분석용 마커 개발

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콩은 우리나라의 전통 식생활 문화에서 단백질을 공급하는 중요한 식량작물로서 영양학적 가치뿐만 아니라 지력유지 및 증진, 논에서 벼 대체작물 활용 등의 측면에서 중요한 작물로 재배되고 있다. 그런데 우리나라는 콩의 발생기원지에 속하여 유전적 다양성이 높은 만큼 발생하는 병의 종류도 다양하여 기후변화에 따라 다양한 병의 돌발적인 발생 위험이 내재되어 있다. 그 가운데 콩 들불병(*Pseudomonas amygdali* pv. *tabaci*)은 불마름병과 함께 우리나라에서 콩의 생육후기에 발생하는 대표적인 세균병으로 수량 감소를 초래하는 것으로 알려져 있는데 약제 방제의 효과가 미미하여 저항성 품종을 재배하는 것이 피해를 줄이는 가장 효과적인 방법이다. 이러한 이유로 최근 콩 들불병 저항성 계통 육성 체계를 확립하고자 연구를 진행하고 있는데, 다양한 변이체들을 포함하는 콩 들불병 병원균 자체에 대한 정보가 부족한 상황이다. 본 연구에서는 들불병 수집 균주들을 대상으로 GBS(genotyping by sequencing)분석을 실시하였고 이 데이터를 기반으로 실험의 편의성을 고려하여 아가로즈 젤 기반에서 분석이 가능한 분자마커(Insertion-deletion; Indel)를 개발하였다. 개발된 분자마커는 14세트이며 PCR을 수행하고 제한효소(Sma I)로 절단하여 그 사이즈와 조각수에 대한 정보를 이용할 수 있다(Cleaved amplified polymorphic sequences; CAPs). 국내외에서 수집된 45점의 콩 들불병 균주들을 대상으로, 개발된 분자마커를 적용하여 다형성을 분석한 결과, 균주들의 다양성에 대한 동일한 정보(동일한 패턴)를 제공하는 분자마커를 제외하고 11종의 분자마커 세트를 사용하는 것이 효율적임을 확인하였다. 들불병 균주들의 특성을 확인할 수 있는 방법은 여러 가지가 있겠지만 본 연구에서 개발된 분자마커를 활용하면 간편하고 신속하게 유전적 다양성을 확인할 수 있어, 신규로 수집되는 균주들의 다양성 및 발생 균주들의 모니터링에도 활용할 수 있을 것으로 기대된다.

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Identification, classification, and expression analysis of the receptor-like protein family in tomato

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Receptor-like proteins (RLPs) are well-known to have crucial roles in plant development and defense response against pathogens. But a few RLPs in tomato (*Solanum lycopersicum* L.) have been functionally characterized though 176 genes encoding RLPs, which have been identified in the tomato genome. To further predict the possible role of tomato RLPs, we performed genome-widely classification and transcriptome analysis. Phylogenetic comparisons revealed that the tomato RLPs were divided into eight subgroups and evolved independently compared to those in Arabidopsis. The localization and physical clustering analyses showed that tomato RLPs were expanded primarily through tandem duplication events. Through analyses of tissue specific RNA-seq data, 71 RLPs were expressed in at least one of the following tissues: root, leaf, bud, flower, or fruit, of which several showed tissue specific expression. In addition, tomato RLP expression profiles after infection with different pathogens showed distinguishable gene regulations to disease induction and resistance response by bacteria and virus. Notably, Some RLPs were highly and/or unique expressed in susceptible tomato to pathogen, suggesting that the RLP could be involved in disease response, possibly as a host-susceptibility factor. Our study could provide an important clues for further investigations into the function of tomato RLPs involved in developmental and response to pathogens.

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Genome-wide identification and transcriptional co-regulation analysis of receptor-like protein genes in pepper (*Capsicum annuum*)

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Receptor-like proteins (RLPs) are cell surface receptors, and it is well known to be involved in plant development and defense. To study the characterization of RLPs in pepper, we identified and analyzed RLPs using pepper genome and transcriptome. A total of 438 RLP genes were identified in the pepper genome. CaRLPs were divided into 11 subgroups showing differential expansion. Phylogenetic comparison with Arabidopsis RLPs revealed that pepper and Arabidopsis RLP families evolved independently. Furthermore, transcriptome of RLP genes showed dynamics of global gene expression changes during either plant growth stages or pepper-pathogen interactions. Through transcriptomic data of biotic treatments, we constructed multi-dimensional co-expression network for predicting RLP gene functions by functional modules. Several pathogen-responsive regulatory module of CaRLPs were identified through integrating the co-expression network and function enrichment tool.s, which cover variable function such as immune responses, metabolism, transcriptional regulation. We expected that the results would be useful keys for functional analysis of RLPs in pepper.

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Development and evaluation of clustered resistance gene analogs based markers linked to the resistance locus to *Phytophthora capsici* in hot Pepper

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Phytophthora capsici (*P. capsici*) is one of the destructive soil-borne oomycete in *Capsicum spp.* To date, Resistance against *P. capsici* in pepper is controlled by numerous quantitative trait loci (QTLs). The majority of the QTLs have been identified on chromosome 5. For this major QTL. Several molecular markers have been developed but they are still limit to search for *P. capsici* resistance pepper germplasm and further characterization of resistance gene. In this study, we attain QTL region (6.2Mbp – 139.2Mbp) using integrated genetic and genomic data with previously developed molecular markers located on chromosome 5. After then, we re-analyzed domain structure of genes to select candidate resistance gene analogs (RGAs) which has 19 RGAs on extended QTL region. These RGAs are divided into 15 NBS-LRRs (nucleotide binding site leucine rich repeats), 3 RLKs (receptor like kinases) and 1 RLPs (receptor like proteins). To mining single nucleotide polymorphism between *P. capsici* resistance and susceptible germplasm, we performed multiple sequence alignment and then we developed 11 RGAs based markers. We confirmed that the 11 molecular markers are closely linked to the major QTL for *P. capsici* resistance through the high resolution melting analysis. Among the 11 molecular markers, M6 is verified as the highest co-segregation marker against *P. capsici* (86.7%). These could be helpful to characterization of resistance gene against *P. capsici* and investigation of the *P. capsici* resistance germplasm.

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복합내병 다수성 조생종 벼 ‘아이에스592비비(IS592BB)’

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‘아이에스592비비(IS592BB)’는 다른 생태형에 비해 내병성이 약한 조생종 벼의 내병성을 증진하기 위해 개발되었다. 2008/09년 동계에 최고품질 다수성 조생 품종인 ‘운광’을 모본으로 하고 ‘운광’과 벼흰잎마름병 및 줄무늬잎마름병 저항성 유전자를 보유하고 있는 ‘SR31206-12’계통을 교배한 F₁을 부분으로 삼원교배하여 교배번호 HR28420을 부여하였다. 2009년부터 2013년까지 계통육종법을 수행하면서 병원성이 강한 벼흰잎마름병 K3a균계에 대한 생물검정과 벼흰잎마름병과 줄무늬잎마름병에 대한 저항성 유전자 도입 확인을 위한 DNA 분자표지 선발을 통해 저항성 유전자가 집적된 계통을 선발해 나갔다. 조생종으로 내병성이 증진되었으며 농업형질이 양호한 계통을 선발하여 2014-2015년 생산력검정시험을 수행하였다. 생산력검정시험에서 ‘조평’보다 출수가 2-3일 늦은 조생종이며 벼흰잎마름병 저항성 유전자 *Xa3+Xa21*과 줄무늬잎마름병 저항성 유전자 *Stv-b¹*이 집적되어 있어 벼흰잎마름병과 줄무늬잎마름병에 대한 저항성이 향상된 우량 계통 HR28420-34-2-2-1을 선발하여 ‘익산592호’라 계통명을 부여하였다. ‘익산592호’는 2015-2017년 3년간 실시된 지역적응성 검정시험 결과 조생종으로 단간 내도복 다수성 특성을 가지고 있으면서 도열병 저항성과 함께 벼흰잎마름병과 줄무늬잎마름병에 대한 내병성이 증진되었다는 점이 인정되어 2017년 12월 직무육성 신품종 선정심의위원회에서 조생종의 내병성 증진을 위한 중간모본으로 선정되었고 ‘아이에스592비비(IS592BB)’로 품종명을 명명하였다. ‘아이에스592비비(IS592BB)’는 복합내병 다수성 중간모본으로 조생종의 내병성 증진을 위한 육종소재로서 조생종 벼 육종사업에 다양하게 활용되고 있다.

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덩굴쫄김병 및 흰가루병 저항성 멜론대목 ‘뚝심’ 육성

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멜론 덩굴쫄김병과 검은점뿌리썩음병에 저항성인 유전자원을 계통 선별하여 ‘PI414723’을 모본으로 하고 검은점뿌리썩음병 저항성 유전자원 ‘PI614467’을 부분으로 교배하여 덩굴쫄김병과 검은점뿌리썩음병에 저항성인 대목용 멜론 ‘뚝심’을 육성하였다. 뚝심은 덩굴쫄김병과 흰가루병에 저항성이며, 검은점뿌리썩음병에 중간정도 저항성을 나타낸다. 유묘의 배축길이는 대조품종과 비교하여 길며, 떡잎크기는 큰편이다. 잎자루 길이는 길고 잎자루 자세는 반직립이다. 과형은 난형이고 과피색은 녹색을 띠다가 성숙할수록 녹색으로 되며 과피에 점이있고 점의 밀도는 높았다. 과육색은 황색빛 백색이고 당도는 11°Brix정도로 대비종보다 낮았다. 2016년 여름재배와 2017년 봄재배에서 뚝심을 대목으로 이용하였을 때 멜론의 수량 및 품질이 무점목 재배와 비교하여 비슷한 수준이었다. 멜론 재배 시 토양병해 발생으로 생산성이 감소되고 있는 지역에 뚝심을 대목으로 이용하여 점목 재배시 안정적인 생산이 가능할 것이다.

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New BB resistance gene confirmation by QTL fine mapping using 7K SNP-chip in bi-parental population

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Bacterial blight (BB) disease by the *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) is one of most severe factor regarding rice yield loss in most of rice cultivation countries especially in Asia. Deployment of cultivar with the resistance gene to BB is known as the most effective way to control the disease. However the evolution of new *Xoo* or pathotypes changed by single gene dependent abuse often result in breakdown of the resistance. Thus, efforts for searching new novel *R*-gene with sustainable BB resistance has been constantly required. In this study we have identified three QTLs on chromosomes 1, 4, and 11, respectively, with 493 F₂ individuals from across between P6 and Ilpum using 7K SNP-chip. Of these one major QTL *qBB_11* on chromosome 11 explained 61.58 % of the total phenotypic variance in the population, with an LOD value of 113.59 harboring SNPs 11964077 and 11985463. The single major *R*-gene which is recessive to BB was designated as *xa44(t)* and was narrowed down to 470 kb segment franked within 27.98Mbp to 28.45Mbp. The results may suggested useful information to understand BB resistance mechanism and provide DNA marker for MAS breeding to improve BB resistance in rice.

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GWAS for detecting relative gene to apple blotch disease in apple

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Apples are important agricultural crops in worldwide. Apple Marssonina blotch that is usually called Apple Blotch disease is one of major apple diseases known in Korea and is caused by *Diplocarpon mali*. Apple Marssonina blotch occurs on leaves and fruits, which lowers fruit quality and makes early defoliation of leaves leads to lower tree growth. 'Fuji' and 'Hongro' are main apple cultivars in Korea and these are known as susceptible to apple Marssonina blotch. But relative genome study has been rare. Genome-wide association study (GWAS) is useful for searching for related genes to the target trait. This study was carry out to detect candidate genes affection resistance to apple Marssonina blotch establish basic data for genomic study in future. From May, large quantity of conidia was produced, we monitored severity of infection on leaf of 730 apple germplasm until October and scored on a six scale follow to 'Agricultural science technology research analysis standard reference'(RDA). Results of pathogenicity showed 1.9% Immune(I) and 4.2% resistant(R), 23.0% Moderately resistant(MR), 28.1% Moderately susceptible(MS), 26.0% Susceptible(S), 16.7% Highly susceptible(HS), respectively. SNPs of 187 core collection are called by using Genotyping-by-Sequencing (GBS) and are filtered thru TASSEL-GBS pipeline with apple reference genome. We performed GWAS analysis with SNPs data.

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MAB를 이용한 운광벼 줄무늬잎마름병 근동질 계통 육성

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경상남도 밀양시 점필재로 20 국립식량과학원 남부작물부 논이용작물과

고품질벼인 운광벼의 단점을 개선하기 위해 줄무늬 잎마름병에 저항성을 보이는 해당쌀을 2회 여교배하여 선발된 YR32548에 다시 해당쌀을 교배하여 BC₂F₁ 24 개체를 얻었다. BC₂F₁ 및 BC₂F₁ 식물체에서 InDel 7 마커로 유전자형을 검정한 결과 이형접합체가 각각 12, 11개체 이었으며, χ^2 -test 결과 1개의 유전자 검정교배 시 이론적인 분리비 1 : 1 에 적합한 것으로 나타났다. 즉, 1개의 우성유전자로 밝혀진 줄무늬잎마름병 저항성 유전자가 인디카 품종 Modan에서 유래되었지만, 인디카/자포니카 원연교잡에서 발생할 수 있는 연관불균형(linkage equilibrium) 또는 분리변형(segregation distortion)은 발생하지 않는 것으로 판단되어진다.

선발된 11개체에 대하여 background selection을 위한 유전자지도 작성을 위해 KASP Marker 315개를 이용하여 다형성 검정을 실시한 결과 23.2%인 73개의 마커에서 양친간의 다형성이 검정되었고, 이를 이용하여 11개 개체에 대한 유전자형 검정을 실시하였다. 선발된 계통은 평균 6.6개의 이형접합체와 1.3개의 해당쌀의 염색체 단편이 이입되어 있었으며, 평균 단편이입률은 이형접합체 포함 20%로 80%이상 운광벼로 회복되었음을 확인할 수 있었다. 육종에서의 MAB의 이용은 목표형질의 개량에 있어 목표 형질을 소실시키지 않고, 시간과 비용을 절감할 수 있다는 점에서 그 효율성이 증명되고 있다. 선발된 개체는 2018년 하계에 운광벼, 해당쌀과 농업적 특성을 비교할 예정이며, 애멸구 접종 후 줄무늬잎마름병 생물검정을 실시할 예정이다.

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Genetic analysis of bakanae disease resistance of Samgwangbyeo

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Bakanae disease has become a serious threat in almost all rice cultivation regions worldwide. The incidence of bakanae disease is increasing with temperature rise due to global warming, and the advent of fungicide-resistant strains has rendered disease control difficult. We performed bioassay of bakanae disease resistance with 47 rice varieties by in vitro seedling screening method. Samgwangbyeo showed the highest resistance with Nampyeongbyeo. We crossed Samgwangbyeo with a susceptible variety, Junambyeo, and developed an F2 population. A genetic map comprising 132 KASP markers which are polymorphic between the parents was constructed with 188 F2 plants. The total distance of the genetic map was 1,863.3 cM, and the average distance between markers was 15.27 cM. Bioassay of 188 F3 families derived from the F2 plants was also performed by in vitro seedling screening method. The mortality rate of the F3 families ranged from 0 to 100 %, while that of Samgwangbyeo was 1.7% and that of Junambyeo was 83.3%. These data will be utilized in mapping QTLs of bakanae resistance in Samgwangbyeo, which may contribute to breeding bakanae disease resistant rice varieties.

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Roles of OsWRKY67 in basal and XA21-mediated resistance in rice

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Numbers of studies last twenty years have emphasized the unordinary role of WRKY family in plants, remarkable in retroactions to environmental stimuli. Among a hundred of WRKY genes in rice, at least twelve were determined to regulate defense response either in positively or negatively fashion. Here we show that *OsWRKY67* emerges as a member contributing in resistance to various pathogens in rice. The activation of *OsWRKY67* gained by T-DNA tagging significantly improved resistance against *Magnaporthe oryzae* and *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) whereas *OsWRKY67* RNAi lines significantly reduced resistance. *OsWRKY67* was then functional deciphered in XA21-mediated resistance as a negative regulator, characterized by the abolishment of XA21-mediated resistance in *OsWRKY67* RNAi. Overexpression of *OsWRKY67* in rice confirmed enhanced disease resistance, but revealed a restriction of plant growth with high levels of *OsWRKY67* protein. Quantitative PCR reveals numbers of PR genes are strikingly up-regulated if *OsWRKY67* is enhanced meanwhile our transcriptional activity assay and localization that *OsWRKY67* is a transcriptional activator. Accordingly, our study offers an additional WRKY candidate into transcription factor category for crop genetic improvement.

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Quantification of ingested plant subcellular fractions and dsRNA by *Frankliniella occidentalis* for the establishment of RNAi-based control system

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Frankliniella occidentalis is one of the polyphagous pest damaging flowers and leaves of horticultural and agricultural crops. Due to its wide host range and rapid development of insecticide resistance, *F. occidentalis* is extremely hard to control by conventional insecticides, thus requiring an alternative control measure. RNA interference (RNAi)-based control strategy has been developed to control various phytophagous chewing pests. However, no successful case of RNAi-based control has been reported for sucking pests including thrips. In this study, as the basic information for the establishment of ingestion RNAi against thrips, feeding amount and time course of plant subcellular fractions by *F. occidentalis* were determined by quantitative PCR (qPCR). *F. occidentalis* adults were starved for 24 h and then fed with kidney bean leaf for 48 h. Thrips were then collected every 6-h interval, their genomic DNA was extracted and the ingested fractions of chloroplast and nuclear were quantified using rubisco and 5S rRNA genes as markers, respectively. The ingested amount of rubisco and 5s rRNA genes increased rapidly until 6 h after feeding and then slightly reduced over time. Detection of both genes confirms that *F. occidentalis* ingests both chloroplasts and nucleus along with cytosol during sucking. Relative ratio between two marker genes detected in thrips (1 : 24) was different from that of kidney bean tissue itself (1 : 8000), suggesting that thrips ingested nucleus along with cytosol more selectively compared to chloroplasts. Finally, two different feeding systems (sliced bean and leaf-disc) were tested as double-stranded RNA (dsRNA) delivery methods, and the ingested amount of test dsRNA (pQE30) was quantified using qPCR.

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Genome-wide association analysis of flowering time genes with nested association mapping (NAM) population in soybean

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We developed a Korean soybean [*Glycine max* (L.) Merr] Nested-Association Mapping Population (NAM) and conducted a Genome-Wide Association Study (GWAS) with flowering time. To develop the NAM population, Daepung was used as hub parent and 27 soybean varieties were chosen as founder parents, based on their genetic diversity. Total of 2,619 recombinant inbred lines of 27 combinations were produced. The 180K Axiom® SoyaSNP array Chip was employed for genotyping of NAM population.

We investigated the flowering time in three environments, Cheonan in 2015 and 2016, and Jeonju in 2016. The each flowering time in 3 environments were normally distributed, even though some lines showed different flowering time in different environment. First, to identify the flowering time-related genes/QTL, the genetic linkage map was constructed using each RILs, and QTL analysis was performed. Highly saturated genetic map was composited with a total length of 4,407 cM and an average distance of SNP marker was 0.15 cM.

A QTL analysis results showed that QTLs from each population was not identical in 23 RILs and 3 environments. To employ more polymorphic SNPs in genetic linkage map construction and QTL identification, GWAS was conducted using 23 RILs. Interestingly, the results showed that identified QTLs were identical in all 3 environments. The major QTLs were identified on chromosomes 6, 10, and 12, and minor QTLs were identified on many other chromosomes. Among them, QTLs on the chromosomes 6, 10 and 19 were in good agreement with previously reported soybean flowering time locus, E locus. Also many other newly identified QTLs were detected.

In summary, constructed Korean soybean NAM population and following GWAS analysis showed that GWAS with NAM population is a highly accurate genes/QTL identification method, and has improved capability to gene identification and great potential for noble genes/QTLs identification, comparing to traditional QTL identification procedure using single RIL population.

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콩에서 자외선(UV-B) 저항성 유전자원 탐색 및 유전양상 규명

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기후환경변화에 따른 오존층파괴는 식물의 생화학적 대사기구 장애를 일으킨다. 이에 대비하여 자외선(UV-B)에 저항성을 보이는 콩 유전자원을 지속적으로 발굴하고, 발굴된 저항성 유전자를 신속하고 안정적으로 신품종에 도입하기 위한 UV-B 저항성 유전자의 근접마커 개발 및 후보유전자 확보로 금후 고자외선 환경 하에서도 안정적인 작물생육과 수량 확보할 수 있는 기반을 마련코자 본 연구를 추진하였다. 본 연구에서는 국내의 수집보관종인 재배콩 및 야생콩 유전자원 1,500여점과 UV-B 저항성 유전분석을 위해 감수성 자원과 저항성 자원을 인공교배하여 만든 F₂ 집단으로 저항성 검정을 실시하였다. 검정방법은 다수의 기 연구자가 수행한 바와 같이 UV-B 인공 처리를 위해 UV lamp에 diacetate 필름을 처리(UV-C 제거)하여 만들었으며, 조사량은 선행연구결과 콩에서는 10kJ 이상처리 시 감수성품종과 저항성 품종간에 차이를 보이고 있어 본 실험에서도 10kJ/m²/day 전 후로 처리하였다. 국내 수집 콩 유전자원 중 재배종 1,276점, 야생종 186점을 대상으로 UV-B 인공조사를 통한 저항성 검정 결과 익산10호 등 재배종 5점과 야생종 9점에서 저항성 반응을 보이는 자원을 확보하였고, 감수성 자원인 대풍콩과 신평달콩을 저항성 자원으로 발굴된 익산 10호와 인공교배하여 확보한 F₂ 집단에 UV-B 인공조사 후 피해증상으로 유전분석을 실시한 결과 엽형과 엽색 및 전체 피해정도 등 모든 형질에서 저항성과 감수성이 1 : 3의 분리비를 보여 자외선 저항성 유전자는 단일자이며 열성유전함을 확인하였다. 본 실험 결과에서 확인한 UV-B 저항성 자원과 유전분석결과는 추후 정밀 검정을 통해 관련 유전자 확보와 더불어 분자육종방법을 활용한 UV 저항성 품종개발에 유용하게 활용될 것으로 판단된다.

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콩 탈립성 연관 SNP마커를 활용한 내탈립성 계통선발

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콩에서 탈립성은 수량감수의 직접적인 원인이며 저항성 계통을 선발하기 위한 특성검정도 매우 번거롭고 많은 시간이 소요되어 육종과정에서 저항성계통 선발에 큰 어려움이 있다. 따라서 본 연구에서는 내탈립 콩 품종개발에 활용 가능한 분자마커를 개발하고 이를 활용하기 위한 연구를 수행하였다.

본 연구에서는 활용한 콩 탈립성 연관 SNP Marker는 Lee 등(2017)이 RIL Line에서 개발한 qPDH1-KS 유래 SNP를 활용하였다. SNP probe의 재현성을 검증하기 위해 참을×대원 F₃ 56계통을 3반복으로 하여 Genotyping 후 결과를 비교하였고, 국내생산 SNP probe의 육종집단에서 적용 가능성을 검증하고자 참을×대원, 황금을×대원의 초기세대 F₃ 166계통과 지역적응시험 및 생산력검증시험계통 52계통에 대해 Oven - dry 방법을 통한 탈립성 검정을 실시하고 이를 genotyping 결과와 비교하였다. 본 실험에서 활용한 SNP genotyping은 국내 기술진에 의해 개발(SFC)된 probe를 사용하였고, SNP detection은 RT-PCR (StepOne Plus)로 진행하였다.

실험결과, F₃ 56계통을 이용한 마커의 재현성 검정에서 3회 모두 동일한 결과를 보여 이용된 SNP 및 genotype 기술의 안정성이 확인되었다. 또한 분리세대에서 실내검정을 통한 포장검증 표현형과 SNP genotype 비교 결과, 초기세대 F₃ 166계통에서 92.9%의 정확도를 보였고, 다양한 모부본으로 이루어진 지역적응성/생산력검정용 52계통에서는 100%의 정확도를 나타내었다.

본 연구를 통해 국내에서 개발된 탈립성연관 SNP marker 및 국내 개발 Probe가 콩에서 내탈립성 계통 선발에 매우 높은 정확도 보여 DNA마커를 활용한 내탈립성 계통 선발의 가능성을 확인하였다. 금후 이러한 기술은 콩에서 분자육종을 통한 우수한 신품종의 조기육성 및 관련기술 확산에 크게 기여할 것으로 판단된다.

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Detection of the disease resistance genes using GWAS in grape vine

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Grapes have cultivated worldwide, especially grown for brewing purposes and accounting for about one-third of the world's fruits production. However, grape ripe rot disease caused by *Colletotrichum spp.* is an economically important disease in grape production. Therefore, we conducted a study to identify the trait associated with grape disease-resistant and performed genome-wide association study(GWAS) for pheno/genomics using grape core collections. Firstly, we conducted phenotypic characterization to prove the pathogenicity of the fungal isolates *Colletotrichum acutatum* and *C. gloeosporioides* which were inoculated onto healthy grape leaves. Results of pathogenicity test from 844 grape cultivars(obtained from RDA Korea) showed 726(87%) susceptible and 118(13%) resistance, respectively. Secondly, we selected 350 cultivars (118 resistance and 232 susceptible cultivars) and constructed the Genotyping-By-Sequencing(GBS) library with 96 barcode sets to find the disease-resistant related(NB-LRR) genes. After that, the experiment was carried out to select the candidate genes, phenotype data converted into analyzed format data and performed GWAS analysis with GBS data(using TASSEL software). As a results of GWAS, we identified 6 resistance-related candidate genes for *C. gloeosporioides* and 7 candidate genes for *C. acutatum* using filtered 77,126 SNPs by their trait. Among them, only 2 candidate genes were included disease resistance LRR family protein. However, it is necessary to confirm the current results which are actually related or not to resistance genes. Therefore, additional studies should be carried out to confirm resistance genes which are related to current candidate genes.

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Genome-wide investigation and expression analysis of F-box genes in wheat development stages

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F-box gene family, as one of the largest gene families in plants, plays crucial roles in regulating plant development, reproduction, cellular protein degradation and responses to biotic and abiotic stresses. However, comprehensive analysis of the F-box gene family in wheat (*Triticum aestivum* L.) has not been analyzed yet. We identified a total of 1,796 F-box genes in wheat genome and these genes were further divided into various subgroups based on specific domains, such as FBA, FBD, DUF, Kelch, Tub, PP2 Arm, cupin_8 Actin, LysM, Myb-binding, pro-isomerase and WD40 domains. In addition, The F-box genes were physically mapped on the 42 wheat chromosomes and duplication events were investigated. F-box genes exhibited functional specificity based on GO analysis, and 47 % of the F-box genes were significantly enriched in ubiquitin-like protein transferase activity (GO:0019787). Transcriptome and digital expression analysis revealed differential expression patterns of F-box genes which were specifically expressed in various developmental stages and tissues. The genome-wide analysis of F-box genes provides new opportunities for characterization of candidate F-box genes and elucidation of biological roles in growth and development in wheat.

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Functional analysis of plant transcription factor related to disease resistance

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We isolated *NAC* transcription factor related to disease resistance of bacterial and fungal pathogens, *Xanthomonas oryzae* pv. *oryzae* (*Xoo*), *Magnaporthe grisea* and *Fusarium fujikuroi*. *NAC* (NAM, ATAF, and CUC) transcription factors are plant specific gene family and they are involved in plant growth, development, and stress tolerance. This transcription factor family has five groups (I–V). On the basis of phylogenetic analysis, isolated and selected *OsNAC* genes (*OsRXI58*, *OsRXI69*, and *OsRXI85*) fell into group II, III and IV, respectively. To investigate their biological function in the rice, we constructed vector for overexpression in rice, and then generated transgenic rice, respectively. *NAC* gene expression of overexpressed transgenic rice lines were analyzed by northern blot or RT-PCR, respectively. Analysis of disease resistance to the bacterial leaf blight, blast, and bakanae disease pathogen, *OsNAC*-overexpressed transgenic rice lines showing high expression level of *OsNAC* gene were shown more resistant than wild type. These results suggest that *OsNAC* genes may play regulatory role during bacterial and fungal pathogen infection.

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Development InDel molecular markers for distinguishing between Korean cymbidium and Chinese cymbidium

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In domestic, Korean Cymbidium (*Cymbidium goeringii*) is belonging to Orchidaceae Cymbidium, perennial plant. Distinguishing the Korean cultivar from other national cultivars is difficult. Therefore, we selected 23 In/Del regions that have difference more than 10bp sequence among 370 InDel region which is identified between Korean cymbidium and China cymbidium (NC_028524) for development of cultivar distinguishing system. To develop Korean cymbidium specific markers, We detected adaptable marker by using the 12 Korean cymbidium and 12 Chinese cymbidium for develop specific marker through using selective region. Inel 48067 showed a moderately PIC value (0.24) in Korea cymbidium, InDel 78919 showed a high PIC value (0.58) in Chinese cymbidium. Especially, InDel 1520 didn't have polymorphism because of appeared only 205bp band in Korea cymbidium, it showed high PIC value (0.45) and didn't appeared 205bp band in Chinese cymbidium. When InDel merker was used with SSR marker, it would be powerful for distinguishing more than use only one marker. This study was performed by support of IPET (815004-3).

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Genome-wide characterization of the *Brassica rapa* genes encoding serine/arginine (SR)-rich proteins: expression and alternative splicing events by abiotic stresses

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Serine/arginine-rich (SR) gene family members can diversify the transcriptome and proteome of eukaryotes by facilitating the alternative splicing (AS) of precursor messenger RNAs. Herein, we investigated the evolutionary dynamics, AS patterns, and expression levels of the *Brassica rapa* SR (*BrSR*) gene family in young seedlings treated with abiotic stresses. A comparative genomic analysis identified 25 *BrSR* genes at 18 Arabidopsis loci and three *BrSR-like* genes at two Arabidopsis loci. Thirteen of these loci were singletons, while seven loci carried paralogs. All the duplicated pairs were determined to be under purifying selection pressure. The expansion of the *BrSR* gene family was found to be the result of segmental duplications only. Additionally, the expression levels of 78.6 % (22 of 28) and the AS patterns of 60.7 % (17 of 28) of the *BrSR* genes were altered in response to abiotic stresses. Among the analyzed abiotic stresses, oxidative, cold, and heat treatments induced the largest expression changes, while cold and heat stresses caused most AS events. Our findings provide insights into the evolutionary dynamics of *BrSR* genes following polyploidization events, and provide an important resource for future studies aimed at characterizing the specific function(s) of *BrSR* genes in plant growth, development, and defense.

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Cloning and characterization of two phytochelatin synthases in rice (*Oryza sativa* cv. Milyang 117) that respond to cadmium stress

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Cadmium (Cd) is one of the most toxic heavy metals and a non-essential element to all organisms, including plants; however, the genes involved in Cd resistance in plants remain poorly characterized. To identify Cd resistance genes in rice, we screened a rice cDNA expression library treated with CdCl₂ using a yeast (*Saccharomyces cerevisiae*) mutant *ycf1* strain (DTY167) and isolated two rice phytochelatin synthases (*OsPCS5* and *OsPCS15*). The genes were strongly induced by Cd treatment and conferred increased resistance to Cd when expressed in the *ycf1* mutant strain. In addition, the Cd concentration was 2-fold higher in yeast expressing *OsPCS5* and *OsPCS15* than in vector-transformed yeast, and *OsPCS5* and *OsPCS15* localized in the cytoplasm. *Arabidopsisthaliana* plants overexpressing *OsPCS5/-15* paradoxically exhibited increased sensitivity to Cd, suggesting that overexpression of *OsPCS5/-15* resulted in toxicity due to excess phytochelatin production in *A. thaliana* plants. These data indicate that *OsPCS5* and *OsPCS15* are involved in Cd tolerance, which may be related to the relative abundances of phytochelatin synthesized by these phytochelatin synthases.

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Analysis of salt-tolerant by M₂ generation EMS variation-induced maize inbred lines

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The EMS induced mutants has been used for disease resistance, abiotic stress, and quantitative including yielding ability. The two maize inbred lines treated with 0.3%, 0.5%, 0.7%, and 0.9% EMS respectively for 8 h. The results of phenotyping analysis of mutagenized maize population in each treatment condition that we couldn't obtained M₂ generation seeds from condition treated with 0.7% and 0.9% EMS(v/v) for 8 h. otherwise, it is shown variable phenotypic variation in conditions with treated 0.5% EMS(v/v) for 8 h, however we could obtained mutagenized M₂ generation seeds for a salt-tolerant analysis. A total of 1041 independent M₂ familiar of EMS-induced maize inbred mutants were investigated for salt tolerance. We selected salt tolerance maize inbred lines from mutants populations treated with 0.7% NaCl for 3 weeks in the greenhouse. A salt tolerant mutants was identified in M₂ mutant populations. We generated whole-genome sequencing data to the two maize inbred mutants for genetic variation analyses of salt-tolerant enhanced in mutant populations. we expect to the result which is significantly impacts genetic studies of these maize inbred lines as comparative genomics.

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내염성 증진 사료용 벼 교배계통의 *Saltol* 유전자간 상관 관계 분석

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염분은 작물의 수확량을 줄이는 주요 비생물적 스트레스 중 하나로 알려져 있다. 따라서 간척지와 같이 염 농도가 높은 토양에서 사료용 벼의 재배를 위해서는 내염성이 증진된 사료용 벼의 개발이 필요하다. 이러한 내염성이 증진된 사료용 벼의 개발을 위하여 목양과 IR64를 교배하여 얻은 58 계통에 대해 우선 내염성이 우수한 계통을 선발하기 위하여 기내배양 실험을 실시하였다. 기내배양에 의한 염 처리 방법은 교배종으로 사용한 목양, IR64, 포카리, FL478 품종을 H₂O, 0.1, 0.2, 0.3, 0.4% NaCl 농도에서 2주간 재배하여 생육 상태를 분석한 결과 염 농도가 0.3% 이상이 되면 뿌리 생장이 거의 되지 않았다. 또한, 0.3% 배지에서 1주와 2주간 재배하여 염이 전혀 없는 배지에 옮겨 식물체의 회복 상태를 확인한 결과 0.3% NaCl 에서 1주간 재배한 후 물로 옮긴 배지에서는 거의 정상적으로 회복이 되었으나, 같은 조건에서 2주간 재배한 것에서는 정상적인 회복이 되지 않았다. 위 실험 조건을 바탕으로 목양과 IR64의 58 교배 계통을 이용하여 0.3% NaCl 배지에서 2주간 재배하여 식물 생장을 관찰한 결과 58 계통 중 대조군인 목양과 IR64 보다 더 잘 생육하는 11 계통을 선발 하였다. 이들 선발 계통들에 대해 벼의 내염성 관련 유전자로 알려진 *Saltol* 유전자의 19개 마크를 이용하여 목양과 IR64의 *Saltol* 유전자의 삽입 여부를 PCR을 이용하여 확인하였다. 19개 프라이머들 중 목양과 IR64의 *Saltol* 유전자가 명확하게 구별되는 6개의 프라이머를 이용하여 선발된 11 교배계통에 대해 *Saltol* 유전자의 삽입 타입을 결정하였다. PCR 결과 11 계통 중 4 계통이 목양과 IR64의 *Saltol* 유전자가 동시에 삽입되어 있는 것을 확인하였고, 4 계통은 IR64 유전자가 삽입되어 고정된 타입, 2 계통은 목양 유전자가 삽입되어 고정된 타입으로 확인되었으나 1 계통은 프라이머에 따라 목양과 IR64 *Saltol* 유전자가 각각 다르게 나타나는 결과를 보였다. 위 실험결과를 토대로, 기내배양에 의해 선발된 11 교배계통들에 대해 토양에서도 유사한 내염성 결과가 나오는지에 대해 확인 중에 있다. 또한 선발된 11 교배계통들에 있어 목양 또는 IR64 타입의 *Saltol* 유전자간 내염성 증진과의 상관관계를 분석할 예정이다.

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Biological responses of cowpea plants after gamma-ray and proton-beam irradiation

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Cowpea (*Vigna unguiculata* L.) is rich in vitamins (B1 and B2), lysine and polyphenols, which are good for muscular growth and development, anticancer and anti-aging in human. In addition, this crop is suitable for cooking with rice, rice cakes, soups and stews. In this study, morphological responses were investigated in cowpea plants with two different types of radiations, the proton-beam and the gamma-ray. Seeds of Okdang cultivar were exposed to 100, 200, 300, 400 and 500 Gy of gamma-ray and proton-beam, respectively. After 5 days of sowing, the germination rate tended to decrease with increasing dose regardless of the type of radiation, but all treatments showed more than 90% germination rate after 10 days of sowing. The survival rate decreased significantly over 300 Gy. The survival rates of proton beam and gamma ray at 500 Gy were 35% and 27%, respectively. The half-lethal dose (LD₅₀) of Okdang was 327 Gy in gamma ray and 330 Gy in proton beam. The plant height and the fresh weight of shoot tended to decrease with increasing dose in both radiations with a significant difference from the control group except 100 Gy of gamma-ray in fresh weight. This study will be valuable as a basic research to compare the mutagenic effects of two different types of radiation in cowpea.

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Distribution of gene-based polymorphisms in tropical maize by using RNA sequencing

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Maize has high food and industrial value, but has difficulties in research because of their complex and huge size genome. Nested association mapping (NAM) was constructed to better understand maize genetics. However, most studies were conducted using the reference genome B73, and only a few studies were conducted on tropical maize. We analyzed the genetic characteristics of Ki3, one of the NAM parent lines, which are tropical maize for various genetic studies using RNA sequencing and bioinformatics tools. As results, a total of 30,526 genes were expressed, and expression profile were constructed. In addition, high-density polymorphisms including 408,193 single nucleotide polymorphisms (SNPs), 22,367 multiple nucleotide polymorphisms (MNPs) and 83,793 insertions and deletions (InDels) were found compared to reference genome. Among them, 14.2 % of polymorphisms (73,172) were passed non-synonymous test which could alter amino acid sequences. A total of 15,396 expressed genes have non-synonymous polymorphisms. Our results offer resources for development of gene-based marker and will help to genomic studies of maize.

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Transcriptional network regulation of BES1/BZR1–TPL–HDA19 in Brassinosteroid signaling pathway

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A plant steroid hormone, Brassinosteroids (BR), is essentially involved in diverse growth and developmental processes in whole life cycles of plants. The BR related transcription factors, BES1 and BZR1, regulate a range of global gene expressions in response to BR and several external signaling cues. However, the molecular mechanisms of BES1/BZR1-mediated transcriptional reprogramming are still unclear. In this study, we elucidate that protein complex formation of BES1/BZR1 with Histone deacetylase19 (HDA19) via evolutionary conserved EAR motif is essential for regulation of BR signaling related gene expressions. Defects in BR related functions of EAR motif mutated BRI1-EMS-SUPPRESSOR 1 (BES1) and BRASSINAZOLE-RESISTANT 1 (BZR1) were completely recovered by artificial fusion of either SRDX, TPL or HDA19 proteins. RNA-seq analysis of *bes1-DmEAR* and *bes1-DmEAR-HDA19* overexpression plants supported the essential roles of HDA19 activity for BES1/BZR1-mediated BR signaling regulations. In addition to BR related gene expressions, the BES1-HDA19 transcription factor complex is importantly involved in development, defense and abiotic stress related to drought stress tolerances. Our data suggest that activation of BR signaling pathways is integrated to complex formation of BES1/BZR1 with HDA19 for fine-tuning of BR related gene networks in plants.

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Physiological and molecular evaluation of Cheongho Byeo for salinity tolerance at the seedling stage

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Salinity is a major factor limiting crop productivity worldwide. Salinity tolerance is a complex agronomic trait and diverse mechanisms are associated with different aspects of salt stress. *Saltol* is a major QTL associated with seedling stage salt tolerance, and *OsHKT1;5* within the *Saltol* locus is known as a key gene responsible for maintaining high shoot K^+/Na^+ ratio (*SKC1*) under the salt stress in rice. Cheongho Byeo is a moderate salt tolerant Korean rice cultivar developed for adaptation to the Gyeonha reclaimed saline land, but the molecular components underlying salt tolerance is not well characterized. In the present study, genotyping analysis of *Saltol* locus of Cheongho Byeo and other Gyeonha rice varieties was conducted by direct sequencing of *OsHKT1;5* gene and PCR with simple sequence repeat (SSR) markers. The *OsHKT1;5* alleles found in the Gyeonha rice varieties are different from those of salt tolerant Indica rice, Nona Bokra or FL478. This indicates that *SKC1* allele is not incorporated in those Korean rice cultivars. It is noted that SSR marker RM3412 showed polymorphism among rice varieties with different salt tolerance, suggesting that genomic variation of this region may contribute salinity tolerance difference. Differential degree of salt-induced expression of *OsHKT1;5* gene was observed among rice varieties. Morpho-physiological evaluation of Cheongho Byeo and confocal Na^+ imaging analysis in root tissues using CoroNa Green is currently undergoing. Supported by grants (PJ01247603 and PJ01318203) from RDA.

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Identification of *OsRF1*, a salt-responsive RING zinc-finger-encoding gene, conferring drought and salt tolerance in rice

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Drought and Salinity are major important factors affecting growth and productivity of rice. Some RING zinc-finger proteins, such as XERIC0 in *Arabidopsis*, have been reported to enhance drought and salt tolerance by increasing abscisic acid (ABA) biosynthesis. Here, we reported a newly identified gene encoding a RING zinc-finger protein which involved in drought and salt stress response in rice. From microarray analysis, a salt stress-induced C₃HC₄ type RING finger gene was selected for further analyses and designated *OsRF1*. To investigate its roles in drought and salt stress response, *OsRF1* overexpressing rice (OsRF1-OE) was constructed. Soil-pot assay indicated that OsRF1-OE was more tolerant to drought and salt stress compare to wild-type. In leaf-water loss assay, OsRF1-OE exhibited decreased water loss rate compare to wild-type, suggesting that the drought tolerance trait of OsRF1-OE due to its lower water loss rate. Measurement of endogenous ABA content using TQ LC/MS revealed that the endogenous ABA content of OsRF1-OE was higher than that of wild-type regardless of salt stress. Consistent with this, expression level of some ABA biosynthesis genes and ABA-responsive genes were higher in OsRF1-OE than in wild-type. Further yeast two-hybrid assay indicated that the OsRF1 proteins interact with several PP2C proteins directly. The combined results suggested that OsRF1 confers drought and salt tolerance in rice by inducing ABA signaling via increasing ABA biosynthesis and direct interaction with PP2C proteins. Supported by grants from RDA.

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Ectopic expression of an ABA receptor, which functions specifically under high ABA concentrations, enhances drought tolerance in rice

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Overexpression of ABA receptors has previously been reported to enhance drought tolerance, but also to cause stunted growth and decreased crop yields. Here, we screened the signaling activity of monomeric ABA receptors under various ABA concentrations using a transient expression system in rice. Among the ABA receptors, an OsPYL/RCA had the lowest ABA-responsive signaling activity. Further, transgenic rice overexpressing the OsPYL/RCAR showed neither an ABA-sensitive nor an osmotic stress-tolerant phenotype in plate assay, and had similar stem heights and total seed yields compared to those of the control rice cultivar. In yeast two-hybridization and biomolecular fluorescence complementation experiments, the OsPYL/RCAR required a higher concentration of ABA to interact with protein phosphatases compared to other ABA receptors. Under high-ABA treatment conditions, the OsPYL/RCAR was also able to repress phosphatase activity, despite having much lower activity than OsPYL/RCAR5. Notably, transgenic rice overexpressing the OsPYL/RCAR exhibited enhanced drought tolerance, lost less water and showed no effect on growth compared to the wild type. Stress marker genes were induced more than in wild type only under very high concentrations of ABA. We conclude that the OsPYL/RCAR is functional as an ABA receptor only under high concentrations of ABA or harsh stress conditions. Thus, transgenic rice over-expressing OsPYL/RCAR showed drought tolerance, (i.e., harsh stress conditions) but exhibited no defects under normal growth conditions. These results lay the foundation for a new strategy to improve abiotic stress tolerance of crop without yield penalty.

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Overexpression of a member of OsDREB1 subfamily, OsDREB1H confers cold stress tolerance in rice

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Plants adapt to adverse environments through molecular and physiological responses such as ABA signaling pathway, stomatal regulation or root elongation. Gene expression regulation is also one of major responses of plants against adverse environment. Several transcription factors are identified as master switches to induce the stress tolerant genes. DREBs is one of the important abiotic stress tolerant transcription factors. Those are evolutionary conserved in plants and a subfamily of AP2/ERF superfamily. Rice might have two different kinds of DREB groups, OsDREB1 and OsDREB2 which consists of 11 and 6 members in genome. We tried to characterize an unidentified member of DREB1, OsDREB1H which is induced cold specifically. This gene is induced only in the cold stress condition and expressed in leaf sheath and leaf blade but not in root and flower. Transgenic rice overexpressing this gene presents strongly cold tolerance and growth retardation like other transgenic rice overexpressing OsDREB1 genes. However, the transgenic rice doesn't show drought and salt tolerance. Cold responsive genes were induced much in transgenic rice overexpressing DREB1H. Promoters of those induced genes also can be induced by OsDREB1H in protoplasts. Thus, this OsDREB1H is a typical CBF/DREB1 member functioning specifically in cold stress. This gene can be very useful to develop transgenic rice for cold stress tolerance.

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Overexpression of *PsGPD* from *Pleurotus sajor-caju* enhances tolerance to salt stress in rice

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Plants often face a variety of biotic and abiotic stresses that influence their development, growth and productivity. Salt stress is particularly an important abiotic stress that seriously affects plant growth and development. Transgenic potatoes expressing glyceraldehyde-3-phosphate dehydrogenase (GPD), isolated from the oyster mushroom, *Pleurotus sajor-caju*, had increased tolerance to salt stress. The over-expression of *PsGPD* in *PsGPD*-OX transgenic rice was confirmed by quantitative RT-PCR and western blot analysis. To elucidate the role of *PsGPD* in stress tolerance, responses of *PsGPD*-OX transgenic rice plants to salt stress conditions were examined. *PsGPD*-OX #5, #6, and #17 lines were treated with salt stress on MS medium containing 100 mM or 200 mM of NaCl for 5 and 14 days. Morphological analysis revealed differences between the three transgenic *PsGPD*-OX rice and the wild-type rice. The germination rates of the three transgenic *PsGPD*-OX lines of rice were significantly higher than that of the wild type rice, indicating that they were more tolerant to 200 mM NaCl than the wild type rice. In addition, the three transgenic *PsGPD*-OX rice lines had significantly longer length of root and shoot compared to the wild type rice. These results suggested that overexpression of *PsGPD* improve more tolerance to salt in rice.

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Overexpression of *BrTST53* Gene improves tolerance of rice plant to salt stress

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Plant is frequently exposed to various abiotic stress. Salt stress is particularly an important abiotic stress that seriously affects plant growth and development. *BrTST53* gene, a putative stress-related gene isolated from *Brassica rapa*, was used to generate overexpression transgenic rice. The over-expression of *BrTST53* in *BrTST53*-OX transgenic rice was confirmed by quantitative RT-PCR and western blot analysis. To elucidate the role of *BrTST53* in stress tolerance, responses of *BrTST53*-OX transgenic rice plants to salt stress conditions were examined. *BrTST53*-OX #12, #28, and #32 lines were treated with salt stress on MS medium containing 100 mM or 200 mM of NaCl for 5 and 14 days. Morphological analysis revealed differences between the three transgenic *BrTST53*-OX rice and the wild-type rice. The germination rates of the three transgenic *BrTST53*-OX lines of rice were significantly higher than that of the wild type rice, indicating that they were more tolerant to 200 mM NaCl than the wild type rice. In addition, the three transgenic *BrTST53*-OX rice lines had significantly longer length of root and shoot compared to the wild type rice. These results suggest that the *BrTST53* gene played an important role in the tolerance of rice to salt stress. Therefore, it might be a potential target for the purpose of improving salt tolerance of rice and other crops.

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Transcriptome analysis of pre-harvest sprouting (PHS) in Korean wheat (*Triticum aestivum*)

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Pre-harvest sprouting (PHS) is the precocious germination condition of grains while the spike is still in the mother plant. Because PHS in wheat drastically reduced the quality and economic value of wheat grain, the improving PHS wheat is one of the most important breeding goal in Korean wheat breeding program. In this study, we performed comparative expression analyses of genes related to phytohormone biosynthesis and signaling, especially ABA and GA, in two Korean wheat cultivars with different responses to PHS (tolerant/susceptible) using high-throughput RNA-seq technology. In order to perform RNA-seq, Two Korean cultivars of common wheat, 'Keumgang' (Geuru/Kanto75//Eunpa, PHS sensitive, Korea RDA accession no. IT213100) and 'Woori' (Geuru/OI, PHS resistant, Korea RDA accession no. IT175538) were analyzed using Hi-Seq 2500. A total of 123 unigenes were related to the biosynthesis or signaling of ABA, gibberellic acid, indole-3-acetic acid, and cytokinin, and 1862 of differentially expressed genes (DEGs) were identified and categorized into eight groups. The majority of DEGs were involved in sugar-related processes, which interacted with ABA signaling in PHS-induced grains of the PHS-tolerant cultivar. These findings indicate that ABA-related genes are key regulators of dormancy and germination in winter wheat and provide insight into PHS-induced changes in the expression of plant hormone-related genes.

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재배안정성과 밥맛이 우수한 조생 최고품질 벼 ‘해들’

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우리나라 식량자급률 제고를 위해 중부지역은 다양한 식량작물이 재배되고 있으며 이러한 작물들을 효율적으로 재배하기 위해 다양한 작부체계가 필요하다. 작부체계의 성공을 위해서는 작물 재배기간이 중첩되는 것을 피해야 하고 이를 위해 벼를 일반재배보다 빨리 재배하는 조기재배 또는 늦게 재배하는 만기재배에 적응할 수 있는 벼 품종 개발이 필수적이다. 또한 중부지역에 오랜 기간 재배되고 있는 외래품종의 교체를 위해 도정특성과 쌀 품질이 우수한 품종개발 역시 필요하다. 중부지역에 적응하는 밥맛과 재배안정성이 우수한 조생품종 개발을 목적으로 ‘해들’은 고품과 강원4호를 각각 모부본으로 하여 2007년에 교배되었다. 세대단축을 위해 F₁ 세대의 약을 배양하여 AC3세대에서 초형과 쌀품질이 우수하고 도열병 및 흰잎마름병 저항성을 보인 SR31523-HB3111-195-3을 선발하여, 수원588호의 계통명을 부여하였다. 2년간의 생산력검정시험과 3년간의 지역적응시험 결과 그 우수성이 인정되어 2017년 직무육성 신품종 심의회에서 최고품질벼로 선정되었다. ‘해들’은 조생종으로 밥맛과 재배안정성이 우수하여 생산자부터 소비자까지 만족할 수 있고, 다양한 작부체계에 적응할 수 있는 품종으로 역할이 기대된다.

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Arabidopsis NAC103 transcription factor is involved in the DNA damage response in *sog1* mutant

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DNA double-strand breaks (DSBs) are toxic lesion that can lead genetic instability and can be occurred by gamma rays and genotoxic stress in plants. To preserve chromosomal integrity from DNA damage such as DSBs, plants have a DNA damage response (DDR) system that regulates programmed cell death (PCD), DNA repair, and cell cycle arrest. However, in plants, it was little unknown about transcription factors are involved in the DDR system. In this study, we confirmed that transcript of DDR-related genes and *NAC103* gene was increased in gamma rays- and genotoxic stresses-treated wild type. In addition, the expression of DDR-related genes, such as *Rad51*, *GRG*, *RPA1E*, *BRCA1* and *PARP1* genes regulated in *NAC103*-GFP overexpression lines and *nac103* mutant, but not changed in *NAC103* overexpression lines. Moreover, generation of true leaves and cell death of roots are decreased in *sog1* and *nac103* mutant compare to wild type under genotoxic stress. Transcriptional activation assay and chromatin immunoprecipitation analysis suggested direct or indirect interaction of *NAC103*-GFP with promoters of DDR-related genes. Furthermore, expression of DDR-related genes was induced in *NAC103*-GFP OX lines and *NAC103* OX lines of *sog1* mutant under genotoxic stress. Taken together, these results demonstrate that *NAC103*, which is regulated by *SOG1*, serve as a part of regulator of DDR under DNA damage condition.

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Ortholog gene of *OshCI1*, *Sorghum bicolor* heat-induced RING finger E3 ligase

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The general negative effect by global warming is affect on plant survival due to the damaging effect of high temperatures on plant development. However, it is far little known that functions of RING E3 ligase in response to high temperature in plants. To identify genes required for the heat stress response in the cereal crops, we found that the *Sorghum bicolor* (sorghum) ortholog of *Oryza sativa* heat and cold induced (*OshCI1*), SbHIRP1 protein, which is highly induced under high temperature condition in sorghum. Subcellular localization results showed that SbHIRP1 was mainly associated with the cytosol and moved to Golgi apparatus when exposed to high temperature conditions. In addition, results of Bimolecular fluorescence complementation (BiFC) and yeast two-hybrid (Y2H) assay showed that SbHIRP1 physically interacted with ortholog partner proteins of *OshCI1*, i.e. SbbHLH, Sb14-3-3 and SbbGLU1, at cytoplasm within the cell. Moreover, *in vitro* ubiquitination assay revealed that SbHIRP1 ubiquitinates each of three interacting proteins. Therefore, SbHIRP1 is induced by heat stress and suggests that it's activation as an e3 ligase.

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Analysis of physiological response and protein expression in Korean F1 maize hybrids at flowering stage under water deficit stress

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Despite its relevance, transcript regulation, protein regulation, and the physiological status of plant under water deficit are not well understood in F1 hybrid maize developed in Korea. In this study, F1 hybrid maize exposed to water deficit conditions by withholding water for 10 days at flowering stage. In both Ilmichal (Ilmi) and Gwangpyeongok (GPOK), the water deficit stress severely caused to reduce relative leaf water content and decrease leaf area by about 36 and 45%, respectively. Stem length and total dry matter of aerial parts of the water deficit-stressed plants was decreased in Ilmi and GPOK, respectively. Root dry matter accumulation was only reduced by about 25 % in GPOK. SPAD value and leaf conductance of the water deficit stressed plants severely decreased in both hybrids. 2-DE analyses were compared between well-watered and water-deficient F1 hybrid maize. Differentially expression was observed for 24 protein spots due to water deficit stress. Major identified proteins by MALDI-TOF mass spectrometry were involved in carbohydrate metabolism, stress response, and photosynthesis. Out of the 24 differentially expressed proteins, seven stress responsive proteins were highly expressed in both F1 hybrid by water deficit stress compared to well-watered plants. Interestingly, delta 3,5-delta 2,4-dienoyl-CoA isomerase and bifunctional 3-phosphoadenosine 5-phosphosulfate synthetase 2 were only expressed in GPOK. Otherwise, NAD-dependent epimerase/dehydratase, NAD(P)H-quinone oxidoreductase subunit 2 A, and uncharacterized protein were expressed in Ilmi response to water deficit stress. Semi-quantitative RT-PCR analysis showed that mRNA expression level of most of genes encoding the identified proteins was well correlated with their protein abundance, suggesting their water deficit-dependent transcriptional regulation in F1 hybrid maize at flowering stage.

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Identifying salt stress response genes during germination stage in rice (*Oryza sativa* L.) using Genome-wide association study

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Rice yield is influenced by various factors, Salt is one of crucial factor. In this study, we conducted GWAS analysis with 137 varieties of rice core set to identifying genes which response to salt stress during germination in rice. Seeds were germinated and grown under 250mM NaCl solution for 10 days in a growth chamber with 12°C, 40% of relative humidity. After 10 days, we measured 137 varieties seeds of germination rate, germination speed, germination energy, germination uniform rate and shoot length. These phenotype data were analyzed by GWAS. As a result, We found 11 SNPs markers related with germination under salt stress. Two candidate genes for germination rate, 2 candidate genes for germination speed, 3 candidates genes for germination uniform rate, 2 candidate gens for germination energy and 2 candidate genes for shoot length were detected by GWAS analysis.

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Evaluating the major agronomic characters of four forage crops at Saemangeum-reclaimed land of Jeollabuk-do Province

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The main objective of this study was to evaluate the four forage crops at the reclaimed land of Jeollabuk-do Province based on the evaluation of plant height, tiller, fresh weight, dry weight, and K/Na ratio. Four crops such as barley, rye, triticale, and italian ryegrass in this study were cultured at the reclaimed land. During cultivation period, the field was evaluated for moisture (%), electrical conductivity (EC, ds/m), and hardness (kg/cm²) 13 times. The moisture ranged from 5.37 to 36.51. The EC level was 0.45~1.27. The soil hardness showed 0.45~1.27 value. In vegetative period, a plant height (48.7 cm) of rye was the highest over the others. With regard to tiller number, italian ryegrass showed the greatest tillering capacity with 5.7 on average. But, there was no statistically significant difference. As compared to a dry weight per plant, barely showed the heaviest measurement as 1.64 g, italian ryegrass lowest as 0.38 g. During reproductive growth period, a plant height of rye was much higher than that of other crops. It is similar to the result of vegetative period. A tiller number was same in both barley and italian ryegrass with 3.4 on average. A fresh weight was high in the order of italian ryegrass (10.16 kg/m²) > rye (5.53 kg/m²) > triticale (4.2 kg/m²) > barley (4.1 kg/m²). A average dry weight of rye and Italian ryegrass was 1.8 and 1.81 kg/m², respectively, which was significantly high over that of the others. At non-reclaimed land, a K/Na ratio was nearly equal to rye, triticale, and italian ryegrass. But, its level (159.4) of rye was the highest compared to that of the others. A barley showed a heavy imbalance of growth in the reclaimed land. The heading stage of barley was the fastest. Based on a K/Na ratio, it could be concluded that the rye is a suitable to produce a coarse forage in the reclaimed land. In the immediate future, the feed value of forage crops will be analyzed.

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벼 정조 저장 중 저장조건이 도정특성 변화에 미치는 영향

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벼 정조 저장 중 저장조건에 따라 최고품질 벼 품종의 도정특성 변화에 미치는 영향을 평가하기 위하여 저온(15°C), 저온밀봉, 상온 조건에서 저장한 벼 품종의 도정특성, 수분함량, 현미의 경도 및 밥의 윤기치 등을 조사하였다. 저장 중 밥의 윤기치는 저장 전 대비 감소하는 경향이었고 저온저장보다 상온저장에서 밥의 윤기치 감소 정도가 더 심한 경향이 있었다. 저장 전 시료의 수분함량은 12.5~14.6% 이었고 저장 중 수분함량 변화는 저온밀봉, 상온, 저온저장 순으로 감소하는 정도가 심하였으며 현미의 경도는 저온밀봉, 상온, 저온저장 순으로 수분함량이 감소하는 정도에 따라 높게 나타났다. 저온저장의 경우 현미의 수분함량이 낮고 현미의 경도가 높아 찌라기 발생률이 높았으며 현미를 백미로 도정할 때의 현백률이 높게 나타났다. 따라서, 백미를 색채 선별할 때 색채 선별 불완전비율 또한 높아졌다. 그러나 상온 및 저온밀봉 조건에서 저장한 시료는 저장 전과 비교해도 도정특성에는 큰 차이가 없었다. 상온저장보다 저온저장 조건에서 찌라기 비율 및 현백률이 높아진 이유는 상온저장에서는 대체로 정조의 수분함량이 낮아지는 정도가 적은 반면 저온저장에서는 상대습도 조절이 안되는 저장고에서 찬바람을 이용해 온도가 조절되는 조건으로 저장 1개월 만에 8~9%로 빠르게 수분함량이 감소하고 현미의 경도가 높아졌기 때문이다. 수분함량이 낮은 상태에서 도정을 하면 찌라기 발생률이 높고 도정이 잘 되지 않아 색채 선별 과정에서 색채미로 선별되어 완전미 도정수율이 낮아지는 원인이 된다. 따라서, 저장시설 부족으로 상온에서 야적할 경우 쌀의 미질이 나빠지기 때문에 15°C 이하의 조건에서 저장함으로써 미질 저하를 줄일 수 있으나 완전미 비율을 유지하기 위해서는 저장고 내의 상대습도를 조절할 수 있는 시설을 갖추어야 할 필요가 있다.

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Effect of salt stress on germination and seedling growth in soybean

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High salt concentration is known to affect seed germination, nodule formation, seedling growth, and reduce soybean yield. The objective of the present study was to investigate the effect of NaCl concentrations on water uptake of seeds, germination, seedling growth, fresh weight, and dry weight in soybean. A total of 16 soybean salt tolerant and susceptible accessions (8 *G. max* and 8 *G. soja*) were utilized in the present study. Two replicates of seeds were grown within paper towels (30 seeds/replicate) pre-moistened with a range of NaCl solution (0mM, 100mM and 200mM) and placed vertically in plastic trays into a dark plant growth chamber at $25 \pm 2^\circ\text{C}$ for 8 days. The water uptake of seeds was measured 24 hours after sowing. The germination was recorded every 24 hours for 8 days. Seedling growth rate and fresh weight were measured 4, 6, and 8 days after germination. The results showed that the highest water uptake percentage was observed in *G. soja* tolerant accessions at 100mM and 200mM NaCl concentrations. The final germination percentage in all accessions was the same as control at 100mM NaCl concentration, whereas at 200mM germination decreased 29.4%. The *G. max* accessions showed higher germination percentage than *G. soja* at 200mM NaCl. The total average seedling growth, fresh and dry weights reduction in all soybean accessions was 49.0% and 10.8%, 41.0% and 10.1%, 51.1% and 23.3% of the control at 100mM and 200mM NaCl concentration, respectively.

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유묘기 습해처리에 따른 테오신트의 생체량, SPAD 변화 및 유전자 발현 양상

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최근 내습성 관련한 인자의 도입을 위하여 옥수수 야생종인 테오신트(teosinte)를 이용한 연구가 진행되고 있다. 따라서 본 연구에서는 옥수수 야생종인 테오신트(*Zea diploperennis* 등 6종)의 내습성 유용유전자를 현재 재배되는 옥수수로 도입 가능성을 타진하고자 수집된 테오신트를 대상으로 유묘기에 습해처리 후 식물체 생체량, SPAD값 변화 및 유전자 발현 양상을 알아보려 수행하였다. 유묘기 습해처리에 따른 테오신트의 뿌리 생체량은 *Zea mays* subsp. *Parviglumis*을 제외한 나머지 테오신트 수집종에서 습해 처리후 3일까지는 증가하는 경향을 나타내지만 습해 처리후 6일째에서 감소하는 경향을 나타내었다. SPAD값에 따른 엽록소 함량측정 결과에서 습해처리 후 상위엽에 비하여 하위엽에서 측정된 SPAD 값의 감소가 더 크게 나타났다. 그러나 다른 수집된 테오신트에 비하여 *Zea diploperennis*은 유묘기 습해 처리에 따른 SPAD 값의 감소율이 가장 낮게 나타났다. 습해 처리에 따른 유전자 발현 양상은 각각의 수집된 테오신트에서 반응 정도가 차이가 있었으며, 내습성 관련된 AP2-EREBP-transcription factor 180, Alcohol dehydrogenase 1, Alcohol dehydrogenase 2 등에서 발현이 높았다. 따라서 생체량 변화와 유전자 발현 양상을 검토해 보았을 때 수집된 테오신트에서 습해 저항 유전자가 있을 것으로 추정되었다.

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qVDT11, a major QTL that positively regulates tillering in rice under drought stress condition in field

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Rice is important cereal crops and staple foods worldwide. Drought is the most serious abiotic stress limiting rice production. However, little progress has been made in the genetic analysis of drought tolerance, because it is a complex trait controlled by a number of genes and affected by various environmental factors. We evaluate rice grain yield of Nagdong and Samgang under two different field conditions, rain-fed, irrigation. Grain yield of Nagdong decreased by 53.3% from 517 kg/10a to 241 kg/10a when compare to irrigation condition. By comparison, grain yield of Samgang decreased by 23.6% from 550 kg/10a to 420 kg/10a. To identify QTLs for drought tolerance, we examined visual drought tolerance (VDT) and relative water content (RWC) using a doubled haploid (DH) population consisted of 101 lines derived from a cross between Samgang (a drought tolerance variety) and Nagdong (a drought sensitive variety). Three QTLs for VDT were located on chromosomes 2, 6, and 11, respectively, and explained 41.8% of the total phenotypic variance. *qVDT11*, flanked by markers RM26765 and RM287, explained 19.9% of the phenotypic variance with LOD score of 7.1 and an additive effect of -1.0 . To determine QTL effects on drought tolerance under rain-fed paddy conditions, seven DH lines were selected according to the number of QTLs they contained. Of the drought tolerance associated QTLs, *qVDT2* and *qVDT6* did not affect tiller formation, but *qVDT11* increased tiller number. Tiller formation was most stable when *qVDT2* and *qVDT11* were combined. These results suggest that *qVDT11* is important for drought tolerance and stable tiller formation under drought stress condition in field.

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Genome-wide analysis of auxin efflux carrier protein family in rice reveals the close association with nitrogen stress response

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Auxin efflux carrier protein family genes play roles in the transport of auxins from the leaves to the roots. however, the biological functions in rice have not been well studied. In this study, we tried to find out functional roles of auxin efflux carrier protein family genes in rice through the diverse transcriptome analysis in the phylogenetic context. These transcriptome data include anatomical meta-expression profiles and differential expression patterns under hormone, abiotic stress, and nitrogen supplement. In rice, there are 12 auxin efflux carrier protein family members and phylogenetic analysis classified these members to four clades. Then, we analyzed the expression patterns in various tissues and organs for ACE genes using both meta-expression data and qRT-PCR. As a result, *OsPIN1a*, *OsPIN1b*, *OsPIN2*, *OsPIN5c*, and *OsPIN9* showed the highest expression in the root. *OsPIN1c* and *OsPIN1d* were expressed highly in the young panicles. When nitrogen was supplemented with nitrogen-deficient plants, microarray showed that expression levels of four auxin efflux carrier protein family genes were significantly induced, indicating that auxin efflux carrier protein family in rice are strongly associated with nitrogen utilization. To identify the molecular mechanism for enhancing the nitrogen use efficiency in rice, we are undergoing functional studies for rice auxin efflux carrier protein family genes.

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miRNAome analysis in flood-tolerant soybean Cheongja-3

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Flooding is a one of the most critical factor has influence on decrease in crop growth and productivity. Soybean (*Glycine max*) is a crop relatively sensitive to wet soil environment, causing poor root respiration and nutrition uptake.

MicroRNAs(miRNAs) are known to serve as key regulators of gene expression in relation to biotic and abiotic stress. To investigate the composition of miRNAome of Cheongja-3, known as flood-tolerant soybean, small RNA libraries from control samples (non-flood treated) and flood-treated samples (10 days) were constructed and sequenced by Illumina Hiseq sequencing. After size classification of small RNAs, the 24nt RNAs showed the highest proportion of 26% among the small RNAs ranged from 18 to 30nt. For further investigation to identify candidate miRNAs, sequence similarity search was conducted using miRBase (<http://www.mirbase.org>, release 22). A total of 512 sequences were matched to the known miRNAs of *Glycine max* (WS82), and 90 sequences to the miRNAs of *Arabidopsis thaliana*. Of them, 55 sequences were detected in both *G. max* and *A. thaliana*. Our results in this analysis will be helpful to identify candidate miRNAs in Cheongja-3, as well as the comparative miRNAome study with soybean WS82 and other related species.

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Screening of drought- and flood-tolerant soybeans in core populations and EMS-treated 'Pungsannamul' mutant population

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Drought and flood are the major abiotic stresses affecting crops yield and production stability. Soybean (*Glycine max* (L.) Merr.) is an important leguminous crop known as a sensitive to drought and flood. The purpose of present study is to screen genetic variation in drought- and flood-tolerant accessions and utilize them as genetic resources for the development of high yielding drought- and flood-tolerant varieties. In the present study, we used leaf scorch score (LSS) index to identify tolerant accessions. A total of seven hundred and seventy one (386 accessions *G. max* and 385 accessions of *G. soja*) accessions of soybean core population in Korea were screened for drought tolerance in greenhouse condition. Out of them, 21 accessions showed very tolerant phenotype for drought screening. In case of flood tolerance screening, a total of three hundred and eighty lines of EMS population were tested and eight lines showed tolerant phenotype. In further studies, the tolerant lines isolated will be utilized for the breeding programme to identify the genetic resources involved in the drought and flood tolerance.

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Enhancement of soybean drought tolerance by genetic transformation

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YUCCA6 gene was introduced to produce drought tolerant transgenic soybean plants via *Agrobacterium*-mediated transformation using the improved half-seed method. The presence of the gene in transgenic plants were confirmed by PCR and Southern blot analysis, and the expression was investigated by RT-PCR. Transgenic line #2, #3 and #5 were tolerant to drought stress while non-transgenic plants were withered completely. Line #2, #3 and #5 were not affected remarkably by water deficit condition and lead to enhanced drought tolerance due to the prevention of cell membrane damage and maintenance of chlorophyll content. Moreover, the enhanced drought tolerance in transgenic lines resulted in reduced transpiration rate and low ROS content.

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현사시나무에서 AN1/A20 zinc finger family 유전자의 분리 및 내염·내건 특성 구명

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Stress-associated proteins(SAPs)을 암호화하는 AN1/A20 zinc finger family 유전자는 다양한 스트레스에 반응하여 발현되는 것으로 알려져 있다. 본 연구에서는 현사시나무에서 AN1/A20 도메인을 갖는 19개의 유전자(AN101~AN119)를 분리한 다음 염과 건조 스트레스 처리에 의해 2배 이상 발현이 변화하는 8개의 유전자를 선발하였다. 선발된 유전자의 발현을 각각 증가 또는 억제시킨 형질전환 현사시나무를 만들었다. 건조 및 염 스트레스를 처리하고 광화학효율을 조사한 결과, AN101, AN111, AN112 그리고 AN119의 유전자 발현이 억제된 형질전환 현사시나무에서 내염성의 증가를 확인하였다. 한편 AN105의 발현이 증가된 형질전환 현사시나무는 내건성이 증가하였다. 따라서 현사시나무의 AN1/A20 zinc finger family 유전자는 내염성 및 내건성이 증진된 기능성 임목을 개발하는데 유용하게 활용 될 것으로 기대된다. 현재, 형질전환 현사시나무에서 내염성 및 내건성이 증진된 기작을 구명하기 위해 유전자 발현정보 분석 등을 수행 중에 있다.

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Soybean NAC transcription factors promote the lateral root formation and enhance drought and salt stress tolerance in overexpressed transgenic Arabidopsis plants

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NACs are plant-specific transcription factors which play crucial roles in plant development and biotic and/or abiotic stress responses. This study was performed to characterize functions of a soybean *NAC* gene, *GmNAC109* in stress response and lateral root formation. DNA sequence of *GmNAC109* showed the highest identity with *ATAF1* (*Arabidopsis Transcription Activation Factor 1*) which regulates both abiotic and biotic stress response. In soybean, expression of the *GmNAC109* gene was significantly induced by salt stress, especially in root tissue. Similarly, overexpression of *GmNAC109* in Arabidopsis plants resulted in higher tolerance to drought and salt stress. The stress response-related genes, such as *DREB2A*, *COR15A* and *ABI5* were positively regulated by *GmNAC109* in the transgenic Arabidopsis plants. Besides, overexpression of *GmNAC109* significantly enhanced the lateral root formation which is known to be regulated by auxin pathway and auxin signaling-related genes, *ERF5*, *AXR3* and *ARF2* were up-regulated in roots of the transgenic Arabidopsis plants. This indicates that *GmNAC109* may also be involve in auxin signal pathway to regulate hairy roots formation. Our results provide a basis for genetic manipulation to develop promising soybean lines by improving tolerance to abiotic stress.

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Analysis of QTL interaction for low-temperature germinability using progenies derived from an interspecific cross in rice

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Low-temperature germinability (LTG) is one of the most important traits in direct seeding method for rice cultivation. In our previous study, five QTLs controlling the LTG were identified using BC₄F₈ population derived from an interspecific cross between a Korean elite line Hwaseong and *Oryza rufipogon* (IRGC 105491). These five *O. rufipogon* QTL alleles increased the LTG and were located on chromosomes 1, 3, 4, 10, and 11 (*qLTG1*, *qLTG3*, *qLTG4*, *qLTG10*, and *qLTG11*). To examine the interaction between QTLs, we selected one progeny, CR1022, which has both *qLTG1* and *qLTG3* *O. rufipogon* alleles with Hwaseong genetic background. CR1022 was crossed with Hwaseong and 769 F₂ plants were developed. Six different genotype groups for *qLTG1* and *qLTG3* were selected from F₂ population using flanking SSR and InDel markers. Seeds of six genotype groups were incubated at 13°C in the growth chamber for LTG phenotyping and germinated seeds number was counted. Phenotyping results showed that the *O. rufipogon* alleles at *qLTG1* and *qLTG3* increased the LTG, respectively. Moreover, plants containing both *qLTG1* and *qLTG3* from *O. rufipogon* showed the highest LTG score. A two-way ANOVA indicated significant interaction between *qLTG1* and *qLTG3*, indicating that the two QTLs possibly regulate the LTG in the same pathway. The *qLTG3* locus was closely located with the known *qLTG3-1* (Os03g0103300) gene. In addition, the sequence variation of *qLTG3-1* gene was found between Hwaseong and *Oryza rufipogon* and it might be responsible for the variation of LTG in CR1022. Because *qLTG1* locus is not yet cloned, further studies on molecular mechanism of *qLTG1* and *qLTG3* will be carried out in the future. Hence, understanding the genetic and molecular interaction of these QTLs will be useful in rice research and breeding especially in the development of better direct seeding varieties with LTG.

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Marker development of the genes/QTLs related to biotic and abiotic stress tolerances

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Rice is the staple food for half of the world population and is mainly grown in stress-prone rainfed regions where rice plants regularly suffer from various abiotic and biotic stresses. Rice production is likely to be more unstable in the future due to climate change. To cope with this, varieties capable of increasing stress tolerances need to be developed rapidly. Here, we selected genes and QTLs for climate-change related traits such as *Sub1* and *AG1* for submergence, *DTY* for drought, *Saltol* for salinity, *Pup1* for root system and *Pb1* for blast resistance. DNA polymorphisms of target genes or QTLs were found by comparing trait-specific SNPs/InDels between target-gene donors and elite recipient varieties using the SNP-Seek(<http://snp-seek.irri.org/>) database and the related literatures. To develop the allele-specific markers, SNPs/Indels information were used to design KASP (Kompetitive Allele Specific PCR) and PCR gel-based markers. These developed markers were applied to genotyping segregation populations including donor and recipient varieties for marker validation. The subsequent phenotyping will be performed for five abiotic stresses including and one biotic stress. The allele-specific markers developed in this study would be very useful for developing varieties tolerant to biotic and abiotic stresses.

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Mitogen Activated Protein Kinase (MAPK)-related genes that increase cadmium contents in rice

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Cadmium is one of the toxic substances exposed to the environment, threatening organisms including human beings and major crops through the natural circulation process. Cadmium contaminates most agricultural lands exposed by phosphate fertilizers, irrigation water, waste incinerator, contamination such as mines, *etc.* In particular, disease caused by cadmium are potential chronic features at the level of low toxicity. Generally, when rice is exposed to heavy metals such as cadmium, enzymes (MAPKKK, MAPKK and MAPK) involved in the phosphorylation reaction are induced in vivo. In particular, MAPK is known to be activated for details of Cd-resistant cultivars than Cd-susceptible cultivars. Therefore, in this study, we conducted genome-wide related research and eQTL analysis for breeding of low-cadmium rice varieties of the rice core-set of Kongju National University.

Os01g0621600 and Os01g0607900 have the same function as the MPK5 (Mitogen-activated protein kinase 5) gene and affect cadmium genes such as OsMTP1 (Cation Diffusion Facilitator protein; Translocation of Zn, Cd and other heavy metals), Os08g0379200 (K/ Mg/ Cd/ Cu transporter family protein).

As a result of the sequence analysis of Os01g0621600, "Group12" had an average cadmium content of 1.8374 $\mu\text{g kg}^{-1}$ ($p < 0.0001$) which was the highest than the other groups, and amino acid was substituted valine to methionine at the 24,785,497 position. "Group4" of Os01g0607900 had an average cadmium content of 1.7196 $\mu\text{g kg}^{-1}$ ($p < 0.001$), which was the highest than the other groups. and it had deletion and amino acid substitution at the 23,980,869 and 23,981,207 position.

Thus, the group with high cadmium content of Os01g0621600 and Os01g0607900 is presumed to be Cd-resistant. Also, mutations in these genes are expected to reduce MAPK activity and cadmium content.

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Characterization of BSP protein family from *Triticum aestivum* L. and its expression under the high temperature

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Common wheat (*Triticum aestivum* L.) is the most cultivated crop species in the world. Wheat is frequently exposed to heat stress during grain development periods, which resulted in reduction of grain filling period, starch deposition and also grain size. In this study, plants were subjected to high temperature stress (34°C/31°C, day/night) for 5 days at eight days after flowering. A putative gene which was annotated as barley pr17c precursor and was belonged to the BSP family showed a higher transcriptional level during grain development under heat stress in qRT-PCR. Total 15 BSP family member genes in *Triticum aestivum* can be grouped into six phylogenetic clades, which were further confirmed by the following sequence analyses and motif structures. Based on the 51 identified homologs in seven Poaceae families, they were associated with six phylogenetic clades of *Triticum aestivum*. The defensive role of BSP family in relation to plant defense against pathogenesis has been widely studied. Here, we revealed that BSP family genes are also important responsive genes under the high temperature.

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OsMDHAR3 gene affects salt stress tolerance and grain yield under natural field conditions

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The monodehydroascorbate reductase (MDHAR), which is responsible for growth and development and stress response in plants, is a key enzyme in the maintenance of ascorbate (AsA) pool through the AsA – glutathione (AsA – GSH) cycle and is induced by abiotic stresses. It has highly conserved regions containing FAD- and NAD(P)H-binding domains. In particular, NAD(P)H is a significant electron donor in the AsA – GSH pathway. In this context, we introduced RNA interference (RNAi) to determine the functional role of *Oryza sativa* L. *japonica* MDHAR isoform 3 (*MDHAR3*) and developed transgenic (*mdhar3*) rice plants in which the NAD(P)H domain was silenced. The *mdhar3* rice plants were more sensitive to salt stress than the wild-type (WT) plants. In addition, the *mdhar3* rice plants showed decreased ability for environmental adaptation because of an imbalance in the redox homeostasis and reduced AsA pool. These plants showed increased hydroperoxide levels and ion leakage, and decreased chlorophyll content and ascorbate/dehydroascorbate ratio under the paddy field conditions; they also exhibited a reduction in the total biomass and grain yield. These results suggest that *MDHAR3* plays a critical role in the intrinsic resistance, as well as in the sensitivity of seed maturation and productivity, of rice plants to environmental stresses, thereby, indicating the functional importance of NADH in MDHAR activity, *in vivo* and *in vitro*.

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Fine mapping and identification of candidate genes associated with low-temperature germinability using derived from a cross between *Oryza sativa* and *Oryza rufipogon*

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Seed germination is being delayed or inhibited under several kinds of stress such as temperature, salt, and osmotic pressure. High germination rate for low-temperature is an important factor in growing rice. In direct-seeded method in rice, low-temperature germinability is considered as one of the factors for stable plant stand establishment in temperate regions and high altitude areas. Previously, we detected the *qLTG1* as the quantitative trait locus (QTL) that plays a vital role in controlling tolerance to a low temperature in seed germination stage using progenies derived from a cross between *Oryza sativa* (cv. Hwaseong) and *Oryza rufipogon* (Rufi). The *qLTG1* was detected and located between in CRM23-CRM15 on chromosome 1 within 56.4 kb region harboring 10 genes. To identify the genes targeted by *qLTG1*, the expression profiles of the identified candidate genes and germination behavior of *qLTG1* under different low-temperature condition were investigated and compared to HS, Rufi, and TR5 (BC₃F₇). These results indicated that *qLTG1* showed tolerance for several abiotic stresses such as salt, drought and low temperature. The *qLTG1* for low-temperature germinability would be useful in rice breeding programs especially in the development of lines possessing low-temperature germinability.

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Changes of germination rate on seed germplasm of maize, sorghum, and cowpea after long-term conservation

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The seeds of maize (*Zea mays* L.), sorghum (*Sorghum bicolor*), and cowpea (*Vigna unguiculata*) were examined the germination rate after 10 years of long-term storage (-18 °C) conservation. For maize seeds, 4,463 accessions were examined and germination rate of 1,512 accessions was decreased with below 15% of initial germination rate. For 183 accessions of maize, germination rate was decreased with above 15% of initial germination rate after 10 years of long-term storage, which is needed to be rejuvenated. Germination rate of 1,404 accessions was increased and showed no change for 1,364 accessions after 10 years of long-term storage. For sorghum seeds, 830 accessions were examined and germination rate of 345 accessions was decreased with below 15% of initial germination rate. For 21 accessions of sorghum, germination rate was decreased with above 15% of initial germination rate after 10 years of long-term storage, which is needed to be rejuvenated. Germination rate of 368 accessions was increased and showed no change for 96 accessions after 10 years of long-term storage. For cowpea seeds, 497 accessions were examined and germination rate of 127 accessions was decreased with below 15% of initial germination rate. For 34 accessions of cowpea, germination rate was decreased with above 15% of initial germination rate after 10 years of long-term storage, which is needed to be rejuvenated. Germination rate of 238 accessions was increased and showed no change for 98 accessions after 10 years of long-term storage.

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Identification and marker development of Cucumber's chilling tolerance related genes by Next Generation Sequencing

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For identification of chilling tolerance related genes, three chilling susceptible Cucumber inbred lines and two chilling tolerant Cucumber inbred lines were used as materials and sequenced using Illumina Miseq. Reference genome sequences were collected from NCBI GenBank and annotation data was downloaded from cucumber genome database. Through read mapping analysis to reference Cucumber genome data, all nuclear, chloroplast, and mitochondrial genome sequences of five Cucumber inbred lines were compared to each other. As a result totally 26,579 common polymorphic sites were identified between chilling tolerant and susceptible lines. Among all of 26,579 polymorphic sites, 1,182 sites were located in CDS regions of nuclear genome and two polymorphic sites were in intron regions of mitochondrial genome sequences. We also conducted candidate gene approach to identify the cold tolerance gene. A total of 16 genes were selected for candidate cold tolerance responsible genes in two Cucumber inbred lines. We developed 12 dCAPs markers one from each candidate gene based on these polymorphic analysis results. Candidate genes and developed markers will be valuable resource for molecular breeding of Cucumber. This work was supported by Korea Institute of Planning and Evaluation for Technology in Food, Agriculture, Forestry and Fisheries (IPET) through Agri-Bio industry Technology Development Program, funded by Ministry of Agriculture, Food and Rural Affairs (MAFRA) (grant number 116076-03-3-HD0b0).

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Evaluation of anaerobic germinability and relative expression analysis of anaerobic-responsive genes in rice germplasm

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Direct-seeded rice cultivation (DSC) is getting farmer's attention due to its low water requirements and labor's cost. In temperate regions, DSC is followed by flooding by irrigation or heavy rainfall creating anaerobic conditions for seed germination. In such anaerobic conditions, successful seedling establishment requires rapid coleoptile growth to ensure access to oxygen near the water surface. However, not all rice varieties can tolerate anaerobic conditions; only tolerant accessions with strong anaerobic germinability (AG) can germinate and elongate their coleoptiles to escape from anaerobic conditions. Due to the limited availability of highly tolerant genotypes, there is an urgent need to select diverse rice germplasm with enhanced AG. In this study, we evaluated 185 rice accessions from six subpopulations for germination rate (AGR) and coleoptile length (ACL) under anaerobic conditions. The highest average AGR (60%) and longest average ACL (2.13 cm) were observed in *tropical japonica* and *temperate japonica* germplasm, respectively. We identified highly-tolerant and -susceptible accessions and compared relative expressions of AG-related genes with well known tolerant variety 'KHO' via quantitative real-time PCR. The proton pyrophosphatase (*OVP3*) and rice alpha-amylase (*RAmy3D*) were expressed at significantly higher levels in the strong accessions than 'KHO' and susceptible accession. In general, *OVP3* was expressed at the highest levels in all strong accessions, whereas the expression level of rice ethylene-response element binding protein (*OsEREBP1*) and alcohol dehydrogenase 1 (*ADH1*) did not significantly differ among accessions. These findings could be helpful for breeders and lay the foundation for further genetic analysis.

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애기장대 유래 비생물학적 스트레스 저항성 유전자들을 이용한 고온 저항성 벼 형질전환체 육성

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식물은 성장하면서 다양한 환경 스트레스에 노출되며, 이러한 스트레스는 식물생육에 영향을 끼친다. 현재 계속되는 지구 기후 변화로 인한 기온상승과 극단적 기상변동 등은 농업에 부정적인 영향을 미쳐 작물의 수확량 감소를 초래하는 직접적인 원인이 되고 있다. 따라서 식물의 비생물학적 스트레스 저항성을 증진시키는 것은 환경조건의 변화 시에도 식물 성장과 발달을 유지하여 안정적 생산을 가능하게 해 줄 것이다. 벼의 고온 스트레스 저항성 증진할 목적으로, 본 연구에서는 애기장대에서 유래된 비생물학적 스트레스 저항성 관련 후보유전자 6종 (*NDPK2*, *GolS1*, *PRE1*, *YUCCA6*, *Hsp101*, *CBF1*)들을 벼유래 화기조직 특이적 및 상시발현을 유도하는 4종의 프로모터(*TDF1*, *RMP1*, *OsLPS1*, *UBQ14*)들과 결합시킨 형질전환용 벡터들을 제작하였다. *Agrobacterium*을 이용한 조직배양으로 미성숙 배로부터 캘러스를 유도시켜 재분화를 통해 벼 형질전환체들을 육성하였으며, T0 식물체 genomic DNA의 PCR 분석을 통해 유전자 도입을 확인하였다. 후대에서의 저항성 검정과 PCR 분석을 통해 single copy가 들어간 식물체들을 선발하고 T2세대에서 유효기, 출수기 등 고온 스트레스에 취약한 발달단계에서 저항성을 검정한다. 다양한 후보유전자들을 대상으로 고온저항성 증진에 효과적인 유전자에 관한 연구결과들은 향후 지구 온난화 대비 벼 품종육성을 위한 기초자료로 유용하게 활용될 것으로 기대된다.

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Screening sorghum varieties for salt tolerance

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Sorghum is highly productive crop plant, which can be used for human food, livestock feed and alternative energy resource. The plant has a great adaptation potential to drought, high salinity and high temperature, which are important characteristics of crop growth. Salinity is an abiotic stress that limits both growth and yield of crops. Genotypic differences in salt tolerant exist and exploiting genetic variability to identify salt tolerant genotype is one of the strategies used to overcome salinity. For this purpose some experiment was carried out to evaluate the genetic variation of 136 sorghum genotypes for NaCl salinity response at germination and early seedling stages. Experiments were conducted in Petri plates and plots with 250mM NaCl levels to validate screening tools. Physiological parameters such as germination, shoot and root development were analyzed to identify the salt tolerant of representative line. Nampungchal and Btx623 were categorized as tolerant, SC372 were as sensitive ones. The results affirmed the presence of genotypic variation among the sorghum genotypes for salt tolerance. the selection of suitable lines that can be recommended for saline areas to improve yields.

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CBF1 overexpression confers heat tolerance in Arabidopsis seedlings

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As the world population and grain demand have been increasing, food security is the most urgent matter we face. In addition, environments of the plant growth are predicted to be changed due to global climate changes in the coming decades, which will seriously affect sufficient crop yield. There have been significant efforts to improve plant fitness that can withstand various stress conditions. There have been reports about positive relationship between C-repeat-binding factors(*CBF*) genes expression and cold acclimation. It has been also known that plants overexpressing the *CBF1* gene exhibit growth retardation and late flowering. In this study, we investigated whether *CBF1* gene also plays a role for heat tolerance in Arabidopsis. To this end, we generated transgenic lines harboring an overexpression vector proUBQ14-*CBF1*. We tested 10 day-old seedlings at heat stress conditions and checked their survival rates. Our preliminary results suggest that overexpression of *CBF1* gene confers enhanced heat tolerance at seedling stages. Based on this result we will continue to test heat stress conditions during reproductive stages.

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GWAS and eQTL on preharvest sprouting characteristics of Asian cultivated rice

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Using 378 Asian cultivated rice varieties, we performed GWAS and eQTL analysis independently. The result of GWAS showed that a number of significantly associated SNPs with preharvest sprouting (PHS) response tested in field for two years. eQTL analysis was performed to identify the genetic variants associated with the expression of each gene. Some of the significantly associated SNPs with PHS response by GWAS were also significantly associated eQTL of certain genes indicating the SNPs are involved in PHS response as a way of influencing the expression of specific genes.

Keywords: preharvest sprouting, GWAS, eQTL, Asian cultivated rice

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The Development of Transgenic Rice Pool Over-expressing Full Length Genes related to Stress Response in *Oryza sativa*

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We have developed the transgenic pool of over-expressing full length genes in rice to investigate the functions of rice genes and to create the resources applicable for the molecular breeding program as a fundamental approach for crop improvement.

The overexpression vector *pB2GW7* was modified for the construction of destination vector in the use of the insertion clones of a cDNA library. It is constructed from the stress-related genes induced in rice under the condition by the treatment of both abiotic and biotic stresses. All the retrieved sequences of clones from the cDNA library were scanned and determined using data of Rice Genome Annotation Project. Only a full-length insertion fragments were selected from the clones of the constructed cDNA library, and the selected full-length genes for the transgenic lines are approximately over 400. The *Agrobacterium* strain LBA4404 harboring the modified *pB2GW7* vector was introduced into embryogenic rice calli (*Oryza sativa* L. Japonica), and then the transgenic lines were preliminarily obtained by *Agrobacterium*-mediated transformation and regeneration method. Phenotypic observation of the positive T1 transgenic plants showed that a few of these transgenic lines exhibited potentially obvious phenotypes (yellowish leaves, more branches etc.). Subsequent phenotypic analysis is underway to demonstrate that these phenotypes were due to the overexpression of rice genes.

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Variation in early plant height in wild and cultivated soybean (I)

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Soybean (*Glycine max*) and wild soybean (*G. soja*) are annual legumes of Fabaceae family. Plant height is an important characteristic trait in soybean germplasm and cultivated soybean for evaluation. In this study, four elements were used to assess variation of early plant height in wild and cultivated soybean. Wild accessions 375 and 395 cultivated soybean used for a field experiment to identify and evaluate for plant height at early stage. The experiment was laid out in complete randomized design (RCBD) with three replications. Secondly, we evaluated the correlation between planting dates to the plant height in wild soybean. Third, the effect of four plant hormones GA₃, GA₃₊₄, GA₄₊₇ and prohexadione-calcium (inhibitor of GA synthesis) were used with four different concentration 0, 10, 20, and 40μM in three different plant groups for instance (fast-growing, slow-growing and cultivated soybeans). Finally, we evaluated the segregation pattern for plant height when crossing between fast-growing and slow-growing accessions. In addition to plant height we examine other agronomic traits, such as the number of nodes, the number of stem diameter, the number of branches per plant after 30 days of planting. The result of tendency showed that the bioactive GA₃ and GA₃₊₄ were detectable to the elongation increased of three plant groups. Concentration 40μM. was found to be best among four treatments. Our results provide important information for rapid growth trait in wild soybean and a useful trait for evaluation plant height in soybean.

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Variation in early plant height in wild and cultivated soybean (II)

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Soybean (*Glycine max*) and wild soybean (*G. soja*) are annual legumes of Fabaceae family. Understanding genetic and environmental effect on plant height is important for soybean production. In this study, core collections including 375 wild accessions and 395 cultivated soybeans were used for a field experiment to identify and evaluate for plant height at early stage. The experiment was laid out in complete randomized design (RCBD) with three replications. Secondly, we evaluated the correlation between planting dates to the plant height in wild soybean. Third, plant hormones, GA₃, GA₄, and prohexadione-calcium (inhibitor of GA synthesis), were used to figure out the effect on plant height with four different concentrations 0, 10, 20, and 40μM in three different plant groups (fast-growing, slow-growing and cultivated soybeans) for instance. The result showed that there was big variation in early plant height in wild soybean and the bioactive GA₃ was detectable to the elongation increased of three plant groups. Our results provide important information for rapid growth trait in wild soybean and a useful trait for evaluation plant height in soybean.

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Differential protein expressions of soybean leaves under waterlogging stress at early vegetative stage

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Waterlogging (WL), a major environmental stress, is a severe constraint on crop growth and productivity in many regions and situations. Waterlogging can reduce the photosynthesis rate, induce oxidative stress, accelerate leaf senescence, inhibit plant growth and finally lead to crop yield loss. The present study was conducted to investigate the morpho-physiological and proteome responses of three- and five leaf stage of soybean to WL stress. The domestic cultivar, Uram was used to test the waterlogging stress. In the experiment of 3-leaf stage soybean, stem length, chlorophyll contents were decreased when the plants were exposed to WL stress. The 5-leaf stage experiment was similar to the 3-leaf experiment. In the waterlogging for 4 days, the stem length and chlorophyll contents showed significant change among other treatments. Characteristic related to leaf showed treatments was smaller than control regardless to soils. The results observed from experiment 1, 2 and 3 were considered to be influenced by the waterlogging stress more in the 5-leaf stage soybean, and as the waterlogging treatment progressed, the waterlogging stress influenced the growth difference between control and treatment. A total of 30 protein spots were analyzed using LTQ-FI ICR MS. As a result, 9 proteins were up-regulated in the treatment group and 4 proteins were down-regulated. Analysis of LTQ-FI ICR MS showed that 50% of the proteins involved in RNA processing, translation, biological process. Malate dehydrogenase protein and Glyceraldehyde-3-phosphate dehydrogenase protein increased the level of protein expression in 3 and 5-leaf stage under waterlogging stress. These proteins are known to function as antistress agents. The expression of oxygen-evolving enhancer protein 1 related to photosynthesis was increased in treatment than control. Superoxide dismutase protein related to response to oxidative stress showed high expression level in 5-leaf stage treatment. These results suggest that waterlogging directly impairs photosynthesis and photorespiration.

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Proteome analysis of sesame leaves under waterlogging stress at an early vegetative stage

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Waterlogging is a common adverse environmental condition that limits plant growth and one of the major abiotic stresses affect in sesame (*Sesamum indicum* L.) yields resulting in increases of relative ion leakage, lipid peroxidation and in vivo H₂O₂ content. The purpose of this study was to explore the protein expression patterns of sesame leaves under waterlogging stress. The plant height, stem length, chlorophyll content exhibited gradually decrease while chlorophyll and H₂O₂ content increased significantly in response to waterlogging stress. More than 300 protein spots were detected on 2-DE from 10-leaf growth stage and 20 protein spots were differentially altered, and their abundance was significantly responsive to waterlogging treatment, with more than a 1.5-fold change in intensity. In case of flowering stage, more than 400 protein spots were identified and a total of 31 protein spots that exhibited more than a 1.5-fold changes in intensity. Of 31 proteins 16 proteins were found to be up-regulated and 15 proteins were down-regulated under waterlogging stress. These findings shed light on the complex mechanisms underlying waterlogging tolerance in sesame.

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Responses of leaf proteins in Azuki bean at early vegetative and reproductive stage to waterlogging stress

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Waterlogging of soil is a major limiting factor for crop growth in humid regions. Prolonged rainy period or heavy rainfall in the field with poor soil drainage significantly reduces the seed yield of grain legumes. To explore the morpho-physiological and unravel the molecular tolerance mechanism of two- and five leaf stage of Azuki bean to waterlogging stress. The plant height, stem length, chlorophyll contents were decreased when the plants were exposed to waterlogging stress. In the 2-leaf stage, more than 400 protein spots were detected on 2-D gels, and quantitative image analysis revealed a total of 43 protein spots that exhibited more than a 1.5-fold changes in intensity whereas 23 differentially expressed proteins were successfully analyzed using MALDI-TOF/TOF MS analysis. Among these proteins, a total of 14 proteins showed increased expression, and 9 proteins showed decreased expression in the treated samples compared to their levels in untreated seedlings. However, in the 5-leaf stage proteome, 29 protein spots were found to be expressed differentially upon waterlogging stress, with more than 1.5-fold differences in abundances between the control and waterlogging-treated samples. A total of 16 proteins were increased significantly while 13 proteins were decreased abundances. The abundance of the most identified protein species from the leaves that function in stress response and metabolism was significantly enhanced, while protein species involved in transcription and regulation were severely reduced.

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Genome-wide identification and characterization of bZIP transcription factor gene family in mungbean (*Vigna radiata* (L.) R. Wilczek)

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Basic region-leucine zipper (bZIP) transcription factor family is one of the largest families in plant species, and is known to play crucial roles in plant development from various signaling responses to organogenesis. Because of its significance, genomic studies of bZIP transcription factor (TF) have been conducted in many important plant species, such as Arabidopsis, rice and maize. Mungbean (*Vigna radiata* (L.) R. Wilczek), although recognized as one of the major crops in Asia for its high level of protein and vital micronutrients, has not been studied for its identification and characterization of bZIP TF. Recently, reference genome sequence of mungbean has been published. In this study, based on the mungbean genome sequence and annotations, bZIP TF genes in mungbean were identified using sequence similarities of known Arabidopsis bZIP TFs, and further verified with domain search. Based on the neighbor-joining tree constructed from bZIP TF sequences of Arabidopsis and mungbean, mungbean bZIP TF clades were classified and other conserved motifs were analyzed. Additionally, possible gene duplications and sequence variations within regions of bZIP TF sequences were found with synteny analysis of mungbean genome. To check expression level variations of bZIP TF genes among four tissues of mungbean, including leaf, flower, pod and root, expression heatmap was built using RNA-Seq data. With the first genome-wide study of bZIP TF genes in mungbean, the data can further be utilized to elucidate the mechanisms behind various stress responses and development of mungbean.

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Chromosome investigations on three tetraploid of *Chrysanthemum* species through FISH analysis

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Chrysanthemum is popular for the beauty of its flowers and the health benefits it offers. The good keeping quality with the different varieties of flowers has made its mark in the floricultural industry in Korea and in the other parts of the world. Karyomorphological study is performed on three tetraploid species of chrysanthemum by employing fluorescence in situ hybridization (FISH) technique using rDNA probes. The three species have a chromosome number of $2n=4X=36$. FISH results showed 8 and 4 signals of 45S and 5S rDNA in *Chrysanthemum boreale*, *Chrysanthemum indicum*, and *Chrysanthemum zawadskii*. The number and distribution of rDNA signals which are all located in metaphase chromosomes between *C. boreale* and *C. indicum* are more conserved. This may suggest that the genomic components of the 2 tetraploids are mostly homogeneous. The karyotype formulae of three polyploids are $27m+9sm+0st+0t$, $23m+13sm+0st+0t$, and $25m+9sm+2st+0t$. The karyotypes of three species are found to be symmetric. This implies that the three chrysanthemums are primitive or primordial species. The cytological information coupled with molecular analysis are vital for the elucidation of the genetic make-up of plants and to better understand their phylogenetic relationship.

Keywords: FISH karyotype ploidy, symmetry, rDNA

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A rice B-box protein, OsBBX14, finely regulates anthocyanin biosynthesis in rice

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Anthocyanins are important pigments that influence the quality of fruits and flowers. Anthocyanin biosynthesis is regulated by transcription factors and other proteins working in concert to finely tune the expression of genes involved in the flavonoid biosynthetic pathway. In rice (*Oryza sativa*), the R2R3 MYB transcription factor (TF) OsC1 and a bHLH TF, OsB2, were previously reported to control anthocyanin biosynthesis in vegetative tissues and seeds, respectively; however, the regulatory mechanisms of the anthocyanin biosynthesis TFs remain largely unknown. In this study, we identified OsBBX14, a homolog of *Arabidopsis thaliana* B-box domain protein 22 (AtBBX22), and investigated its function. The transcript level of *OsBBX14* was high in pigmented rice seeds and gradually increased as the seeds matured. The ectopic expression of *OsBBX14* in *Arabidopsis* resulted in a dramatic increase in anthocyanin accumulation in seedlings. Using a steroid receptor-based inducible activation system, OsBBX14 was found to partner with OsHY5 to directly activate the transcription of *OsC1*. Furthermore, OsBBX14 was found to physically interact with OsHY5; the second B-box domain of OsBBX14 and the bZIP domain of OsHY5 were sufficient for their interaction. Taken together, these results show that OsBBX14 interacts with OsHY5 to induce and fine tune the expression of *OsC1*, and thereby regulates anthocyanin biosynthesis.

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Molecular characterization of transgenic plants using Next Generation Sequencing and confirmation of insert in breeding combined trait products using sequencing analysis

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Molecular characterization of crops produced by transformation has traditionally been conducted using Southern blot analysis which has been used to determine T-DNA insert and copy numbers, the presence or absence of backbone (sequence outside of the T-DNA) and to demonstrate generational stability of the T-DNA insert. With the advancement of high-throughput Next Generation Sequencing (NGS) technology, efficient characterization of the transgene incorporated into the plant genome is now feasible by sequencing the entire plant genome. By generating NGS data with sufficient coverage depth followed by sequence read mapping to the plasmid vector, inserted plasmid sequence and flanking genomic sequence are identified. Through the analysis of mapped reads over multiple breeding generations, conclusions equivalent to those of Southern blot analyses, including insert number, copy number, absence of backbone and generational stability can be drawn. Stacked products are produced by conventional breeding of fully characterized single events to combine two or more GM traits into a single plant. Considering the nature of conventional breeding, a repeated full molecular characterization of each insert is not necessary as the transgene DNA behaves no differently than endogenous plant DNA. Therefore, transgenic events in a breeding stack can be confirmed by comparing the “fingerprint”, a blot that demonstrates the presence of an intact T-DNA insert and flanks, between the stack and the parental single event. Same conclusions can also be obtained through direct sequencing of the T-DNA insert and flanking genomic DNA in the stack when compared to the T-DNA insert and flanking genomic DNA in the parental single.

Due to recent advances of DNA sequencing and bioinformatics technology, there is an emerging opportunity to use NGS for the molecular analysis of both single event and stacked event transgenic crops. NGS and direct sequencing yield conclusions that are comparable to those of Southern blotting without radioactive hazards and artifacts that are frequently observed in Southern blotting.

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Genome-wide identification of RLK and RLP gene family in radish (*Raphanus sativus* L.)

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Radish, *Raphanus sativus* (2n = 18), belong to the Brassicaceae family, is one of the main economic vegetable in the world. However, the continuously threatened by devastating diseases, climatic variation and environmental stress which are affecting yield and quality of radish. In this study, we conducted genome-wide analyses of radish for two types of pattern recognition receptors which mediate a wide range of processes, including development, disease resistance, initiate an immune response, hormone perception, and self incompatibility. A total of 44 receptor-like kinase (RLK) and 10 of receptor-like protein (RLP) genes are identified in the genome of radish. RLK and RLP gene families each include different s-locus, G-lectin, PAN-2 and kinase functional domains. While a large number of RLPs resembling the extracellular domains of RLKs are also found in the radish genome. A phylogenetic analysis separated these genes into four groups. Group 1 and 3 mainly comprise of kinase domain and group 2 mainly comprise of G-Lectin domain and group 4 with PAN domain. Characterizing this gene family will be useful for the genetic improvement of radish.

Keywords: *Raphanus sativus*, receptor-like kinase (RLK), receptor-like protein (RLP), phylogenetics

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Anthocyanin content and antioxidant activity in several varieties of *Sorghum bicolor* (L.) Moench

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Sorghum bicolor (L.) Moench contains various phenolic compounds such as anthocyanin. We classified eleven sorghum accessions into five groups by seed color and measured antioxidant activity as well as the contents of total phenolic compounds (TPC) and anthocyanin in sorghum grains. The seed color was related to TPC content, but not to monomeric anthocyanin content. Moreover, the overall patterns of antioxidant activity levels in DPPH or ABTS assay were similar to those of the TPC content. We analyzed statistical correlations between TPC and anthocyanin contents, and antioxidant activities. The TPC and anthocyanin contents were statistically significant for positive correlation ($P < 0.05$), and the TPC content showed strong positive correlation against the DPPH and ABTS antioxidant activities. We expect that our results provide the basic data for breeding of sorghum varieties containing large amounts of antioxidants.

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Physicochemical properties and eating quality of cooked rice in low amylose content under freezing storage

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This study was carried out to investigate the physicochemical properties and eating quality under freezing temperature storage in low amylose content rices. For textures of eating quality, the five cooked rice samples were restored by microwave for 2.5 mins from storage of freezing temperature(-18°C) for 6, 24 and 48 hours. In physicochemical analysis, the amylose contents were ranged from 5.14 to 16.62%. And 'Baekogchal'(amylose 5.14%) showed the lowest value in peak, hot paste and cold paste viscosity as it is glutinous rice. 'Baegjinju'(amylose 9.75%) and 'Saeilmi'(amylose 16.62%) were the highest in breakdown viscosity and setback viscosity, respectively. The water absorption index of 'Baekogchal' was the highest level. In eating quality, all the cooked rice samples showed increased textural properties except hardness after 6 hours of freezing storage. Interestingly, the hardness of 'Miho' was increased while the others were decreased after freezing storage. Furthermore, 'Miho' showed not much difference compared to other rices in springiness, gumminess, chewiness and cohesiveness under the freezing storage. Under the freezing and thawing conditions. 'Miho', 'Baegjinju' and 'Saeilmi' showed increased lightness while 'Baekogchal' was decreased after 48 hours. In this study, we observed that 'Miho' showed a good textural properties for eating quality and color values under freezing storage. Therefore 'Miho' can be more acceptable in the refrigerate foods such as lunch box and processed freezing foods which are distributed under the low temperature.

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TALEN-based gene editing to produce herbicide-resistance *bar* knockout rice lines

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Gene editing technologies such as transcription activator-like effector nucleases (TALENs) and CRISPR/Cas9 systems have been developed to create targeted DNA double-strand breaks (DSBs) in many crop plants. DSBs are mainly repaired by error-prone nonhomologous end joining (NHEJ), which often caused small insertions or deletions at break site to generate knockout mutations. Here, TALENs were engineered to target and disrupt the herbicide-resistance *bar* in two donor plants of Bt-resistance transgenic rice and herbicide-resistance transgenic rice. A total of 10 and 30 of rice plants were respectively regenerated from both donors. Sanger sequencing and *bar* elisa analyses indicated that four and 18 mutant plants from Bt-resistant rice and basta-resistant rice respectively showed various indel mutations and SNPs at target gene, but not at TALEN target site. Mutant plants carrying only the desired DNA sequence change but not the TALEN transgene would be selected from segregations in the T1 and T2 generations. These TALEN-mediated *bar* gene knockout mutant lines will be used to study substantial equivalence to non-transgenic donor rice variety 'Dongjin' in the further study.

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Biochemical analysis of the role of leucine-rich repeat receptor-like kinases and the carboxy-terminus of receptor kinases in regulating kinase activity in arabidopsis thaliana and brassica oleracea

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Protein post-translational modification by phosphorylation is essential for the activity and stability of proteins in higher plants and underlies their responses to diverse stimuli. There are more than 300 leucine-rich repeat receptor-like kinases (LRR-RLKs), a major group of receptor-like kinases (RLKs) that plays an important role in growth, development, and biotic stress responses in higher plants. To analyze auto- and transphosphorylation patterns and kinase activities *in vitro*, 43 full-length complementary DNA (cDNA) sequences were cloned from genes encoding LRR-RLKs. Autophosphorylation activity was found in the cytoplasmic domains (CDs) of 18 LRR-RLKs; 13 of these LRR-RLKs with autophosphorylation activity showed transphosphorylation in *Escherichia coli*. BRI1-Associated Receptor Kinase (BAK1), which is critically involved in the brassinosteroid and plant innate immunity signal transduction pathways, showed strong auto- and transphosphorylation with multi-specific kinase activity within 2 h of induction of *Brassica oleracea* BAK1-CD (BoBAK1-CD) in *E. coli*; moreover, the carboxy-terminus of LRR-RLKs regulated phosphorylation and kinase activity in *Arabidopsis thaliana* and vegetative crops.

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중만생 내병성 강화 발아현미용 기능성 거대배아미 ‘큰품’

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최근 쌀 과잉 생산과 소비 감소의 구조적 문제로 인해 농가 소득감소, 정부재정부담 가중 등으로 한시적으로 쌀 생산조정제가 ‘논 타작물 재배 지원 사업’으로 시행되고 있다. 이에 풍흉에 따라 취사선택할 수 있는 사료용과 가공특성 겸용 용도다양화 품종개발이 요구되고 있다. 또한 세계적으로 비만 및 성인병 예방 기능성 간편식품의 수요가 증가 추세에 있으며, 우리나라에서도 건강 기능성이 우수한 발아현미를 이용한 간편식 제품화에 관심이 증대되고 있다. 발아현미는 발아과정에서 질감이 부드러워지고 GABA 등 기능성 성분이 증가되어 치매, 비만 및 성인병 예방에 효과적인 식품이다. 이번에 개발한 거대배아미 ‘큰품’은 출수기가 8월 10일이고 기존 거대배아미인 ‘큰눈’에 비해 흰잎마름병(균계 K1, K2, K3), 줄무늬잎마름병 저항성을 가지고 있어 내병성이 강화되었고 수량성(534kg/10a)이 ‘큰눈’에 비해 10% 향상되었다. 또한 동시발아율이 높고 제품화 시 쌀눈탈락율이 낮아 발아가공에 적합한 품종이다. 또한 ‘큰눈’에 비해 외관품위가 맑고 깨끗하며 현미의 폴리페놀 등 항산화성분과 항산화활성은 ‘큰눈’보다 높아 국민 건강증진 및 기능성 가공식품 소재로 활용할 수 있어 재배농가 및 가공업체 소득증대에 기여할 것으로 기대된다. 덧붙여 곡질의 특성을 다양화 할 수 있는 소재로도 활용 가능하여 사회경제적 여건에 따라 변화무쌍한 시대에 용도를 다변화 할 수 있는 품종개발에도 이용 가능하다. 본 연구는 농촌진흥청 연구사업(세부과제명: 쌀 용도다양화를 위한 맞춤형 벼 품종개발, 세부과제번호: PJ013150032018)의 지원에 의해 이루어진 것임.

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Study about gene flow and stability assessment in GM rice

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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. Recent global abnormal weather, desertification associated with global warming, dry land soils, and salinization of ground water associated with the large-scale agricultural irrigation agriculture all demonstrate that the agricultural environment is deteriorating rapidly. In agriculture, the rice is the one of important things. Many farmers and scientists have long tried to increase the yield of rice. One type of technology has given rise to a host of concerns and questions, namely GMOs. The significance of environment change and genetic safety has been recently recognized by the commercialization of GM crops. The scientific evidence concerning the environmental and health impacts of GMOs is still emerging, but so far there is no conclusive information on the definitive negative impacts of GMOs on health or the environment. Nevertheless, public perceptions about GMOs in food and agriculture are divided with a tendency toward avoiding GM food and products in many developed and developing countries. Also Korea is one of that country and is not allow the GMOs now. So I studied whether these GMOs are actually dangerous for environment and whether there are differences in cultivar characteristics such as germination test with TTC tetrazolium, germination test in frozen soil and gene-flow test with glufosinate and strip-bar test. These experiments will indicate that drought-tolerant GM rice may be used to detect genetic safety and evaluation standards in GM rice progeny.

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Evaluation of role of chorismate mutase in aromatic amino acid and secondary metabolites biosynthesis by using yeast functional expression system

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Chorismate mutase gene isolated from rice was cloned and functionally expressed in yeast. This gene encodes a bifunctional protein of 125 amino acids and 13.77 KDa molecular mass. It possesses catalytic activity and catalyzed a very main step of converting an intermediate metabolite chorismate to prephenate and furthermore to phenylalanine and tyrosine which are the ultimate sources of secondary metabolites synthesized in shikimate pathway. Not only Phe and tyr are essential compounds for protein synthesis but also secondary metabolites have a predominant value in plant growth promotion and defense against environmental stresses. To functionally express the target gene were cloned in an episomal plasmid of RS series and pRS42k was designed with PGK promoter and CYC1 terminator sites resistant to gentamicin. This plasmid used as a shuttle vector i.e. multiply both in *E. coli*, DH5 α and *S. cerevisiae* D452-2 strain were used for multiple copies of insert and functional expression respectively. Quantitative analysis of aromatic amino acid biosynthesis confirmed that expression of CM gene significantly increases phenylalanine 26% and tyrosine 24%. HPLC analysis revealed that expression of CM gene in transformed strain increases secondary metabolites than non-transformed strain and also demonstrated that the rate of secretion of secondary metabolites to liquid media was higher than that of accumulation inside the cell. Western blot analysis also shows that recombinant protein related to CM gene was significantly expressed in transformed strain as compare to wild type strain.

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Construction of genetic map by EST-SSR markers and QTL analysis of major agronomic characters in hexaploid oat (*Avena sativa* L.)

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Cultivated oat, *Avena sativa* L., is a self-pollinating, disomic, hexaploid ($2n = 6x = 42$) species. The genome of hexaploid *Avena* species consists of three basic subgenomes, referred to as the A, C, and D genomes, each of which contains seven pairs of chromosomes. The objective of this study is to construct the genetic map of cultivated hexaploid oat by EST-SSR markers and QTL analysis of major agronomic characters. Total RNA from both oats cultivars (seonyang and daeyang) were extracted from young leaves after 1 month of growing process using Trizol reagent. 100 mg of each leaf cultivars samples were well grind in LN₂ after cutting using sterilized scissor and liquid nitrogen (-120 °C). Measured the RNA concentration (seonyang: 938.4 ng/ μ L and 1199.1 ng/ μ L and daeyang: 2066.0 ng/ μ L and 790.2 ng/ μ L. RNA samples (10 μ L) from both cultivars were then utilized for cDNA synthesis. From the samples checked in gel electrophoresis were excised the DNA fragment (cutting) with scalpel by gel extraction. Apart from this process another 100 oats cultivars were sowing and each DNA were extracted after 26 days of growing process according to Solgent Co.,Ltd instructions.

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Evaluation of East Asian oat (*Avena sativa* L.) genetic resources based on major nutritional ingredients and agricultural traits

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One of most important global food trends is 'health'. Oat is rich in protein and lipids compared to other grains, and contains a large amount of dietary fiber, β -glucan. Korean domestic consumption of oat, one of 'top 10 super food', is rapidly increasing due to the high nutritional value. However, the researches on evaluation of cultural and functional characteristics of oat genetic resources as breeding material has been insufficient because oat has been studied as feeds rather than food. Therefore, this study aims to provide information of agricultural traits, physicochemical property (crude proteins, lipids, fibers), and the most important nutritional ingredient, β -Glucan of 142 oat germplasms from Korea, China, and Japan which are maintained in National Agrobiodiversity Center (NAC) to be used as basic research as oat breeding. On morphological characteristics, Korean oats were averagely headed and matured earlier than Chinese and Japanese ones. Most of oat accessions were not suitable for double cropping with rice. But, 7 accessions including IT151107 (Korea-origin) was matured before mid June which could be cultivated with paddy rice in Korean Southern region. IT166575 (1.8g, Korea-origin) and IT128790 (4.2g, China-origin) were the accessions having the lightest and the heaviest 100 seed weight, respectively. There were also some accessions having colorful outer glum as brown or even black (IT162928, Japan-origin). Such resources having unique characteristics could be useful as breeding sources. The ranges of protein, lipids, fiber, and β -glucan contents of oat germplasms in this study were from 11.6% to 22.9%, from 1.4% to 12.0%, from 2.3% to 5.7%, and 0.80% to 2.69%, respectively. Chinese oats had averagely higher protein (17.1%) and β -glucan (4.1%) contents than Korean (15.9%, 3.7%) or Japanese ones (15.6%, 4.0%). Korean oats had averagely higher lipids (5.7%) and fiber (1.8%) contents than Chinese (4.9%, 1.3%) or Japanese (4.0%, 1.3%) ones. IT166594 (China-origin), IT166584 (China-origin), IT129802 (China-origin), and IT151108 (Korea-origin) showed the highest levels of protein, lipids, β -Glucan, and fiber content, respectively. These resources having high content of major nutrients can be useful breeding sources for functional oat food materials

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User-friendly common platform using genotype, phenotype and chemotype for managing tartary buckwheat genetic resources

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Genetic resources of tartary buckwheat (*Fagopyrum tataricum* Gaertn.) preserve useful genetic variation, yet they remain untapped due to lack of genetic markers. In this study, we used high throughput next-generation sequencing (NGS) data in order to unravel the genetic resources for developing buckwheat as a highly functional food crop. Overall, 26 core resources of tartary buckwheat has been collected from six countries including China, India, and Nepal. A comparative genomic study has explored a large number of InDel (insertion/deletion) markers required for developing common platform. Bioinformatic analysis revealed 171,926 and 53,755 homo- and hetero-InDels, respectively. Among them, 50 *in silico* polymorphic InDels from 26 accessions were selected by gel electrophoresis, which were converted as barcode types by comparing amplicon polymorphisms with the reference sequence. In order to make user-friendly common platform for genotype, phenotype and chemotype resources, we incorporated genotypic data with that phenotype and chemotype (rutin content) data of 26 buckwheat accessions. As a user friendly system, the homology between the accessions can be visualized in both one (1D) and two dimension (2D) as blocks. Our platform could be not only used in genetic research and breeding programs but also used for efficient resource management system in buckwheat.

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Molecular footprints of adaptation and high flavonol content in tartary buckwheat revealed by a draft genome analysis

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Tartary buckwheat possesses more interesting nutrient profiles, including higher levels of flavonoids compared to the common buckwheat. In this study, we report a draft genome assembly of a high-rutin tartary buckwheat (*Fagopyrum tataricum*), which included 43,771 protein-coding gene models captured in 526 million base-pairs (Mbps). The diploid genome showed a signature of a single whole genome duplication dated before its divergence from common buckwheat (*F. esculentum*) and after the divergence from Amaranthaceae family crop species. Comparative analyses identified an enrichment of transcription factors among *Fagopyrum* specific gene families. The genome of tartary buckwheat included higher copy numbers of genes encoding enzymes synthesizing precursors of rutin than those of common buckwheat and Amaranthaceae family crops. Notably, we identified an inverted tandem duplication of gene loci encoding paralogs of flavonol synthase 1 (FtFLS1) that showed flower-specific expression patterns in the tartary buckwheat. The inverted tandem duplication was also present in the co-linear region in the genome of grape, another species known for high flavonol content, but absent in genomes of common buckwheat and Amaranthaceae crops. The tartary and common buckwheat genomes included uniquely expanded additional copies of enzymes representing specialized metabolic profiles specific to each species. The tartary buckwheat genome has expanded gene families encoding nitrate and phosphate transporters as well as enzymes synthesizing phenylpropanoid and terpenoids, exemplifying an adaptive strategy that optimize growth with a buildup of defense molecules low in nitrogen and phosphorous in a nutrient-poor habitat. Our draft genome, the pan-genomes of buckwheat and the comparative analyses with other plant genomes provide insight and resources for studying the genomic basis of adaptive evolution specially related to flavonoids.

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Inheritance of fertility restoration of male-sterility conferred by cytotype y and identification of instability of male fertility phenotypes in onion (*Allium cepa* L.)

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A novel onion (*Allium cepa* L.) cytoplasm, cytotype Y, was found in a previous study. Cytotype Y contained unique stoichiometry of *coxI* and *orf725*, a candidate gene responsible for male-sterility induction in onions. A S₁ segregating population was produced from a single plant selected from PI273626. Although male-fertility segregated in this population, the ratio significantly deviated from single-gene inheritance. However, genotypes of RF31446 marker perfectly linked to *Ms* locus controlling fertility restoration completely matched with male-fertility phenotypes, indicating that male-fertility restoration of male-sterility conferred by cytotype Y might be determined by the *Ms* locus. One plant derived from the S₁ population showed discrepancy between male-fertility phenotype and RF31446 genotype. Although the RF31446 genotype was homozygous recessive, reduced amount of pollen grains were observed in anthers. Many pollen grains of the unstable male-sterile plant were deformed. Analysis of 13 molecular markers flanking the *Ms* locus showed no crossover between the *Ms* locus and the RF31446 marker. Ten more unstable male-sterile plants were identified from open-pollinated progenies of the unstable male-sterile plant. Viable seeds were successfully produced from unstable male-sterile plants, indicating that pollen grains of the unstable male-sterile plants were partially viable. In addition, an umbel containing unstable male-fertile flowers was identified from one of maintainer lines, although both male and female organs might be sterile in these flowers.

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Compositional variability in diverse maize hybrids (Literature review)

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Maize (*Zea mays*L.) is known as a highly genetically diverse species, which is reflected in the considerable natural variability in composition. The paper reviewed here provides an in-depth compositional analysis of a set of hybrids based on Nested Association Mapping (NAM) founder lines and landraces that were selected for their genetic diversity, and documents the variability in the levels of a large set of grain components.

25 inbred lines selected to represent genetic diversity in maize (NAM inbreds) and 24 inbred lines derived from a diverse collection of landraces were hybridized with B73, an inbred line that has a high-quality reference genome. These hybrids were planted in 2012 in a replicated trial at a single location in the United States. Components from the harvested grain were analyzed for proximates, fiber, minerals, amino acids, fatty acids, tocopherols, β -carotene, phytic acid, and raffinose.

Results reported in the publication demonstrated that while composition segregated by group (ex. tropical vs. temperate varieties) extensive variation existed across all grain components assessed for both the NAM and landrace hybrids, reflecting the underlying genetic diversity of these lines. The results from these hybrids are important because they provide a first survey of grain composition in hybrids from two important genetic resources, the NAM founder lines and landraces.

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Evaluation of gene flow from Bt transgenic rice to non-GM rice

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Genetically modified (GM) crops have been developed worldwide through the recombinant DNA technology and commercialized by global agricultural companies. Until now, GM crops have not been cultivated commercially in Korea. Commercialization of GM crops requires a compulsory assessment of environmental risk associated with the release of GM crops. This study was conducted to evaluate the frequency of pollen mediated gene flow from Bt transgenic rice (Agb0101) to japonica non-GM rice (Nakdongbyeo), indica non-GM rice (IR36), and weedy rice (R55). A total of 729,917, 596,318 and 230,635 seeds were collected from Nakdongbyeo, IR36, and R55, respectively, which were planted around Agb0101. Selection of the hybrids was determined by repeated spraying of herbicide and Cry1Ac1 immunostrip assay. Finally, the hybrids were confirmed by PCR analysis using specific primer. The hybrids were found in all non-GM rice and out-crossing ranged from 0.0005% at IR36 to 0.0027% at Nakdongbyeo. All of hybrids were located within 1.2 m distance from the Agb0101 rice plot. The meteorological elements including rainfall and temperature during rice flowering time were found to be important factors to determine rice out-crossing rate. Consideration should be taken for many factors like the meteorological elements of field and physiological condition of crop to set up the safety management guideline to prevention of GM crops gene flow.

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CEPR1 receptor kinase and gene expression in regulating carbon/nitrogen balance in *Arabidopsis thaliana*

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Plants adjust to changing conditions and make decisions based on sensing substances such as water, light, external nutrients and internal nutrient reserves. Plants also utilize long distance signaling mechanisms for a variety of biological processes. Environmental responses can also involve peptides and Leucine-Rich Repeat Receptor-Like Kinases (LRR-RLKs). In *Arabidopsis*, CEP1 peptides, unrelated to CLE peptides, are synthesized and move through the xylem to shoots, where they are perceived by the two LRR-RLKs CEPR1 and CEPR2, resulting in long-range stimulation of root growth in nitrogen rich conditions. In addition, cytoplasmic domains of Flag-CEPR1 also autophosphorylate on threonine and tyrosine residues and thus are dual-specificity kinases.

Primary root length of wild type seedlings was inhibited by cep1 peptide treatment under normal growth condition. Comparison of WT and cep1/2 double knock-out mutants after treatment of cep1 peptide in terms of primary root length shown that cep1/2 double mutants was not response to cep1 peptide treatment compare to root length of WT seedlings. As another interesting results, we monitored expression pattern of genes, possibly related to regulation of sugar/nitrate balance under cep1 peptide treatment *in vivo*. Among genes investigated, transcripts level of PPK, PPC2, CYP79F1 and NRT2.1 are increased with cep1-dependent manner. Theseresult demonstrated that cep1 is interconnected to nitrate uptake and root growth in *Arabidopsis*.

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Selection of New Soybean Strain with *ti* and *rs2* recessive allele

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Soybean [*Glycine max*(L.) Merr.] seed is an important dietary source of protein, oil, carbohydrates, isoflavones, and other nutrients for humans and animals. But, antinutritional factors in the raw mature soybean are exist. Kunitz trypsin inhibitor (KTI) protein and stachyose are main antinutritional factors in soybean seed. The genetic removal of the antinutritional factors will improve the nutritional value of black soybean seed. The objective of this research was to breed a new strains with the traits of lacking of KTI protein and low content of stachyose. Presence or absence of KTI protein was detected based on Western Blot technique. Content of stachyose in mature seed was detected by HPLC. Total five new strains (603-1, 603-1brown, 603-2, 625, and 694) with KTI protein free and low content of stachyose were developed. Four strains(603-1, 603-2, 625, and 694) have yellow seed coat and hilum. One strain(603-1brown) has brown seed coat and white hilum. Plant height of 603-1 strain was 65cm and 100-seed weight was 29.2g. Plant height of 603-2 strain was 66cm and 100-seed weight was 26.2g. Plant height of 625 strain was 64cm and 100-seed weight was 27.1g. Five strains selected in this research will be used to improve new cultivar with KTI protein free, and low content of stachyose.

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Development of New Soybean Strain with Large Seed Size and *ti* and *lox* recessive allele

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Soybean [*Glycine max* (L.) Merr.] seeds contain protein, carbohydrate, oil, vitamins, minerals, and many functional components. Anthocyanins from black soybean seed coat are known to have many pharmaceutical effect. Soybean cultivar with large seed size and black seed coat is needed by soybean farmer. But, antinutritional factors in the raw mature soybean are exist. Soybean Kunitz trypsin inhibitor and lipoxygenase proteins are well known as antinutritional factors. Lipoxygenase is responsible for the beany flavor and Kunitz trypsin inhibitor (KTI) protein is responsible for the inferior nutritional quality of unheated or incompletely heated soybean meal. The objective of this research was to breed a new strains with black seed coat, large seed size, and lacking of lipoxygenase and KTI protein. A few parents were used. Presence or absence of KTI protein was detected based on Western Blot technique and absence of lipoxygenase protein were selected by SDS-PAGE analysis. New strain with black seed coat, large seed size, and lacking of lipoxygenase and KTI protein was developed. Plant height of new strain was 48cm and 100-seed weight was 36.0g.

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Isoegomaketone-related genes revealed by RNA-Seq in mutant cultivar of *Perilla frutescens* var. *crispa*

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Perilla frutescens var. *crispa* (Labiatae), which is known as ‘Cha-Jo-Ki’ in Korea, ‘Zi-Su-Ye’ in China, and ‘Shiso’ in Japan, is widely cultivating in East Asia. It has been used as a medicinal herb and oil production. A new radiation mutant cultivar *P. frutescens* var. *crispa* (vs. Antisperill) was developed recently, which has a 25-fold higher content of isoegomaketone (IK) than wild type. The IK of perilla has an effect for arthritis. For determining and evaluation of IK related genes between Antisperill and wild type, we performed RNA-seq with three growth stages in both perilla cultivars. In total, 132,943 transcripts and 36,995 representative transcripts were identified in three repetitive mRNAs. Of the 36,995 representative transcripts, 25,510 (69.96%) sequences had similarity with the GO, KOG, and KEGG amino acid sequences. We identified 65, 131, and 230 differentially expressed genes (DEGs) between the mutant and wild type in 70, 94, and 122 days after sowing, respectively. With the exception of redundancy, a clustering analysis was performed using 362 unigenes. Among these genes, 110 homologs of *P. frutescens* terpenoid biosynthesis pathway related genes were identified and seven genes were related to monoterpenoid biosynthesis, which is thought to be the pathway of IK. However, the correlation between the seven candidate genes and IK contents depending on the growth stage should be compared in a further study.

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Variation block browser for functional crops

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In genomics era, genetic assisted breeding is more effective tool, which improves the crops cultivation from different environmental factors and prevent from revenue loss. Cross breeding of different phenotypes is resulted with new cultivars by the DNA recombination. Those, Cultivars are evolved with low levels of genetic diversity in specific genome loci with high recombination rate. Those regions are filled with high dense of nucleotide variations, and these regions are called as “Variation Blocks” (VB). These variations blocks are highly interlinked with the phenotypes. Here, we established barcode system approach based on insertions/deletions (InDel) markers of crop cultivars. The VBs were mined by analyzing whole genome data cultivars followed by putative InDels in the VB regions were identified for the development variation block browse. In addition, the changing of the VBs in a chromosomal level can be quickly identified due to investigation of the reshuffling pattern between cultivars. This browser is more useful for detecting the recombinant loci and trait associated marker, which are more effective for agricultural traits and to identify agronomical important genes, which could use for gene cloning applications. Moreover, VB browser facilitate genome wide VB visualizations using genome browsers. VB browsers is publicly available as Cropsquare (<http://cropsquare.net/index.do>).

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Development of kompetitive allele specific PCR (KASP) markers in *Dendrobium* genotypes derived from mutation breeding

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The genus *Dendrobium* is the third largest in the Orchidaceae, comprising approximately 1,190 species worldwide. *Dendrobium* plants are among the most prevalent orchids for horticultural industries and about 40 *Dendrobium* species have been used in traditional medicine from Eastern Asia including Korea, China, and Japan. Recently, new *Dendrobium* mutant lines showing several distinctive characteristics for stem, leaf and flower colors and/or dwarf have been developed by mutation breeding technology in Korea. In this study, we evaluated genetic variations in *Dendrobium* genotypes using single nucleotide polymorphism (SNP) markers generated from genotyping-by-sequencing (GBS) analysis and to develop a Kompetitive Allele Specific PCR (KASP) assay for a set of SNPs. GBS analysis was conducted with 18 *Dendrobium* genotypes, consisting of seven mutant lines and eleven commercial cultivars. A total of 517,660 high-quality union loci were detected, which contained 443,305 homozygous SNPs and 74,355 heterozygous SNPs. A set of 37,721 filtered SNPs was used to perform a phylogenetic analysis, which showed that there were clear differences among the *Dendrobium* genotypes based on their species. The ten KASP assays were successfully developed to distinguish among the *Dendrobium* genotypes. This study demonstrated that the KASP method is an economically efficient tool for mutant screening in *Dendrobium* breeding programs.

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Development and validation of kompetitive allele specific PCR (KASP) assay in *Rubus* mutant genotypes

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Rubus is an economically important berry crops because of its potential health benefits on human. Recently, several *Rubus* mutant genotypes showed improved agronomic traits such as thorneless, higher fruit yields and disease resistance obtained from gamma-ray. This study investigated genetic diversity and variations in *Rubus* mutant genotypes using single nucleotide polymorphism (SNP) markers generated from genotyping-by-sequencing (GBS) analysis and to develop a Kompetitive Allele Specific PCR (KASP) assay for a set of SNPs in *Rubus* mutant genotypes. A GBS library of 14 *Rubus* genotypes, consisting of seven hybrid mutant lines, four blackberry mutant lines, and three original genotypes, were sequenced on the Illumina HiSeq2000 platform. A total of 50,831,040 reads of clean data were generated, and the trimmed length ranged from 116,380,840 to 509,806,521 bp, with an average of 228,087,333 bp per line. A total of 19,634 high-quality SNPs were detected, which contained 11,328 homozygous SNPs and 8,306 heterozygous SNPs. A set of 1,504 SNPs was used to perform a phylogenetic analysis, which showed that there were clear differences among the *Rubus* genotypes based on their origin. The genetic diversity matrix (GDM) revealed variability among the mutant genotypes ranging from 0.010 to 0.375. The six KASP assays were successfully developed to distinguish among the original genotypes and mutant genotypes in *Rubus* hybrid. This study demonstrated that the SNP and KASP method is an economically efficient tool for mutant screening in *Rubus* breeding programs.

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시스템합성생명공학연구사업 성과활용과 확산을 위한 실용화 추진 연구

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시스템합성생명공학사업단은 1-2단계 차세대바이오그린21사업을 통해 고부가가치 유용물질 생산용 슈퍼농생물체 개발 및 산업화를 위한 기초·원천 기술 개발 연구과제들을 수행하고, 우수한 논문 및 산업재산권 등의 성과를 거두었으나 기술이전 등을 통한 연구성과 확산 및 실용화 추진 노력이 필요한 실정이다.

본 연구에서는 사업단 수행과제로부터 도출된 총 390건의 산업재산권 성과를 분석, 국내외 기업으로의 기술이전 촉진 및 성과확산이 가능한 유망 핵심기술들을 선별하고, 최신 기술동향 및 시장동향 조사를 통한 타겟 시장 및 수요기업 발굴과 기업 맞춤형 개별 기술, 또는 관련 기술의 기술패키징을 통한 효율적 성과확산 추진 체계를 구축하고자 한다.

시스템합성생명공학사업단 선행과제 도출 대량 산업재산권은 SMART3 특허등급평가로 분석, 권리성, 기술성, 활용성 분야의 특허등급을 종합적으로 평가하여 실용화 유망기술을 객관적 지표로 1차 선별하였다, 그 결과, 2018년 1월 현재 국내등록 유지특허 247건 중 총점 등급 BBB등급이상 기술은 총 102건(42%)이었고, 기술분류체계에 따라 분석하면, 분자육종소재 개발연구 기술이 총 65건, 기능성물질생산 시스템 44건, 기능성 소재 응용기술 77건 등으로 전체 특허의 약 77%이었고, 미생물제재 등 검출/진단 기술 등 기타기술도 약 25건으로 파악되었다. 따라서, 사업단의 중점추진목표와 부합하는 고기능성 산업용소재 생산을 위한 미생물과 식물 시스템 개발 기술을 중심으로 국내 화장품, 의약품, 건강기능성 식품 산업분야로의 성과 확산이 유망한 기술을 기술이전 대상으로 삼고, 온-오프라인 기술마케팅을 위한 SMK 제작 및 기술이전을 위한 연구자-사업단-수요기업간의 네트워크 연계를 구축할 예정이다. 또한, 3단계 수행과제 중 1-2단계 연계 또는 신규로 선별되어 수행되는 과제에서 창출될 미래 성과들을 기술사업화에 활용하기 위한 전략적 지식재산권 포트폴리오 구축 등을 지원할 것이다.

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TRAP markers can be used to determine mutation frequencies induced by gamma radiation in faba bean (*Vicia faba* L.)

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This study was to survey the radiosensitivity of gamma-ray on seed of faba bean as well as identify genetic variation and mutation frequency among the mutants by TRAP markers. Ten elite faba bean lines were irradiated with gamma rays (50–700 Gy), and the germination and survival rate, as well as representative morphological traits were measured. The extent of DNA damage was investigated using comet assay, and TRAP markers were used for evaluation of genetic variation, genetic diversity and mutation frequencies. The germination rate decreased at doses greater than 100 Gy. The survival rate and morphological traits decreased as the radiation dose increased. The comet assay revealed that increasing doses of gamma rays decreased head DNA levels. The phylogenetic and PCA indicated that the 555 individuals belonged to eight major groups. Genetic variations between the control and mutants were limited to the intra-group. The mutation frequencies were related gamma dosages in each mutant line. The optimal gamma dosage were revealed by 100–150 Gy. The TRAP markers were distinct separated mutant lines and showed association between mutation frequency and gamma dosages. This study will be very useful for faba bean mutation breeding and may be applicable to other crops breeding strategy.

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A WUSCHEL homeobox transcription factor, OsWOX13, enhances drought tolerance and triggers early flowering in rice

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Plants have evolved strategies to cope with drought stress by maximizing physiological capacity and adjusting developmental processes such as flowering time. The WOX13 orthologous group is the most conserved among the clade of WOX homeodomain-containing proteins and is found to function in both drought stress and flower development. In this study, we isolated and characterized *OsWOX13* from rice. *OsWOX13* was regulated spatially in vegetative organs but temporally in flowers and seeds. Overexpression of *OsWOX13* (*OsWOX13-ov*) in rice under the *rab21* promoter resulted in drought resistance and early flowering by 7–10 days. Screening of gene expression profiles in mature leaf and panicles of *OsWOX13-ov* showed a broad spectrum of effects on biological processes, such as abiotic and biotic stresses, exerting a cross-talk between responses. Protein binding microarray and electrophoretic mobility shift assay analyses supported ATTGATTG as the putative *cis*-element binding of *OsWOX13*. *OsDREB1A* and *OsDREB1F*, drought stress response transcription factors, contain ATTGATTG motif(s) in their promoters and are preferentially expressed in *OsWOX13-ov*. In addition, *Heading date 3a* and *OsMADS14*, regulators in the flowering pathway and development, were enhanced in *OsWOX13-ov*. These results suggest that *OsWOX13* mediates the stress response and early flowering and, thus, may be a regulator of genes involved in drought escape.

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Identification of QTLs associate with flowering time using a GBS-SNP-based high-density map in *Perilla*

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Perilla seeds are good source of polyunsaturated fatty acids such as DHA and EPA, ALA. Accumulation of oil contents in *perilla* are closely related to flowering time (FT). Three traits which associated with flowering time, days to visible flower bud (DtoFB) and days to flowering (DtoF), days to maturity (DtoM) are positively correlated (68% to 86%). To identify FT QTLs, F2 populations were developed by an interspecific cross between *P. citriodora* and *P. hirtella*. Through genotyping-by-sequencing (GBS) of 96 F2 populations, a total of 9,607 SNP markers were identified, of which 2,518 markers were grouped into 10 linkage groups spanning 1309.39 cM with an average distance of 0.56 cM. Using this map, QTL analysis was performed and two DtoFB QTLs, three DtoF QTLs, and one DtoM QTL were detected. In addition, orthologue gene analysis with known genes involved in the regulation of FT among the crop species is underway. These result might be useful tools for *perilla* breeding to develop new *perilla* varieties with high content of polyunsaturated fatty acid.

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Evaluation of Genetic Diversity in Korean rice varieties as revealed by SSR markers

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Molecular markers are useful tools for evaluating genetic diversity and determining cultivar identity. In this study, we examined the genetic distance among Korean rice varieties using allele frequencies and a genetic diversity analysis with Simple Sequence Repeats (SSRs) markers. The analysis of the genetic diversity and genetic relationships of 243 Korean rice varieties was varied out using 20 SSRs markers. A total of 268 alleles were detected, ranging from 6 to 32, with an average of 13.45 alleles per locus, and averages of gene diversity (GD) of 0.5554. Seven SSR markers were selected as key markers for discrimination among Korean rice varieties. As the results, 243 varieties (100%) were discriminated by using acrylamide gel and fragment analyzer-based markers. In conclusion, this study provides useful basic data that can be utilized in Korean rice varieties breeding and development. In addition, we will have to manage and conserve as a valuable genetic resource, without losing diversity of Korean rice varieties.

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Identification of SNP related to leaf-angle traits using a genome-wide association study in rice (*Oryza sativa* L.)

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Leaf traits are always key issue to investigate in plant research. In this study, we conducted to investigate a morphological trait in 294 rice accessions including Korean breeding lines. We also carried out a genome-wide association study (GWAS) to detect significant single nucleotide polymorphism markers and candidate genes affecting major agronomic traits. A Manhattan plot analysis of GWAS using morphological traits showed that phenotypic and statistical significance was associated with a chromosome in each group. The significance of SNPs that were detected in this study was investigated by comparing them with those found previously studied QTL regions related to agronomic traits. As a result, SNP (S8-19815442), which is significant with regard to leaf angle, was located in the known QTL regions. To observe gene mutations related to leaf angle in a candidate gene, Os08g31950, its sequences were compared with sequences in previously selected rice varieties. In Os08g31950, a single nucleotide mutation occurred in one region. To compare relative RNA expression levels of candidate gene Os08g31950, obtained from GWAS analysis of 294 rice accessions and related to lateral leaf angle, we investigated relative levels by selecting 10 erect leaf-angle varieties and 10 horizontal leaf-angle varieties and examining real-time PCR. In Os08g31950, a high level of expression and various expression patterns were observed in all tissues. Also, Os08g31950 showed higher expression levels in the erect leaf-angle variety group and higher expression rates in the leaf than in the root. The candidate gene detected through GWAS would be useful in the development of new rice varieties with improved yield potential through future molecular breeding

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콩 조직배양 callus에서 isoflavone 축적 확인

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이소플라본은 콩에 함유되어 있는 주요한 기능성 성분으로 phyto-hormone 역할을 한다. 그동안 이소플라본은 콩 종실, 콩 잎 등에서 함량 분석 실험이 수행되었을 뿐 조직배양에서의 응용에 관한 연구는 없었다. 따라서 콩 callus에서의 이소플라본 축적을 확인하고자 본 연구를 수행하였다. 콩 장려품종 대풍2호의 종자에서 배아를 적출하고 소독한 후 MS 배지에 치상하여 callus를 유도하였다. Callus 유도는 첨가된 식물생장조절제에 따라 반응이 달랐으며, 성장조절제는 또한 callus의 계대배양 기간에도 영향을 미쳤다. 배아를 치상한 1개월 후 callus를 수확하여 HPLC를 사용하여 이소플라본 함량을 분석하였다. 전체 이소플라본 함량은 여러 가지 처리에 따라 1,280~2,140ug/g 변이를 보였다. 또한 총 12가지 이소플라본 종류 중 malonylglucosides의 함량이 전체 함량의 80% 이상을 차지하여 malonylglucosides가 콩의 주된 이소플라본임을 알 수 있었다. 한편, 식물생장조절제 처리에 따라 이소플라본 함량이 달라짐을 확인할 수 있었다. 이와 같은 결과를 볼 때 추후 조직배양을 통하여 이소플라본을 대량생산할 수 있으리라 판단된다.

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찰옥수수 출사후 일수에 따른 지방산 조성 및 Phytosterol 함량 변화

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찰옥수수의 출사후 일수 경과에 따른 종실의 지방산조성과 phytosterol의 함량변화를 구명하여 고품질 찰옥수수 생산을 위한 기초자료로 활용하고자 본 연구를 수행하였다. 본 시험에 사용된 찰옥수수는 국립식량과학원에서 육성된 일미찰과 흑진주찰 2품종이었고, 출사후 일수 경과에 따라 5회(21, 24, 27, 30, 33일) 시료를 채취하여 백립중, 지방산조성 및 phytosterol 함량을 검토하였다. Phytosterol의 분석을 위해서는 시료를 saponification 처리후 비누화 반응이 유도되지 않은 불검화물(unsaponifiables)을 취하여 BSA[N,O-bis(trimethylsilyl)acetamide], pyridine, hexane을 순차적으로 가하여 TMS 유도체화 하였고, HP-5ms capillary column으로 분석을 하였다. 본 시험을 수행하여 얻어진 결과를 요약하면 다음과 같다. 출사후 일수가 경과할수록 찰옥수수 종실의 조지방 함량은 지속적으로 증가를 하였고, 흑진주찰은 일미찰보다 조지방 함량이 다소 높았다. 출사후 일수의 경과에 따른 지방산의 조성비는 뚜렷한 변화를 보였는데, palmitic(C16:0) 및 linoleic acid(C18:2)는 점차 감소되었으나, oleic acid(C18:1)는 증가되는 것으로 나타났고, 흑진주찰은 일미찰에 비해 불포화지방산(USFA)의 조성비가 다소 높은 것으로 나타났다. 출사후 일수가 경과할수록 총 phytosterol의 함량은 증가되었으나 품종간 총 함량의 차이는 보이지 않았다. 그러나 phytosterol의 조성비는 품종간 차이를 보였는데, 일미찰은 β -sitosterol > stigmasterol > campesterol 순으로 조성비가 높았으나, 흑진주찰은 β -sitosterol > campesterol > stigmasterol 순으로 조성비가 높았으며, 성분별로 볼 때 campesterol 및 β -sitosterol 함량은 품종간 차이가 없었으나 stigmasterol은 흑진주찰이 일미찰에 비해 함량이 높은 것으로 나타났다. 출사후 100립중 증가비율에 따른 조지방, USFA 및 phytosterol의 증가비율의 관계를 검토한 결과 100립중이 증가할수록 조지방 및 phytosterol 함량도 증가되었으나, USFA의 조성비는 변화가 적었다.

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튀김부피 및 수량성이 높은 팝콘용 옥수수 신품종 ‘기찬팝콘’

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국내 팝콘옥수수는 대부분 수입에 의존하고 있으며, 매년 10,000톤 정도가 수입되어 극장 및 놀이공원 등에서 소비가 되고 있다. 옥수수연구소에서는 수입산 팝콘원료를 대체하기 위하여 1997년부터 튀김옥수수 연구를 시작하여 현재 오륜팝콘, 지팝콘, 오륜2호를 개발하여 국내 재배농가에 보급하고 있다. 하지만 수입산에 비해 높은 생산가격으로 수요가 확대되지 못하고 국내산을 선호하는 소비자층을 중심으로 소비가 되며 원료공급을 위한 재배단지가 전국적으로 20ha정도 조성되어 있다. 국내산 품종의 품질을 높이기 위해 2017년부터 지역특화과제로 수확 후 관리 기술개발을 위해 저장온도 및 저장방법 등 표준화 기술을 개발하여 국내산 팝콘품질을 수입산과 대등하게 높여 나가고 있다. 국산 품종의 소비를 높이기 위해서는 생산비를 낮추고 수량이 높은 품종을 개발하고, 재배가 쉬운 품종을 개발한다면 팝콘원료의 수입을 대체할 수 있을 것이다. 따라서 본 연구는 튀김부피 및 수량성이 높은 품종을 개발하고자 수행하였다. “기찬팝콘”은 튀김용 모집단에서 분리된 GP6를 모본, GP3를 부분으로 하여 개발하였으며, 수량성은 “오륜팝콘” 대비 6%증수한 489kg/10a로 수량이 높으며, 도복지수는 1로 “오륜팝콘”의 3보다 낮아 내재해성도 강하며, 100립중은 15.6g으로 “오륜팝콘” 16.2g보다 소립인 특성을 갖고 있다. 튀김부피는 알곡 수분이 11.0~12.0%일 때 “기찬팝콘”이 33.7cm³/g로 “오륜팝콘”의 31.1cm³/g배보다 높아 가공용으로도 적합한 특성을 가지고 있어 앞으로 농가에 보급하여 재배단지를 확대하면 수입산을 대체할 품종으로 기대한다.

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Characterization of complete chloroplast genomes of *Adenophora triphylla* and *Codonopsis lanceolata*

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Adenophora triphylla and *Codonopsis lanceolata* have been used as a valuable medicinal sources and food in East Asia. However, both plants are difficult to be distinguished due to its similarity in morphology. The chloroplast (cp) genomes of both pharmaceutical plants were revealed and analyzed to investigate phylogenetic relationships and discover potential molecular markers for its authentication. We performed phylogenetic analysis indicating considerable distance between *A. triphylla* and *C. lanceolata*. In this analysis, the potential DNA markers based on the cp genome sequences were demonstrated. We identified potential DNA markers that carry Insertion/Deletion (*InDels*) that are able to identify these two species around genic-intergenic regions of *ycf2*, *ndhB*, *rps7*, and *ycf1* loci. The cp genomes identified in this study would serve as useful tools for fundamental molecular understanding and future authentication of *Adenophora* and *Codonopsis* species. This research was supported by a grant (17162MFDS065) from Ministry of Food and Drug Safety, Korea, in 2018.

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Characterization of complete chloroplast genomes of *Hemerocallis fulva* and *Veratrum japonicum*

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Chloroplast (cp) genome sequence has been served as a valuable source for understanding evolutionary history and developing molecular markers. The cp genomes of *Hemerocallis fulva* (medicinal plant) and *Veratrum japonicum* (inedible toxic plant) were revealed and analyzed to investigate phylogenetic relationships and discover potential molecular markers for its authentication. Phylogenetic analysis was indicated considerable distance between *H. fulva* and *V. japonicum*. We developed the potential DNA markers based on the cp genome sequences in this research. The five potential DNA markers including Insertion/Deletion (*InDels*) could be able to discriminate these two species around genic-intergenic regions of *psbA*, *psbL*, *atpA*, *psbZ*, *psbM*, *psbD*, and *rps14* loci. The cp genomes identified in this study would help as useful tools for fundamental molecular understanding and future authentication of *Hemerocallis* and *Veratrum* species. This research was supported by a grant (17162MFDS065) from Ministry of Food and Drug Safety, Korea, in 2018.

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Analysis of transferability of kenaf EST-SSR marker to other *Hibiscus* genus and their use in studying genetic diversity

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Hibiscus belong to Malvaceae family consist of about 300 species such as *H. cannabinus*, *H. sabdariffa*, and *H. rosa sinensis*. However, the limitation of molecular markers have brought about low genetic diversity and relationship of *Hibiscus* germplasm resources. This study showed that we screened and evaluated transferability of 102 EST-SSR markers derived from kenaf to other 18 *hibiscus* species. One-hundred and one EST-SSR markers were successfully amplified. Among them, 100 markers showed polymorphism to 94 genetic resources/cultivars in the *hibiscus* genus. As a result, transferability rates varied from 82.35% (*H. trionum*) to 98.04% (*H. ponticus*) and the average revealed 89.02%. A total of 827 alleles were generated from the use of 101 EST-SSR markers, and the number of alleles ranged from 1 (RBRC_Hc_ES_73) to 16 (RBRC_Hc_ES_80) per locus and the average was 8.6. The PIC values ranged from 0 (RBRC_Hc_ES_73) to 0.86 (RBRC_Hc_ES_95), and the average was 0.5608. Moreover, we identified the genetic relationship among 18 *hibiscus* species. According to UPGMA clustering and a PCoA analysis, 18 *hibiscus* species were classified into three clusters. Cluster I contained one species (*H. acetosella*), cluster II included two species (*H. sabdariffa* and *H. radiates*), and the remaining 15 species were clustered in Cluster III. The population structure with 94 genetic resources/cultivars was divided into three groups as well. In this study will be useful resources to evaluate genetic diversity and population structure of unclear germplasm among the *hibiscus* genus.

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Characterization of complete chloroplast genomes of *Kalopanax septemlobus* and *Zanthoxylum ailanthoides*

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The chloroplast plays a crucial role in maintaining life on Earth. Chloroplast genomes from a variety of land plants has enhanced our understanding of intracellular gene transfer, chloroplast biology, conservation, evolutionary history, diversity, and the genetic basis by which chloroplast transgenes can be engineered to enhance plant agronomic traits. The cp genomes of *Kalopanax septemlobus* and *Zanthoxylum ailanthoides* were analyzed to investigate phylogenetic relationships and to discover potential molecular markers for their recognition. We were able to distinguish these two species around the genic-intergenic regions with a potential DNA marker developed based on the sequence of chloroplast genomes. The cp genomes identified in this study would serve as useful tools for fundamental molecular understanding and future authentication of *Kalopanax* and *Zanthoxylum* species. This research was supported by a grant (17162MFDS065) from Ministry of Food and Drug Safety, Korea, in 2018.

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Bx7 유전자와 밀의 단백질 함량 간의 상관관계 분석

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밀의 단백질 함량과 조성은 빵, 면과 같은 밀의 가공에 매우 큰 영향을 미친다. 밀의 단백질 함량은 유전적, 환경적인 영향을 받지만, 유전적 요인이 큰 것으로 알려져 있다. 빵용 특성을 갖는 밀은 5+10 단백질 조성을 기본적으로 갖고 있어야 하며, 최근 7번 단백질이 밀의 단백질 함량을 높이는 것으로 알려져 있다. 특히 Bx7^{OE} 유전자를 갖는 밀의 단백질 함량이 높아지는 연구결과들이 보고되고 있다. 따라서 본 연구는 밀의 가공특성에 맞는 밀 품종 개발에 유용하게 사용할 수 있는 자원 개발을 위해 국내뿐만 아니라 북한, 몽골 등 외국 자원을 포함하고 있는 유전자원에 대하여 Bx7^{OE} 유전자와 관련된 분자마커를 평가하였다. 608개 자원 평가 결과를 통해 7개 자원에서 Bx7 유전자가 과발현 하는 것을 확인하였다. 7개 계통은 북한, 일본 등 여러 지역에서 수집된 자원들이 포함되어 있었다. 이들 계통의 평균 단백질 함량은 평균 12.5%로 확인되었으며, 특히 7번 단백질의 함량이 뚜렷하게 높아지는 것을 확인하였다. 앞으로 실제 종자를 이용하여 단백질, 회분, 글루텐, 침전가와 같은 밀의 품질특성과 유전자 간의 상호관계를 밝혀내고, 뛰어난 자원을 선발할 수 있는 표지인자를 개발한다면 밀 육종프로그램에 매우 유용하게 이용될 수 있을 것으로 생각된다.

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Application of TRAP markers to genetic diversity and relationship in soybean mutant lines

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Soybean [*Glycine max* (L.)] is the most widely grown grain legumes in the world, which is widely used as the major sources of vegetable oils and plant proteins. Despite the economic importance of soybeans, there have been no TRAP marker system studies on genetic relationships between/among mutant lines. To develop a strategy of Mutant Diversity Pool (MDP) conservation, a study on the genetic diversity of 210 soybean mutant lines (8 cultivars and 202 mutants) was performed through a TRAP analysis. TRAP was conducted using sixteen primer combinations. The highest polymorphism level (86.96%) was obtained using a MIR157B + Sa4, whereas the lowest polymorphism level (31.03%) was obtained using a B14G15B + Ga3. Phylogenetic and principal component analysis (PCA) analyses indicated that the 210 lines belong to five groups based on the 16 combination TRAP markers. AMOVA showed 21.0% and 79.0% variations among and within the population, respectively. Overall, the genetic similarity of each cultivar and its mutants were higher than within other mutant populations. Our results suggest that the TRAP marker system may be useful for assessing the genetic diversity among soybean mutants and help to improve our knowledge of soybean mutation breeding.

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Population genetic structure and genetic diversity of peanut (*Arachis hypogaea* L.) collections

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Peanut is an allotetraploid because the single recent polyploidization caused significant decrease in genetic diversity. Development of SNP-based markers such as CAPS that for PCR amplification of DNA restriction enzyme analysis are widely applied in next-generation sequencing (NGS). This study aimed 1) to evaluate the availability of SNP markers and 2) to identify the peanut genetic diversity and structure populations using molecular markers and 96 peanut accessions from Peru, China, Argentina, Brazil, and Korea for data analyses. A total of 30 CAPS markers from 13 different chromosomes were selected, and twenty-eight of the CAPSs were in intergenic and two CAPSs were in coding sequence. PCR amplifications were conducted in 20 μ L reactions. PCR product was digested with enzyme (AseI, DraI, HpaII, MseI, MspI, PstI, Taq. I) and were resolved on 1.5 % agarose gels to detect the polymorphism. Genetic relationship among 5 different origin groups was evaluated using Neighbor-joining tree and population structure. Principle Coordinate Analysis and Analysis of Molecular Variance were performed based on genetic distance matrix. As a result, the high genetic dissimilarities were observed between Korea and other 4 countries; genotypes between other countries had F_{ST} values range 0.15 to 0.25 mean moderate differentiation; genotypes Brazil and Argentina had the lowest genetic dissimilarity. This means that Korean peanut varieties have fewer common origins with others, while those from the other four regions have more closely related origins.

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Roles of perilla heading date gene, pfHd3a, in flowering time

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Perilla (*Perilla frutescens*) is an annual plant and grown in Asia. As one of important oil crops, its seeds are used to make a product and leaves are used as a vegetable, nevertheless, much is unknown about research of perilla. we already found a gene in RNA-seq results which may play a role in flowering time, and it was identified to be an ortholog of OsHd3a in rice. Hd3a promote heading under short-day conditions. Here, we focused on function of pfHd3a. Since tissue culture system using agrobacterium was developed, we made a pfHd3a-overexpressing plant in perilla using agrobacterium-mediated transformation. Also, we constructed knock-out mutant using CRISPR/Cas9 genome editing system. A reproducible shoot was induced from hypocotyl explants on MS basal medium supplemented with 3.0 mg/l 6-Benzylaminopurine (BA), 0.01mg/l indole-3-acetic acid (IAA), 250mg/l cefotaxime, 500mg/l carbenicillin and 1.2 mg/l PPT and candidates were selected. Rooting was induced on half-strength hormone-free MS medium. The transformants were confirmed by PCR of PPT resistance region. Next generation seeds were used for flowering phenotype check compared wild type under daylength condition.

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Plastidal ribosomal protein caused albino, seedling death phenotype in rice

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The plastid ribosomal proteins (PRPs) are essential for plastid protein biosynthesis, ribosome biogenesis and chloroplast development. To identify the leaf senescence mutants in rice, we screened T-DNA insertional mutant lines and isolated three different albino, seedling death phenotype mutants. Two mutants, PRP1 and PRP2 phenotypes were co-segregated with T-DNA by genotyping analysis. PRP1 and PRP2 ribosomal proteins encode the large subunit components of chloroplast 50S ribosomal proteins, which contain chloroplast localization signal peptides, respectively. GUS assay showed that expression of PRP1-GUS detected in the root, sheath and leaf blade in seedling stage.

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The plastid ribosomal proteins (PRPs) are essential for plastid protein biosynthesis, ribosome biogenesis and chloroplast development. To identify the leaf senescence mutants in rice, we screened T-DNA insertional mutant lines and isolated three different albino, seedling death phenotype mutants. Two mutants, PRP1 and PRP2 phenotypes were co-segregated with T-DNA by genotyping analysis. PRP1 and PRP2 ribosomal proteins encode the large subunit components of chloroplast 50S ribosomal proteins, which contain chloroplast localization signal peptides, respectively. GUS assay showed that expression of PRP1-GUS detected in the root, sheath and leaf blade in seedling stage.

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Utilization of *Mutator* transposable elements for waxy and common maize breeding program

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Maize (*Zea mays* ssp. *mays*) is among the most predominant food sources in the grass family (Poaceae), along with wheat (*Triticum aestivum*) and rice (*Oryza sativa*). Also, maize is an economically important crop and serves as a primary component of biofuels and animal fodder, as well as a source of byproducts used in textile, adhesive, and papermaking industries. Based on both endosperm and kernel constitution, maize can be classified into two categories, non-glutinous (common maize) and glutinous (waxy maize). In Korea, demand for both the types of maize is high and will increase exponentially in coming years. The maize genome is primarily composed of transposable elements, for which large and stable insertions generate variations that reflect selection during evolution. *Mutator* (Mu) transposon superfamily, a class of DNA transposons, is the most complex and active element in maize genome suggesting a unique role in plant evolution. In the present study, we have designed, a novel set of Mu-specific primers based on terminal invert repeats (TIR) and utilized a transposon insertion display method (MU-TD) for genotyping. Based on this method we have analyzed the distribution pattern of Mu insertion in teosinte (wild relative), sorghum (distant relative) and few domesticated maize accessions (dent, sweet and waxy). While 17% of the Mu insertion appeared to be fossil insertion shared between teosinte and maize, there is substantial evidence of recent activity of Mu element in investigated species. Apart from it, our other objective was to utilize the newly developed system for linkage analysis, identifying QTLs for yield-related traits, association mapping and to estimate genetic diversity in waxy and common maize. Results demonstrate the efficiency of the new system (Mu-TD) which will be useful for future maize breeding.

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Genetic mapping and characterization of a stunted growth mutant in rice

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In this study, we identified a stunted growth mutant from a *japonica* rice cultivar, Samgwang, treated with N-methyl-N-nitrosourea (MNU). The mutant showed dwarf, narrow leaf and sterile panicle. The retardation growth of the mutant initiated at the seedling stage and became severe at the reproductive stage. The plant height was reduced by 34% compared to that in wild type and showed significantly decreased first five internode length. The width of flag leaf was reduced by 46% compared to that in wild type. Anatomical analysis of the leaf suggested that less number of the vascular bundles and epidermal cells caused narrow leaf. Also, mutant plants showed low pollen viability and complete sterility. Genetic analysis indicated that the mutation was controlled by a single recessive gene. The F₂ generations of a cross between mutant and Milyang23 were used for mapping. Candidate region was detected to a short arm of chromosome 5 near the marker S05000 and S05032 via BSA method. The mutant was fine-mapped at an interval of 84kb flanked by the markers NC0501.48 and NdC0501.56. Sequencing of the region identified that the mutant carries 11bp insertion in the third exon of LOC_Os05g03550, a gene which contains two SANT domains related to histone deacetylation. The insertion led to premature stop codon in cDNA. Accordingly, a novel gene that cause inhibition of plant growth was isolated and the results may provide a basis for functional studies of the gene associated with growth and development of rice.

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Comprehensive transcriptome analysis of *Ligularia fischeri* to identify isoforms and biosynthesis genes associated with medicinal components

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Ligularia fischeri is a popular edible herb in Korea containing broad ranges of pharmacologically important compounds. It is used in traditional medicine for treating infectious and inflammatory diseases. Despite its importance as herbal medicine, there are no transcriptome/genome sequences available in the public database limiting its research at molecular level. To address this issue, *L. fischeri* leaf transcriptome was sequenced using Pacific Biosciences single molecule long-read isoform sequencing platform. We identified 60,646 polished, high-quality non-redundant full-length transcripts with a total length of 116.5Mb. Among these 27,453 transcripts were annotated to known genes in different species based on non-redundant and uniprot database. Functional classification using Gene ontology identified 11,279 transcripts of which majority were associated with the cellular and metabolic process. The Kyoto Encyclopedia of Genes & Genomes pathway analysis identified 1332 transcripts encoding 160 enzymes related to secondary metabolism with a higher number of transcripts for biosynthesis of antibiotics. Furthermore, we observed alternate splicing, in a total of 1,030 transcripts covering a total of 2250 isoforms with a variable of 2-11 isoforms. This data led us to identify 117 transcripts containing 271 isoforms involved in various metabolic pathways along with 36 transcripts containing 84 isoforms involved in various stress responses. This is the first detailed transcriptome analysis of *L. fischeri*. The resulting transcriptome along with the identified alternative splicing events provides insights into the biological process including the genes related to biosynthesis of characteristic secondary metabolites. This data will be valuable resource as transcriptome reference for further studies in the genetics and breeding of *L. fischeri*.

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Understanding the sensory characteristics of aromatic rice breeding line using an electronic nose

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Aromatic rice is a variety of rice with nice aroma and flavor. These rice were much higher price than high quality non-aromatic rice in international market. This study was performed to investigate the differences among the 31 varieties of aromatic rice and characterization of aromatic rice breeding line by using a GC-based electronic nose. We was conducted to optimize the analysis condition quantify the 2-acetyl-1-pyrroline(2AP) in the brown aromatic rice. The results of e-nose analysis showed that 2AP contents of Aromi and Jeonbuk10 were higher than those of domestic resources. As a result of SIMCA analysis of Jeonbuk10, We confirmed Daohuaxiang2 which was used as a crossbreeding combination of Jeonbuk10 showed the most similar aroma to Jeonbuk10. So this study would be useful to the fragrance analysis system for the aromatic rice breeding as objective data in the future.

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Compositional analysis of wheat LMW-GS using aroona near-isogenic lines and a set of standard cultivars by 2-DGE, MS/MS and RP-HPLC

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It is well known that the composition of low-molecular weight glutenin subunits (LMW-GS) in wheat flour is important for end-use quality. However, the contributions of specific LMW-GS to quality have been difficult to assess because of the complexity of LMW-GS within a cultivar as well as the allelic variation between cultivars. Thus, the accurate and reliable determination of LMW-GS alleles in wheat germplasm is very important for breeding efforts. To locate individual LMW-GS corresponding to different alleles encoded by the *Glu-A3*, *Glu-B3* and *Glu-D3* loci, we analyzed a set of 15 near isogenic lines (NILs) from Aroona containing unique LMW-GS alleles in the same genetic background. Proteins in glutenin fractions were separated by two-dimensional gel electrophoresis (2-DGE) and the resulting protein patterns were compared to the pattern from Aroona. For most lines, the identifications of protein spots corresponding to LMW-GS alleles were consistent with results using a set of standard wheat cultivars for *Glu-3*. However, some spots in lines containing the *Glu-B3b*, *Glu-B3g* and *Glu-D3c* alleles differed from the previous study. To confirm their identities, these spots were excised from 2-D gels, digested with chymotrypsin and subjected to tandem mass spectrometry (MS/MS). We also developed a practical and optimized method for RP-HPLC analysis of LMW-GS using a Waters Xbridge BEH, C4 peptide column that results in better resolution than previous studies. The results will be used to identify LMW-GS alleles in germplasm prior to breeding and to screen for desirable LMW-GS alleles in wheat quality improvement.

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Development of wheat transformation methods by advanced particle bombardment in a Korean wheat cultivars "Keumkang"

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By establishing a system that can efficiently induce transgenic plants using plant tissue culture and molecular biology techniques, it can be applied to wheat to produce crops with useful traits. But wheat is considered a plant that is recalcitrant to genetically modify because of its low transgenic efficiency and genotype dependency. Therefore, various wheat transformation methods are underway to increase efficiency. So far, studies of transformation methods based on the characteristics of Korean wheat cultivars have been reported mainly on the regeneration efficiency and the confirmation of transient expression in embryogenic callus, and studies of systematic transformation method have rarely been progressed. Therefore, the aim of this study was to establish transgenic plants in Korean wheat cultivar "Keumkang" which try to introduce the centrifuges and embryo axis excision as well as the conventional methods to increase the transformation efficiency by biolistic method. Immature embryos (IEs) between the 13th and 23th days of DPA were dissected and used for transformation. A total of 9,030 IEs were tested with gold particle bombardment to introduce the GFP gene. The phosphinothricin (ppt) resistance test, the incidence of callus and the rate of green spot occurrence in Keumkang wheat were checked according to whether embryo axis was removed or not. Based on results of this study, it will provide valuable information for further development and commercialization of transgenic wheat.

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국내 귀리 탈부특성에 따른 품질연관성 분석

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귀리(*Avena sativa* L.)는 세계적으로 벼과 작물 중에서 밀, 옥수수, 벼, 보리 다음으로 생산량이 많은 작물로 대부분이 가축사료로 쓰이나, 종실은 단백질과 지질이 풍부하고 체내 이용률이 높은 식이섬유인 베타글루칸이 3~6% 들어있어 식용으로도 그 가치를 인정받고 있다. 귀리는 탈곡 후 종실의 껍질 유무로 구분되는데 겉귀리는 종실에 내영과 외영이라는 껍질이 있고 쌀귀리는 껍질이 없다. 이런 이유로 겉귀리는 수확 후 껍질을 탈피하기 위한 노력이 필요하지만 쌀귀리는 탈곡과 함께 껍질이 제거되어 식용으로 사용하기 유리하여 우리나라에서는 쌀귀리를 식용으로 이용하고 있다. 하지만 종실의 껍질을 제거한 후에는 겉귀리와 쌀귀리가 외관적으로 비교가 잘 되지 않고 도입되는 귀리가 국내산 쌀귀리와 판별이 어려운 실정이다. 이에 겉귀리와 쌀귀리의 탈부특성과 품질이 연관성이 있는지 알아보기 위해 본 연구를 수행하였다. 시험 재료는 국내에서 재배되고 있는 겉귀리 7품종과 쌀귀리 5품종 총 12품종을 이용하였으며, 겉귀리와 쌀귀리의 탈부 여부는 수확 후 탈곡기를 이용해 탈곡되어 나오는 종실의 껍질의 유무로 탈부성을 확인하였다. 조단백질 함량은 질소/단백질 분석기(Kjeltec 8400)를 이용하였고, 조지방은 조지방 자동 추출기(SoxtecTM 2050)를 이용하여 정량하였다. 베타글루칸은 Megazyme kit를 이용하여 분석하였고, 지방산 조성은 Gas Chromatography를 이용해 분석 하였다. 그 결과 단백질은 쌀귀리가 13.45~16.56% 함량 분포를 나타내었고 겉귀리는 12.95~15.31% 함량 분포를 나타내었으며, 지방은 쌀귀리가 7.26~10.34%의 함량분포를 나타내었고 겉귀리는 7.53~10.82% 함량분포를 나타내었다. 식이섬유인 베타글루칸은 쌀귀리가 4.19~5.05%의 함량 분포를 나타내었고 겉귀리는 3.49~5.60%의 함량 분포를 나타내어 귀리 품종 간에는 품질특성이 차이가 나타났으나 쌀귀리와 겉귀리를 구분 할 수 있을 정도는 아니었다. 지방산 조성 비율은 쌀귀리가 겉귀리에 비해 올레인산(C18:1, Oleic acid)과 스테아르산(C18:0, Stearic acid)이 높은 비율을 나타냈으며, 겉귀리는 쌀귀리에 비해 리놀레산(C18:2, Linoleic acid)과 리놀렌산(C18:3, Linolenic acid)이 더 높은 비율을 보였다.

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The effect of the chemical components and glyoxylate cycle-related gene expression on sprouting speed of soybean seed

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Sprouting speed of soybean [*Glycine max* Merr (L.)] seed is various among genotypes. It has been known that the contents of lipid and sugars were changed in the germination process and several enzymes relating to glyoxylate cycle were also activated during germination of oil seeds. These factors seemed to be associated with energy distribution mechanism in soybean seed. To determine important factors for sprouting speed of soybean seed, four genotypes with different chemical composition and sprout characteristics, 'Pungsannamul', 'Wonheug', 'S04 (low saturated fatty acid, SFA)' and 'S11 (high SFA)', were grown for soybean-sprout in dark chamber for five days with 20°C air condition and irrigating water 3 minutes per every 4 hours. Sprout characteristics, amounts of chemical components (lipid, fatty acid and sugar) and the level of gene expression (ICL : isocitrate lyase enzyme gene) of cotyledon were investigated during the sprouting process. Sprout length of 'Wonheug' was 20.1cm and much higher than other genotypes. Lipid and sugar contents in seed were different among soybean genotypes, but significant variation of their contents during sprouting process was not observed. The fatty acid composition was also not changed during sprouting process. The level of ICL gene expression of 'Wonheug' was highest with a value of 15.76(p<0.01) in 1-day old sprout as compared to that of 'Pungsannamul(2.66)', 'S04(1.82)', and 'S11(1.10)'. These results showed that the contents of lipid and sugar and the composition of fatty acid were not major factors to determine sprouting speed of soybean. The level of ICL gene expression might be related to the sprouting speed in soybean.

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Identify component difference of tea cultivars using fourier transform infrared(FT-IR)

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Many functionality roles are widely known about tea leaves such as amino acids like theanine and polyphenol like catechin can help psychological stability or prevent various illness. These components are contained different volume depending on tea cultivars and cultivation style. For breeding new cultivars which are contained many or unique functionality components, we tried to distinguish domestic and foreign tea cultivars using extracted components from fresh tea leaves. FT-IR analysis were performed about 26 tea cultivars including 10 domestic tea, 12 Japanese tea, 3 Taiwan tea and 1 Chinese tea. According to spectra result, significant spectra were identified on three spectrum range and some cultivars had remarkable spectra. Part of cultivars like Yabukida, Meiryoku, Sangnok were assumed certainly different from others and many of cultivars which were nearly located from each other were identified following results of Principal Component Analysis(PCA), Partial Least Squares Discriminant Analysis(PLSDA) and Hierarchical Cluster Analysis(HCA) dendrogram. These results mean tea cultivar which have similar characteristics are appeared similar components. Thus, breeding line and characteristic were important for composing various component and this results will provided basic information for breeding new functionality tea cultivars. We will perform metabolome analysis about target component by adding actual measurement data of polyphenol contents in further study.

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유전체편집 기술 활용 Glucoraphanin 고함량 브로콜리 계통 육성

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배추과 작물에서 주로 발견되는 glucosinolates 유래의 분해산물은 인체 내에서 항암 작용을 하거나, 돌연변이를 억제하는 등 다양한 생리활성 효과를 나타낸다고 알려져 있다. 현재까지 120 여종의 glucosinolate가 다양한 배추과 작물에서 밝혀졌다. 특히 glucosinolate는 식물체가 상처를 받을 경우 myrosinase 라는 효소 작용으로 isothiocyanate, glucose, 산성 황산염 등으로 분해된다고 알려져 있다. 이 중에서 isothiocyanate는 강한 항암, 항균, 살충 작용과 같은 생체방어 반응을 유도하는 것으로 알려져 있다. 브로콜리 (*Brassica oleracea*)는 배추과 작물로 항암, 고혈압 예방, 심혈관 질환 예방을 비롯한 다양한 효능이 있다고 알려지면서 타임지가 선정한 세계10대 푸드 중 하나에 속하기도 한다. 따라서 국내에서도 2000년도 이후 소비량이 급속히 증가 되고 있는 실정이다. 브로콜리의 대표적인 기능성 물질은 sulforaphane (S-methylsulfanylbutyl isothiocyanate)으로 알려져 있다. 브로콜리는 sulforaphane의 전구 물질인 glucoraphanin을 합성해서 축적하고 있다가, 조직이 기계적인 상처를 입을 경우 myrosinase에 의해 분해되면서 sulforaphane과 sulforaphane nitrile을 함께 생성된다고 알려져 있다. 따라서 브로콜리가 가지는 다양한 생리활성 효능은 glucoraphanin 함량과 비례한다고 여겨지며, 함량을 높이는 시도가 진행되어왔다. 최근에는 기존 품종 대비 glucoraphanin 함량이 2-3 배 증가된 품종이 개발되어 시장에 출시되는 상황이다. 영국 연구진에 의해서 Glucoraphanin 함량은 높은 야생brassica (*Brassica villosa*) 자원이 수집되었고, 이후 15 년간의 반복적인 교배를 통해서 2011년 “Beneforte” 라는 품종이 몬산토에서 출시되었다. 하지만 전통적인 교배 육종을 통해서 glucoraphanin 고함량 품종을 육성하기에는 너무나 많은 제약 요인이 많다. 따라서 본 연구진은 CRISP/Cas9이라는 최신 유전자 편집 기술을 육종 계통에 직접 적용하여 단기간에 Glucoraphanin 함량이 증대된 브로콜리 품종을 육성하고자 한다.

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MBW complex mediates the transcriptional regulation of anthocyanin biosynthesis in rice

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Anthocyanins, pigments that accumulate in flowers and fruits, have attracted a lot of attention due to their antioxidant properties. Anthocyanin biosynthesis is transcriptionally regulated by the MBW complex composed of R2R3-MYB, bHLH, and WD40. To identify the regulatory mechanism in anthocyanin production in rice, here, the molecular and functional properties of three rice homologues corresponding to the three components of the MBW, OsC1 (R2R3-MYB), OsB2 (bHLH), and OsTTG1 (WD40) were investigated. We analyzed the subcellular localizations of these proteins, showing that OsC1 and OsB2 localized in nucleus, and OsTTG1 localized in cytoplasm as well as nucleus. Yeast two-hybrid showed the interaction between each component of the MBW. In addition, the gene expression with steroid receptor-based inducible activation system revealed that the transcript levels of anthocyanin biosynthetic genes were increased by co-expression of the three genes. These results suggest that anthocyanin biosynthesis in rice could be directly activated by MBW complex composed of OsC1, OsB2, and OsTTG1. Complementation analysis of *tt2*, *tt8* and *ttg1 Arabidopsis* mutants showed that anthocyanin and proanthocyanidin accumulations in their seeds were recovered by *OsC1*, *OsB2*, and *OsTTG1* expression, respectively, and trichome development in the leaf of *ttg1* was restored by *OsTTG1* expression. These indicate that OsC1, OsB2, and OsTTG1 can be a functional combination as an MBW complex in planta, and the MBW regulatory machineries are well conserved in dicot and monocot plants.

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Redesign of starch biosynthetic pathway in rice by genome editing toward human diets

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Starch is a major component of human diets. The physio-chemical properties of starch influence the nutritional value of starch and the functional properties of starch containing foods. A population of 233 breeding lines of rice was analysed for variation in 17 rice starch synthesis genes, encoding seven classes of enzymes, including ADP-glucose pyrophosphorylase (AGPases), granule starch synthases (GBSS), soluble starch synthase (SS), starch branching enzyme (BE), starch debranching enzyme (DBE) and starch phosphorylase (SPHOL) and phosphate translocator (GPT1). To obtain variant plants with diverse starch structure in endosperm, we used the CRISPR / cas9 system for the starch biosynthesis-related 22 genes, respectively. Sixty-nine Cas9 vectors constructed by selecting three sgRNAs for each of the 22 genes were introduced by the *Agrobacterium* method and obtained 3960 transgenic T0 plants. As a result of the NGS analysis of the transgenic plants, 2900 plants were selected with 75% of the mutated plants at the target site. In the compilation of genes, base addition and deletion were observed at the target site. Homo, Hetero and Bi genes were also found. Homo plants breed T1 seeds and 60 T1 seeds were seeded to discriminate resistance and susceptibility with 4 ppm Barstar treatment. Also, the presence of T-DNA was reaffirmed by a bar-strip kit from susceptible individuals. Among the susceptible plants, individuals with very normal phenotype were selected and recognized as Null line. The amylose and amylopectin contents in the Null lines were varied and it could be used as a rice breeding material with double mutant breeding and new type of starch constitution.

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Korean soybean (*Glycine max*) core collection: Identification of genetic diversity, morphological traits, population structure, and genome-wide association study by Axiom 180k SoyaSNP Genotyping Array

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Developing a core collection in soybean, one of the most important crop resources worldwide, is an important and valuable task. Here, we developed a Korean soybean (*Glycine max*) core collection consisting of 430 accessions, using Affymetrix Axiom[®] 180k (180,961) SoyaSNP genotyping array and GenoCore method. In addition, we performed genetic diversity, morphological trait and population structure analyses to construct the core collection from a total of 2,872 collections. Furthermore, to evaluate the representative nature of the developed core collection for entire germplasm accessions, genome-wide association studies (GWAS) for various important, agronomic traits were conducted and compared. Sample call rates less than 97% were excluded, along with duplicate samples with more than 99.9% similarity, according to genotype analysis using Axiom[®] 180K SoyaSNP from the entire collections. As a result, we constructed the core collection of genetic diversity that reflects 99% of the total collections, including 430 soybeans. Finally, we developed the Korean soybean core collection, approximately 15% of the total collection. The Korean soybean core collection developed in this study was divided into 6 groups based on a population structure analysis. Further, morphological aspects of the Korean soybean core collection were confirmed to represent an average of 18.1% of the total collection. In addition, we validated the core collection through GWAS for already known controlling genes such as days to flowering, flower color, pubescence color, and growth habit. Consequentially, the Korean soybean core collection developed in this study should provide useful material for both soybean breeding programs and GWAS.

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Transcriptome analysis using Iso-Seq provides a comprehensive view of fruit development in *Schisandra chinensis*

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Schisandra chinensis (Omiija) is a fruit-bearing vine, and its purple-red berries are described as having five tastes. In particular, the seeds contain lignans, having beneficial effects on health. To obtain transcriptomic data that offers a more comprehensive view of fruit development in *S. chinensis*, we generated genome-wide transcriptome data from different tissues using PacBio isoform sequencing (Iso-Seq) technology. A total of 132,856 assembled transcripts were generated with an average length of 1.9 kb and high assembly completeness. Of those unigenes, 71.6% were predicted to be complete full-length (FL) ORFs and exhibited a high gene annotation rate. Furthermore, we successfully identified unique full-length genes involved in polyphenol synthesis. Based on these unigenes, we have identified the expression change of genes from different ripening stages of fruit, thus extrapolating regulatory networks genes, especially regulators, related to polyphenol synthesis. In conclusion, our results suggest that long-read, full-length or partial-unigene data with high-quality assemblies are invaluable resources as transcriptomic references in *S. chinensis* and can be used for comparative analyses for fruit development in closely related medicinal plants.

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A blue single freesia (*Freesia hybrida* Hort.) 'Blue Angel'

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Freesia (Freesia hybrida Hort.) 'Blue Angel' was developed for the cut flower in the National Institute of Horticultural Herbal Science in 2017. This hybrid was crossed and selected from a seedling of '04C3-43' and 'CV06C3-009' with single blue and pink petals, respectively, in 2010. Morphological characteristics of the selected freesia hybrid were investigated for 5 years from 2011 to 2016, and then it was named 'Blue Angel' in 2017. 'Blue Angel' has blue single petals (RHS, VG84A). The average flower width is 5.8 cm and the average yield is 6.0. The growth of the plant shows vigorous and the average height is 114.7cm. The average number of floret per stalk was 11.7, and 9.8 cm length that of control cultivar 'Cascade', 10.3 and 10.2 cm length, respectively. The average days to first flowering of 'Blue Angel', 118.7 days and the average vase life and yield is 12.3 days and 6.0 cormlets per plant, respectively.

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A pink double freesia (*Freesia hybrida* Hort.) 'Pink Bubble'

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Freesia (Freesia hybrida Hort.) 'Pink Bubble' was developed for the cut flower in the National Institute of Horticultural Herbal Science in 2017. This hybrid was crossed and selected from a seedling of 'Kristie' and the seedling of 'Michelle' and 'Rpssini' crossed with 'White Lace' in 2010. Morphological characteristics of the selected freesia hybrid were investigated for 5 years from 2011 to 2016, and then it was named 'Pink Bubble' in 2017. 'Pink Bubble' has pink double petals (RHS, RPN57A). The average flower width is 5.8 cm and the average yield is 5.0. The growth of the plant shows vigorous and the average height is 104cm, and it is higher than about 16 cm that of control cultivar 'Honeymoon'. The average number of floret per stalk was 10, and stalk was 9.0 cm length that of control cultivar 'Honeymoon', 10 and 10.3 cm length, respectively. The average days to first flowering of 'Pink Bubble', 118 days and the average vase life and yield is 11.7 days and 5.0 per plant, respectively.

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Polymorphic analysis of chloroplast genomes and 45S nrDNAs reveals genetic diversity of *Perilla* species

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Perilla species have been known to belong to the Lamiaceae family of plants and are widely grown in East Asia. They also have been taken as a traditional herbal medicine or a functional food for a long time. To find single nucleotide polymorphisms (SNPs) in *Perilla* species and analyze a phylogenomic relationship, we determined the complete sequences of the chloroplast genome (cpDNA) and 45S nuclear ribosomal DNA (45S nrDNA) of six cultivated and three wild *Perilla* species. The complete cp genome ranged in size from 152,588 bp to 152,656 bp and the length variation in cp genomes was 68 bp. The length of the 45S nrDNA ranged from 6,235 bp to 8,303 bp and the main variations of length differences was caused by the intergenic spacer (IGS) region. Comparative analysis of the cp genome sequences of nine *Perilla* species revealed low genetic diversity at the intra- and inter-species level. Using SNP analysis of cpDNA, we detected 42 synonymous SNPs (sySNPs) from 27 genes and 37 non-synonymous SNPs (nsSNPs) from 15 genes. A comparison of the 45S nrDNA sequences revealed two SNPs in the 18S rRNA, five SNPs in the 26S rRNA, three SNPs and two InDels in the internal transcribed spacer (ITS) 1 region, and six SNPs in the ITS 2 region. Our phylogenomic analysis suggests that the tetraploidization of *Perilla* cultivars may have arisen from the *P. citriodora* genome. The genotyping data from this study may be used to develop molecular markers associated with useful traits for use in *Perilla* breeding.

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Comparison of assembly protocol for *Brassica rapa* genome

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As an increasing number of plant genome sequences become available, it is clear that gene content varies between individuals, and the challenge arises to predict the gene content of a species. However, the high quality assembled genome is important for understanding the genome structure, genetic variation and evolution on crop species. Here, we present the comparison of different sequencing platform and *de novo* assembly protocol for *Brassica rapa* cultivar chiffu genome. For this, we generated two types sequencing data. 1) short-reads paired-end data from Illumina HiSeq4000 platform (385.23X). 2) Long-reads Single Molecule Real Time (SMRT) data from PacBio Sequel platform (61.64X). Furthermore, we assembled *B. rapa* genome using three different tools, in order to achieve high quality assembly (Platanus [Illumina short-read] - 391Mb, CANU [PacBio long-read] - 353Mb, FALCON-Unzip [PacBio long-read] - 320Mb). We observed that, the assembled genome size was less than the estimated genome size (452Mb) of *B. rapa* based on *k*-mer measurement. In addition, assembly results revealed that the contig N50 size was longer in long-read assembly than short-read assembly. To address the assessment and completeness of assembled genomes, we used BUSCO and CEGMA tools revealed complete matches of single copy orthologs in *B. rapa*. Finally, we confirmed the assembled *B. rapa* genome with the previously reported *B. rapa* (Chiifu-401-42) genome using QUAST for assessment. Besides, our results are the first step towards efficient comparison of assembly protocol and highlight the potential sources of error in future production of a *B. rapa* pangome.

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유색밀 ‘아리흑’의 색소 특성 및 영양성분 분석

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경남 밀양시 점필재로 20, 농촌진흥청 국립식량과학원 남부작물부 논이용작물과

유색밀은 종피에 자색 또는 흑색이 착색되어 색을 띠는 밀이다. 유색밀 아리흑을 실험재료로 사용하여 색소성분과 영양성분을 분석해 일반밀 금강밀과 비교하였다. HPLC를 이용해 안토시아닌 색소 계열별 함유량을 비교했을 때 아리흑에서는 C3G(cyanidin-3-O-glucoside)가 1.53 μ g/g, Pn3G(peonidin-3-O-glucoside)는 0.38 μ g/g 검출되었고, 금강밀에서는 검출되지 않았다. 아리흑의 DPPH 라디칼 소거활성을 측정했을 때, 40% MeOH에서 30분에 5.32 \pm 2.22%, 60분에 19.45 \pm 2.82%였고, 80% MeOH에서는 30분에 12.18 \pm 0.83%, 60분에 22.06 \pm 3.18%로 금강밀보다 높게 나타났다. 통밀가루로 분쇄한 후 알칼리 가수분해 방법을 이용해 결합형 탄닌과 총페놀성화합물, 항산화능 등을 분석한 결과, 유색밀의 결합형 탄닌 함량은 423.33 \pm 83.27(μ g catechin Eq./g), 총페놀성화합물 함량은 1587.88 \pm 18.37(μ g GAE/g)로 모두 금강밀의 탄닌 함량 207.50 \pm 20.62(μ g catechin Eq./g), 총페놀성화합물 함량 839.39 \pm 17.21(μ g GAE/g)보다 높게 나타났다. Trolox equivalent antioxidant capacity(TEAC) 항산화능 측정 결과 유색밀은 1456.25 \pm 28.64(μ g trolox Eq./g)로 금강의 150.42 \pm 4.77(μ g trolox Eq./g)보다 높았다. 아리흑과 금강밀 통밀가루의 무기이온 함량 비교 결과, 칼슘 성분은 아리흑에서 35.65mg/100g로 금강밀보다 5.95mg/100g 높았고 철은 4.76mg/100g로 금강밀보다 1.844.76mg/100g 높았으며, 인은 284.5mg/100g로 금강밀보다 61.6284.5mg/100g 높았다. 그러므로 유색밀을 통밀로 활용하여 가공품을 만들 경우 기존의 일반밀보다 기능성성분 및 영양성분이 풍부할 것으로 생각된다.

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카로티노이드를 함유한 노랑찰옥수수 ‘황금맛찰’

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황금맛찰은 자식계통 KY37을 종자친(모본)으로 하고 KY29을 화분친(부본)으로 하는 단교잡종 찰옥수수이다. 황금맛찰은 2012년과 2014년 수원에서 생산력검정시험을 수행하였고 2015년 ~ 2017년 전국 5개 지역에서 지역적응시험을 수행하였으며 2017년 농촌진흥청 직무육성 신품종 선정위원회에서 그 우수성이 인정되어 직무육성 신품종으로 선정되었다.

황금맛찰은 카로티노이드를 함유하고 있어 이삭의 색이 황색이고 줄기에 굴곡이 있으며 수염에 안토시아닌 색소가 강하게 발현된다. 황금맛찰은 출사일수가 69일로 표준품종인 일미찰보다 2일 빨랐고 착수고는 낮았으며 분지수는 적었다. 이삭길이는 일미찰과 유사하였고 이삭폭과 착립장률은 다소 작았다. 황금맛찰은 깨씨무늬병, 그을음무늬병, 조명나방 등 병해충저항성과 내도복성에서 일미찰과 차이가 없었으며 황금맛찰의 10a당 이삭수와 이삭중은 각각 6,389개/10a, 1,246kg/10a으로 일미찰과 유사하였다. 황금맛찰의 베타카로틴 함량은 16.4 μ g/100g으로 일미찰보다 8배이상 높았고 과피두께, 백립중, 전체기호도 등에서는 일미찰과 유의한 차이는 없었다. 황금맛찰은 찰옥수수 열성유전자(wx)를 보유하고 있어 일반옥수수, 초당옥수수(sh, sh2, bt 등), 단옥수수(su, se) 등 다른 종류의 옥수수 꽃가루로 수정되면 고유한 특성이 사라지므로 반드시 시간적 혹은 공간적으로 격리 재배하여야 하고 조명나방에 감수성이어서 적기방제가 필요하며 품질이 우수한 찰옥수수 생산을 위하여 적기에 수확(출사후 22~23일)하여야 한다. 본 연구는 농촌진흥청 연구사업(세부과제명 : 식용옥수수 우량 계통육성시험, 세부과제번호 : PJ012497022018)의 지원에 의해 이루어진 것이다.

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기능성 두유 제품 생산을 위한 “약선콩” 관능 평가

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강원도농업기술원에서 육성한 비린내 없는 기능성 소립검정콩 “약선콩”을 이용한 고품질 기능성 두유 생산을 위하여 일반적으로 시중에 유통되는 쥐눈이콩과 비교하여 두유가공 시 관능성을 평가하였다. 이는 특수목적 콩 육성 후 현장 실용화를 위해서 육성 품종의 기능성 물질 특성 뿐 아니라 소비자가 직접 접하는 제품 형태의 관능성 평가 결과를 수반하여 산업화하기 위함이다. 관능성 평가는 기존제품 대비 약선콩 두유의 맛품질 경쟁력을 파악하기 위하여 서울 및 수도권 거주 30-50대 여성들을 대상으로 관능평가 전문가인 (주)센소메트릭스에서 수행하였다. 평가방법은 블라인드 검사로 객관적 결과 도출 후 시장에서 인식되는 상품성 수준 파악을 위하여 제품컨셉을 제공한 후 같은 방식으로 평가하였다. 제품컨셉은 「이번에 제공되는 제품은 예로부터 건강에 더 좋다고 알려진 국산 검은콩(쥐눈이콩)만 껍질채 갈아 넣어 약콩의 풍부한 영양성분을 그대로 담았습니다. 또한 설탕이나 유화제 등을 첨가하지 않아 더욱 건강한 제품입니다.」이다. 주요 관능속성 평가는 맛에 대한 종합기호, 외관, 향미, 입안느낌, 뒷맛의 세부기호를 평가하였고, 인지강도와 희망강도는 두유맛, 고소한맛, 단맛, 비릿함, 목넘김 부드러움, 텁텁함 속성을 평가하였다. 결과분석은 SensMine(센소메트릭스)를 활용하였으며, 종합 선호 결과는 각 시료에 대한 선호 선택 빈도를 선호 유의차 검정(Binomial Test)하여 95% 신뢰수준 차이에서 비교분석하였다. 기호 및 강도 평가 결과는 LSD(Least Significant Difference) 방법으로 95% 신뢰수준에서 다중비교 검정하였다. 관능품질 개선 방향에 대해서는 종합기호도와 관능속성의 인지 및 희망강도 반응값에 대해 Ideal Profile Method(IPM) 방법으로 분석하였다. 종합평가 결과 약선콩 제품은 기존 재래종 제품에 비하여 종합선호, 기호는 물론 세부기호에서 높게 평가되었다. 세부속성 강도에서 약선콩은 대표적인 긍정속성 중 하나인 목넘김부드러움의 경우 뚜렷하게 강하고, 부정속성 중의 하나인 비릿함은 뚜렷하게 약한 것으로 평가되어 관능속성 프로파일 관점에서 유리하였다. 이러한 결론은 약선콩 두유제품은 기능성 측면과 함께 맛품질 측면에서도 높은 경쟁력을 가진 것으로 평가된다.

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Induced coiled branch (*cbr*) mutant in Arabidopsis by overexpression of a novel E3 ubiquitin ligase gene

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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 coiling branches. 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 ubiquitinated 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.

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Development of a DNA barcode database for scientific authentication of raw materials for food safety: Current status and recent progress

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DNA barcodes developed from organellar genomes in mitochondria or chloroplast have been playing important role in distinguishing authentic food materials from fraud ones. Our primary objective is to develop a comprehensive DNA barcode database, which will serve as a resource for future scientific authentication for food safety. In order to build such database, we used Tripal open-source database infrastructure. The Tripal-based DNA barcode database consists of three interconnected modules: search, profile, and analysis. These modules make the database enable both single marker review and batch analysis with multiple kinds of data and multiple species. To date, we have deposited more than 200 barcode markers designed from mitochondrial and chloroplast genomes. Equipped with specialized functional modules and modernized visualization tools, and populated with multiple kinds of data, our database will provide a quick and easy data analysis platform for both industry and academia. This research was supported by a grant (17162MFDS065) from Ministry of Food and Drug Safety, Korea, in 2018.

Keywords: Chloroplast genome, DNA barcode marker, Database, food authentication

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분자마커를 활용한 베타카로틴 고함유 옥수수 계통 선발

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강원도 홍천군 두촌면 장남길 26 강원도농업기술원 옥수수연구소

베타카로틴(β -carotene)은 동물의 대사작용을 통해 비타민A로 전환될 수 있는 카로티노이드에 속하는 주요 성분으로 시각과 관련된 망막질환과 백내장 등의 예방에 매우 중요한 역할을 한다. 카로티노이드는 주로 빨강색, 노란색, 주황색 과일 또는 채소에 많이 함유되어 있으며 심장병 및 암에도 의학적 효과가 있다고 한다. 최근 이러한 식물의 천연 색소, 식이섬유, 단백질 원료 등을 활용하기 위한 연구가 진행되고 있으며, 색소 성분의 함량이 높은 품종 육성이 육종가의 주요 목표가 되고 있다. 본 연구에서는 국제밀옥수수연구소(CIMMYT)에서 개발한 베타카로틴 생성에 관련된 hydroxylase 1(*cr1RB1*) 유전자를 선발하기 위한 두 가지 분자마커를(5'TE, 3'TE) 활용하여 F₃ 분리세대(17Cr) 옥수수의 계통을 분석 및 선발하였다. 또한, 선발된 계통에 대한 베타카로틴의 함량을 평가하고자 고성능 액체 크로마토그래피(HPLC) 분석을 실시하였다. 본 연구에서는 704개의 분리계통을 평가하였고, 각각의 DNA는 앞에서 추출하여 *cr1RB1*-3'TE, 5'TE 두 개의 프라이머로 분석하였다. 분석 결과 한 개의 특이 증폭밴드를 가진 39계통을 선발하였다. 선발된 계통 및 그렇지 않은 계통들을 베타카로틴 함량 분석을 한 결과 17Cr243 계통에서 최고 38.6 $\mu\text{g/g}$ 의 베타카로틴이 검출되었고, 이 수치는 선발되지 않은 계통들을 분석한 함량 중에서 불검출을 제외한 최저 함량인 1.6 $\mu\text{g/g}$ (17Cr422)에 비해 약 24배 높았다. 본 연구의 결과를 통해 *cr1RB1* 분자마커를 활용한 베타카로틴 고함유 옥수수 계통 선발은 색깔을 통한 육안으로 선발하는 육종방법에 비해 시간과 노력이 절감되며 정확한 선발을 할 수 있을 것으로 기대된다.

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Metabolic regulation for high production of syringin in *Arabidopsis thaliana*

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Syringin, sinapyl alcohol 4-*O*-glucoside, is well known as a plant-derived bioactive monolignol glucoside. In *Arabidopsis*, recombinant chimeric protein UGT72E3/2 has been previously reported to lead to significantly higher syringin production than the parental enzymes UGT72E2 and UGT72E3. In this study, we demonstrated that the production of syringin in *Arabidopsis* leaves can be enhanced through metabolic regulation. To enhance metabolic flow through the phenylpropanoid pathway and maintain a high homeostatic concentration of sinapyl alcohol in the plant leaves without cosuppression, we combined various *UGT72E-Myc* with *F5H* encoding ferulate 5-hydroxylase or/and *Myb58* encoding the lignin biosynthesis transcriptional activator in a single vector. The results showed that transgenic plants expressing simultaneously *UGT72E3-Myc+F5H+Myb58* accumulated syringin 3 ~ 6 times more in their leaves compared to transgenic plants expressing *UGT72E3-Myc+F5H* or *UGT72E3-Myc+Myb58*. More importantly, transgenic plants expressing *UGT72E3-Myc+F5H+Myb58* exhibited the highest ratio of syringin to coniferin, suggesting that is optimal combination of genes on regulating metabolic flow for syringin production in plants. We also are attempting to transform this multiple gene expression vector into several mutants blocking the metabolic branch pathways from phenylpropanoid pathway, such as *chs* mutant deficient chalcone synthase that catalyses the flavonoid/isoflavonoid biosynthesis pathway and *aldh* mutant deficient aldehyde dehydrogenase that bypasses sinapyl aldehyde to sinapate instead of sinapyl alcohol. These metabolic regulation methods are of value in the development crop plants efficiently producing biologically active secondary metabolites.

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Identification of a new *Sg-9* gene responsible for the DDMP-saponin biosynthesis in soybean

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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 its 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 along with two cultivars, Pungsannamul and Uram to study the segregation and genetic linkage analysis, respectively. The segregation analysis showed that the mutant phenotype is controlled by a single recessive gene. The position of locus (*Sg-9*) involved in the biosynthesis of DDMP deficient saponins was mapped using bulk segregation analysis and fine mapped on chromosome 16 (130 kb) between two SNP markers. The genomic sequencing of *Sg-9* gene showed a single nucleotide polymorphism in PE2248 (G626A) and PE2371 (C137T) mutant lines and new alleles were designated *sg-9-a* and *sg-9-b*, respectively. Allelism test between two mutants PE2248 and PE2371 exhibited that the mutation sites lie on the same gene. The enzymatic assay showed that mutant recombinant proteins showed lower glycosyltransferase activity than wild-type *Sg-9*. Further, tissue-specific expression study indicated that *Sg-9* expression corresponds to the accumulation of DDMP saponins in soybean seeds. These results support that *Sg-9* is likely to play a role in the biosynthesis of DDMP saponins in soybean.

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Expression of F-box proteins and their interacting proteins in wheat grain development

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F-box protein is components of SCF ubiquitin ligase complex, serves as substrate adaptors to mediate the degradation of a large number of regulatory proteins involved in diverse processes. F-box protein plays important roles in the regulation of various development processes in plants. About 1796 F-box genes have been identified in the wheat genome, but their detailed functions remain unknown. We isolated five F-box protein genes from wheat grain development. The cDNAs encoding *TaKFB1*, *TaKFB2*, *TaKFB3*, *TaKFB4*, and *TaKFB5* contained 364-, 450-, 354-, 383-, and 457-bp open reading frames, respectively, and all deduced TaKFBs contained a F-box domain (IPR001810) and Kelch repeat type 1 domain (IPR006652) except TaKFB2. The *TaKFBs* showed elevated expression during grain development stages of color pigmentation. To clarify how TaKFBs and SKP proteins combine in wheat, we examined whether the 5 TaKFB proteins showed specificity for 6 SKP proteins using a yeast two-hybrid assay. And also, a yeast two-hybrid screen performed to search for proteins capable of binding the TaKFB proteins identified an interaction with partner of paired. To examine the subcellular localization of TaKFBs, we transiently expressed TaKFB-GFP fusions in tobacco leaves; the TaKFB-GFP fusions were detected in the nucleus and the cytoplasm. These results will provide useful information for further functional studies on wheat F-box proteins and their possible roles.

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Comparison of agricultural and physicochemical traits from tropical and subtropical legume crops

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This study was conducted to provide information by evaluating the nutritional and functional components as well as the agricultural characteristics related to the possibility of growing tropical and subtropical minor legume crops in Korea. The materials were used 260 accessions including lentil(68 acc.), lima bean(48acc.), chick pea(72acc.) and guar(72acc.). Four Legume crops were sown on 14th March, and planted on 10th April 2017, at green house in Nongsaeng myeongro, Jeonju city. Days to flowering were ranged from 48 to 85 days, those of lentil was the shortest with 48 days, those of lima bean was the longest with 85 days. The average days of growth were ranged from 82 days(lentil) to 164 days(guar). The maturity period was mostly distributed from the last of May to the middle of September. The flowering days of common bean controls, Gangnangkong # 1 and Shinseondu were 55 days and 54 days, days of growth of those were 102 days and 98 days, respectively. The average 100 seed weight by crops was 2.2g of lentil, 80.5g of lima bean, 22.9g of chick pea, 3.8g of guar. The average of crude protein contents in legume crops was ranged from 17.5% to 26.4%, the highest in guar, and the lowest in chick pea. The average of crude oil contents in legume crops was generally low from 0.8%(lentil, lima bean) to 4.3%(chick pea). The crude protein contents of common bean controls was between 17.2 % and 19.7 %, 0.9-1.0 % of the crude oil, and 4.0 % of the crude fiber. The average of crude protein and crude fiber contents in legume crops were higher than common bean and the crude oil contents of those were similar with that. According to the characteristics of tropical and subtropical legume crops, lima beans, chick pea and guar was possible to grow in Korea, but the lentils needed to reconfirm. total sixty eight accessions of lentil were used in this study, 58 accessions of them can be harvested and 29 accessions of which can be obtained enough yield for evaluation. The agricultural characteristics of tropical and subtropical legume crops do not differ much from those of control common bean. In addition, legume crops were excellent than common bean in physicochemical properties. Therefore tropical and subtropical legume crops, chick pea, guar and lima bean seem to be useful to utilize in domestic.

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Overexpression of *IbMYB1a* gene in soybean increased high content of anthocyanin

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Anthocyanin, flavonoid-based natural pigment, is contained in flowers and fruits of plants. Anthocyanins are anti-oxidant and anti-cancer agents when ingested by humans. *IbMYB1a* gene derived from *Ipomoea batatas*, is a transcription factor that promotes enzymatic activity of anthocyanin biosynthetic pathway. To use soybean as antioxidant, transgenic plant was created by inserting *IbMYB1a* gene into soybean genome along with over-expression promoter. Transgenic plant (T₀) was produced by using modified half-seed method, and PCR analysis of T-DNA was performed to confirm the insertion of *IbMYB1a* gene. Among transgenic T₁ plants, line #6 plant showed dark purple color. Moreover, high level of gene expression was verified in line #6 plant by using RT-PCR. Leaves of the transgenic plants were analyzed by HPLC. As a result, anthocyanin content of the line # 6 was 160-times higher than wild type soybean. Transgenic line #6 plant (T₁) was grown to identify the phenotypic change. Line #6 plant was strongly purple, but leaves were dry and consequently failed to produce flowers. In addition, we are identifying phenotype by germinating line #7 plant seeds, which anthocyanin content is measured 14-times higher than wild type soybean.

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OsSTK1 enhances the intrinsic GTPase activity of OsNug2 through binding and phosphorylating its serine 209

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The Nug protein family is an important part of GTPases which involves in ribosome biogenesis, cell proliferation, and cell growth. Recently, We characterized a rice (*Oryza sativa*) nuclear/nucleolar GTPase 2 (OsNug2), which belongs to the YlqF/YawG family of GTPases, playing a role in maturation of pre-60S ribosomal subunit. Yeast two-hybrid screening, using OsNug2 as bait, was carried out to find out potential interaction factors, and rice serine/threonine kinase 1 (OsSTK1) was identified as a candidate. When recombinant OsSTK1 was added into OsNug2 assay reaction mixtures, OsSTK1 increased the intrinsic GTPase activity of OsNug2 significantly. The kinase assay of OsSTK1 *in vitro* reveals that, OsSTK1 strongly phosphorylated serine 209 of OsNug2. Yeast complementation test result in a *GAL::OsNug2(S209N)* mutant-harboring yeast strain, exhibited a growth-defective phenotype on galactose medium at 39°C, divergent from that of a yeast strain harboring *GAL::OsNug2*. The intrinsic GTPase activity of mutant OsNug2(S209N) was similar to that of OsNug2, but could not be enhanced upon weak binding of OsSTK1. Our findings reported here suggest that OsSTK1 functions as a positive regulator of OsNug2 through binding and enhancing the GTPase activity of OsNug2, and that the phosphorylation of serine 209 of OsNug2 is essential for the complete function of OsNug2 in ribosome biogenesis.

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Variety discrimination of 'Fuji' and its somatic mutation cultivar by InDel and AS-PCR primer using re-sequencing

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Abstract Domesticated apple (*Malus × domestica* Borkh.) is one of the most widely cultivated and loved temperate fruit crops in world. One of domesticated apple 'Fuji' (Ralls Genet × Delicious) apple is favorite apple cultivar to Koreans has been very famous after it was promoted in 1958, Japan. But, 'Fuji' apple has genetic problem that cause restriction high quality fruit production. To solve these 'Fuji' apple's problems, various and numerous somatic mutation cultivars were bred and selected. These somatic mutation cultivars are classified with three major group of fruiting spur group, early season group, and coloring group. However, 'Fuji' and its somatic mutation cultivars have genetic similarity and not much different phenotype too. For these reason, it has hard to the identification of between 'Fuji' and its somatic mutation cultivars. Therefore, in this research, we identify variety genetic diversity different between 'Fuji' and its somatic mutation cultivars by using Re-sequencing. We used Re-sequencing using 'Golden Delicious' apple genome to reference genome. Insertion/deletion (InDels) and Single nucleotide polymorphism(SNP) of 'Fuji' apple and its somatic mutation cultivars were discovered. we selected and designed the Indel marker and Allele specific PCR (AS-PCR) primer out of several markers considering reproducibility and resolution power. And data from result had selected and had converted into InDel markers and allele specific PCR primers to used it for identify between 'Fuji' and its somatic mutation cultivars. And, the results obtained with InDel markers and AS-PCR primers which distinguish 'Fuji' and its somatic mutation cultivars will be advanced that helpful to 'Fuji' somatic mutation cultivar breeders.

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Distribution of capsaicinoid contents in pepper core collection understanding genetic association

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Pungency is an unique trait that only pepper (*capsicum* spp. genus) has. Pepper's pungency is originated from its secondary metabolite, capsaicinoids that are valuable for industrial and medical purpose. Although several studies have identified loci that control capsaicinoids contents, still it is difficult to utilize on a breeding program and shows low efficiency since the trait controlled by QTL. Combining with high density SNP marker and statistical prediction model, genomic selection (GS) has been proposed as a solution to limitations of QTL mapping in plant breeding. To construct GS model of capsaicinoids contents, 351 pepper core collection were used to quantify its pungency level during 2 years. Genotype was obtained from genotype by sequencing (GBS) data which provides 168,714 SNPs. Four capsaicinoids compound (capsaicin, dihydrocapsicin, capsiate, dihydrocapsiate) were extracted from the mature fruits and quantified its pungency level by HPLC analysis. Through GBS genotype data, we conducted population stratification based on principle component analysis (PCA) in which pepper core collection divided into four sub-populations. Through HPLC analysis, we obtained overall capsaicinoids level distribution sorted by species. To Compare these two data set, we plotted a capsaicinoids compound level heatmap with phylogenetic tree that shows correlation between genotype and phenotype. Results of this experiment, ultimately, could be used to construct an accurate genome-wide selection model as an explanatory variable. Furthermore, it could provide information in which breeders can choose specific core collection for pungency trait pre-breeding.

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The complete chloroplast genomes of six *Ipomoea* species and indel marker development for the discrimination of authentic pharbitidis semen (seeds of *I. nil* or *I. purpurea*)

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Ipomoea species (morning glories) are economically valuable as horticultural species and scientifically valuable as ecological model plants to investigate mating systems, molecular evolution, and both plant-herbivore and plant-parasite interactions. Furthermore, the dried seeds of *I. nil* or *I. purpurea* are used in Korean traditional herbal medicines. In this study, chloroplast (cp) genomes were sequenced from six *Ipomoea* species, namely, *I. nil* and *I. purpurea* and, for the first time, *I. triloba*, *I. lacunosa*, *I. hederacea*, and *I. hederacea* var. *integriscula*. The cp genomes were 161,354 -161,750 bp in length and exhibited conserved quadripartite structures. In total, 112 genes were identified, including 78 protein-coding regions, 30 transfer RNA (tRNA) genes, and four ribosomal RNA (rRNA) genes. Comparison of the six *Ipomoea* cp genomes revealed locally divergent regions, mainly within intergenic spacer regions. In addition, the protein-coding genes *accD*, *cemA*, and *ycf2* exhibited high sequence variability and were under positive selection ($Ka/Ks > 1$), indicating adaptive evolution to the environment within the *Ipomoea* genus. Phylogenetic analysis of the six *Ipomoea* species revealed that these species clustered according to the APG IV system. We uncovered high-resolution phylogenetic relationships between Ipomoeaeae. Finally, indel markers (IPOTY and IPOYCF1) were developed for the discrimination of the important herbal medicine species *I. nil* and *I. purpurea*. The cp genomes and analyses in this study provide useful information for taxonomic, phylogenetic, and evolutionary analysis of the *Ipomoea* genome, and the indel markers will be useful for authentication of herbal medicines.

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Comparison of sesame seed qualities grown in field and in the greenhouse

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Sesame is cultivated in both in the field and in the greenhouse followed postharvest of vegetables and fruits. Sesame seeds contain 50% oil, 25% protein and 0.5% lignan content. It is considered as valuable vegetable oil, easy to extract as roasted, as well as refined unroasted oil. In this study, we evaluated the variation of seed quality of sesame grown in field and greenhouse conditions. We analyzed crude fat, crude protein, lignan contents and fatty acid composition of twelve cultivar 'Ansan', 'Daheuk', 'Dodam', 'Galmi', 'Hwangbaek', 'Jinki', 'Jinyul', 'Kangheuk', 'Pyeongan', 'Sangbaek', 'Seodun', 'Yangbaek'. The cultivar 'Seodun' showed the highest crude protein and oleic acid composition of 31.2% and 49.2%, respectively. The cultivar 'Sangbaek' showed the highest crude fat of (52.4%) content whereas, 'Yangbaek' showed the highest lignan content (6.31mg/g). Estimated crude protein, crude fat, lignan and fatty acid contents of sesame seeds were varied among cultivars and influenced by environment. The crude protein, lignan and linoleic acid contents were relatively high whereas, crude fat and oleic acid contents were slightly low when grown in greenhouse condition. The results showed that sesame seeds grown in the greenhouse had higher quality than those grown in the field.

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Development of web-based database for phenotype data management

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The development of Next Generation Sequencing (NGS) technique and bioinformatics skills have led a dramatical increase of genomic data. This information can be used to develop comprehensive and precise molecular markers for breeding since thousands upon thousands of SNPs are extracted from NGS dataset. To use of these data for molecular breeding the linkage of the information to phenotype data is an essential requirement, however phenotype information seem relatively insufficient to utilize genome information in agriculture. Thus, we developed a new module for management of phenotype data in the existing web-based database, 'Phenome and Genome Database for Breeding (PGDB)' that can search molecular markers associated with traits of interest. At present, the types of phenotypes are divided into a total of 42 traits of tomato, and user can input these data in bulk through CSV files or input them individually for each item using web interface. In addition, phenotype images are also stored in it. In the future, we will link seed numbers commonly used among related researchers for clear management of these information. These features from this study can allows seed company and breeders to manage phenotype information of their seeds and then could be extended further to various crops.

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Anti-oxidant, phenolic/flavonoid compounds, anti-elastase and anti-collagenase activities of extracts from *Citrus unshiu* at various stages of fruit development and tissues

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Citrus fruits are well-known as an important dietary source of nutrients and health-promotion. It is widely distributed in the tropical and subtropical regions in the world and also Jeju island in south korea. Several studies have reported anti-oxidant activity and phenolic compounds in commercially available citrus species but not yet investigated for various stages during fruit development and tissues. Aging of human skin is an inevitable biological phenomenon by intrinsic and extrinsic factors as accumulation of reactive oxygen species (ROS) which leads to the activation of elastase, collagenase and hyaluronidase. So far, the extract from several plant, such as rice, alfalfa and tea etc, have been investigated for elastase, collagenase and hyaluronidase inhibitory activities, but anti-aging assay from the extract of citrus fruit have not been elucidated yet. In this present study, anti-oxidant activity and total phenolic/flavonoid content of Citrus unshiu extract during fruit development and tissues were evaluated as well as inhibitory activities of elastase and collagenase. And we also investigated the total carotenoid and chlorophyll a/b content

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Differential expression analysis of RNA-seq with respect to capsaicinoid biosynthesis in the pericarp tissue of *Capsicum chinense*

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The pungent flavor of chillies is induced by capsaicinoids found only in the genus *Capsicum*. Capsaicinoid biosynthesis occurs in the placental epidermis cells, secreted towards the outer cell wall, and finally accumulate “blisters” located on the placenta surface. However, extremely pungent pepper such as *C. chinense* ‘Trinidad Moruga Scorpion’, extreme character of chilli is owing to a volatile phenolic amine ‘Capsaicin’, a molecule which is responsible for the pungency of chilli peppers and found mainly in the placenta as well as fleshy tissue of the fruit. The goal of the present study was to identify putative genes involved in controlling capsaicinoid biosynthesis in the pericarp by analyzing changes in global gene expression patterns. RNA-seq was used to analyze the expression profiles in the pericarp tissue over three developmental stages of three *Capsicum* cultivars with different capsaicinoid content: a highly pungent cultivar *C. chinense* ‘Trinidad Moruga Scorpion’, a pungent cultivar *C. chinense* ‘Habanero’, and a non-pungent *C. annuum* ‘Early Calwonder (ECW)’. Changes in gene expression patterns were determined by comparing two cultivars at each developmental stages: 18 days after pollination (DAP), 34 DAP, and 45 DAP. We identified genes differentially expressed in the pericarp of ‘Scorpion’ compared to ‘Habanero’ 1,437, and 1,717, and 676 were up-regulated while 1,195, 1,313, and 654 were down-regulated at 18, 34, and 45 DAP, respectively. Additionally, to functionally categorize DEGs, these DEGs were mapped to terms in the KEGG database. Furthermore, we analyzed the expression patterns of 12 genes of known function in the capsaicinoid biosynthesis pathway. Multiple genes including Pun1, pAMT and KAS were up-regulated in the pericarp of ‘Scorpion’. Increasing capsaicinoid content is an important objective of pepper breeding. Our comprehensive transcriptional overview will be helpful for revealing genes involving capsaicinoid biosynthesis in the pericarp, and thus enhancing the capsaicinoid content in the whole fruit.

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Gene expression analysis varying apple peel color and pattern between ‘Fuji’ and ‘Benishogun’

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To overcome genetic weakness of ‘Fuji’ leading pale coloration, its enhanced somatic mutants were widely cultivated including ‘Benishogun’. In order to examine whether apple peel phenotype difference between cultivars was due to expression of anthocyanin and carotenoid biosynthesis related genes, RNA was isolated from fruit skin samples during six developmental stages and cDNA was synthesized immediately. And then, that was analyzed by quantitative real time PCR. The results generally showed that the expression level of most genes were increased at maturity stage. But there was a significant difference between ‘Fuji’ and ‘Benishogun’. In case of eight anthocyanin involved genes, *MdCHI*, *MdF3'H*, *MdMYB10* and *MdGST* and about three carotenoid involved genes, *MdZISO*, *MdCRTISO* and *MdLCY-ε* highly expressed in ‘Benishogun’ than ‘Fuji’. These observations may have increased the accumulation of anthocyanin and carotenoid in ‘Benishogun’ inducing diverse apple skin phenotype.

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Development of SNP marker associated with fruit traits using GWAS in apple

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Fruit breeding is imperative that new cultivars are selected to have outstanding consumer appeal. To improve fruit quality, it is necessary to confirm association between genetic and fruit traits useful for fruit breeding. Genome-wide association study(GWAS) that links molecular genetic information with phenotypic information is a method that is being used in various fields today, and it can be used to search for genes that are related to the target trait of the genome. In this study, using GBS(genotyping-by-sequencing) data of NGS technology generated from 308 apple germplasm, GWAS was performed to indentify SNPs associated with fruit traits. High association level SNPs were confirmed on chromosome 9 about skin color and were identified on chromosome 16 about acidity. The results of this study will can be proposed candidate gene and marker including SNP associated with fruit traits. Also, application of molecular markers developed through phenotypic and genomic analysis to apples mating population will be able to select useful individuals and used as the basis of apple molecular breeding.

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A Comparison of two *de novo* GBS pipelines for a large genome

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With the fast development of NGS technology and the decline in prices, various genotyping methods based on sequencing have been developed. In particular, Genotyping-By-Sequencing (GBS) technology has been used in genotyping of agricultural organisms since 2011 and has become a useful technology in agricultural plant research since the announcement of the TASSEL-GBS pipeline in 2014. The GBS pipeline is divided into the referenced-base method and the *de novo* method, depending on whether the reference is used. However, many agriculturally important crops have large genomes due to polyploidy and a huge number of repeat sequences but have no reference genome. At present, Stacks and UNEAK support the *de novo* method. Studies have shown that the two pipelines work relatively well in diploid and medium-sized genome plants, but the performance of the pipelines for the large genomes is not clear. In this study, we tested the pipelines with a bread wheat genome (*Triticum aestivum*) which has large hexaploidy genome(15.3 Gb). The results show both pipelines have a proper performance for the large genomes but need to be improved.

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Comparative analysis of synteny between plants to improve the quality of a genome sequences which is a base of modern breeding technologies

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The genome sequence is a base of the modern breeding technologies such as genomic selection. Notably, it is more important to obtain high-quality genome sequence for a crop which has complex genome structure. Up to date, to improve a genome assembly quality, there were many tries to use information of synteny generated by speciation and a (whole) genome duplication which are general evolutionary events in plants. However, the most usages of synteny information are determining of order and orientation of contigs(scaffolding), but there was no noticeable report in a determination of the length of a junction between contigs(gap). Herein, to address the possibility that the synteny is used to determine gap length, we identified synteny regions between 23 representative plant genomes and compared the features such as the number of genes and the length. The results such as a distribution of the length difference show that the information can be used to improve a genome assembly.

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Maturation rate of inflorescence stem determines the direction of stem growth in Solanaceae

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Apical shoots dominantly grow upright to maintain the top position until stems are fully mature or terminate to reproductive stems such as pedicel and floral stem. Plant stems have a critical time point to react to gravity or light vectors. In Solanaceae, shoot architecture has been remarkably diverged, developing sympodial (inflorescence) shoot carrying single flower to both sympodial shoot and inflorescence producing compound flowers. To understand this divergence, we hypothesize that the direction of sympodial growths were decided by maturation rates. In tomato, new sympodial shoot take place of main erect stem after primary shoot transition to inflorescence and terminate to flowers. Here we show tomato inflorescence could be shifted to sympodial shoot growth with erect growth in mutants, indicating inflorescence meristems can be reverted to vegetative status by the delayed maturation in the meristem. *mc sp* double and *s* single mutant developed inflorescence growing upright, which is similar that of *S. peruvianum*. Erect type inflorescences reverted to vegetative state were produced in *sft*, *mc*, and *j* background. Moreover, *sft*, *j* double produced only sympodial shoots carrying single flower, which is similar to the sympodial shoot of *N. benthamiana*. Interestingly, molecular state of inflorescence meristems indicated delayed maturation of the meristems in *s* mutant and *sft* mutant. Therefore, we suggest that sympodial shoot meristem and sympodial inflorescence meristem might have been evolved by variations in maturation state and activity of erect growth response on each young stem in Solanaceae.

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Assessment of potential environmental risks of transgene flow in smallholder farming systems in Asia: *Brassica napus* as a case study in Korea

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With increasing GM crops imports and exports worldwide, the concern of transgene flow and environmental risks from GM crops is growing. Particularly in Asia including Korea which has smallholder farming system, concerns about ecological impact of GM crops on non-target organisms, such as their closely-related relative species are high. However, few studies about environmental risks of GM crops have been conducted under smallholder farming systems in Asia with diverse crops in co-existence. Thus, in this study, two-year field study was conducted to assess potential environmental risks deriving from transgenic flow glufosinate-ammonium resistant (GR) *Brassica napus* to its conventional relatives, *B. napus*, *B. juncea*, and *Raphanus sativus* under simulated smallholder field conditions in Korea. Screening with glufosinate-ammonium was conducted on F1 hybrids, and PCR analysis was also conducted to detect bar-specific gene introgression. The result showed that hybridization frequency ranged between 0.007% (75m) to 2.33% (2m) for *B. napus*, and 0.025% (16m) to 0.076% (2m) for *B. juncea*. No gene flow was observed to *R. sativus*. Results suggest that long-distance gene flow from GR *B. napus* to *B. napus* and *B. juncea* is unlikely, but gene flow can potentially occur between adjacent fields where the smallholder farming systems exist.

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국내 육성 콩 품종의 이소플라본 조성별 함량 변이 분석 및 자원 선발

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경상남도 밀양시 점필재로 20 국립식량과학원 남부작물부

콩 이소플라본은 건강기능성 식의약 소재로서 중요한 생리활성 성분이다. 국산콩의 소비촉진과 수입산과의 차별화를 위해 본 연구에서는 용도별 국내 육성 주요 콩 품종에 대한 이소플라본 함량을 분석하고 원료곡 자원 선발 및 육종 기초자료로 활용하고자 한다. 장류·두부용, 나물용 등 용도별 구분된 총 44개 품종을 시험재료로 국립식량과학원 대구시험지에서 2016~2017년 수확한 콩 종자의 이소플라본 총량 및 조성별 함량을 HPLC로 분석하였다. 이소플라본 총량 및 조성별 함량 변이에 대한 품종간 차이가 인정되고, 시험년도는 daidzein과 genistin 성분 함량을 제외하고 유의성이 인정되었다. 전 품종의 2년간 평균 이소플라본 함량은 2,935 $\mu\text{g/g}$ 이며, 용도별 품종군 평균 함량은 나물용(3,850.4 $\mu\text{g/g}$) > 장류용(3082.8) > 유색콩(2345.8) > 울콩류(1,298.6) 순이었다. 2년간 이소플라본 함량에 대한 44개 품종의 순위상관은 고도로 유의하였으나($r=0.92^{***}$), 함량 변이에 대한 품종과 시험년의 상호작용 효과도 유의하였다. 나물용 품종 ‘소원콩’이 전체 공시품종에서 함량이 가장 높았고(5,226 $\mu\text{g/g}$), ‘신화’(4,956)와 ‘소록’(4,830)이 높은 수준을 나타내었다. 장류·두부용 품종에서는 ‘대풍’(4,962 $\mu\text{g/g}$)이 가장 높고 ‘대풍2호’(4,619), ‘새금’(4,602), ‘우람’(4,305) 순이었다. 반면, ‘태광콩’, ‘새단백’, ‘단백콩’ 등은 1,500 $\mu\text{g/g}$ 미만으로 낮았다. 생육기간이 짧고 대립인 울콩류와 안토시아닌 함량이 높고 대립인 검정콩 품종은 이소플라본 함량이 낮은 경향이였다. 이소플라본 조성 성분 비율은 malonyl계 배당체(평균 2,437 $\mu\text{g/g}$)가 전 함량의 83.0%로 가장 높고 glucoside(9.5%), aglycon 비배당체(5.4%), acetyl계 배당체(2.1%) 순으로 낮았다. 검정 소립콩 ‘소청자’ 등을 제외하고 종자 크기가 작을수록 이소플라본 함량은 증가하는 경향이였다. 단기성 콩을 포함한 품종별 파종~성숙기까지의 생육일수는 이소플라본 함량 변이와 유의한 상관을 보였으나($r_{2016}=0.40^{**}$, $r_{2017}=0.44^{**}$), 개화기~성숙기까지의 생육일수는 유의성이 없었다. 품종별 개화이후 성숙기까지의 기온이 높을수록 이소플라본 함량은 낮은 경향을 보여 역의 상관관계를 나타내었다. 향후 이소플라본 함량이 안정적으로 높거나 낮은 품종을 식품 및 산업 소재화함으로써 시장과 소비자의 다양한 기능성 신수요 창출 및 지원이 기대된다.

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Construction of linkage maps in octoploid strawberry based on SNPs discovered by GBS method

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The cultivated strawberry, *Fragaria x ananassa*, is an allo-octoploid species ($2n = 8x = 56$) with an estimated genome size of 708-720 Mb. Although strawberry is one of the important vegetable crops in Korea, the complex structure of the genome prevented research in genomics of strawberry. However, advances of genomics in *Fragaria* has been made by releasing genome sequences of diploid *F. vesca* and octoploid *F. ananassa*. In this study, we constructed linkage maps of strawberry families using single nucleotide polymorphism (SNP) markers discovered by genotyping-by-sequencing (GBS). Three *F. ananassa* varieties were used for development of two F2 cultivated strawberry families: ‘Benihoppe’ x ‘Chandler’ (‘BC’) and ‘Benihoppe’ x ‘Doyonoka’ (‘BD’). We compared the SNP discovery results when utilizing two reference genomes. In ‘BC’ population, a total of 192,649 and 2,245 SNPs were obtained for *F. vesca* and *F. ananassa* respectively. In ‘BD’ population, a total of 165,893 and 748 SNPs were obtained for *F. vesca* and *F. ananassa* respectively. A linkage map for ‘BC’ population consisted of 25 linkage groups possessing 145 high-quality SNPs identified from *F. ananassa* reference genome and total map length was 686 cM. 134 SNP markers obtained by mapping to *F. vesca* reference genome were used for a linkage map of ‘BD’ population and the total length of seven linkage groups was 1,234 cM. In addition, we showed the complementary application of two reference genome according to SNPs to be analyzed. This SNP-based linkage maps will be helpful for the genetics and breeding of allo-octoploid strawberry.

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메밀 유전자원 재배시기별 생육특성 및 플라보노이드 함량 비교

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메밀은 마디풀과(polygonaceae)의 메밀속에 속하는 일년생 초본으로 야생종을 포함하여 20여 종이 확인되고 있다. 현재 재배되고 있는 메밀 재배종은 보통메밀(*Fagopyrum esculentum* Moench)과 쓴메밀(*Fagopyrum tataricum* Gaertn., 타타리메밀) 등 두 종이 주류를 이루고 있으며 우리나라에서는 보통메밀이 주로 재배되어 왔다. 본 연구는 농업유전자원센터에서 보유중인 메밀 유전자원 183점을 봄, 여름에 파종하여 재배시기별 생육특성과 플라보노이드 함량을 비교하기 위해 수행되었다. 봄, 여름 파종은 각각 2017년 4월 14일과 8월 17일에 전주 소재 농업유전자원센터 포장에 하였으며 개화기, 성숙기, 주경절수, 충분지수, 백립중 등 5개 농업형질을 조사하였다. 봄 파종시 개화기는 대부분 5월 25일 전후하여 파종일로부터 약 40일이 소요되었고 성숙기는 6월 말부터 7월 중순까지 분포하였다. 여름 파종시는 9월 15일 전후 개화하여 파종 후 30-35일이 소요되었고 10월 말에 성숙하였다. 종자 생산과 관련된 주경절수와 충분지수는 봄 파종과 여름 파종에서 많은 차이를 나타냈으며 봄 재배시 영양생장이 왕성하여 가을 재배보다 많은 주경절수와 충분지수가 조사되었다. 그러나 백립중에서는 여름 파종이 봄 파종보다 무거운 경향을 보여 주경절수, 충분지수와 백립중 간 부의 상관관계가 있었다. 일반메밀 유전자원을 국내 수집지별로 나누어 조사한 결과 주경절수와 충분지수는 봄, 여름 파종 모두에서 전남 수집자원이 가장 많았으며, 강원, 경남, 경북, 전북, 충북 수집자원과 유의성있는 차이를 나타내었다. 강원, 충북 수집자원은 제일 낮은 주경절수와 충분지수를 보였으나 백립중은 가장 높게 조사되었다. 성숙 종자의 플라보노이드 함량을 조사한 결과 봄 재배 자원은 0.22 mg/g을 나타내었고 가을 재배 자원은 2배 높은 0.44 mg/g의 함량을 보여 가을 재배시 더 높은 플라보노이드를 축적함을 알 수 있었다. 수집지역별로는 전남 수집자원이 봄, 가을 재배 모두에서 가장 높은 플라보노이드 함량을 보였으며, 봄 재배시 지역간 유의성있는 함량 차이가 나타났지만 가을 재배에서는 비슷한 경향을 보여 봄 재배가 메밀 유전자원의 플라보노이드 함량 차이에 더 많은 영향을 미치는 것을 확인하였다.

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설갱벼의 분상질 유전자 *flO14(t)*에 관한 유전분석 및 유전자 지도 작성

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일품벼의 MNU 돌연변이처리로 육성된 설갱벼의 분상질(floury)에 관여하는 유전분석 및 DNA 연관마커를 개발하고자 정상 품종인 새일미벼와 설갱벼가 교배된 F1식물체에서 채종한 F2종자의 현미를 내어 유전분석을 위한 표현형을 조사하였다. 분상질과 정상형의 각각 35개, 115개로서 1:3으로 분리하였으며($\chi^2=0.222$, $p=0.637$), 1개의 열성유전자에 의해 지배됨을 확인하였다. 또한 설갱의 분상질 유전자 지도 작성 및 연관마커를 탐색을 위해 370개의 KASP마커 이용하여 모부분 다형성을 분석하였다. 다형성을 보인 153개 마커로 연관분석용 Frame map을 작성하였ek. 또한 열성형질인 분상질 식물체 12개체를 선발하여 recessive class analysis 방법으로 유전자형을 분석한 결과 3번 염색체의 단완에 KJ03_017(6.0Mb) ~ KJ03_029(12.0Mb)사이의 분자마커와 연관성이 높은 것을 확인하였다. BC1F2집단으로 분자마커와 표현형의 연관분석을 수행한 결과 3번 염색체 RM218(8.3Mb)와 KJ0329(12.3)사이 설갱벼의 분상질 유전자가 존재하는 것을 확인하였다. 또한 3번 염색체 10.1Mb에 위치한 Indel마커 RD03-25는 분상질 유전자와 조환가가 1.2%로 밀접히 연관되었음을 확인하였다. 이는 현재까지 알려진 분상질 유전자와 다른 새로운 위치에 존재하고 있어 이유전자를 *flO14(t)*로 명명하였다.

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Genetic analysis of *Purple pericarp (Prp)* and *Purple Leaf (Pl)* traits of rice

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Rice *Purple pericarp (Prp)* and the *Purple leaf (Pl^w)* traits were analyzed. Rice *Prp* trait is controlled complementary gene interaction of *Pb* and *Pp*. The *Pl^w* trait is resulted by the epistatic interaction of *Pl* gene with a complementary gene. Dominant *Pb* allele encodes OsB1 protein and expressed in seed specific mode for purple color determination in seed pericarp. The *Pl* gene is expressed OsB2 protein in purple leaf. Both OsB1 and OsB2 contain a helix-loop-helix (HLH) domain for transcription factors. However, it is still ambiguous that both genes are involved in expression of anthocyanins in both seed and/or leaf. We identified *Pl^w* trait was governed by a dominant *Pl* allele encoding a functional OsB2 protein molecule for purple leaf only. In molecular level, recessive alleles of these two traits were caused by frame-shift mutations. In phenotypes, we identified that purple color phenotypes in different tissues either seed pericarp or leaf were determined by the gene expression patterns of *Pb* and *Pl* genes. Differentiated gene expression of *Pb* and *Pl* were resulted in differential accumulation of anthocyanin in specific tissues. Because these two genes having very similar domain structures, it may be possible share the same complementary gene in genetics. Here we defined that the two genes are high homologous but different manners in tissue specific regulation resulting in purple seeds(*Prp*) was produced by *Pb* gene but purple leaf (*Pl*) was produced by *Pl* gene.

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Identification and application of genome-wide SNPs using genotyping by sequencing (GBS) of 119 *Panax ginseng* accessions

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Panax ginseng is a valuable medicinal plant, as containing various ginsenosides which have many benefits to human health. A lot of pharmacological studies for the herb have been carried out for a long time, however, genomic studies are fewer because of unusual slow growth and complex genome characteristics. To construct molecular breeding basis for ginseng, genetic researches using various genetic resources are demanded. We analyzed various 119 ginseng breeding lines using genotyping by sequencing (GBS) technique to elucidate genetic variations and develop useful markers. Through mapping to reference sequence, 173,138 SNPs were identified. Among them, high quality of 1,229 SNPs (0% missing data, 5 minimum depth) were used for analysis of population structure. As a result, the accessions were clustered into four populations. Also, phylogenetic analysis showed that 14 cultivars were evenly distributed in various groups. It indicated that ginseng breeding lines have abundant genetic diversity and these variations could be used as valuable information for further breeding researches. Consequently, we identified abundant genome-wide SNPs and elucidated population structure using the 119 ginseng accessions. These results will be used for genome wide association studies about diverse agricultural traits and for development of useful markers which applicable to other ginseng genetic resources for breeding. This work was carried out with the support of "Cooperative Research Program for Agriculture Science & Technology Development (PJ01311901)" Rural Development Administration, Republic of Korea.

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Genetic variation of Major Carotenoids and fruit characteristics of 250 tomato germplasm

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This study evaluated the content variation of major carotenoids in 250 tomato germplasm also with agricultural fruit characteristics to search for good quality breeding resources. One hundred and three accessions among 250 accessions using in this study are wild species including *Solanum pimpinellifolium*, *S. habrochaites*, *S. peruvianum*. The number of *Solanum lycopersicum* var. *lycopersicum* and *S. lycopersicum* var. *cerasiforme* are 101 and 46, respectively. Three individual carotenoids, lutein, lycopene, and β -carotene were quantified using fully matured tomato fruits at harvest using HPLC. The lutein content of 250 tomato germplasm showed a variation ranging from nt(not detected) to 9.3 mg/100g, DW. The lycopene contents were varied from 19.3 to 640.7 mg/100g, DW. The content of β -carotene was evaluated from 19.2 to 122.9 mg/100g, DW. The nine accessions including IT173895 could be selected as potential high-lycopene resources over 500 mg/100g, DW. IT173863 showed the highest soluble solid content with 14.0 ± 0.6 °Brix. These accessions could be used as potential breeding resources with respect to contents in sugar or functional chemicals, and further research is needed for the antioxidative and anticancer activities.

Keywords: carotenoid, tomato, HPLC, lycopene, β -carotene, lutein

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Search for clues to delaying tomato fruit ripening by sound wave through transcriptome analysis

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We previously reported that sound wave delays tomato fruit ripening by altering the expression of gene in ethylene biosynthesis. Here, we evaluated the molecular mechanism underlying this delaying fruit ripening by performing RNA-sequencing analysis of tomato fruits at 6 h, 2 days (d), 5 d and 7 d after 1 kHz sound vibration treatment. Bioinformatic analysis of differentially expressed genes and non-coding small RNAs revealed that some of these genes are involved in plant hormone and cell wall modification processes. Ethylene and cytokinin biosynthesis and signalling genes were downregulated by sound vibration treatment, whereas genes involved in flavonoid, phenylpropanoid and glucan biosynthesis were upregulated. Our results indicate that sound vibration helps delay fruit ripening through the sophisticated regulation of coding and non-coding RNAs and transcription factor genes. On the other hand, as the quality of life has improved, interest in secondary metabolites such as vitamin C, flavonoid and anthocyanin etc. We treated to alfalfa with various sound wave frequency, treatment time, and treatment period. Sound wave treated alfalfa sprouts had higher vitamin C content than non-treated sprout vegetables. To identify the mechanism of vitamin C content increase by sound wave, the expression pattern of vitamin C biosynthesis-related genes in sound-treated alfalfa sprouts was analyzed by qRT-PCR.

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Development of SNP array in single copy genes of *Brassica oleraceae* for MAB

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Brassica oleraceae is one of the 10 most cultivated crops in the world. According to report, in *Brassica oleraceae*, the competitiveness of Korean traditional breeding is world-class. With more advanced molecular breeding, Korea is expected to have global competitiveness in *Brassica oleraceae*. For development of SNP array, resequencing data of 44 accessions is mapped to reference genome. More than 3 million SNPs that is genotyped from more than 40 accessions are filtered. After filterings that are mean to enhance the accuracy of markers, 3446 SNPs that are from genic regions are filtered. Since paralogous sequences can interfere fluorescent signal, SNPs with flanking sequences that have paralogous sequences in other regions are filtered. From 849 SNPs in single copy genes, 240 markers that are distributed throughout the genome to represent genome, are designed. After SNP array experiments, 192 markers that have high accordance rate with resequencing data are selected and these markers are utilized to 92 samples from LG farmhannong. 150 markers that can be used in MAB are selected finally with criteria of No call rate and clustering form of data points. Phylogeny tree that is drawn with 150 markers shows group 1 and group 2 that are consisted with cabbage and other *Brassica oleracea* subspecies each, are classified well and match with phenotype data well. These result shows these markers are working well and can be utilized to facilitate breeding period instantly.

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채종원산 소나무의 소나무재선충병 감수성 변이

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서로 다른 환경 조건에서 자란 동일한 채종원산 소나무(*Pinus densiflora*) 가계들이 소나무재선충(*Bursaphelenchus xylophilus*)에 인공적으로 감염된 후 감수성 및 병진전에 어떤 차이를 보이는지 알아보려고 본 연구를 수행하였다. 국립산림과학원 산림생명자원연구부 온실(982본)과 경남산림환경연구원 포지(1,079본)에서 동일한 병원성 재선충 균주로 인공접종을 실시한 결과, 온실 접종묘 평균 감염률은 91.5%, 진주 포지 평균 감염률은 19.2%를 보여 큰 차이를 나타냈다. 특히 강원13은 온실 실험에서 전체 평균 감염률에 비해 17% 정도 낮은 감염률을 보여 다른 가계에 비해 내병성이 높은 가계로 확인되었으며 강원72는 감수성이 가장 높은 가계로 나타났다. 지역별로 감염성에 큰 차이를 보인 주요 원인으로는 나지묘 vs. 포트묘라는 차이점과 포지 vs. 온실이라는 묘목 생장 조건 차이에 따른 것으로 사료되며 특히 소나무재선충은 24~25°C에서 가장 번식이 왕성하므로 인공접종 후 온도 차가 가장 중요한 limiting factor 인 것으로 여겨진다. 두 지역에서 가계별 감수성을 비교해 보면 그 순위가 유사한 것으로 나타났는데 이는 소나무재선충에 대한 유전적 감수성이 환경 차에도 불구하고 확연히 나타남을 알 수 있다. 성숙목에 대해 인공접종을 실시하여 내병성을 보이는 개체를 선발하는 것이 가장 이상적이긴 하나 선발하기까지 걸리는 시간적 제약 등 여러 가지 문제로 인해 묘목 인공접종을 통해 소나무재선충병 내병성 품종 육성을 추진하게 되는데, 본 연구 결과로 비추어 묘목을 이용하더라도 나지묘와 포트묘, 온실과 포지 간 소나무재선충에 대한 감수성에 큰 차이가 있음을 전제로 수행되어야 할 것으로 본다.

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Deciphering the complex wheat gliadin proteins: basic study to application for development of allergen-reduced wheat

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Gliadin proteins are a major component of wheat flour and important determinants of bread making quality, but also present significant health problems for consumers with celiac disease or wheat allergies. In the present studies, we have attempted to explain the biochemical and molecular bases of these complex and unfavourable properties, and to develop strategies for their elimination. Firstly, to construct proteomic reference map, we extracted ethanol-soluble gliadin fractions from flour of the Korean bread wheat cultivar Keumkang. Proteins were separated by 2-dimensional gel electrophoresis (2-DGE) and individual spots were excised from gels, digested with chymotrypsin and subjected to tandem mass spectrometry (MS/MS). α -, γ - and ω -gliadins were identified as the predominant proteins in 31, 28 and one of 98 spots, respectively. Protein sequences were analyzed for specific epitopes related to celiac disease and food allergy. Secondly, to assign the individual gliadins to their chromosome encoded, we performed profiling of gliadins from Chinese Spring and its aneuploid lines missing chromosome 1 and 6 (and 6 short arms) using SDS-PAGE, A-PAGE, 2-DGE and MS/MS. In RP-HPLC, all peaks except one peak could be explained, but some bands (spots) could not be explained in SDS-PAGE, A-PAGE and 2-DGE. In particular, 11 out of 33 gliadin spots were not assigned in 2-DGE experiments. To confirm the identities of 11 unassigned spots, eleven individual spots were excised from 2-D gel, digested with chymotrypsin and subjected to MS/MS analysis. Unexpectedly, these spots were identified gamma and alpha gliadins of group 1 and 6 chromosome. The results may imply that certain regulatory mechanism may be involved in the regulation of gliadin protein expression. Thirdly, a new wheat mutant missing proteins encoded at *Glu-B3* and *Gli-B1* loci was discovered among double haploid lines obtained from a cross between the Korean wheat cultivars Keumkang and Olgeuru. Absence of the *Glu-B3* LMW-GSs, w-5 gliadins and some γ -gliadins was determined by SDS-PAGE, 2-DGE and MS/MS. The deletion of *Glu-B3* and *Gli-B1* loci was also demonstrated using structure gene specific and loci specific DNA markers. Basic agronomic traits, protein content, dough mixing properties and bread loaf volume of DH20 and parental wheat cultivars were evaluated in field-grown wheat over a two year period. This mutant will be useful as a valuable resource for breeding efforts to reduce allergenic potential. Finally, we have attempted a transformation strategy to apply it directly to Korean commercial wheat cultivar 'Keumkang', along with the breeding strategy by obtaining the DH20 double haploid mutant lines. So far not only there is no transformation research on the Korean commercial wheat cultivar 'Keumkang', but also studies of systematic transformation method in 'Keumkang' have rarely been progressed. Although the transformation efficiency is as low as ~1%, we succeeded to establish transgenic wheat. Our study contributes to a better understanding of how the heterogeneity of gliadins among wheat cultivars influences the immunogenic potential of the flour and also provides us with a valuable information to find and/or produce hypoallergenic wheat lines with reduced levels of harmful gliadin proteins using either breeding or biotechnology approaches.

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A novel RING type E3 ligase, CaASRF1, positively regulates drought tolerance via modulation of CaAIBZ1 stability in *Capsicum annuum*

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Plants have evolved complex defense mechanisms to adapt and survive under adverse growth conditions. Abscisic acid (ABA) is a phytohormone that plays a pivotal role in the stress response, especially regulation of the stomatal aperture in response to drought stress. Here, we identified the pepper *CaASRF1* (*Capsicum annuum* ABA Sensitive RING Finger E3 ligase 1) gene, which regulates drought stress tolerance via ABA-mediated signaling. We found that CaASRF1 contains a C3H2C3 type RING finger domain, which functions as an E3 ligase by attaching ubiquitins to the substrate target proteins. *CaASRF1* expression was enhanced after exposure to ABA, drought, and NaCl. Loss-of-function in pepper plants and gain-of-function in Arabidopsis plants revealed that CaASRF1 positively regulates ABA signaling and the drought stress response. Moreover, CaASRF1 interacted with and was associated with degradation of the pepper bZIP transcription factor CaAIBZ1 (*Capsicum annuum* ASRF1-Interacting bZIP transcription factor 1). Contrary to CaASRF1 phenotypes, *CaAIBZ1*-silenced pepper plants and *CaAIBZ1*-overexpressing Arabidopsis plants exhibited drought-tolerant and drought-sensitive phenotypes, respectively. Taken together, our data indicate that CaASRF1 positively regulates ABA signaling and the drought stress response via modulation of CaAIBZ1 stability.

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Late embryogenesis abundant protein, CaLEA5, positively regulates the drought tolerance and ABA signaling in *Capsicum annuum*

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Plants are sessile organisms; hence they constantly respond to environmental stress for their growth and development. The regulation of transpiration via stomata plays crucial roles in plant adaptation to environmental stresses, particularly drought stress. Lots of enzyme encoding genes involved in regulation of transpiration via modulating stomatal opening/closure. Here, we demonstrate that CaLEA5, encoding a late embryogenesis abundant protein, is critical regulator of transpirational water loss in pepper (*Capsicum annuum*). The expression level of *CaLEA5* in pepper leaves was up-regulated after exposure to abscisic acid (ABA) and drought. The phenotype analysis showed that *CaLEA5*-silenced pepper and *CaLEA5*-OX plants exhibited reduced and enhanced drought tolerance, respectively, accompanied by an altered transpiration rate. Furthermore, the ABA sensitivity were significantly reduced in *CaLEA5*-silenced pepper, but increased in *CaLEA5*-OX plants compared with control plants, which resulted in opposite response to drought stress. Taken together, our data indicate that CaLEA5 positively regulates the ABA signaling and drought stress tolerance.

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A DEAD-box RNA helicase, RH8, is critical for regulation of ABA signaling and the drought stress response via inhibition of PP2CA activity

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Abscisic acid (ABA) is major plant hormone involved in regulating abiotic stress responses. Several studies have established that an ABA-signaling transduction pathway—from ABA perception to response—functions in plant cells. The group A PP2Cs constitute core components of ABA signaling, and they negatively regulate ABA signaling and stress responses. Recent studies have identified and functionally analyzed regulators of PP2C activity; however, the precise regulatory mechanisms remain unclear. In the present study, we used a yeast two-hybrid (Y2H) screening analysis to identify the DEAD-box RNA helicase RH8, which interacted with PP2CA in the nucleus. *rh8* knockout mutants exhibited ABA hyposensitivity and drought-susceptible phenotypes characterized by high levels of transpirational water loss via reduced stomatal closure and decreased leaf temperatures. However, *rh8/pp2ca* double mutants showed ABA hypersensitivity and drought-tolerant phenotypes, indicating that RH8 and PP2CA function in the same ABA-signaling pathway in the drought stress response; moreover, RH8 functions upstream of PP2CA. In vitro phosphatase and kinase assays revealed that RH8 inhibits PP2CA phosphatase activity. Our data indicate that RH8 and its interacting partner PP2CA modulate the drought stress response via ABA-dependent signaling.

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Transcriptome analysis of dwarf soybean suggests the association of carbon metabolism with dwarf phenotype

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Soybean growth is one of the most important traits for high yield breeding development. We selected normal and dwarf phenotype soybeans, which are F4 recombinant inbred lines from a cross between *G. max* (Peking, female) and soybean *G. soja* (male), and compared the gene expression associated with growth type. Whole transcriptome sequence was generated by Illumina HiSeq2500 sequencing platform. A total of more than thousand genes were identified to be highly differentially expressed between normal and dwarf mutant lines. The dwarf phenotype showed less expression of photosynthesis- and protein biosynthesis-related genes than normal phenotype. Interestingly, plastid-related genes are rarely expressed in the dwarf phenotype. Given that chloroplast, one kind of plastids, performs photosynthesis in plants, the dwarf phenotype seems to have low photosynthetic efficiency. Moreover, most of photosynthesis related genes such as thylakoid reaction and Calvin-Benson cycle were less expressed in dwarf phenotype than normal phenotype. Sucrose and other metabolites produced by the photosynthesis process have been found to interact with hormones to regulate and integrate many plant metabolic processes. We expect that these candidate genes will be useful for subsequent studies on plant growth.

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HCRs, anti-crossover proteins restrict crossover number in *Arabidopsis*

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Meiotic crossover recombination affects genetic diversity in population and is a critical tool for breeding. During meiosis, meiotic DSBs are repaired to reciprocal crossovers through class I and class II pathways. Anti-crossover factors such as FANCM, RECQ4 and FIGL1 were known to restrict crossovers in class II pathway dependent manner. However, the mechanism underlining how crossover number is limited to one to three along chromosome remains unexplored. We performed a high throughput genetic screening of *higher crossover rate (hcr)* mutants by using fluorescent seed-based system, enabling the measurement of crossover frequency in individual plants. We found that *hcr* mutants (*hcr1*, *hcr2*, *hcr3*) were new anti-crossover mutants by genetic analysis and deep-sequencing. We present characterization of *hcr2* and *hcr3* mutants, including mapping of them and their effects on crossover frequency in defined intervals along chromosomes.

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Characterizing substrate specificity of guanosine deaminase from *Arabidopsis thaliana*

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Nitrogen is an essential element for growth and reproduction of plant. In the past decade, it has been characterized in plants and many microbes that purine, a nitrogen-rich compound, is subject to enzyme-dependent degradation and the resulting products are ammonia and/or urea. In brief, the ureide pathway in plants is capable of utilizing urate, an early product from purine degradation, as substrate and undergoes sequential enzyme reactions to produce ammonia, glyoxylate, and/or urea. This ureide pathway has been suggested as one of the possible metabolic pathway for recycling nitrogen in plants. Unlike the downstream of purine catabolism by ureide pathway, the early biological events for purine degradation have been studied recently. In *Arabidopsis thaliana*, among those early events in purine degradation, guanosine deaminase (GSDA), a plant-specific enzyme, was characterized to be responsible for converting guanosine into xanthosine. Product xanthosine is then catalyzed into xanthine for further conversion into urate, a substrate for the ureide pathway. Presence of plant specific GSDA is very unique, because in most organisms guanine serves as a substrate of guanine deaminase (GDA) to produce xanthine. In order to understand substrate specificity of GSDA from *Arabidopsis thaliana* (AtGSDA) and its mechanistic features, we are undergoing structural studies of AtGSDA. In particular, AtGSDA is related in sequences to GDA but differs in its function. Specifically, they contain catalytic residues common for the cytidine/deoxycytidylate deaminase superfamily but their substrate specificities are unclear. Our analyses will provide structural basis for substrate specificity of AtGSDA and characterize enzyme mechanism in the early events of purine degradation in plants. This work was supported by Next Generation BioGreen 21 program of Rural Development Administration (Plant Molecular Breeding Center) of Republic of KOREA.

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A study of allelic diversity underlying flowering-time adaptation in soybean cultivars using a variation block analysis

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Flowering time adaptation is a major breeding goal in soybean (*Glycine max* L.), yet they remain untapped due to the genetic linkage between the few useful alleles and hundreds of undesirable alleles. To investigate the genetic architecture of flowering time, a variation block analysis of flowering time was conducted with a diversity panel comprising 96 soybean cultivars and inbred lines grown in three agroecological conditions. In total, 7,087 variation blocks (VB) were mined by analyzing whole genome sequencing data of 96 soybean genotypes. Phenotypic associations with flowering time and seed yield were calculated in the panel over the year 2016-2017. We identified 290 VB's associating with the onset of flowering among all soybean cultivars. Three clusters were inferred by STRUCTURE analysis, which is in good agreement with a neighbor-joining tree. In addition, soybean orthologs for a number of candidate genes for adaptation were detected, including soybean maturity locus *E1*. Further, backcross recombinant inbred lines (BC₂F₃, 'Hwangkeum' X 'Daepoong') exhibited significant variations in their onset of flowering, with a range of 18-20 days due to obvious difference in *E1* locus. Hence, VB analysis of candidate regions suggested that, selection of genes involved not only in flowering time but also in other trait may have high impact on diverse soybean cultivars. Furthermore, our study provides a valuable framework to improve the genetic resources of crop plants under changing environments.

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Role of chloroplast dynamics in plant innate immunity

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Chloroplasts play an essential role in producing immune signals in plant cells upon pathogen's attack beside their major role of using sunlight to provide energy for plant growth and development. Chloroplasts dynamically change their characteristics, proliferation, and positions in cells. Remarkable change of their morphology is to produce thin tubular structures, stromules, in cells faced to the various stress conditions. However, molecular function of stromules and the regulatory mechanism of stromule production remain elusive. Recently, we observed that active repositioning of the chloroplast close to nucleus occurs in the cells undergoing immune responses to bacterial and viral pathogens. Interestingly, numerous stromules were observed to extend toward the nucleus and attach their tips to the nucleus in the infected cells. Further study revealed that dynamic stromule induction is a part of plant immune responses and cytoskeletons in the infected cells might regulate the rapid changes in stromule length and position. In summary, we propose that stromule might provide a path to transfer signaling molecules from chloroplast to the nucleus as well as a driving force to translocate chloroplast body close to nuclei during plant innate immunity.

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Plant pathogen effectors suppresses reactive oxygen species signaling networks in plants

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Microbial pathogens have evolved protein effectors to promote virulence and cause disease in host plants. Pathogen effectors delivered into plant cells suppress plant immune responses and modulate host metabolism to support the infection processes of pathogens. Reactive oxygen species (ROS) act as cellular signaling molecules to trigger plant immune responses, such as pathogen-associated molecular pattern (PAMP)-triggered immunity (PTI) and effector-triggered immunity. In this review, we discuss recent insights into the molecular functions of pathogen effectors that target multiple steps in the ROS signaling pathway in plants. The perception of PAMPs by pattern recognition receptors leads to the rapid and strong production of ROS through activation of NADPH oxidase Respiratory Burst Oxidase Homologs (RBOHs) as well as peroxidases. Specific pathogen effectors directly or indirectly interact with plant nucleotide-binding leucine-rich repeat receptors to induce ROS production and the hypersensitive response in plant cells. By contrast, virulent pathogens possess effectors capable of suppressing plant ROS bursts in different ways during infection. PAMP-triggered ROS bursts are suppressed by pathogen effectors that target mitogen-activated protein kinase cascades. Moreover, pathogen effectors target vesicle trafficking or metabolic priming, leading to the suppression of ROS production. Secreted pathogen effectors block the metabolic coenzyme NADP-malic enzyme, inhibiting the transfer of electrons to the NADPH oxidases (RBOHs) responsible for ROS generation. Collectively, pathogen effectors may have evolved to converge on a common host protein network to suppress the common plant immune system, including the ROS burst and cell death response in plants.

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Potyviral CP-interacting proteins facilitate potato virus X infectivity by interacting with viral protein and RNAs.

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Host proteins of *Nicotiana benthamiana* interacting with potato virus X (PVX) RNA stem-loop 1 (SL1) structure were identified by northwestern blot in previous study. Based upon previous results and *N. benthamiana* genome sequences draft, we identified two proteins, Potyviral CP-interacting protein 2a (NbcPIP2a) and Potyviral CP-interacting protein 2b (NbcPIP2b) that contains five amino acid differences. Electrophoretic mobility shift assay (EMSA) showed the interaction between PVX structures and two NbcPIPs. We observed that NbcPIPs bind to PVX SL1(+), SL1(-), and 3' SL. Especially, NbcPIP2a strongly interacted with PVX 3' SL structure than SL1(+) and SL1(-). Bimolecular Fluorescence Complementation (BiFC) was investigated to determine protein-protein interaction between two proteins and PVX viral proteins. By BiFC, we confirmed that NbcPIPs bind to only PVX coat protein (CP) in planta. Transient over-expression of NbcPIP2a and NbcPIP2b in *N. benthamiana* increased accumulation of GFP expressing PVX in local area. In protoplast experiment, PVX replication was also increased by transient overexpressed NbcPIP2a. Overexpression of NbcPIP2a positively affected systemic movement of PVX in *N. benthamiana*, whereas NbcPIP2b overexpression did not affect systemic movement of PVX. RNAi-mediated silencing experiment showed that PVX replication was hampered in NbcPIPs-silenced protoplast. These results suggest that PVX exploits a host protein NbcPIP2a than NbcPIP2b for local replication and systemic movement by interacting with SL cis-elements in PVX RNA and CP subunit.

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Homeobox transcription factor OsZHD2 promotes lateral root growth in rice by inducing ethylene and auxin biosynthesis

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Lateral roots are the most important component of the root system. Their functions include the acquisition of water and nutrient elements, anchorage of the plant, and biosynthesis of hormones. Although auxin plays a major role in their development and growth, the regulatory elements for its biosynthesis in lateral roots have not been well elucidated. Using rice, we identified an activation tagging line of a zinc-finger homeobox gene, *ZHD2*, which has longer-than-normal lateral roots. Because *ZHD2* did not alter the density of lateral roots, it appears to function mainly in their emergence and elongation. When compared with the wild type (WT), the overexpressing plants absorbed nitrogen at a higher rate and grew better under a nitrogen deficiency. Knockout mutations of *ZHD2* did not show any visible phenotypic alterations. However, double mutations of *ZHD2* and *ZHD1* reduced lateral root growth. To investigate how *ZHD2* induces lateral root development, we performed transcriptome analyses of roots from activation tagging line *ZHD2-D* and the WT when sampled at the initiation stage. Genes for ethylene biosynthesis were up-regulated in *ZHD2-D* and those plants also had higher levels of ethylene than in the WT. Results from our ChIP assay suggested that *ZHD2* interacts with the chromatin of *SAM2* and *ACS5*. This implies that ethylene biosynthesis genes are controlled by *ZHD2*. We also generated transgenic rice plants expressing *DR5::GUS* in the WT and *ZHD2-D*. Histochemical staining indicated that expression of the *DR5* reporter was greater in *ZHD2-D* than in the WT, especially at the root tip. This demonstrated that *ZHD2* also affects auxin biosynthesis. These observations show that *ZHD2* enhances lateral root development by influencing the biosynthesis of both ethylene and auxin.

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Regulation of chloroplast development by alternative splicing

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Plastid-encoded RNA polymerase (PEP) plays an essential role in chloroplast biogenesis by regulating the transcription of chloroplast genes. Recent findings show that the PEP interacts with PEP-associated proteins to form PEP complex, and the formation of PEP-complex is key to controlling the activity of PEP to regulate expression of chloroplast genes and chloroplast development. *FSD3* encoding iron superoxide dismutase is a PEP-associated protein. We found that *FSD3* gene produces *FSD3*, a original form of *FSD3*, and *FSD3S*, a splicing variant of *FSD3* by alternative splicing. Transcript level of *FSD3* was higher than that of *FSD3S* in young leaves carrying well-developed chloroplasts, but lower in old leaves carrying senescent chloroplasts, gerontoplasts. Additionally, the enrichment of *FSD3* and *FSD3S* transcripts was differently regulated in response to light, a key environmental factor governing chloroplast development. The transcript level of *FSD3* increased in response to light, while the transcript level of *FSD3S* increased in response to darkness. The *FSD3* and *FSD3S* transcripts encode proteins with identical N-termini, but different C-termini, and we found that the C-terminus of *FSD3S* exhibited higher hydrophobicity than that of *FSD3*. Further bioinformatics analysis revealed that the higher hydrophobicity of *FSD3S* is caused by a transmembrane domain, which is highly conserved in the TM domain proteins of plants. These findings suggest that *FSD3S* is a transmembrane proteins unlike *FSD3*, and its function in chloroplast development might be different from that of *FSD3*.

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식물분자육종사업단 연구개발 성과물의 실용화 추진 연구

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전통유전육종 기술과 첨단 식물분자육종 기술을 융합하여 고품질, 다수성 기후변화 대응 신품종 작물개발 연구를 수행하는 차세대바이오 그린21사업 식물분자육종사업단은 안정적인 식량자원 확보를 통한 국가 안보 강화를 이루고, 국내 농생명바이오산업 분야의 활성화를 위한 우수 연구개발 성과 활용 방안을 모색하고 있다. 본 연구에서는 1-2단계(2011-2017년) 수행과제로부터 도출된 총 260건의 산업재산권과 86건의 농업형질 개선 효과가 있는 신품종 작물 품종보호출원 성과들을 종합 분석하여, 성과확산 및 실용화 추진대상으로 유망 산업재산권 52건과 슈퍼홍미, 고프라보노이드 벼 등 우수 신품종을 1차 선발하였다. SMART3특허등급평가는 국내등록 유지 특허를 대상으로 권리성, 기술성, 활용성 부분을 평가하여 대량 산업재산권 성과물에서 핵심특허를 선발하는 방법으로 널리 활용되고 있다. 분석일 현재 기준 국내 등록 특허로 유지되고 있는 사업단 도출 특허 172건은 기술분류체계에 따라 분자육종소재 개발연구 기술 109건, 형질도입/조직배양기술 26건, 검출/진단 기술 23건이었고, 기능성물질생산 시스템, 기능성 소재 응용기술, 그리고 기타 기술은 각각 1, 9건, 4건으로 분류되어, 식물분자육종사업단의 최종 연구목표에 맞는 연구개발 성과물이 도출되었음을 알 수 있었다. 172건 중 SMART3 총점 BBB등급이상의 특허는 52건으로, 분자육종소재 개발연구 기술 36건, 그 외 기술은 총 16건이었고, 전반적으로 권리성은 높으나, 활용성이 낮은 기술이 다수인 탓에 총점등급이 하향되었음을 알 수 있었다. 특히, 기후변화대응 생물학적/비생물학적 스트레스 저항성 분자육종 소재 개발 기술과 분자표지 기반 품종구별 및 병저항성 품종 선발 등 다양한 정밀분자육종 기술이 BBB등급이상의 우수기술로 다수 포함되어 있었다. 따라서, 해당 분야의 최신 기술동향 및 시장동향 조사를 통한 타겟 시장 분석과 성과확산을 위한 수요기업을 발굴하고, 수요기술과 유사 관련 우수기술들의 패키징 및 맞춤형 기술홍보자료를 제작 및 기술마케팅을 통한 성과확산을 진행할 예정이며, 연구자-사업단-수요기업간 네트워크 형성에 기반한 실용화 추진체계 구축은 개별기술의 기술이전시 발생하던 규모적 한계와 절차적 한계를 극복할 수 있을 것이다.

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Effector-assisted breeding methodology for bacterial wilt resistance in pepper

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Ralstonia solanacearum (*Rso*) is a causal agent of bacterial wilt disease in Solanaceae crops and especially for pepper, which is second most important vegetable crop in Korea but no efficient genetic control has been identified. For tracking new genetic source of resistance in pepper, screening phenotypes of segregation by infection assay is used, however, *Rso* infection assay has limitations due to influence of the environment on disease development, host genome complexity and the genetic diversity inherent to *Rso* strains. To supplement the limitations, we develop a powerful methodology termed effector-assisted breeding to improve disease resistance in pepper against *Rso*. This approach relies on scoring the specific recognition of an avirulent effector by the matching resistance (*R*) gene which trigger hypersensitive response (HR), a form of programmed cell death that can be easily observed on pepper leaf. To establish single effector delivery system into pepper leaves, we conducted preliminary experiment using AvrBsT, a well-known avirulent effector from *Xanthomonas euvesicatoria*. We assayed two delivery systems, *Agrobacterium tumefaciens*-mediated transient transformation and non-pathogenic *Pseudomonas fluorescens*, (Pf0-1) which carry a functional type III secretion system (T3SS) in a commercial cultivar of pepper. As a result, the recognition of AvrBsT transferred by both single-effector delivery systems induced HR in commercial pepper leaves. Using this delivery system, we plan to identify avirulent *Rso* effectors and use them to screen the presence of matching *R* gene in recombinant inbred pepper lines. This approach will simplify and speed up the fine mapping of resistance loci, and the development of molecular markers tightly linked to bacterial wilt disease resistance in pepper.

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Identification of MRFs as an unusual type of translation regulators that are involved in plant mRNA translation under low energy conditions

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Control of global translation activity is critical for cellular adaptation to fluctuating growth conditions and environmental stimuli, especially photosynthetic produced sugar level in plants. Therefore, photo-autotrophic plants adjust a valance of translation efficiency with cellular sugar availability through massive transcriptional modulation and phosphorylation of the translation machinery by Target of Rapamycin signaling. Here, we report that *Arabidopsis thaliana* MRF (MA3 DOMAIN-CONTAINING TRANSLATION REGULATORY FACTOR) family genes encode translation regulatory factors under TOR control, and their functions are particularly important in energy-deficient conditions. Four MRF family genes (MRF1 – MRF4) are transcriptionally induced by dark and starvation (DS). Silencing of multiple MRFs increases susceptibility to DS and treatment with a TOR inhibitor, while MRF1 overexpression decreases susceptibility. MRF proteins interact with eIF4A and co-fractionate with ribosomes. MRF silencing decreases translation activity, while MRF1 overexpression increases it, accompanied by altered ribosome patterns, particularly in DS. Furthermore, MRF deficiency in DS causes altered distribution of mRNAs in sucrose gradient fractions, and accelerates rRNA degradation. MRF expression, and MRF1 ribosome association and phosphorylation are modulated by cellular energy status and TOR activity.

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Functional characterization of chloroplast-targeted RbgA GTPase in higher plants

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Ribosome Biogenesis GTPase A (RbgA) homologs are evolutionarily conserved GTPases that are widely distributed in both prokaryotes and eukaryotes. In this study, we investigated functions of chloroplast-targeted RbgA. *Nicotiana benthamiana* RbgA (NbRbgA) and *Arabidopsis thaliana* RbgA (AtRbgA) contained a conserved GTP-binding domain and a plant-specific C-terminal domain. NbRbgA and AtRbgA were mainly localized in chloroplasts, and possessed GTPase activity. Since *Arabidopsis rbgA* null mutants exhibited an embryonic lethal phenotype, virus-induced gene silencing (VIGS) of *NbRbgA* was performed in *N. benthamiana*. *NbRbgA* VIGS resulted in a leaf-yellowing phenotype caused by disrupted chloroplast development. NbRbgA was mainly co-fractionated with 50S/70S ribosomes and interacted with the chloroplast ribosomal proteins cpRPL6 and cpRPL35. NbRbgA deficiency lowered the levels of mature 23S and 16S rRNAs in chloroplasts and caused processing defects. Sucrose density gradient sedimentation revealed that NbRbgA-deficient chloroplasts contained reduced levels of mature 23S and 16S rRNAs and diverse plastid-encoded mRNAs in the polysomal fractions, suggesting decreased protein translation activity in the chloroplasts. Interestingly, NbRbgA protein was highly unstable under high light stress, suggesting its possible involvement in the control of chloroplast ribosome biogenesis under environmental stresses. Collectively, these results suggest a role for RbgA GTPase in chloroplast rRNA processing/ribosome biogenesis, affecting chloroplast protein translation in higher plants.

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Interspecific comparison of *Angelica* species using chloroplast indel markers developed from *Angelica gigas* Naki.

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Angelica species is a representative medicinal plants and it has been used in traditional herbal therapies. The *Angelica* species used in herbal medicine varies by country according to specific regulations, i.e. *A. gigas* Nakai in Korea, *A. sinensis* Diels in China, and *A. acutiloba* Kitagawa in Japan. Because of the similarity between the names, "Danggui", they can be confused in the traditional medicine markets. In this study, twenty-four chloroplast insertion or deletion (CPInDel) markers were developed for the classification of *Angelica* species using chloroplast DNA sequences of *A. gigas*. Primer sets were designed from flanking sequences of the discovered InDel loci using CLC Main Workbench (version 6.8.4) with the following parameters: primer length = 18~26 bp (Opt. 23 bp); GC% = 50~70% (Opt. 60%); Ta = 55~62°C (Opt. 58°C); product size range = 120~300 bp. Polymorphism and genotype analysis of thirteen *Angelica* species were performed using the CPInDel markers. The 24 CPInDel markers developed in this study could be used for genetic diversity analysis and classification of *Angelica* species.

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Functional properties of an alternative, tissue-specific promoter for rice NADPH-dependent dihydroflavonol reductase

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A deletion analysis of the *Oryza sativa* dihydroflavonol reductase (DFR) promoter defined a 25 bp region (-386 to -362) sufficient to confer pericarp-specific expression of a β -glucuronidase (GUS) reporter gene in transgenic rice. Site-specific mutagenesis of these conserved sequences and subsequent expression analysis in calli which transiently expressed the mutated promoter::GUS gene showed that both bHLH (-386 to -381) and Myb (-368 to -362) binding sites in the DEL3 (-440 to 70) promoter were necessary for complete expression of the GUS gene including the tissue-specific expression of DFR::GUS gene. The GUS gene was expressed well in the mutated Myb (-368 to -362) binding site, but not as strong as in normal condition, implying that the Myb is also necessary to express GUS gene fully. Also, we found the non-epistatic relation between Rc and DFR. There were no changes of expression patterns GUS under the Rc and rc genotypes. Thus, DFR expression might be independent of the presence of functional Rc gene and suggested that Rc and Rd (DFR) share the same pathway controlling the regulation of flavonoid synthesis but not a direct positive transcriptional regulator of DFR gene.

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Brassinosteroids-controlled local auxin homeostasis is essential for xylem differentiation and wood formation in tomato

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Brassinosteroids (BR) are plant steroid hormones playing crucial roles in diverse growth and developmental processes in plant life cycles. The canonical BR signaling and its crosstalks with other signaling pathways are involved in pleiotropic regulation of plant growth and development. However, their biological roles in one of the most important crops, tomato (*Solanum lycopersicum*), are largely unknown. Here, we performed comparative physiological and in-silico analysis between cultivated wild-type tomato, BGA and a BR biosynthetic mutant, micro-tom (MT). As previously reported, the BR-deficient MT tomato displayed stunt growth phenotypes and we further revealed abnormal xylem development in tomato stem tissues. These BR-defective phenotypes were completely recovered by either exogenous epi-BL treatments or complementation of BR biosynthetic and signaling components. Conversely, impaired BR signaling pathways in tomato by overexpressing *SI*GSK3s or knocking-out *SIBR11* with a CRISPR-Cas9 genome editing system were resulted in more severe defects in the xylem developments. Using RNA-seq and bioinformatic analysis of a BR defected MT tomato plant, we confirmed the correlation between BR signaling pathways and diverse development or stress related gene networks. Furthermore, we successfully selected and analyzed a putative novel direct target gene for the BR-mediated xylem development. The molecular functional studies of the novel target gene showed that BR directly modulate auxin homeostasis during the xylem formation. In this study, we reveal BR-mediated novel molecular networks for plant vascular developments and signaling integration with auxin in the important crop tomato plant.

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Transcriptome analysis and development of EST-SSR markers from *Codonopsis lanceolata*

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Codonopsis lanceolata has been used for a long time in the private sector since its efficacy and safety had been proven in East Asian countries including Korea, China, and Japan. In Korea, most of them are cultivated in mountain farms and they are prescribed as therapeutic characteristics in oriental medicine. However, the cultivation remains only at the farm level, and the basic genetic studies are inferior to the element and efficacy studies. Although *C. lanceolata* is also a high-efficiency crop, but standard cultivar was not developed yet. Therefore it needs to establish an early screening system for genetic resources that can be used for breeding. In this study, we developed SSR (Simple Sequence Repeat) markers based EST (Expressed Sequence Tag) by analyzing the transcriptomes of *C. lanceolata* and hope the markers could be used for the breeding and trait-related genes discovery from *C. lanceolata* in the futures.

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Identification of a novel seed specific glycine rich protein Dor1, which regulates seed dormancy in rice

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Seed dormancy is an important agronomic trait affected by complex genetic and environmental interactions not yet comprehensively understood. By screening of rice mutants generated by a Ds transposable element, we identified a viviparous mutant *dor1*. Caryopses of the *dor1* mutant display opaque endosperm with abnormal morphology of aleurone layers, and germinate faster at developing stages as well as in mature state. A single insertion of Ds element was found at the second exon of a novel gene *Dor1*. The viviparous and opaque phenotype of *dor1* mutant caryopses was complemented by reintroduction of the *Dor1* gene. Ectopic expression of the *Dor1* gene in transgenic rice and Arabidopsis enhanced seed dormancy. Dor1 preferentially expressed in the seed embryo and aleurone cells and showed no homology with known proteins except a short glycine-rich domain. We determined that Dor1 protein is capable to bind to the GA receptor protein GID1 and other hormone sensitive lipase. The *dor1* mutant featured a hypersensitive GA-response of α -amylase gene expression during seed germination. The combined results suggested that Dor1 protein is a putative negative player of GA signaling operated in the maintenance of seed dormancy. Supported by grants (PJ01321801 and PJ01247601) from RDA.

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Systemic network analysis to gain candidate genes regulating seed storage proteins in rice

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The accumulation of transcriptomic data from diverse stress conditions, development stages, organs and cultivars and gene co-expression network analysis can provides precise information for identifying the function of novel genes. Up to now, we have gathered 210 transcriptome datasets resulted from Agilent rice 44K DNA chip in NCBI GEO and our research team. Systemic network analysis among oxylipin-related genes including *lipoxygenase (LOX)*, *allene oxide synthase (AOS)*, *hydroperoxide lyase (HPL)*, *allene oxide cyclase (AOC)* and *12-oxo phytodienoic acid reductase (OPR)* provided candidate genes participating a novel oxylipin pathway. Indeed, the characteristic analysis of protein encoded by the candidate gene showed that the gene participate in the new oxylipin pathway (9-lipoxygenase pathway), indicating that the network analysis of gene to gene using transcriptome could be a powerful approach to mine novel genes regulating rice seed storage proteins such as prolamin, glutelin and globulin. For the network analysis, Pearson correlation analysis was performed between genes encoding prolamin, glutelin and globulin and all genes (43494) on rice DNA chip. We selected genes with high correlation coefficient value, annotated their functions, and then found genes involved in rice seed storage proteins.

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Post-translational modifications of E3 SUMO ligase AtSIZ1 are specifically regulated by heat and drought stresses

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Sumoylation regulates numerous cellular functions including the localization, level and stability of various proteins in plants as well as animal systems. However, the regulatory mechanisms controlling E3 SUMO ligase are poorly understood. Here, sumoylation and ubiquitination of the Arabidopsis E3 SUMO ligase AtSIZ1 was specifically regulated by abiotic stresses. AtSIZ1 ubiquitination was induced by exposure to heat stress in transgenic plants overexpressing the E3 ubiquitin ligase COP1. In addition, AtSIZ1 ubiquitination was strongly enhanced in transgenic plants overexpressing SUMO isopeptidase ESD4 under heat stress. By contrast, drought stress induced sumoylation rather than ubiquitination of AtSIZ1 and sumoylated forms of AtSIZ1 accumulated in *esd4* and *cop1-4* mutants. Moreover, *siz1* mutants were found to be tolerant to heat and drought stresses. Our data indicate that ubiquitination and sumoylation of AtSIZ1 in response to abiotic stresses depend on the activities of COP1 and ESD4, and that the activity and stability of AtSIZ1 can be specifically controlled by different abiotic stresses.

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고추 앞에서 AGI(a-glucosidase inhibitor) 활성 분석 방법 개선

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당뇨병은 전 세계적으로 심각한 문제가 되는 질병 중의 하나이며 그 환자수가 매년 급격히 증가하고 있다. 당뇨병은 인슐린의 분비량이 부족하거나 정상적인 기능이 이루어지지 않는 대사질환의 일종으로 혈중 포도당의 농도가 높아지는 고혈당을 특징으로 하며 이 때 심각한 합병증을 유발한다. 알파-글루코시데이스(α -glucosidase)는 이당류를 단당류로 분해하여 소장에서의 탄수화물 흡수를 촉진시키는 효소이다. AGI(α -glucosidase inhibitor)는 이 분해 효소의 활성을 억제하여 탄수화물의 흡수 속도를 지연시켜 체내의 혈당을 낮춰주는 기능을 한다. 현재 의료용으로 사용되는 경구 혈당 강하제는 미생물로부터 추출한 것들이며 소화기 장애와 같은 부작용을 초래하기도 한다. 때문에 경구 혈당 강하제를 대체할 천연물질을 찾고자 많은 선행연구들이 진행되었다. 그 중 고추에서 AGI 함량이 높다는 보고가 있었으며 고추의 과실보다 잎에서 더 높은 활성을 보인다는 결과가 있었다. 이러한 결과를 바탕으로 AGI 고활성 잎전용 고추 품종을 육성하고자 하며 이를 위해 고추 잎에서 AGI 활성 분석 방법의 확립이 필요하다. 기존에 알려진 AGI 활성 분석 방법을 따라, 추출용매로 에탄올을 사용하면 잎의 엽록소도 같이 추출되어 AGI 활성을 측정하는데 문제가 되었다. 이러한 문제를 해결하기 위해 첨가된 α -glucosidase 및 기질(pNPG) 용량을 변화시켜 실험을 수행하였고, 또한 추출되는 엽록소를 줄이기 위해 에탄올 대신에 물로 추출하는 실험도 수행하였다. 고추 과실에서 추출 용매로 물과 에탄올을 사용하였을 때 AGI 활성 정도가 비슷하였지만, 고추 잎에서는 두 추출 용매를 사용하였을 때 AGI 활성에 차이를 보였다. 또한 에탄올에서 추출된 엽록소의 흡광도 값을 낮추기 위하여 마지막 단계에 sodium carbonate로 희석되는 양을 다양하게 하여 분석하여 보았다. 희석되는 양을 두 배로 늘린 결과 엽록소의 흡광도 값이 약 1/6로 감소하였다. 개선된 분석 방법을 사용하면 에탄올에 의해 추출되는 엽록소에 크게 영향을 받지 않고 AGI 활성을 분석할 수 있었다.

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Investigation of bacterial wilt pathogen effector diversity and interactions with host plants

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Ralstonia solanacearum(Rso), the causal agent of bacterial wilt disease, is one of the most devastating phytopathogens. With a surprisingly broad host range, it threatens more than 200 plant species, including major crops such as potatoes, tomatoes, peppers, etc. It is so genetically heterogeneous in nature that it is difficult to develop disease resistance against it. Rso translocate special molecules (known as effectors) into their plant host cells in order to effectively suppress plant immunity. One of the most important objectives for plant breeding is to confer disease resistance. These days, effectors are used as an uprising tool to breed disease resistance, referred to as effector-assisted molecular breeding. We aim to comparatively analyze Rso genomes and investigate their effector diversity and its interactions with host plants. We sequenced 30 Rso strains, which were isolated from different host plants in different geographic regions of South Korea. We applied comparative genomics approach to investigate the phylogenetic structure of this strain set and currently we report that, surprisingly, these strains show high level of genetic diversification and significant phylogenetic distances even in a single phylotype. We also screened wild-type potato plants and their relatives against the Rso Korean strains and identified avirulence gene candidates based on the comparative genomic analysis. The gene candidate constructs would be cloned or synthesized to be tested whether they can induce plant disease resistance. We hope it contribute to the development of effector-assisted disease resistant potato breeding system so expect it to accelerate breeding for disease resistant lines.

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Study on *OsGT1* (*Oryza sativa* *Grassy Tiller1*) determining branching in rice

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Enhancing yield has been a major challenge of agriculture. In rice, tiller number is one of the important biomass and yield components. A maize mutant *grassy tillers1(gt1)* increases lateral branches in maize. The *GT1* gene encodes a class I homeodomain leucine zipper (HD-Zip) protein. In maize, the *gt1* expression is induced by shading and is dependent on the activity of *teosinte branched1(tb1)*, a major domestication locus controlling tillering and lateral branching. To estimate the biological role and agricultural utility of *gt1* in rice, rice homologue (*OsGT1*) has been isolated and its overexpressors and RNAi lines were generated. Field data have shown that *OsGT1* overexpressors reduce the number of tillers and panicles while RNAi lines increase them, compared to ones of wild type. Since shade signal is an important factor in determining lateral branching, the relationship between *OsGT1* and shade avoidance has been explored. Plants have been grown under 50% shading in the field. Also, double genetic combinations with phytochrome mutants (*phyA*, *B*, and *C*) are being examined for tillering phenotype. These researches could provide insights in determining the action of *OsGT1* on branching and shade avoidance in rice. This research is supported by the Plant Molecular Breeding Center of PostBiogreen 21

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Association between sequence variants in panicle development genes and the number of spikelets per panicle in rice

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Balancing panicle-related traits such as panicle length and the numbers of primary and secondary branches per panicle, is key to improving the number of spikelets per panicle in rice. Identifying genetic information contributes to a broader understanding of the roles of gene and provides candidate alleles for use as DNA markers. Discovering relations between panicle-related traits and sequence variants allows opportunity for molecular application in rice breeding to improve the number of spikelets per panicle. In total, 142 polymorphic sites, which constructed 58 haplotypes, were detected in coding regions of ten panicle development gene and 35 sequence variants in six genes were significantly associated with panicle-related traits. Rice cultivars were clustered according to their sequence variant profiles. One of the four resultant clusters, which contained only indica and tong-il varieties, exhibited the largest average number of favorable alleles and highest average number of spikelets per panicle, suggesting that the favorable allele combination found in this cluster was beneficial in increasing the number of spikelets per panicle. Favorable alleles identified in this study can be used to develop functional markers for rice breeding programs. Furthermore, stacking several favorable alleles has the potential to substantially improve the number of spikelets per panicle in rice

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Rapid identification of HMW-GS in common wheat varieties by MALDI-TOF-MS

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High-molecular weight glutenin subunits (HMW-GSs) play an important role in bread making quality. In this study, matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF-MS) was established to identify HMW-GSs. Four major factors influencing mass spectra including solvent components, resolving volume, matrix II components and treatment with alkylation reagent in glutenin extraction were optimized using HMW-GS of Chinese Spring. To obtain accurate molecular weights for individual HMW-GSs, 24 standard wheat cultivars covering all HMW-GSs in hexaploid wheat were analyzed 3 times using this optimized MALDI-TOF-MS method. 38 Korean wheat cultivars previously determined using RP-HPLC and SDS-PAGE were used to verify the allelic compositions. 675 wheat crossing blocks that were harvested by RDA National Institute of Crop Sciences were also used to analyze the composition of HMW-GSs. Results showed that some varieties have 1Ax2*, 1Bx7^{0E}, 1Bx17+1By18, 1Dx5+1Dy10 which are specifically associated with good bread making quality. Although 3-5 subunits are usually expressed in common bread wheat cultivars, but two lines have only two subunits. HMW-GSs of a wheat cultivar are analyzed within one minute by MALDI-TOF-MS, so it is expected to be suitable for the high-throughput analysis of HMW-GSs. MALDI-TOF-MS will be useful to improve end-use quality in wheat breeding programs.

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The rice Rolled fine striped encodes CHD3/Mi-2 chromatin remodeling factor and is involved in scavenging reactive oxygen species during leaf development

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In rice, moderate leaf rolling increases photosynthetic competence and raises grain yield; therefore, this important agronomic trait has attracted much attention from plant biologists and breeders. However, the relevant molecular mechanism remains unclear. Here, we isolated and characterized *Rolled Fine Striped* (*RFS*), a key gene affecting rice leaf rolling, chloroplast development, and reactive oxygen species (ROS) scavenging. The *rfs-1* gamma-ray allele and the *rfs-2* T-DNA insertion allele of *RFS* failed to complement each other and their mutants had similar phenotypes, producing extremely incurved leaves due to defective development of vascular cells on the adaxial side. Map-based cloning showed that the *rfs-1* mutant harbors a 9-bp deletion in a gene encoding a predicted CHD3/Mi-2 chromatin remodeling factor belonging to the SNF2-ATP-dependent chromatin remodeling family. *RFS* was expressed in various tissues and accumulated mainly in the vascular cells throughout leaf development. Furthermore, *RFS* deficiency resulted in a cell death phenotype that was caused by ROS accumulation in developing leaves. We found that expression of five ROS-scavenging genes (encoding catalase C, ascorbate peroxidase 8, a putative copper/zinc superoxide dismutase, a putative superoxide dismutase, and peroxiredoxin IIE2) decreased in *rfs-2* mutants. Western-blot and chromatin immunoprecipitation (ChIP) assays demonstrated that *rfs-2* mutants have reduced H3K4me3 levels of ROS-related genes. Loss-of-function in *RFS* also led to multiple developmental defects, including pollen development, grain filling, and root development. Our results suggest that *RFS* is required for many aspects of plant development and its function is closely associated with epigenetic regulation of genes that modulate ROS homeostasis.

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EMF1 acts as a transcriptional repressor of *VIN3*, a gene required for sensing long-term winter cold for flowering

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The suppression of floral repressor, FLOWERING LOCUS C (*FLC*), is a crucial mechanism for the promotion of flowering in *Arabidopsis*. *VERNALIZATION INSENSITIVE 3* (*VIN3*) encoding a PHD finger domain protein is associated with the epigenetic repression of *FLC*. The induction of *VIN3* is mediated by long-term winter cold, called vernalization, but how *VIN3* is transcriptionally regulated is poorly understood. Here we show that EMF1 recruits a HISTONE DEACETYLASE 19 (*HDA19*) and directly suppresses *VIN3* by histone deacetylation. To find upstream regulator of *VIN3*, we performed mutagenesis and isolated a mutant which exhibiting reduced activation of *VIN3*. A *VIN3* hyposensitive mutant, called *rev79* (*reduced activation of VIN3*), contains a T-DNA at the promoter region of *EMBRYONIC FLOWER 1* (*EMF1*), and *EMF1* is overexpressed in *rev79*. So we named this mutant *emf1-101D*. *emf1-101D* had a similar *VIN3* induction pattern during the vernalization, but the level of transcription was reduced compared to WT. Consistently loss-of-function mutant, *emf1-1* and *emf1-2*, showed higher expression of *VIN3* at both with and without vernalization. We further demonstrate that EMF1 forms a protein complex with *HDA19* and *hda19* mutant showed higher expression of *VIN3*. To better understand how EMF1 regulates target gene, *VIN3*, we examined the dynamics of histone modification patterns during vernalization and found that histone H3 and H4 acetylation were reduced at *VIN3* locus in *emf1-101D*. Thus, our data suggest that EMF1 controls vernalization sensitivity through histone deacetylation of *VIN3*.

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Molecular approach to develop novel plants optimizing the shade avoidance syndrome (SAS)

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Plants absorb photosynthetically active radiation (PAR, 400-700 nm) to generate carbohydrates for the energy source. The chlorophylls of leaves selectively absorb the red (R) and blue light, whereas they reflect and transmit the far-red (FR) light. Total light intensity or R:FR ratio are reduced in the dense vegetation. To obtain the unfiltered light, plants in the shade promote the hyponastic growth, hypocotyl elongation and petiole elongation, a response known as the shade avoidance syndrome (SAS). As shade promotes the immature and rapid elongation of leaf-bearing organs and early flowering, SAS affects the vegetable crop yield significantly. In shade-avoiding plants such as *Arabidopsis*, this changes in light quality and quantity are sensed by phytochrome (phy) photoreceptors. Under normal vegetation, active phytochrome (Pfr) interact with phytochrome-interacting factors (PIFs). We have sought ways to regulate SAS for modulating the plant response, so that crop yield can be maintained with compromised responses to shade condition. Expression of some transcription factors, known and unknown, have been regulated by transgenics overexpressing them or expressing amiRNAs against them. Transgenic plants under simulated shade conditions have been analyzed. These approach should give us insights on how we can modulate crop plants for preventing significant yield loss due to SAS.

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Diversity of chloroplast genome and development of SSR markers for breeding of *Peucedanum japonicum*

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Peucedanum japonicum, a perennial herbal plant species of Apiaceae family, was initially cultivated as oriental medicine is nowadays being cultivated as healthy edible vegetable. Previous study, we have discovered two types (Long/Short) of inverted repeats (IRs) correlated with the sequence polymorphisms in other regions of chloroplast (cp) genomes through comparative analysis of collected wild accessions. To extend further to this study, we have applied the InDel marker to the collected wild and cultivate *P. japonicum* accessions and learned that the band pattern in the long type *P. japonicum* has lesser variation than the band pattern from the short type *P. japonicum*. For faster and efficient method to differentiate the IR type of each *P. japonicum* accession, we have designed the SNP dCAPS marker in advance to the KASP marker for later experiment. To specifying more intra-species variations as well as genotyping wild accessions of *P. japonicum*, 45S nuclear ribosomal DNA sequences, and simple sequence repeats (SSRs) was examined. Comparative analysis on 45S nuclear ribosomal DNA sequences, resulted three SNP polymorphism has been found, including two types of SNPs located within 26S region. SSR markers was able to detect two type of allele among seven *P. japonicum* accession. Taken together, sequences and polymorphisms identified in this study will be valuable genetic resources that can be applied for molecular breeding of *P. japonicum*. This research was supported by "Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ013238)", Rural Development Administration, Republic of Korea.

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Physiological and biochemical conditions for discrimination between haploid and diploid maize kernels

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Doubled haploids (DHs) in maize breeding programs reduce the time required to generate and evaluate new lines to 2 years or less. However, efficient techniques that accurately discriminate between haploid and diploid maize kernels are required. Here, we investigate the effects of several hormones and chemicals on the germination of haploid and diploid maize kernels, including auxin, cytokinin, ethylene, abscisic acid (ABA) biosynthesis inhibitor (fluridone), ABA catabolism inhibitor (diniconazole), methyl jasmonate (MeJA), and NaCl. Ethylene effectively stimulated the germination of both haploid and diploid maize kernels. The ABA biosynthesis inhibitor fluridone, the ABA catabolism inhibitor diniconazole, and MeJA selectively stimulated the germination of haploid maize kernels. By contrast, gibberellin, 1-naphthaleneacetic acid (NAA), kinetin, and NaCl inhibited the germination of both haploid and diploid maize kernels. These results indicate that the germination of haploid maize kernels is selectively stimulated by fluridone and diniconazole, and suggest that ABA-mediated germination of haploid maize kernels differs from that of diploid maize kernels and other plant seeds.

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고추 Pun1 homologs 들과 매운맛과의 분자생물학적 연구

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고추의 매운맛은 캡사이시노이드 (capsaicinoids) 물질에 의해 나타나며, 그 중 캡사이신 (capsaicin)과 다이하이드로캡사이신 (dihydrocapsaicin)이 양적인 측면에서 주를 이루고 있다. 따라서 캡사이시노이드를 합성하는 Pun1 (acyltransferase) 유전자의 기능이 소실되면 매운맛이 없어진다고 알려져 있다. 매운맛에 대한 최근까지의 연구는 Pun1 유전자에 집중되어 진행되어 왔지만, 고추 유전체 서열분석 결과에 의하면 최소 3개 이상의 Pun1 homologs 가 존재하는 것으로 알려져 있다. 따라서 본 연구에서는 이들 유전자들과 매운맛과의 관계를 규명하고자 한다.

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Investigation of the *in vitro* effects of total extracts from pepper on amyloid production and aggregation

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Alzheimer's disease (AD) involves accumulation, oxidative damage and inflammation and there is currently no clinically accepted treatment to stop its progression. Its risk is known to reduce with increased consumption of antioxidant and anti-inflammatory agents. Fibrillar aggregates of A β are major constituents of the senile plaques found in the brains of AD patients and have been related to AD neurotoxicity. The senile plaques are produced by the sequential cleavage of the amyloid precursor protein by secretases. Recently peppers are noted for their antiaging and cognitive enhancing properties. Thus, in this study, the effects of total extracts from pepper on amyloid production and aggregation *in vitro* were investigated. Our study indicate that pepper could be a possible dietary intervention into the management of AD.

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Investigation of alpha-glucosidase inhibitory activity in different pepper cultivars (*Capsicum annuum* L.)

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Abstract. Plant-based food have been used to treat diabetes mellitus recently, because the number of type II diabetic patient has increased dramatically in worldwide. The effective diabetes prevention is the controlling of postprandial hyperglycemia by α -glucosidase inhibition. This study present data of α -glucosidase inhibitory activity in extracts of 14 pepper fruits (*Capsicum annuum* L.) highly consumed as vegetable in Korea. The pepper fruit extracts were prepared with 70% ethanol and water, subjected to dilution (50 and 25%) prior to α -glucosidase inhibitory assay. Significant differences of α -glucosidase inhibitory activity were not shown between two different aqueous extract. Mee-In and Dda-Go-Ddo-Dda-Go cultivars possessed highest and sustainable inhibitory activity (almost 100%) against α -glucosidase. Whereas, the extracts from Soon-Han-Gil-Sang, Gil-Sang, Sweety, Hyul-Jo K, Shin-Hong, and Ai-Mat showed sharp decreasing pattern between 100 and 50% extract concentration. These results suggest the possibility that existence of unknown inhibitors at different concentration in the different pepper cultivars. Hence, further studies may needed to identify the unknown key α -glucosidase inhibitors in pepper fruits.

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Two circadian rhythm regulators, CIRCADIAN CLOCK ASSOCIATED 1 (CCA1) and LATE ELONGATED HYPOCOTYL (LHY) recognize long-term cold to induce *VERNALIZATION INSENSITIVE 3 (VIN3)* for flowering in *Arabidopsis*

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Vernalization is a process that plants acquire competence to flower after long-term winter cold. How plants recognize long-term cold is still in veil although the molecular mechanism of winter cold memory has been studied well. In *Arabidopsis*, *VERNALIZATION INSENSITIVE 3 (VIN3)*, which confers long-term cold memory by mediating epigenetic silencing of floral repressor(s), is the only known protein-coding gene induced by vernalization. To understand the mechanism how plants sense vernalization, we identified *cis*-element responding to long-term cold from *VIN3* promoter. This *cis*-element is named as VRC (vernalization responding *cis*-element). Plants became vernalization-insensitive when the motif is mutated. We also found CCA1 and LHY, evening element-binding circadian rhythm regulators, are involved in *VIN3* induction during vernalization process. They directly bound to VRC and vernalization-mediated *VIN3* induction was impaired in *cca1 lhy* mutant. The prolonged cold dampens the diurnal rhythms of CCA1 and LHY, thus their level at certain time, i.e. at dusk, gradually increases during vernalization. The altered rhythm of CCA1 and LHY is coincident with *VIN3* expression pattern, which shows peak at dusk. Taken together, *VIN3* transcription is induced by rhythmic change of circadian rhythm regulators, CCA1 and LHY, during vernalization. This study would be adopted for agricultural development. Chinese cabbage (*Brassica rapa pekinensis*) has conserved *VIN3* homologs. We found that among the three *VIN3* homologs in Chinese cabbage, two of them have the conserved VRC. This result implies that Chinese cabbage has conserved vernalization-response mechanism. Therefore, it is plausible to generate vernalization-insensitive, thus more productive, Chinese cabbage by editing *VIN3* homologs.

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Modification of seed colors via LDOX gene editing by CRISPR/Cas9 system in rice

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Genome editing technology have been successfully applied to improve various crop traits such as ZFN, TALEN and CRISPR/Cas9 system. Among them, CRISPR/Cas9 system is now conveniently available as a precise and efficient genome engineering tool. Targeted mutagenesis using CRISPR/Cas9 system is especially useful for plant breeding and gene functional analysis. In this study, we applied the CRISPR/Cas9 system to modify rice seed colors. Binary vectors harboring expression cassettes of Cas9 nuclease, single guide RNA (sgRNA) targeting the leucoanthocyanidin dioxygenase (LDOX) and bar as a selectable marker gene were constructed and developed transgenic rice plants via *Agrobacterium*-mediated methods. Targeted mutations were analyzed in bar-resistant shoots by NGS analysis. Transgenic plants clearly contained DNA mutations such as nucleotide substitutions, insertions and deletions at the target site, which varied depending on the transgenic lines. Also, these mutant lines showed that seed color modified. Therefore, these data will be discussing relationship between modification of seed-color (phenotypic variation) and mutagenesis of target site (genotypic variation) in transgenic plants.

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Genome-wide screening of abiotic stress-responsive long noncoding RNAs in rice

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Recently, long noncoding RNAs (lncRNAs) have emerged as important regulatory factors of diverse biological processes in both plants and animals. However, the number and functional roles of lncRNAs in crops remain largely unknown. In particular, systematic examination of rice lncRNAs involved in abiotic stress responses has not been performed. In this study, we re-analyzed the expression profile of lncRNAs in publicly available rice transcriptome datasets derived from abiotic stress treatments to unveil the potential roles of rice lncRNAs in abiotic stress responses. Overall, we identified 10,831 rice lncRNAs that were significantly altered in shoot and/or root tissues under four different abiotic stresses, including ABA, drought, cold, and high salt. Out of them, 5,516 and 5,315 rice lncRNAs were upregulated or downregulated, respectively, in a highly stress-specific or tissue-specific manner. These stress-responsive lncRNAs were classified into 15 groups from their stress-specific expression patterns. Based on Venn diagram analysis, we observed strong crosstalks between different stress signaling pathways, showing transcriptional regulatory networks underlying lncRNA expression changes in response to abiotic stresses. Lastly, qRT-PCR validation confirmed the differential expression patterns of these lncRNAs under various conditions. This study shows the first comprehensive identification of a group of rice lncRNAs that are involved in abiotic stress responses. The results suggest that rice lncRNAs may play crucial roles in abiotic stress tolerance mechanisms.

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Stable recombinant protein expression in pepper using a broad bean wilt virus 2-based vector system

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While pepper (*Capsicum annuum* L.) is a highly recalcitrant species with respect to current genetic transformation technologies, plant virus-based vectors can provide alternative and valuable tools for transient regulation and functional analysis of genes of interest in pepper. In this study, we established an effective virus-based vector system applicable for over-expression of genes of interest in pepper using broad bean wilt virus 2 (BBWV2). We engineered a single gene insertion cassette between the movement protein and large coat protein-encoding cistrons in RNA2 by modifying the infectious cDNA clone of the BBWV2 strain RP1 (which cause no visible symptoms in pepper) and named it as pBBWV2-OE vector. Successful expression of GFP from the BBWV2 vector was observed in various pepper cultivars and other plant species including *Nicotiana benthamiana*, *Arabidopsis thaliana*, and *Perilla frutescens* var. *japonica* Hara during the early infection stage of the virus. However, the GFP expression level was gradually decreased as viral infection progressed systemically in pepper. To overcome this phenomenon and enhance GFP expression, we sought to examine co-expression of a viral RNA silencing suppressor together with GFP from the BBWV2 vector. To this end, we first engineered an additional gene insertion cassette into pBBWV2-OE and this dual-gene expression vector was named as pBBWV2-OEx2. Next, to investigate the effects of viral RNA silencing suppressors on enhancing gene expression from the BBWV2-based vector, GFP was simultaneously expressed with viral RNA silencing suppressors including the tomato bushy stunt virus p19, cucumber mosaic virus 2b, and flock house virus B2 using pBBWV2-OEx2 in *N. benthamiana* and pepper. The results showed that GFP expression was most effectively enhanced by B2 when co-expressed from the BBWV2-based vector, while 2b has only marginal effect on enhancing GFP expression and co-expression of p19 resulted in increasing symptom severity. This BBWV2-based gene delivery system provides a convenient approach for rapid and simple gain-of-function studies in pepper.

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Comparative analysis on transcriptome and metabolome between insect-resistant wild potato *S. berthaultii* and insect-susceptible potato *S. tuberosum* cv. "Sumi" to identify genes involved in insect-resistance

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Potato is one of the important crops in the world. Cultivated potatoes are vulnerable to insect attacks. However, several wild potato species including *S. berthaultii* are resistant to insect herbivories. To find genes related to insect resistance, we performed a comparative transcriptome analysis between cultivated potato *S. tuberosum* and wild potato *S. berthaultii*. RNA-seq data showed 679 DEGs were up-regulated and 303 DEGs were down-regulated in *S. berthaultii* compared to *S. tuberosum*. Among them, 145 genes were related to biosynthesis of terpenoids and flavonoids, which are well known for insect resistant metabolites. The expression level of genes involved in terpenoids and flavonoids biosynthesis pathways was higher in *S. berthaultii* than *S. tuberosum*, and these results were confirmed by qRT-PCR. GC-MS analysis confirmed that the higher expression of those transcripts in *S. berthaultii* led to the higher accumulation of several terpenoids. These results suggest that secondary metabolites including terpenoids play an important role in plant defense against insect attack.

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Comparative gene expression analysis of seed development in waxy and dent maize (*Zea mays*)

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We used Illumina/HiSeq sequencing to analyses gene expression profiling among the four maize seed at 10 DAP (days after pollination). we generated total 88,993,000 (CM3), 103,817,340 (CM6), 103,139,640 (CM5), 66,978,958 (CM19) sequence reads with read length of about 0.9, 1.0, 1.0 and 0.7 billion bp. We obtained 69.1 (CM3), 71.0 (CM6), 71.2 (CM5), 71.8 (CM19) % high quality reads from the raw data. we compare to the reference RNA sequence in the public DB (NCBI). We revealed that mapped reads were 58%, 63%, 62% and 62% of the EST reference in CM3, CM6, CM5 and CM19. more than 51,000 genes were expressed based on RPKM criteria (over 0.25 value) in each CM3, CM6, CM5 and CM19 inbred lines. In DEG analysis, we found that 3,527 genes were differentially expressed with at least two times with 1,709 up-regulated in waxy maize inbred lines and 1,818 up-regulated in dent maize inbred lines. To identify expressions of DEGs associated with metabolic pathways using MAPMAN, some genes upregulated in waxy and dent were only expressed in independent metabolic pathway for dent upregulated genes, such as cell wall proteins.AGPs, degradation.mannan-xylose-arabinose-fucose (in cell wall), nitrate metabolism, N-degradation (in N-metabolism), synthesis.glutamate family.proline, synthesis.aromatic aa.chorismate, synthesis.histidine, degradation.serine-glycine-cysteine group.glycine (in amino acid metabolism), simple phenols, N misc (in secondary metalbolism), ascorbate and glutathione (in reduction-oxidation), synthesis.pyrimidine, phosphotransfer and pyrophosphatases, deoxynucleotide metabolism (in nucleotide metabolism), non-reductive PP (in OPP), and for waxy upregulated genes such as pectin*esterases (in cell wall), synthesis for aspartate family.lysine, branched chain group.common, branched chain group.leucine specific, serine-glycine-cysteine group.glycine, serine-glycine-cysteine group.cysteine, aromatic aa.phenylalanine and tyrosine and degredation for glutamate family.glutamine, serine-glycine-cysteine group.cysteine, aromatic aa.tryptophan (in amino acid metabolism), trehalose.TPP (in minor CHO metabolism), S-assimilation. The differently expressed gene (DEGs) profiling set and pathway analysis can server to understand of gene regulation depends on kernel types in dent and waxy maize.

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Identification of candidate genes conferring resistance to foxglove aphid in soybean

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The sap-sucking insects infect a wide range of host plants worldwide. The foxglove aphid, *Aulacorthum solani* (Kaltenbach), is a Hemipteran insect that causes serious yield losses in soybean. The objective of this study was to narrow down the *Raso2* region, which is previously identified QTL conferring foxglove aphid resistance, using high-density SNP array, Axiom® 180K SoyaSNP, and identify the candidate genes. The F_{4,8} recombinant inbred lines were developed from a cross between susceptible Williams82 and resistant wild soybean PI 366121, were used to QTL analysis. The antibiosis and antixenosis were evaluated through choice and no-choice assays with total plant damage and primary infestation leaf damage. The high-density genetic linkage map was constructed with total 169,028 SNPs. Using inclusive composite interval mapping analysis, *Raso2* on chromosome 7 narrow down to 3cM, corresponding to 76-kb of genomic region based on the Williams 82 genome assembly (Wm82.a2.v1) including 8 annotated gene models. Furthermore, comparing the nucleotide sequences of eight gene models between both parents, Williams 82 and PI 366121, total 11 SNPs with 4 nonsynonymous substitution were identified. Interestingly, all 4 nonsynonymous substitution were located in *Glyma.07g077700*, which contain NB-ARC domain. In conclusion, we narrow down the *Raso2* up to 76-kb interval, and identified the 4 nonsynonymous SNPs on *Glyma.07g077700* using genome-wide high-density SNP assay. These result could provide the useful information in breeding for new foxglove aphid resistant soybean cultivar.

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Characterization of volatiles and phytonutrients in grains of advanced breeding lines to develop a new fragrant rice variety with superior nutritional value

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Paradigm of Korean rice breeding is recently shifting from yield to palatability and health-beneficial effects. In an attempt to develop a new rice variety superior in both fragrance and nutritional value, 19 candidate advanced breeding lines with aroma properties were selected, and their grain phytochemicals such as tocopherols, squalene, and phytosterols were determined, and their grain volatile profiles were also characterized by using a headspace solid phase microextraction (HS-SPME) combined with an GC/MS. From all fragrant rice breeding lines total 133 volatiles were identified, among which 46 volatiles were found commonly in all tested 19 lines, while 14 volatiles were observed in less than 5 lines. The most frequently and abundantly observed volatile was nonanal, which consisted 16.9 to 34.8% of all identified volatiles in all tested lines. A popcorn-flavoring 2-acetyl-1-pyrroline, the most determinant flavoring compound in rice exhibited 0.3 to 5.6% of volatile compositions in 18 lines. Total tocopherols, tocotrienols, squalene, and total phytosterols contents ranged 5.3 to 33.7, 12.3 to 19.7, 8.1 to 220 ppm, and 154.3 to 514.3 ppm, respectively. Based upon all results describe above, a breeding line JS-29 which showed 3.6% of 2AP composition, 8.8 ppm of total tocopherols, 12.3 ppm of total tocotrienols, 484.3 ppm of total phytosterols, and 15.6 ppm of squalene contents could be selected as the most promising candidate line for a fragrant rice variety with high nutritional value.

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Comprehensive analysis of *R* Gene composition in a *Ctv* locus conferring citrus tristeza virus resistance from the genetic resources of citrus and its relatives

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Regardless of the importance of a viral pathogen, citrus tristeza virus (CTV), in citrus industry, molecular marker tools closely associated with its resistance trait have not been developed yet. A *Ctv* locus, one of at least 2 CTV-resistant loci that was cloned from trifoliolate orange and displayed a distinct feature of enriched *R* gene composition. Based on such molecular characteristics of the genetic locus, we developed multiplex PCR marker sets to specifically detect 7 *R* genes consisting of *Ctv* locus. By using the multiplex PCR marker sets, we surveyed composition of 7 *R* genes consisting of the genetic locus in a total of 156 citrus genetic resources including 12 of Korean citrus landraces. Genetic composition of 7 *R* genes in the locus was variable among the genetic resources. However, all of 7 *R* genes were detected only in both trifoliolate orange, *Poncirus trifoliata* and its derivative cultivar, *P. trifoliata* 'Flying dragon', which have been reported to be resistant to CTV. Multiplex PCR marker sets established in this study would be an effective molecular tool to develop scion or rootstock cultivars with high resistance trait against CTV in citrus breeding program.

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Detection of SNPs among 13 Korean japonica rice varieties using genome sequencing data for SNP marker development

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Plentiful variations in the important agronomic traits such as disease resistance and pre-harvest sprouting exist within Korean japonica rice varieties. Therefore, it is possible to do mapping useful genes with populations derived from crosses between them. But, deficiency of molecular markers discriminating Korean japonica rice varieties has made these efforts difficult. However, abundant SNPs can be revealed between closely related crop varieties by genome sequencing enabling development of sufficient DNA markers. We collected genome sequencing data of 13 Korean japonica rice varieties to detect SNPs among them. The data size varied from 5.8 to 36 Gbp with sequencing depth of 15.5 – 96.6 x. Using CLC Assembly Cell program and Python programs developed in-house, the genome sequence data was processed and SNPs among the varieties were identified. Totally, about 740,000 SNPs were detected. Chromosome 11 showed the highest number of SNPs (163,557) and chromosome 5 showed the lowest number of SNPs (16,017). Currently, we are developing SNP markers to be utilized for gene mapping and marker assisted selection (MAS).

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Identification of structural and regulatory genes involved in anthocyanin biosynthesis that confers the flower color of chrysanthemum

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Chrysanthemums (*Chrysanthemum × morifolium*) exhibit a broad range of flower colors through the accumulation of anthocyanins. In this study, the cDNA sequences of the seven structural genes CmCHS, CmCHI, CmF3H, CmF3'H, CmDFR, CmANS, and CmGT and two regulatory genes CmMYB, Cmbasic-helix-loop-helix (CmbHLH) involved in anthocyanin biosynthesis were isolated from three different Chrysanthemum cultivars, 'OB', 'DP', and 'RM'. Sequence analysis revealed that most of the cDNA sequences have a few variations, but bHLH cDNAs from DP and RM were exactly same as the previously deposited sequence from another cultivar. Gene expression analysis showed that all of the structural genes were highly expressed in the pink flowering (DP) and red flowering (RM) cultivar compared to the white flowering (OB) cultivar. In particular, the transcript levels of CmF3H, CmF3'H, CmDFR, CmANS, and CmGT were most prominent in RM exhibiting the darkest red flower color. To demonstrate the regulatory mechanism of anthocyanin biosynthesis in the florets of Chrysanthemums, yeast two-hybrid was conducted with recombinant MYB, bHLH, and WD40 (TTG1) proteins from OB and RM, which showed that the three regulatory proteins interacted with each other, and this suggests that the anthocyanin biosynthetic pathway could be transcriptionally controlled via MBW complex.

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Genomic structure and genome wide association study for seed weight using Korean soybean landrace and cultivar

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Seed size is one of the factors determining soybean yield. Large seed size is, therefore, preferable trait for most soybean breeders. However, small seed size is also preferred for soybean sprout in Korea. In this research, we studied genetic structure and genetic variances associated with soybean 100 seeds weight using Korean soybean landraces and cultivars. We developed 25,914 SNPs using genotype-by-sequencing and identified that Korean landraces and cultivars were clustered into 3 subgroups. Principle component analysis exhibited that landraces and cultivars were clearly divided into two groups and, cultivars were clustered depending on their usage. Genome wide association study (GWAS) showed that 30 SNPs were significantly associated with 100 seeds weight and were co-localized with 39 QTLs related to seed size. The SNPs were associated with soybean homologs to Arabidopsis seed size genes and seven of them have not been reported in previous soybean GWAS studies. We identified novel genetic factors associated with 100 seeds weight in soybean. This study will contribute to breed soybeans with preferable seed sizes for diverse usage.

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Development of drought tolerant temperate rice varieties utilizing *Pup1* and drought QTLs

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Drought stress in early growing season became serious recent years in Korea. Improvement root vigor and P uptake might be a solution to overcome the problems in that stage. Early establishment by help of those traits will provide the benefits increasing yield of MS11, which is a *japonica* rice variety adaptive to tropical regions. Two QTLs conferring stress tolerance, *DTY2.2* and *Pup1*, were introgressed into MS11 using marker-assisted backcrossing. Background genotyping of pyramiding lines of BC₂F₃ showed that more than 95% of similarity of them to MS11. The finally selected lines were tested and they showed same in normal growth condition in the overall plant type and yield capacity. Drought stress were applied by growing in rainfed condition and MS11-drought tolerant lines showed better yielding. These lines are being grown in normal irrigation, rainfed, terminal drought, high temperature, and salinity conditions by collaborations. The pyramiding of *Pup1* and drought QTLs might provide the meaningful breeding materials for the climate-ready rice development. Further, MS11-QTL lines might be considered for new candidate varieties in problem regions of south-east Asian countries.

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Identification of key plastidic phosphoglucomutase and ADP-glucose pyrophosphorylase isoforms essential for successful fertilization in rice

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To elucidate the starch synthetic pathway and the role of this reserve in rice pollen, we characterized mutations in the plastidic phosphoglucomutase, *OspPGM*, and the plastidic large subunit of ADP-glucose (ADP-Glc) pyrophosphorylase, *OsAGPL4*. Both genes were upregulated in maturing pollen, a stage when starch begins to accumulate. Progeny analysis of self-pollinated heterozygous lines carrying the *OspPGM* mutant alleles, *osppgm-1* and *osppgm-2*, or the *OsAGPL4* mutant allele, *osagpl4-1*, as well as reciprocal crosses between wild type (WT) and heterozygotes revealed that loss of *OspPGM* or *OsAGPL4* caused male sterility, with the former condition rescued by introduction of the WT *OspPGM* gene. While iodine staining and transmission electron microscopy analyses of pollen grains from homozygous *osppgm-1* lines produced by anther culture confirmed the starch null phenotype, pollen from homozygous *osagpl4* mutant lines, *osagpl4-2* and *osagpl4-3*, generated by CRISPR/Cas system, accumulated small amounts of starch, which were sufficient to produce viable seed. Such *osagpl4* mutant pollen, however, was unable to successfully compete against WT pollen, validating the important role of this reserve in fertilization. Our results demonstrate that starch is polymerized mainly from ADP-Glc synthesized from plastidic hexose phosphates in rice pollen, and that starch is an essential requirement for successful fertilization in rice.

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Optimization of TRV mediated CRISPR/Cas9 genome editing in Tomato

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Mutant lines with desirable agronomic traits have important implications for the plant breeding. The advent of CRISPR/Cas9 technology has made genome editing possible in virtually all plant species, including those plant species less amenable to genetic manipulations. However, targeted genome-editing using CRISPR/Cas9 approach in many crop plants is still in progress and optimal strategies need to be developed. In the present study, Agrobacterium mediated stable expression and TRV mediated transient expression systems are being standardized for CRISPR/Cas9 genome editing. As a proof of principle, genome editing in tomato *PDS* gene, a key gene functions in carotenoid biosynthesis pathway is being performed. Additionally, targeted genome editing for loss-of-function in the *eIF4E* and *eIF4E-Iso* genes, which are known to be involved in recessive resistance of potyvirus is underway. For rapid validation of gRNAs, we performed in vivo Cas9 activity analyses and CRISPR-Cas9 efficiency was recorded up to 15%. Agrobacterium transformation efficiency of about 25.0-34.4% was recorded for CRISPR/Cas9-sgRNA-*SIPDS*, *-SleIF4E* and *-SleIF4E-Iso* constructs. Cas9 overexpressing tomato lines have been developed for TRV mediated CRISPR/Cas9 genome editing. This ongoing optimization of stable and transient expression of CRISPR/Cas9 systems has the potential for the development of an efficient procedure for targeted genome editing, and creates a platform to efficiently generate transgene-free tomato and it may provide insights into sophisticated site-specific genome engineering techniques for other crop species.

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Changes in crop productivity induced by new *sp* mutant alleles

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Regulation of shoot growth and termination is a major factor for yield improvement in tomato. *self pruning (sp classic)* mutant inducing shoot termination has been used for breeding field tomatoes for over 90 years. Most recent question addressed that shoot life variation under determinate growth give a new window for manipulating tomato yield in the field. In this study, we isolated new three *sp* mutant alleles from 242 Core Collection (C.C) lines, which show variations in shoot determinacy. One deleterious *sp* mutants, *sp-2798*, resulted in no expression of *sp* represented similar shoot termination with less yield than *sp classic*. A newsingle amino acid substitution mutant, *sp-5732*, produced more sympodial shoots on main shoot and axillary shoots and improved tomato fruit yield up to 42%. Therefore, we suggest that newly discovered *sp* alleles are new resources for manipulating shoot growth and yield of determinate tomato in the field.

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Characterization of the microtubule-associated RING finger protein 2 (*OsMAR2*), acts as a negative regulator in responses to salt stress in *Arabidopsis*

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Environmental stresses such as cold, drought, high temperature, and soil salinity, negatively affect seed germination, vegetative growth, and reproductive development of plants. Soil salinity is the major agricultural problem because cause cellular dehydration and ionic toxicity and leads to a decrease in the productivity of crops. Here, we report on salt-induced RING finger E3 ligase, *Oryza sativa* microtubule-associated RING finger protein 2 (*OsMAR2*). Transcript analysis of *OsMAR2* gene highly expressed at various abiotic and hormone stresses, such as ABA (100 mM), NaCl (200 mM), drought, and heat (45 °C). In addition, in vitro ubiquitination assays demonstrated that *OsMAR2* showed E3 ligase activity by RING C3HC4 type domain. The result of Yeast-Two hybridization and bimolecular fluorescence complementation (BiFC) support that *OsMAR2* interacting with 3 substrates, *O. sativa* Glyoxalase and *O. sativa* Cysteine proteinase 1, at cytosol. Heterogeneous overexpression of *OsMAR2* exhibited sensitive phenotype in compared to control plant under high salinity stress. These results suggest that *OsMAR2* play a negative regulator in salt stress response. you're able not my any help.

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Analysis of Anthocyanins, Chlorophyll and Carotenoid compounds during Seed Development in wheat (*Triticum aestivum* L.)

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For the observation of anthocyanin, chlorophyll and carotenoid deposition during seed development in Yellow (Ye) and Deep Purple (DP) seeds we took samples from the 10, 20, 30 and 40 Days After Pollination (DAP). CRYO-CUT was used to section the seeds in 0.04 mm cryo-sections. Furthermore, we quantified anthocyanins, chlorophyll and carotenoids using spectrophotometry. Results showed that during grain development in Ye seeds that there was not much variation at 10 and 20 DAP – in contrast, however, a white layer formed on DP seeds at 10 DAP. Interestingly, in DP seeds at 10 DAP, anthocyanins were found, but no colors could yet be seen, making us believe that this coat might be related to anthocyanin deposition; furthermore, in DP seeds at 20 DAP, it can be seen that the seedcoat color has covered almost the entire seed (consistent with the cryo-cuts where the chlorophyll stays under the inner layer or, in some places, where the chlorophyll has completely disappeared). During 30 and 40 DAP, in both, Ye and DP, the seed color has fully covered the seeds, yellow and deep purple, respectively. The anthocyanins quantification showed that there are no anthocyanins in the yellow seed; in DP the anthocyanins reduced drastically at 20 DAP and they started increasing gradually until 40 DAP. For Chlorophyll a (Chla), Chlorophyll b (Chlb), Chla/Chlb ratio and Total chlorophyll, data showed consistency with our previous results showing that chlorophyll was being reduced as the grain developed. Carotenoids were higher in Ye seeds, but also DP contained them. Based on these results we conclude that color deposition in wheat depends on the color coat.

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Seed coat color segregation of an F₃ (Yellow x Deep Purple), genetic analysis and temperature effects in wheat (*Triticum aestivum* L.)

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We performed genetic analysis of seed color segregation of an F₃ population with parental lines of Yellow (Ye) and Deep Purple (DP) wheat seeds. Seeds were scored 0 (light yellow) to 9 (deep purple). The best fit was 12yellow:3 brown:1 deep purple for dominant epistasis, with a X² of 2.075 and with a p value of 0.90-0.10. We evaluated the seed color using digital imaging using Adobe Photoshop CS6 (Version 13.0 x 64) by obtaining the CIELAB scores. Values L*, a* and b* represent lightness, red/green and yellow/blue components, respectively. L* scores were higher in Ye, followed by Br and DP, same was in b*; in the case of a* the results were inverted, where DP had higher scores, but results were not significant (P ≤ 0.05). The L* scores show that the lightness between the Br and DP are different with the Yellow one, but not between them; furthermore, in the b* score, all were significant different between each other. Moreover, germination of the clustered seeds (Ye, Br and DP) was performed under cold (» -2°C) and control conditions (18 °C) for a week. From the germination assay we concluded that favorable environmental conditions favor the germination of the lighter colored seeds (Yellow seeds) while hostile environmental conditions favor the germination of deeper colored seeds (Deep Purple).

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Study of gene expression and interacting proteins of wheat MAP Kinase family under cold treatment

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MAPK cascades (MAPK, MKK, MKKK) play crucial role in plant growth and development as well as response to diverse stresses, through regulating the activity of its target protein *via* phosphorylation. In spite of its importance, the components of wheat MAPK family had been uncovered because of its large and complex genome. Recently, with the development of NGS technology, a number of wheat MAPK family genes have been identified and classified depending on their sequence structure. Cold is one of the most severe stresses in winter wheat growth, and wheats have developed a mechanism to enhance cold tolerance, so called cold acclimation. In this study, we observed expressional changes of wheat MAPK genes under cold treatment using public RNAseq data and identified their putative interacting partners *via* yeast-two-hybrid screening. The sequences of wheat MAPK family genes were retrieved from public databases and used as queries to perform BLAST against wheat Refseq v1.0. RNAseq analysis was performed to observe MAPK gene expression changes under normal and cold-treated conditions. Gene expressions of the putative interacting partners were analyzed using qRT-PCR and their interactions were verified through yeast-two hybrid analysis. In this study, the components of the wheat MAPK family and their interacting proteins involved in cold signaling were identified. The elucidation of MAPK-related cold tolerance pathway will help to understand the complex mechanism of cold acclimation.

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Identification of expression levels of arsenic-related genes and genome-wide transcriptome profiling of genes associated with arsenic in arsenic-tolerant rice mutant

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Arsenic (As) is toxic to plants, animals and humans. A large amount of arsenic is emitted from contaminated irrigation water and from arable soil in mine areas. Rice (*Oryza sativa* L.) is one of the major cereals consumed by more than half of the world's population, and rice is also an important route of exposure for humans to arsenic. Because rice has 10 times the arsenic content in the grain than other major crops. However, precise molecular regulations and mechanisms related to the toxicity and tolerance of arsenic in rice are not yet known. In the present study, we developed an arsenic-tolerant type 1 (ATT1) rice mutant by γ -radiation mutagenesis and performed genome-wide transcriptome analysis for the characterization of arsenic-responsive genes. We also compared the expression patterns of WT and ATT1 in arsenic - associated genes already identified in rice. The expression level of the gene that absorbs arsenate (OsPT8) was similar in WT and ATT1 plants. The expression level of the gene (OsABCC1), which isolates Arsenic-GSH complex and arsenic-PC complex into vacuoles in plant body, was higher in root than ATT1 in WT. But in the shoot, WT was more than ATT1. The arsenic contents of root and shoot were compared after arsenic treatment in WT and ATT1 plants. As a result, ATT1 showed higher arsenic content than WT in root, and WT showed higher arsenic content than ATT1 in shoot. In this study, we have developed ATT1, which suggests that further analysis and studies will help reduce arsenic exposure to the food chain by minimizing arsenic accumulation in rice grains.

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야생벼 수량안정성 유전자 분리 및 품종 개발

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야생벼나 잡초벼와 같은 유전자원은 각 지역의 환경조건에 오랜 기간 동안 적응하며 집단을 유지하였기 때문에 여러 가지 저항성이나 불량한 환경에 대한 내성 등 유용한 특성을 갖고 있다. 본 연구는 이러한 야생 유전자원에서 고수량성 등에 관여하는 유용 유전자를 선별적으로 재배벼에 이전시키는 육종방법을 개발하고 우량 품종 육성을 목표로 한다.

야생유전자원의 유용유전자를 활용하기 위하여, 야생벼의 염색체단편이 최소로 이입된 근동질계통을 육성하고 수량안정성 관련 형질연관 QTL을 탐색하였다. 화성/O. rufipogon 조합 계통을 이용하여 종자중 QTL, gw9.1의 후보 유전자로 염색체 9번의 Ascorbate peroxidase 유전자 선발, 형질전환 분석을 통하여 gw9.1이 수량성 및 출수기 특성에 관여함을 밝히고, 저온발아성 QTL, tgl의 후보유전자들을 선발, 발현분석을 통하여 저온발아성에 관여하는 후보 유전자를 선발하였다. 화성/O. minuta 후대계통을 이용하여 까락발달에 관여하는 신규 후보유전자(awn9)들을 염색체 9번 말단 약 96Kb 지역에서 고밀도지도 작성을 통하여 선발하였다. 화성/O. grandiglumis 후대를 이용하여 GW2 (grain width 2) 유전자가 종자중 외에도 엽록소함량을 조절함을 밝혔고, GW2 유전자의 다면발현 효과를 분석 중이다. Nipponbare/kasalath 조합 근동질계통을 이용, 중배축신장에 관여하는 QTL을 탐지하여 초엽 신장성과의 관계를 밝히고, 근동질계통을 이용하여 qMel-3의 고밀도 지도를 작성하였다. 본 연구성과는 농촌진흥청 연구사업 (PJ01321401)의 지원에 의해 이루어진 결과이다.

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Identification and functional analysis of *ASR* genes under drought stress in *Brachypodium distachyon* L.

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Plants are frequently exposed by various environmental stresses, which influence plant growth, development and productivity. *ASR* genes are known to possess ABA/WDS domain, and affect on various stress tolerance. *Brachypodium* is known as monocot model plant and is closely related to important crops such as wheat, barley and sorghum. Although, *ASR* genes is absence in *Arabidopsis*, 5 family genes from *Brachypodium distachyon* were reported to be existed but their functions were still unclear. In this study, we identified 5 *ASR* genes in *Bd21* line using database collection with BLASTP in Phytozome 12. The sequence alignment and phylogenetic analysis were performed to compare the orthologs from other crops. Expression analyses revealed the *ASR* genes responded to abiotic stresses and hormones. To investigate the functions of *BdASRs* in response to abiotic stress, we generated over-expression transgenic plants in *Brachypodium*. Over-expression transgenic line of *BdASR* gene improves drought tolerance and showed higher enzymatic antioxidants activities (SOD, POD, CAT and APX) compare to wild type under drought stress. Also, It showed hypersensitive to exogenous ABA treatment at germination stage. These results suggest the improvement of drought tolerance in *BdASR* transgenics might be ascribed by regulation of ABA signaling, related gene expression and following creased enzymatic activities.

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A genome-wide association study of biomass productivity in core collection of *Miscanthus*

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Miscanthus is generally known to produce large quantity of biomass with low resource consumption and has several agronomic traits such as leaf area, stem traits and heading date, which are strongly related to biomass production. However, *Miscanthus* needs more than three years to evaluate its biomass production capacity due to its slow growth characteristics during the first three years. Thus, breeding strategy using molecular marker selection is essential for shortening breeding period of *Miscanthus*. In this study, we conducted a genome-wide association study (GWAS) between genetic variation and phenotype data related to biomass productivity in 180 accessions of *Miscanthus* core collection. Fourteen agronomic traits related to biomass production and flowering were assessed for four years and they were highly correlated with the estimated biomass yield in the 4th year. Conducting GWAS analysis between selected 34,743 SNPs and phenotype data, 195 SNPs showed significant association with 12 phenotypic traits ($P < 10^{-5}$). Of these, 94 SNPs were selected through by Bonferroni correction and associated with 5 phenotypic traits (number of shoots, stem diameter, leaf dry weight, stem dry weight, and flowering date). In particular, MS_24018 SNP marker showed significant association with five phenotypic variables (3rd and 4th year stem dry weight, 2nd to 4th year stem diameter). It is expected that the results of this study can be used for molecular breeding program of *Miscanthus*. In particular, it can be utilized as the selectable marker for high-yield variety of *Miscanthus* in early stage of breeding.

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Anti-osteoporosis effect of T99 soybean with high isoflavone content

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Soybean isoflavone content has long been considered to be a desirable trait to target in selection programs for their contribution to human health. Soybean and their products (Cheonggukjang and Doenjang) are the most abundant sources of isoflavones in the diet. To develop a soybean crop with high content of isoflavone, a new crop T99 soybean (T99) was made by cross breeding. To compared with total isoflavone content of various soybean crops and their products, we performed HPLC analysis. Total isoflavone concentration of T99 is 2 times higher than other soybean crops. The highest isoflavone content in Cheonggukjang and Doenjang was made with T99. These results suggested that total isoflavone contents were significantly affected by crop. Additionally, we examined whether T99 have a better effect on osteoporosis than other soybean varieties. The alkaline phosphatase (ALP), a biochemical marker of bone formation, activity with Saos-2 cells showed higher activity in T99. In ovariectomized (OVX) animal model, T99 showed the highest anti-osteoporosis effect in biochemical markers of bone turnover and micro CT image compared with other soybean varieties. Therefore, these results suggest that T99 soybean intake may have a potential benefits for bone in post-menopausal women and furthermore, new crop T99 soybean will be competitive in the market of soybean products.

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Development of “Miscold“, a new cold-tolerant *Miscanthus* variety

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Miscanthus x giganteus (Mxg) has been commercially cultivated in Europe and US for biomass production due to its high biomass yield and environmental adaptability. However, despite of such advantages, it has cold-sensitivity which makes it hard to be cultivated in higher latitudes where winter weather is extremely cold and dry. For these reasons, we developed a new triploid *Miscanthus* variety called “Miscold“ with high cold-tolerance in higher latitudes, particularly in Primorski-krai where Korean cropping companies run large farm lands (up to 100,000 ha). “Miscold“ was developed by hybrid breeding method by bulk crossing of diploid *Miscanthus sinensis* and tetraploid *Miscanthus sacchariflorus* parents in 2010. Hybrid seedlings were cultivated from 2011 to 2012, and 37 lines with excellent early growth were pre-selected. For agronomic traits and cold tolerance tests, the 37 lines were tested in Primorski-krai, Russia (N43° 8'), and in Suwon, Korea (N37° 3') simultaneously from 2013 to 2014, and CALS-M-08 line was finally selected and confirmed as a triploid *Miscanthus*, and was named as “Miscold“. “Miscold“ showed better seedling establishment (69%) and winter survival (100%) compared to Mxg (33% and 7%, respectively). “Miscold“ performed better in plant growth and biomass yield; 207 cm tall and 576 g biomass per plant, which are much greater than those of Mxg (158 cm and 71g/plant, respectively).

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Establishment of double-haploid breeding system to produce Korean wheat lines with extra-strong gluten and wheat-*Leymus* addition lines

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Extra-strong gluten is a key factor for bread-making quality. The objectives of this study were to develop 1) Korean wheat lines with extra-strong gluten and 2) wheat-*Leymus mollis* addition lines as genetic resources through double-haploid breeding system for Korean wheat breeding. For production of Korean wheat lines with extra-strong gluten, one Korean wheat landrace with over-expressed Bx7 high molecular gluten subunit (Bx7^{OE}) as extra-strong gluten was found among 310 Korean wheat accessions. The genetic characterization of Bx7^{OE} of the Korean wheat landrace (IT166460) was confirmed with molecular analyses such as SDS-PAGE, RP-HPLC, and DNA sequencing. To introduce of Bx7^{OE} gene into Korean wheat cultivars, calluses were introduced from anthers of the F₂ plants (IT166460 x Bungulla) and F₃ plants (Glenlea, Canadian Western Red Spring wheat with Bx7^{OE} x Dajoong) on CHB3 medium. The frequency of introduction of calluses was 0.5%. The calluses were subcultured. To regenerate green plants, the subcultured calluses were transferred on R9 medium. After plant regeneration, it can be performed pure chromosome doubling by colchicine. For production of addition lines, tetra- or hexaploid wheat was crossed with *Leymus mollis* to introduce wheat-*Leymus* addition lines as genetic resources. After intercrossing, 35 embryos among 240 florets were taken by embryo rescue (frequency:14.6%). Among 35 embryos, 11 hybrid plants were introduced. It is necessary to investigate *Leymus mollis* chromosomes in root meristem cells of the hybrids by genomic *in situ* hybridization.

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벼 분자육종에서 KASP 마커의 활용

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최근에 유전체 분석기술의 범용화에 따라 SNP를 활용한 분자육종기술이 비약적으로 발전하고 있으며, 신속하고 정밀한 대량분석시스템이 구축이 필요한 실정이다. 본 연구는 저비용 고효율 SNP분석 시스템으로 알려진 Kompetitive Allele Specific PCR(KASP) marker가 국내에도 상용화되고 있어 이를 벼 분자육종에 접목하고자 연구를 수행하였다. 유전적 다양성 분석, Marker assist selection(MAS) 및 유용유전자 탐색 등을 통해 활용성을 검토하였다. 250개의 KASP마커를 활용하여 국내 육성 품종 및 계통의 유전적 다양성을 분석한 결과, 자포니카 3그룹과 인디카 및 통일형 1그룹으로 분류되었다. 또한 MAS를 이용한 윤광벼 줄무늬잎마름병 근동질 계통 육성을 위해 BC2F1세대에서 Background selection를 실시한 결과 관행육종의 염색체 치환율(87.5%)보다 더 많이 치환된 계통(92% 이상)을 선발할 수 있었다. 뿐만 아니라, KASP마커를 활용하여 설쟁벼의 분상질 유전자 탐색에 적용하였으며, Recessive Class Analysis(RCA)를 통해 연관영역을 신속하게 위치를 탐색할 수 있었으며, linkage analysis 및 molecular map작성에도 효율적으로 활용할 수 있음을 확인하였다.

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Development of efficient plant regeneration systems in chrysanthemum ‘Ohblang’ and ‘Baekgang’

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New spray and standard chrysanthemum (*Chrysanthemum morifolium* Ramat.) cultivars, ‘Ohblang’ and ‘Baekgang’ were released in 2008 and 2007, respectively, by NHRI, Korea. The flower color of these cultivars is changed or degraded due to high and low temperature during cultivation and distribution process. The changes of flower color cause economic loss due to quality deterioration and decrease in commerciality. Using genetic transformation, the weak point of these cultivars can be overcome. However the establishment of plant regeneration system was pre-requisite for the genetic transformation. Therefore we tried to develop an efficient plant regeneration system from leaf explants of chrysanthemum ‘Ohblang’ and ‘Baekgang’. The effects of plant growth regulators, BA and NAA, were tested to find the optimal conditions for adventitious shoot formation from leaf explants. The explants were cultured on shoot induction medium, MS medium supplemented with 12 combination treatments of BA and NAA, in darkness for 5 weeks and cultured under the 16/8h photoperiod for 4 weeks. In ‘Ohblang’, the highest shoot regeneration was obtained from the explants cultured on the medium with 1.0 mg/L BA and 1.0 mg/L NAA, inducing 75.0% of shoot development and 3.4 shoots per explants. In ‘Baekgang’, the explants cultured on MS medium with 0.5 mg/L BA and 0.5 mg/L NAA produced the highest shoot regeneration with 62.5% of shoot development and 2.8 shoots per explants. When the regenerated shoots were detached from the explants and cultured on MS medium, the shoots were elongated and rooted successfully.

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Development of a new *S* locus haplotyping system based on three tightly linked genes in the *S* locus controlling self-incompatibility in radish (*Raphanus sativus* L.)

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To develop an efficient and reliable haplotype identification system of the *S* locus controlling self-incompatibility (SI) in radish (*Raphanus sativus* L.), polymorphic sequences of the *SLL2* and *SP6* genes, which were located at each border of the *S* core regions, were used together with those of the *SRK* gene, the female determinant of SI. Partial sequences of the *SP6* and *SRK* genes were isolated from 35 diverse breeding lines that showed differential self-incompatibility responses. A total of 25 *SP6* and 29 *SRK* alleles were isolated in this study, and 29 *SLL2* alleles isolated from the previous study were included for the *S* haplotyping. Whereas the phylogenetic tree of the *SP6* alleles showed species-specific clustering patterns, the phylogenetic tree of the *SRK* alleles revealed intergeneric pairing of some *SRK* alleles, although the others showed species-specific clustering. Among 35 breeding lines, 14 had combinations of the unique *SLL2*, *SRK*, and *SP6* alleles, but the others shared a common allele of either *SLL2* or *SP6* genes. Except for two breeding lines that contained the same *SLL2*, *SRK*, and *SP6* alleles, all breeding lines were shown to harbor unique haplotypes that consisted of different combinations of *SLL2*, *SRK*, and *SP6* alleles. When 73 additional diverse breeding lines were analyzed by this new *S* locus haplotyping system, the haplotypes of all breeding lines were clearly identified. In addition, eight new haplotypes that contained different combinations of the *SLL2*, *SRK*, and *SP6* alleles were identified.

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신규 유전자원을 이용한 고추 탄저병저항성 분자표지 개발 및 국내외 품종육성 과제 진도 보고

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전북 김제시 백산면 (주)고추와 육종

본 과제는 “오믹스 기법을 이용한 고추 탄저병 저항성 분자육종 시스템 개발 및 국내외 품종육성” 과제의 주관 과제인 신규 유전자원을 이용한 고추 탄저병 저항성 분자표지 개발 및 국내외 품종육성(고추와 육종, 윤재복)으로 협동과제인 오믹스 기법을 이용한 고추 탄저병 저항성 유전자 분리 및 기능 검증(농업과학원, 박상렬), 영상기반 고추탄저병 저항성 정밀평가시스템 구축 및 활용(농업과학원, 최인찬)과 협동하여 2018~2020년까지 고추 탄저병 저항성 분자표지 개발하고 이를 이용한 국내외 품종육성을 목표로 하고 있다. 국내외적으로 고추 탄저병 및 바이러스병을 포함한 복합내병성 품종 요구도 증가하고 고추 탄저병균의 다양한 변이가 보고되고 있으며, 국립유전자원센터 및 AVRDC 등을 중심으로 신규 저항성 유전자원이 보고됨에 따라 새로운 병원균과 저항성 유전자원을 이용한 유전학적 연구를 통해서 신규 유전자 발굴(분자표지) 및 이를 이용한 품종 육성이 필요하게 되었다. 현재까지 진행된 연구결과는 다음과 같다. 신규 저항성 소재를 개발하기 위해서 탄저병 저항성이라고 확인된 *Capsicum baccatum* 16계통을 도입하고 분자표지 분석과 포장에서 탄저병 발병정도를 조사하여 탄저병 저항성을 확인하였다. *Capsicum baccatum* 유전자지도 작성을 위해 사용한 양친 유전체 ‘Golden-aji’와 ‘PI594137’을 next generation resequencing 방법으로 염기서열을 해독하여 분자표지를 선별하고 그중에서 264개의 SNP maker를 이용하여 연관지도도를 작성하였다. 또한 양친의 NGS resequencing 후 대량 SNP를 탐색하여 총 509개의 HRM 분자표지를 개발하고 고추 유전자지도도를 작성하였고 탄저병 저항성 HRM 분자표지(Cb-HRM337, Cb-HRM140, Cb-HRM131, HRM262, S1221-585, S1464-716, S585-721, HRM91, HRM89)를 개발하였다. 복합 내병성 육종 계통으로는 CMS 모계통으로 F₃-F₁₀, BC₁F₅ 세대에 걸쳐 진행되었고 B계통은 F₃-F₈, BC₁F₈ C계통은 F₃-F₁₀, BC₁F₅ 세대에 걸쳐 진행되었다. GMS 모계는 F₆-F₉, BC₁F₈ 부계는 F₃-F₉ 세대에 걸쳐 진행되었으며 육성된 계통들은 조합능력검정을 위해 각각 조합을 작성하였다. 선행연구결과를 토대로 우수 계통과 조합을 선별하고 선행연구에서 우수조합으로 선별된 품종은 시교사업을 진행하고 있으며 분자표지 개발을 위해 QTL mapping용 집단을 육성 및 GBS분석을 수행한다.

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The Effects of Keunnunjami embryo on lipid meta metabolism

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Rice is high in carbohydrates, fats and proteins, as well as minerals and minerals, and it is about 69 percent of them in embryos. However, they are generally eaten in the form of polished rice. So the embryo is being discarded. Therefore, this study used a variety of pigment rice(Keunnunjami) that contain various physiological activities compared to ordinary rice. It is intended to provide basic data on pigment rice embryo by examining the effects of the substances contained in rice in lipid metabolism. The study divided 24 rats(SD rat) into three groups (C(AIN93M), NB(AIN93M + normal brown rice embryo), KJ(AIN93M + Keunnunjami rice embryo)). The experiment lasted eight weeks. Eight weeks later, blood was collected at sacrifice and the samples were used to measure TG, TC, HDL, LDL, leptin, FFA, and TNF- α . As a result, there was no significant difference between C and NB, but KJ showed significantly lower values than the others. TG had the highest C group and measured in order of NB and KJ. HDL did not show any significant differences between each group. Leptin, TNF-R, had the highest C group, expressed in order of NB and KJ. FFA confirmed that NB was significantly lower and higher in order of B and KJ. Therefore, in this experiment, Keunnunjami embryo was found to have a positive role in reducing blood cholesterol levels and suppressing inflammatory factors.

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The bean pod mottle virus silencing vector triggers acute response in Rsv resistance gene carrying soybean cultivars.

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Functional genomic studies necessitate the use of silencing vectors such as the widely used bean pod mottle virus (BPMV) vector. Such vectors are not supposed to trigger any extreme response in the host so a normal background can allow better studies on the silenced genes without interference of any off-target genes. Soybean cultivar L29, which carries the resistance gene *Rsv3*, exhibits extreme resistance (ER) against the G5H strain of soybean mosaic virus (SMV), but not against the G7H strain. This resistance is controlled by abscisic acid (ABA) and achieved through callose deposition at plasmodesmata. In an attempt to silence few genes in L29, we found the BPMV vector triggers the several genes in the salicylic acid (SA) and the antiviral RNA silencing pathways. Similar response was observed in soybean cultivars Hwangkeumkong and V94 carrying *Rsv1* and *Rsv4* resistance genes, respectively. Interestingly, the Rsv-free susceptible cultivars Somyongkong and Lee74 did not exhibit such strong response in SA and siRNA pathways. In response to BPMV, the levels of ABA genes were not as highly induced as that found in response to G5H in L29 plants. This implies that *Rsv3* might recognize a BPMV-effector in a different mechanism from that of SMV-G5H, leading to the induction of the SA and siRNA pathways. The use of BPMV silencing vector may offer limited workability for studying plant-virus interactions. However, it unveiled that *Rsv3* can activate two different mechanisms controlled by two different hormones.

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Light inhibits COP1-mediated degradation of ICE transcription factors to induce stomatal development in *Arabidopsis*

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Stomata are epidermal openings that facilitate plant-atmosphere gas exchange during photosynthesis, respiration, and water evaporation. Stomatal differentiation and patterning is spatially and temporally regulated by the master regulators SPEECHLESS (SPCH), MUTE, and FAMA, which constitute a central gene regulatory network along with Inducer of *CBF* Expression (ICE) transcription factors for this developmental process. Stomatal development is also profoundly influenced by environmental conditions, such as light, temperature, and humidity. Light induces stomatal development, and various photoreceptors modulate this response. However, it is unknown how light is functionally linked with the master regulatory network. Here, we demonstrate that, under dark conditions, the E3 ubiquitin ligase CONSTITUTIVE PHOTOMORPHOGENIC 1 (COP1) degrades ICE proteins through ubiquitination pathways in leaf abaxial epidermal cells in *Arabidopsis*. Accordingly, the ICE proteins accumulate in the nuclei of leaf abaxial epidermal cells in COP1-defective mutants, which constitutively produce stomata. Notably, light in the blue, red, and far-red wavelength ranges suppresses the COP1-mediated degradation of the ICE proteins to induce stomatal development. These observations indicate that light is directly linked with the ICE-directed signaling module, via the COP1-mediated protein surveillance system, in the modulation of stomatal development.

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Databases for metabolomics-assisted life science

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A set of small molecules, such as metabolites, is both output and input of organismal activities. Metabolite is the most primitive phenotype (output) governed by genome information of the organism. Whereas, the organismal activity is largely affected by the chemicals in the environment (input), such as nutrients, signal compounds, and toxic materials. For example, human health is affected by food intake and food derived materials transformed by intestinal bacteria. Foods are derived from carbohydrates photosynthesized by plants and from their derivatives transformed by other processes such as fermentation and cooking. Metabolomics—technology for comprehensive detection of small molecules—is prospective for monitoring the chemical flow occurring between the organisms, and for the next generation-life sciences based on this. However, due to a limited availability of authentic standards, identification rates of chemicals still remained lower levels, and an overview of metabolome is difficult to depict. We report here a construction of new databases for metabolite identification. Various computational tools for predicting metabolites based on mass spectra obtained by mass spectrometry have been reported so far. However, these tools only provide “candidate lists” with some matching scores, and researchers have to select the correct one from them. As new information for prioritizing the candidates, we developed a database for experimental evidence of detection of known/unknown metabolite peaks, named “Food Metabolome Repository”. An expansion of the sample coverage will facilitate researchers annotating unknown peaks, and understanding the overview of metabolome.

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Ubiquitin-specific protease, CaDUB1, positively regulates ABA signaling and drought tolerance in *Capsicum annuum*

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Abscisic acid (ABA) is a plant hormone that promotes the adaptive mechanisms to environmental stress conditions. The adaptive mechanisms are tightly regulated and complex processes by stress responsive proteins; however, the precise mechanisms that function under adverse conditions remain unclear. Here, we isolated the pepper, which interacts with CaSnRK2.4. The *CaDUB1* was significantly induced after exposure to ABA, drought, and low temperature. Further, the DUB1-GFP fusion constructs localized in the nucleus. Cell free degradation assay exhibited that the CaDUB1 inhibited CaSnRK2.4 degradation. We used *CaDUB1*-silenced plants and *CaDUB1*-overexpressing (OX) plants to elucidate the biological function of CaDUB1 in response to ABA and abiotic stresses. *CaDUB1*-silenced pepper plants and *CaDUB1*-OX Arabidopsis plants displayed drought-sensitive and -tolerant phenotypes, respectively, which were characterized by regulation of transpirational water loss and stomatal aperture. In drought stress condition, the expression levels of pepper stress-related genes were lower in *CaDUB1*-silenced pepper plants and higher in *CaDUB1*-OX plants than control plants. Our findings suggest that CaDUB1 positively regulates the drought stress response via ABA-mediated signaling.

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The function of the alpha 1,3-fucosyltransferase gene on anther and pollen development in rice (*Oryza sativa*)

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N-glycoproteins alter the functions of numerous cell surface proteins participating in adhesion and migration. α 1, 3-Fucosyltransferase (OsFucT) is responsible for transferring α 1, 3-linked fucose residues to the N-glycan of glycoprotein in rice. We characterized a T-DNA-inserted mutant *Osfuct*, by knocking out the α 1, 3-fucosyltransferase (*OsFucT*) gene in rice. The mutant exhibited defects in anther and pollen development. The pollen grains of the mutant were shriveled and significantly smaller in size. Furthermore, the number of pollen grains per anther and viability decreased dramatically in the mutant compared to the wild type. The mutant was shorter, with fewer tillers, and had shorter internode and panicle lengths under field conditions. Matrix-assisted laser desorption/ionization time-of-flight analyses of the N-glycans revealed that the mutant produced N-glycans lacking the core α 1, 3-fucose residue. Mutant complementation revealed that the phenotype was caused by loss of *Osfuct* function. Transcriptome profiling also showed that several genes essential for plant developmental processes were significantly altered in the mutant, including protein kinases, transcription factors, genes involved in metabolism, genes related to protein synthesis, and hypothetical proteins. Moreover, the mutant showed more sensitive to the increased salt concentration than wild-type. Therefore, Identification and characterization of *Osfuct*-interacting partners to dissect the intricate regulatory gene network may shed further insight into the functions of *Osfuct* impaired growth, anther, and pollen development in rice.

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글로벌 농업생명공학 기술 및 활용 정보공유 시스템 구축

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강원도 평창군 서울대학교 평창캠퍼스 그린바이오과학기술연구원

본 연구는 글로벌 농업생명공학 기술 및 활용 관련 실시간 정보공유 시스템 구축을 통한 국내 연구경쟁력 강화 및 효율적 안전관리 방안 수립 지원을 목적으로 수행되었다. 이를 위하여 농업생명공학응용국제서비스인 ISAAA(the International Service for the Acquisition of Agri-biotech Applications)의 글로벌 네트워크인 농업생명공학정보한국센터(Korea Biotechnology Information Center, KBIC)를 운영하면서 글로벌 연구정보를 수집 제공하고 있다. 수집된 정보는 이슈별로 분류 및 번역 후 KBIC의 웹사이트(<http://isaaa-korea.or.kr>)를 통해 공개되고 있으며, KBIC Newsletter로 매분기 600명 이상에게 E-mail로 제공하여 연구원들과 관계자들이 쉽게 이용할 수 있도록 편의를 제공하고 있다. 또한, 국민의 알권리를 위한 대국민 실시간 소통 프로그램도 적극적으로 추진 중이다. KBIC 홈페이지를 통해 일반인들이 궁금해 하는 주요 이슈에 대한 과학적이고 객관적인 정보를 제공하고 있으며, NAVER 등 인터넷 포털사이트에 등록된 질문에 대해 과학적인 정보를 제공하는 등 SNS를 활용한 온라인 소통에도 노력 중이다. 특히, 제공되는 답변과 정보는 생명공학 및 육종전문가들의 자문을 거치는 등 최대한 과학적이고 객관적인 정보제공이 될 수 있도록 노력하고 있다. 이와는 별도로 직접적인 대화를 통한 대중의 궁금증 해소와 다양한 의견수렴을 위하여 주기적인 열린 토론회도 추진 중에 있다. 이밖에, 생명공학기술에 대한 언론기사 분석을 통해 소비자들의 불안 요인과 궁금증 등에 대한 여론을 수렴하고 이에 대한 올바른 정보제공을 위한 노력도 병행하고 있다. 이러한 노력을 통해 우리나라의 농업생명공학기술 경쟁력 확보와 함께 과학적이고 객관적인 정보공유를 통한 농업생명공학 연구 활성화 및 올바른 활용방안 수립 지원에 노력하고 있다.

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Ethephon application increased mineral uptake and development of adventitious roots of soybean (*Glycine max* L) under waterlogging condition

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Waterlogging is the major obstacle for soybean crop productivity worldwide. To adapt waterlogging condition, soybean plants induced various physiological and morphological changes. The present study was focused on root phenotypic changes, particularly adventitious root development in soybean plants under waterlogging condition. As the plants face with anoxia or hypoxia due to low oxygen level of soil under waterlogging. Therefore, plant turns on the various defense strategies such as development of adventitious root, formation of aerenchyma cell in the root. For this reason, we focused on adventitious root development under waterlogging condition. We confirmed different number of adventitious root between contrasting soybean cultivars [waterlogging tolerance (PI408105A), waterlogging susceptible (S99-2281)] under waterlogging condition. Based on our previous results (two contrasting cultivars showed different level of ethylene), we applied ethephon (50 μ M, 100 μ M, and 200 μ M) to soybean plants grown under waterlogging condition. Results showed that contents of essential nutrients were significantly higher in soybean plants treated with 100 μ M ethephon as compared to non-treated plants. Moreover, ethephon application induced adventitious root initiation and increased root surface area compared to that of non-ETP treated soybean plants. In conclusion, ethephon application induced change of uptake of essential nutrient content of soybean plant under waterlogging thus, we hypothesized that the induced changes are might be because of improved root surface area and increased number of adventitious root.

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옥수수에서 유전자 전달기술 확립 및 효율 증진 연구

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전라북도 전주시 완산구 농생명로 370 국립농업과학원 농업생명자원부

본 과제는 글로벌 유전자 개발 및 유용유전자 기능 연구를 하고 이를 기반으로 유전자 등 생명공학 소재의 해외진출 기반을 구축하기 위하여 국내에서 아직 형질전환 기술 확립이 미흡한 옥수수에서 유전자 전달 기술의 효율적인 기술을 확립하기 위하여 수행하고 있다. 이를 위하여 국내외 옥수수 16 품종에 대하여 재배방법 및 재배시기에 따라 미성숙 배를 분리하여 캘러스를 유도한 후 식물체 재분화 효율을 조사하였다. 그 결과 기존에 재분화 및 형질전환이 비교적 잘되는 것으로 보고된 H99, A188, Hi II A, HW3 등의 미성숙배로부터 캘러스 형성 및 식물체 재분화가 높게 나타났다. 이러한 식물체 재분화는 미성숙 배를 분리한 옥수수 식물체의 재배환경 및 상태가 중요한 영향을 주는 것으로 나타났는데 포트나 그린하우스에서 재배했을 때보다 밭 포장에서 재배한 옥수수로부터 분리한 미성숙 배를 사용했을 때 효율이 높게 나타났다. 식물체 재분화 효율이 높은 것으로 선발된 3계통의 옥수수 미성숙 배(크기 1.5-2.0mm)를 분리 후 리포터 GUS 유전자를 포함한 아그로박테리움으로 transient assay을 하여 형질전환 조건을 탐색하였다. 옥수사용 형질전환용으로 pSB11 superbinary vector를 기본으로 한 Ubiquitin 프로모터에 제초제 저항성 유전자(*bar*) 단자엽용으로 변형된 제초제 저항성 유전자(*MoPAT*)를 융합하여 만든 벡터를 제작하여 형질전환에 사용하였다. 현재까지 안정적인 옥수수 형질전환체를 확보하지 못하였으나 향 후 프로모터 재분리 벡터 제작, 감염 또는 공동배양 시 조건 등에 대한 조사 및 유전자 총을 활용한 형질전환 방법도 시도하고자 한다.

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유전자편집 기반 토마토 옹성불임 변이체 개발 및 활용체계 구축

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전라북도 전주시 완산구 농생명로370, 농촌진흥청 국립농업과학원 농업생명자원부

세계적으로 가공용 토마토의 소비가 꾸준히 늘어 종자소요량이 증가하고 있으나, 종자생산 비용이 판매비 보다 높아 효율적인 종자생산체계가 마련이 시급한 실정이다. 교잡종자(F₁ hybrid) 생산에 옹성불임을 적극적으로 이용하는 고추와는 다르게, 국내에서 생산되는 대부분의 토마토 교잡종자는 제웅교배를 통해 생산되는 것으로 알려져 있다. 본 연구에서는 교잡종자 생산비용을 대폭 절감할 수 있는 토마토 옹성불임 활용체계 구축의 일환으로 CRISPR/Cas9을 이용한 옹성불임 토마토 생산을 시도하였다. 먼저, 자연발생 옹성불임인 MS1035 돌연변이의 RNA seq 기반 전사체 분석과 애기장대 및 벼의 옹성불임 유전자와의 비교를 통해 토마토 수술발달에 관여한다고 예측된 유전자 12종을 선발하였다. CRISPR-P 2.0 프로그램을 이용하여, 선발된 유전자의 서열을 표적으로 하는 guideRNA를 제작하고 이를 Two genes-target CRISPR vector(pAGM4723, Addgene)에 도입하였다. 제작된 유전자 편집용 벡터를 토마토 형질전환을 위하여 *Agrobacterium tumefaciens* EHA 105에 도입하였다. 벡터는 NPTII 유전자가 내재되어 형질전환체 선발에 kanamycin을 사용하며, 하나의 Cas9 단백질과 2개의 sgRNA 및 scaffold 서열을 암호화하고 있다. 현재 수술발달에 관여한다고 예측되는 12종의 유전자에 대한 guideRNA를 사용하여 6개의 벡터를 제작하였으며 토마토 중과로 알려진 M82와 홍광에 형질전환을 진행하고 있다. 금후계획으로는 토마토 형질전환체 대량 생산 및 형질전환체와 대조구의 유전체 서열비교를 통해 유전체 편집 유무를 확인하고자 한다. 유전체 편집이 확인된 형질전환체를 대상으로 화기 구조의 분석으로 옹성불임 특성을 확인할 계획이다.

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Characteristics of plant regenerated through Anther Culture using GM rice

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Anther culture technique offers a great opportunities for accelerating breeding progress and improves grain quality characters. Comparing to the conventional method, the production of the double haploids through anther culture is a rapid approach to homozygosity, shortening the timeline required for the development of a new rice cultivars. Haploids are also valuable for the detection and repair of desirable recessive traits to introduced mutation or hybridization. This study was done to characterize gene pool derived from anther culture. Rice anthers cultured using both one-step and two-step culture methods. Callus induction rate was Ilmi, HV8, and HV23 to 17.8, 7.0, 2.8 % in one-step culture, respectively and 23.0, 14.2, 22.3 % in two-step culture, respectively. Plant regeneration rate was Ilmi, HV8, and HV23 to 16.2, 9.5, 2.3 % in one-step culture, respectively, and 13.9, 2.8, 8.7 % in two-step culture, respectively. It takes time plant regeneration 30 days. On average, acclimation treatment for two weeks was enough to adapt to the outside environment. After 60 days, heading is started. From then after 45 days, plants succeeded colchicine treatment were produced seed. The plants were transferred to field Ilmi, HV8, and HV23 to 186, 49, 200. We have successful to developing of global GM rice on the large-scale raising system for excellent events.

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QTL analysis with optical coherence tomography data to bacterial leaf blight in rice (*Oryza sativa* L.)

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Traditional phytopathological analysis requires the destructive sampling of samples because most plant diseases are based on microbial pathogens. So when we find that plants are infected, especially when crop plants are infected, the yield loss is already doomed. So if we can conduct non-destructive monitoring of plants without cutting them, we may be able to prevent plant diseases in advance. And also we can more accurately identify the changes in lesions of various types of plant diseases and conduct targeted studies on different lesion areas by the molecular biological science. In this study, Bacterial leaf blight (BLB) is one of the most serious biotic stress of rice. The earlier the disease occurs, the higher the yield loss. Yield loss due to bacterial blight can be as much as 70% when susceptible varieties are grown. Then we used optical coherence tomography technique to check the leaf morphology and by comparing the data of physiological structure changes before and after inoculation of leaf surface to determine the pathological features in the interior of the rice leaf. And use QTL program to directly identify the target gene region for lesion site by genetic map. Than using plant molecular breeding techniques to make a new rice population can improve the resistance to BLB disease. Also these defense genes can be used for some other areas of molecular biology.

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Gravistimulation on different orientations changes the accumulation pattern of OsPIN genes encoding auxin efflux facilitator in the endodermis of transition zone in *Oryza sativa* seedlings

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The rice (*Oryza sativa* L.) genome contains 12 putative PIN genes encoding auxin efflux transporters, including four PIN1 and one PIN2 genes. Seedlings grown in a horizontal position develop a specialized protuberance on the lower side of the transition zone between the hypocotyl and the root more over in PCR result also show the over expression of OsPIN2 genes in between hypocotyl and root. The gravity-sensing tissue responsible for regulating auxin distribution in the transition zone is thought to be the endodermal cells. To characterize the gravity-stimulated mechanism, the auxin efflux facilitator PIN-FORMED1 (PIN1) in the endodermis was identified and the localization of OsPIN1, PIN2 and PIN3 proteins during the gravimorphogenesis of *Oryza sativa* seedling were examined. Result suggest that the alter pattern of OsPIN accumulation in the endodermis in response to different orientation and gravistimulation influences lateral auxin transport through the endodermis, resulting in asymmetric auxin distribution in the transition zone.

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Development of performing new forms of rice (*Oryza sativa* L.) related to yield and ecology through SNDH population (Double Haploid) by using QTL analysis

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Rice is a staple and one of the most important food crop consumed by almost half of the world's population. Considering the growing increase of the world's population, more rice production is needed as well as early varieties. In this study, QTLs analysis was conducted to show on a physical map, the chromosomal location of the main QTLs involved in the formation of the major's traits of SNDH rice population (Double Haploid) derived from the cross between Nagdong (japonica) and Samgang (indica). Thus, a total of 14 QTLs are detected and localized on 5 chromosomes. The Heading Date alone has generated 5 of these QTLs. The growth of the different lines of this SNH population was also evaluated and the results obtained revealed for the Heading date measured in 2015 that 5 lines were early rice, 82 lines are mid-season rice and 5 lines were late rice. Those obtained from heading date measured in 2016 showed that 20 lines were early rice, 68 lines were mid-season rice and 6 lines were late rice.

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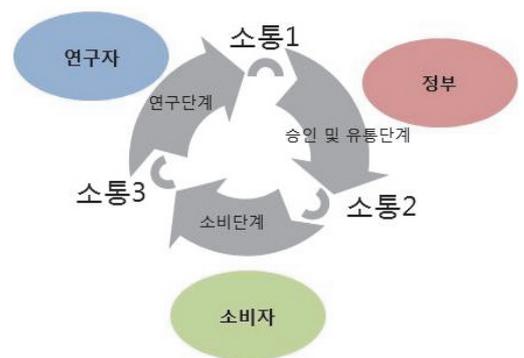
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생명공학(GM)기술에 대한 소통 거버넌스(협치) 전략

김종미

(사)한국공공관리연구원

- 정부지원과 국민의 지지 없이는 연구의 성과를 높일 수가 거의 불가능하므로 생명공학기술의 확산과 소통을 위해서는 무엇보다 상대적으로 전문영역에 해당하는 생명공학기술의 연구자에게 오로지 연구만 요구하는 것이 아니라 기대와 불안이 높아지는 소비자와 정책주도의 정부와 소통과 화합을 위한 거버넌스(협치)가 매우 중요
- 연구자 및 소비자와의 소통을 위한 실증적(인식조사) 분석자료를 바탕으로 정부의 역할 및 협치 전략
 - : 작은 사익추구(이해관계자인 반GMO단체 또는 부정적 연구자)를 위한 부정적 프레임의 확산이 거대한 공익을 포기(상납)하는 어리석음을 깨달을 수 있도록 정보검증 공유 시스템구축
 - : 소비자와 갈등해소 및 소통전략: 정부에 대한 소비자의 의견을 지속적으로 수렴 및 반응을 통한 상호 이해증진과 신뢰제고 (소통2)
 - : 연구자와 갈등해소 및 소통전략: 정부에 대한 연구자의 의견을 지속적으로 수렴 및 반응을 통한 상호 이해증진과 신뢰제고 정부의 정책방향 제시 (소통1)
 - : 정부의 정책방향, 정책의 일관성, 기능배분, 정보제공의 적극성, 표시제를 비롯한 각종 규제강도, 환경 위해성 평가와 인체 안전성 평가 등에 한 인식조사와 요구사항을 바탕으로 소통장벽의 원인규명과 해소를 위한 실증적 진단 및 처방 제시
- 소비자와의 소통을 위한 연구자의 역할 및 협치(governance)전략
 - : 연구자 집단내의 갈등 해소 및 소통전략: 합의(검증)된 용어 및 연구 결과, 효과 등의 정보제공
 - : 소비자와 갈등해소 및 소통전략 : 연구자에 대한 소비자의 의견을 지속적으로 수렴 및 반응을 통한 불안·불신 해소, 신뢰구축, 수요조사를 통한 연구방향 설정(소통 3)



Functional analysis of *Oryza sativa* LATE ELONGATED HYPOCOTYL (*OsLHY*) in controlling of seed development in rice

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In higher plants, a timing of flowering has important role for grain production, in which the optimal timing of flowering leads to increased grain yield. In rice, many flowering time-associated genes and circadian rhythm-associated genes have been identified by plant scientists, but those functions are not clear yet. We have been screened to a various mutants of the flowering associated genes and the circadian rhythm associated genes, and we found an abnormal seed phenotype in *oslhy* mutant.

OsLHY is a homologue gene of arabidopsis *LHY* and CIRCADIAN CLOCK ASSOCIATED 1 (*CCA1*), in which *LHY* and *CCA1* have functional redundancy in arabidopsis, but *OsLHY* (*OsLHY/CCA1*) is just one gene in rice. *OsLHY* is circadian rhythm gene (highly expressed at ZT 0), but the function of *OsLHY* has not been reported yet. In field condition, *oslhy* mutant shows a various defected phenotype as semi-dwarf phenotype, low number of tillers, rolling leaf, and abnormal seed maturation phenotype. Interestingly, abnormal seed development phenotype of *oslhy* mutants can be found from milky stage (about 10 days after heading), and a matured seed shows a brown color, small size, and low maturation rate as *sug-1*, *sug-h*, and *pul* mutant which are involved in starch bio-synthesis pathway. *OsLHY* is MYB-like transcription factor, and locates in nuclei. In micro-array analysis, transcripts level of various starch biosynthesis-associated genes is decreased in *oslhy* mutant than WT, in which *ISA1* (*sug-1*) and *PUL* expression level are significantly decreased in *oslhy* mutant. Taken together, we suggest that *OsLHY* positively regulates transcriptional levels of starch bio-synthetic enzymes, and these regulation is closely involved in seed maturation mechanism in rice.

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Functional analysis of *Oryza sativa* Cryptochrome-Interacting Basic-Helix- Loop-Helix1 (*OsCIB1*) in controlling of leaf angle and grain size in rice

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Cryptochrome-Interacting Basic-Helix-Loop-Helix (*CIB*) plays important roles in various development processes as hypocotyl elongation, flowering, and plastid development in higher plants. It also has been reported that *Glycine Max Cryptochrome-interacting bHLH1* (*GmCIB1*) promotes leaf senescence by activating transcription of senescence-associated genes such as *WRKY DNA BINDING PROTEIN53b* (*WRKY53b*). However, it has not been studied about a function of *OsCIB1* in rice. In this study, we shows a T-DNA inserted mutants, *oscib1-D*, which is highly expressed to *OsCIB1* by 35S promoter inserts in *OsCIB1* promoter region. This gain of function mutant, *oscib1-D*, has a wide leaf angles and long-slender grain phenotype, in which is similar to brassinosteroid (BR) associated phenotype. In real time PCR analysis, we found that over-expressed *OsCIB1* leads to expression of various BR signalling genes, but not leads to BR biosynthesis-related genes. Interestingly, *oscib1-D* plants showed sensitive phenotype to BR, in which we found a increased cell length in adaxial surface of lamina joint in *oscib1-D*, resulting in larger angles. Moreover, we found that the cell elongation-associated genes, as Expansins (EXP's) and Xyloglucan endotransglycosylase/hydrolases (XTH's), were significantly increased in *oscib1-D*. Taken together, these results suggest that *OsCIB1* is involved in the BR signaling pathway, and affects not only leaf inclination but also grain shape by regulating cell elongation-related genes.

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The F-box protein FKF1 inhibits dimerization of COP1 in the control of photoperiodic flowering

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In *Arabidopsis thaliana*, CONSTANS (CO) plays an essential role in the regulation of photoperiodic flowering under long-day conditions. CO protein is stable only in the afternoon of long days, when it induces the expression of *FLOWERING LOCUS T (FT)*, which promotes flowering. The blue-light photoreceptor FLAVIN-BINDING, KELCH REPEAT, F-BOX1 (FKF1) interacts with CO and stabilizes it by an unknown mechanism. Here we provide genetic and biochemical evidence that FKF1 inhibits CONSTITUTIVE PHOTOMORPHOGENIC1 (COP1) dependent CO degradation. Light-activated FKF1 has no apparent effect on COP1 stability but can interact with and negatively regulate COP1. We show that FKF1 can inhibit COP1 homodimerization. Mutation of the coiled-coil domain in COP1, which prevents dimer formation, impairs COP1 function in coordinating flowering time. Based on these results we propose a model whereby the light- and day length-dependent interaction between FKF1 and COP1 controls CO stability to regulate flowering time.

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Development of transgenic rice producing dammarenediol-II of ginseng

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Panax ginseng produces triterpene saponins called ginsenosides, which are classified into two groups by the skeleton of aglycones, namely dammarane type and oleanane type. Among them, Dammarenediol-II is the basic triterpene skeleton in dammarene-type saponin in Panax ginseng. Dammarenediol-II is a useful candidate both for pharmacologically active triterpenes and as a defense compound in plants. This study was conducted to develop transgenic rice plants that produce Dammarenediol-II by overexpression of Panax ginseng dammarenediol-II synthase gene (*PgDDS*). To produce a valuable Dammarenediol-II in rice, recombinant binary vector containing *PgDDS* gene was introduced into rice plants by Agrobacterium-mediated gene transfer. Through Agrobacterium-mediated transformation of rice calli, 63 transgenic plants were obtained. The results of Southern analysis, transgenic plants contained *PgDDS* transgene ranging from one to five copies. The compound of Dammarenediol-II, the products of *PgDDS*, was identified by LC-MS in the T₁ seeds of *PgDDS* transgenic rice plants. Therefore, *PgDDS* transgenic plants can be utilized as a source of pharmacologically active medicinal materials, which suggest that availability of Panax ginseng dammarenediol-II synthase gene could make it possible to engineer ginsenoside biosynthesis to produce ginsenoside aglycones, protopanaxadiol and protopanaxatriol, in transgenic rice plants.

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A N molecular sensor system: a breeding technique for development of high NUE rice under low N conditions

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Nitrogen (N) is an essential nutrient for plant growth and development. N supply from natural soil is insufficient for crop production and rest of N sources are inevitably supplied by N fertilizer. Although N fertilizer induces great benefits in crop yield, overdose of the fertilizer results in a negative impact on the environment. Improvement of N-use-efficiency (NUE) of crops aims to reduce N fertilizer usage while maintaining crop yield. At first, we developed an N molecular sensor system to monitor N status in a rice plant. We identified two genes for allantoin metabolism, *ALLANTOINASE (OsALN)* and *UREIDE PERMEASE 1 (OsUPS1)*, to be highly responsive to N status. *OsALN* was rapidly up-regulated under a low N condition, whereas *OsUPS1* was up-regulated under a high N condition. Taking advantage of their nature in response to N status, we generated N sensors as *proALN::ALN-LUC2* and *proUPS1::UPS1-LUC2* in rice plants. The transgenes mimicked transcriptional regulation of the endogenous *OsALN* and *OsUPS1* genes in response to N status. Importantly, the N sensors showed similar levels of specificity to nitrate and ammonium, inferring the sensing ability of the sensors. Transgenic rice plants with *proUPS1::UPS1-LUC2* sensor showed strong luminescence activity under a high N condition (> 1 mM N source), whereas transgenic plants with *proALN::ALN-LUC2* sensor showed strong luminescence activity under a low N condition (< 0.1 mM N source). Interestingly, >1 mM N substantially increased internal N levels, indicating the luminescence signals of molecular sensors reflect internal N status in rice. With the N sensor-integrated transgenic rice, we generated an EMS mutant population (10,000 individual lines). We are screening the high NUE rice under low N conditions based on the N sensor system and trying to identify key players in rice N metabolism based on bulk segregant analysis and next generation sequencing techniques.

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Seralini's 2012 publication on long term animal study of GMO corn and its effect on the GMO risk communication in Korea

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A French molecular biologist G.-E. Seralini performed a two-year feeding study of GMO corn and Round-up herbicide in rats and reported increases in tumors and mortality among rats fed GMO corn and the Round-Up, published by Food and Chemical Toxicology in September 2012. Numerous independent scientists and regulatory agencies concluded that the study's design was flawed and its findings unsubstantiated. One of the most frequently indicated criticism was that the study used too few rats (10 animals/treatment) to obtain statistically meaningful data, particularly because the strain of rat (Sprague Dawley) used develops tumors at a high rate over its lifetime of about two years. Following widespread criticism by scientists and regulatory agencies over the world, Food and Chemical Toxicology retracted the paper in November 2013 for the reason that its data were inconclusive and its conclusions unreliable. In June 2014 an amended version of the article was republished in Environmental Sciences Europe, a local non-SCI journal. Controversial contents of the article and its impact to the public communications of GMO in Korea are to be presented.

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PAPs-mediated chloroplast development in rice

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Development of chloroplasts largely affects plant growth and productivity because chloroplasts are responsible for photosynthesis and production of biomaterials such as lipids, amino acids and hormones. Transcription of chloroplast genes is a key step determining the development of chloroplasts, and plastid-encoded RNA polymerase (PEP) is a major RNA polymerase governing the transcription of chloroplast genes. PEP regulates transcription of chloroplast genes as a complex involving interaction with PEP-associated proteins (PAPs), suggesting that PAP proteins are essential regulators controlling the activity of PEP and the transcription of chloroplast genes. We attempted to identify 12 PAPs genes in rice whose expressions are suppressed in the rice grown in darkness. To identify key PAP genes in rice, it was attempted to generate CRISPR/Cas9-mediated rice mutants of the 12 *OsPAP* genes. CRISPR/Cas9 system can generate target-specific mutagenesis with the activity of guide RNA. Total 24 guide RNAs were designed for 12 *OsPAPs* mutagenesis (2 independent guide RNAs X 12 *OsPAPs*), and recombined into pRGEB31, a CRISPR/Cas9 binary plasmid. These recombinant DNAs were introduced into rice by rice callus transformation using *Agrobacterium tumefaciens* LBA4404. Additionally, it was also attempted to isolate full-length cDNA of *OsPAPs* for the generation of *OsPAP*-overexpressing transgenic rice. Further analysis of CRISPR/Cas9-mediated *ospap* mutants and *OsPAP*-overexpressing transgenic rice will expand our understanding of PAP-mediated chloroplast biogenesis in rice.

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Optimization of virus induced gene silencing in different petunia cultivars using pepper phytoene desaturase (*PDS*) gene

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Virus-induced gene silencing (VIGS) is widely used for functional analysis of genes in plants. Due to its variation in effectiveness among the plant species, VIGS system was normally optimized using phytoene desaturase (*PDS*) gene as a visible indicator. In this study, we optimized efficient VIGS system for petunia using *PDS* gene isolated from pepper (*Capsicum annuum*) as a visible indicator. Application of the *CaPDS* gene effectively induce gene silencing in petunia cv. Mirage Rose, cv. Mirage Pink, and cv. Picobella Blue. However, silencing effectiveness was observed to be limited by genotypes and inoculation methods because apical meristem application was found to be an appropriate method, while the highest silencing effectiveness was found in cv. Picobella Blue among the cultivars. In addition, it was found that higher silencing effectiveness was associated with higher degradation of the endogenous *PhPDS* mRNA. Moreover, in term of plant age and temperatures, 3-week-old plants grown at 20 °C day/ 18 °C night showed high silencing effectiveness for all cultivars. Taken together, infection of apical meristem of 3-week-old plants grown at 20 °C day/ 18 °C with pTRV2-*CaPDS* exhibited the highest silencing effectiveness for all cultivars. Therefore, this study indicated usage of *CaPDS* for VIGS experiment in petunia and involvement of the different factors in the mechanism influencing silencing effectiveness in petunia, and these results will be helpful to enable high-throughput functional analysis of genes associated with commercially important traits in petunia.

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농업생명공학연구단 도출 생명공학작물 개발성과 분석 및 가치증대 활용방안 연구

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산업화 및 기후변화로 점차 악화되고 있는 농업환경에서 안정적이고 지속적으로 식량자원 확보는 국가안보와 직결되는 문제로 인식되고 있다. 특히, 미국, 중국 등은 기후변화 대응 환경스트레스내성/다수성 생명공학작물 개발연구를 전략적으로 진행하고 있으며, 이와 같은 생명공학작물 종자가 세계 종자시장에서 차지하는 비율도 점차 높아지고 있다.

본 연구는 농업생명공학연구단의 생명공학작물 개발기술 관련 산업재산권 및 육성중인 생명공학작물 이벤트 성과들을 종합 분석하여, 세계 종자시장 진입 및 미래농업 환경에 대응할 수 있는 우수 생명공학 작물개발 기술을 발굴하고, 국내외 다양한 농생명바이오 산업분야로 연구개발 성과물들이 활용될 수 있는 방안을 강구하고자 한다. 차세대바이오그린21사업 1-2단계 선행 연구성과로 출원된 259건의 산업재산권 중 국내 등록유지 특허 109건에 대해 SMART3 특허등급평가로 권리성, 기술성, 활용성 분야를 분석하고 총점 BBB등급 이상의 특허 55건을 실용화 유망 우수기술로 1차 선발하였다. 해당 선발 기술들은 기후변화대응 농업형질 개량을 위한 분자육종소재 개발연구 기술 37건, 형질도입/조직배양기술 7건, 기능성물질생산 시스템 7건이었고, 기능성 소재 응용기술과 검출/진단 기술은 2건으로 나타났다. 특히 생명공학기술로 육성한 식량작물의 재배 및 활용에 관한 규제 심화에 따른 연구개발이 제한적인 현실을 감안하여, 생명공학작물의 활용분야를 국내 의·약학품, 화장품, 건강기능식품 산업 등으로의 재설정하고, 고기능성 산업용 원료 소재 생산 시스템으로서의 생명공학식물 개발연구 성과물을 활용하여 가치 증대하는 방안을 모색하고, 최신 특허동향 및 산업동향 조사 기반 전략적 IP 포트폴리오 및 기술패키징을 수행할 예정이다.

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농업생명공학 분야 과학정보 포털 서비스 구축 연구

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우리 농업의 경쟁력 확보를 위해서는 식량안보 확보 차원의 식량생산 뿐만 아니라 부가가치 창출과 경쟁력 제고를 위한 종자산업 등 농업생명공학을 육성해야 한다. 이를 위해서는 국민들에게 농업생명공학에 대한 객관적이고 투명한 정보 제공과 국민들의 알권리 향상, 지속적인 소통 프로그램 운영을 통한 농업생명공학에 대한 이해 증진과 새로운 기술의 수용성 제고 노력을 통해 국가 발전을 위한 사회적 비용을 절감해야 한다. 최근 국내 미승인 GMO 작물 발견 등 농업생명공학 관련 안전성에 대한 찬반 논쟁이 심화되고, 국민의 안전성에 대한 우려와 안전관리에 대한 요구도 증가하였다. GMO 작물 발견지에 대한 민관협력 안전관리 등으로 국민과의 소통기회가 이전 보다 확대되어 상호 소통을 추진한 결과 농업생명공학에 대한 상호 입장에 대한 이해 부족과 이를 위한 과학적 정보기반 소통의 필요성을 인식하였고 또한 농업생명공학에 대한 정보공개 및 서비스 제공에 대한 국민 요청이 증가하고 있다. 이를 위해서는 농업생명공학에 대한 올바른 과학적 정보를 체계적으로 제공할 수 있는 온라인 포털 정보시스템의 강화와 이를 통한 지속적 과학기반 정보 제공 노력이 강화되어야 한다. 국내 몇몇 사이트에서 GMO 관련 다양한 정보를 제공하고 있으나 농업생명공학 포털 정보시스템에서는 단편적 정보를 포함해 보다 다양한 관점과 시각에서 과학적 이해는 물론 GMO 안전성과 사회적 이슈에 대한 사회적 소통을 위한 콘텐츠 개발을 강화하고 서비스하는 것이 더욱 중요하다. 본 연구에서는 대국민 소통을 목표로 다양한 과학적, 사회적 정보서비스 콘텐츠를 적극 개발 제공할 수 있도록 농림축산용 GMO 정보시스템을 강화하고자한다. 현재 국내외 농업생명공학관련 정보제공 사이트의 정보제공 메뉴와 정보 내용 등 구조분석을 추진 중이며 향후 정보제공 사이트의 구조와 정보 제공 내용 개선을 집중적으로 추진할 계획이다.

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MULTISEEDED affects sorghum grain yield regulating at pedicellate spikelet fertility

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Inflorescence architecture mainly contributes to final grain yield and grain number per panicle (GNP) is a major determinant of grain yield in cereals. Sorghum [*Sorghum bicolor* (L.) Moench] inflorescence is basically composed of one fertile sessile spikelet (SS) and two infertile pedicellate spikelets (PS). To identify regulatory factors involved in the inflorescence architecture, we screened an EMS mutagenesis population from the pedigreed sorghum mutant library. We found inflorescent architecture mutants, named as *multiseeded* mutants, *msdl*_{1,2,3,4}, with gained fertile ability in PS and also an increased number of floral branches. In natural sorghum populations, it is not common that are fertile. A detailed dissection of developmental stages of wild type and *msdl* mutant described that the PS in wild type do not have floral organs, including ovary, stigma, filament and anther, while the *msdl* mutants generate intact floral organ in the sessile spikelet. We found *MSDL* encoded a TCP (Teosinte branched/Cycloidea/PCF) transcription factor using bulk segregant analysis (BSA) of F2 population, and was a strongly enriched expression during inflorescence developmental stages. We proposed that *MSDL* functions to suppress floral organ maintenance at PS during inflorescence development in Sorghum. To explore the regulatory network associated with PS fertility, whole genome expression profiling was performed at 4 different developmental stages in 6 various tissue types between wild type and *msdl*. Whole-genome expression profiling reveals that jasmonic acid (JA) biosynthetic enzymes are transiently activated in pedicellate spikelets. Young *msdl* panicles have 50% less JA than wild-type (WT) panicles, and application of exogenous JA can rescue the *msdl* phenotype. Our results reveal a new mechanism for increasing GNP, with the potential to boost grain yield, and provide insight into the regulation of plant inflorescence architecture and development

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Genome-wide analysis of long non-coding RNAs in radish (*Raphanus sativus*)

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Long non-coding RNAs (lncRNAs) play a vital role in a wide variety of gene regulatory networks related with entire developmental processes and environmental cues. So far, identification and functional analysis of lncRNAs have been limited to several model plant species. Although Brassica species are important vegetable crops, their lncRNAs are not well-predicted thereby only less than 3200 lncRNAs are reported mainly focusing *B. napus*. To explore lncRNAs in *Raphanus sativus*, we analyzed RNA-Seq data generated from distinct 18 tissues and developmental stages that encompass 152 Gb and 1.7×10^9 reads. Of the total 17,448 lncRNA candidates, 12,466 were located in intergenic regions, and 5,022 lncRNAs were in genic. The 11,148 lncRNAs were predicted as antisense while 6,340 were sense RNAs, and mapped on the radish genome ($n=9$, 437.1 Mbp). To identify tissue-specific patterns, we compared the expression levels of lncRNAs derived from 5-week old seedling, 10-week old leaf and root, petal, anther, and pistil. Total 3,230 differentially expressed lncRNAs were obtained. Further, differentially expressed lncRNAs that are related with vernalization were analyzed, and thereby 309 lncRNAs were neo-synthesized and 77 were repressed at the end of 10-week cold treatment. Our predicted lncRNAs will be verified in their expression and functionally analyzed.

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사포닌 생합성 벼의 우수라인 육성

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사포닌은 식물의 이차 대사산물에서 다양하고 풍부한 물질중의 하나로, 인삼, 콩, 도라지, 미나리, 마늘, 양파, 영지버섯, 은행, 칩 등에 풍부하며, 그중 인삼은 생리활성이 가장 높은 진세노사이드 사포닌을 함유하고 있다. 인삼의 주요약리 성분인 사포닌 합성 유전자를 벼에 형질전환하여 사포닌 합성을 유도하였다. 사포닌 합성 벼의 엘리트 라인을 선발하기 위해 약 60라인을 포장에 전개하였다. 모든 라인의 종자를 50립씩 파종하여 2주후 선발마커인 bar 유전자의 삽입을 확인하기 위해 제초제(바스타)를 처리한 후 생존개체를 12주씩 정식하였다. 이 개체들에 대한 유전자삽입 여부, 삽입 copy 수, 삽입위치 등을 분석할 예정이다. 엘리트 라인 중에서 모본과 농업형질이 유사한 계통을 선발하여 후대고정할 예정이다.

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제초제저항성 잔디의 환경모니터링

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GM 작물을 개발 또는 수입하여 환경에 방출하는 등의 재배 또는 상업화를 목적으로 하는 경우에는 반드시 GM 작물의 환경안정성 평가 항목에 따른 과학적인 실험결과를 토대로 안전성 평가심사를 거쳐야만 한다.. 또한, 전 세계적으로 GM 작물의 개발 대상 형질이 점점 다양화되고, 재배면적이 급속하게 증가하고 있으므로, 우리나라도 이러한 GM 작물 개발과 생산에 대비해야 한다. 따라서 작물의 특성 별로 GM작물 안전성을 평가할 수 있는 위해성 평가 모델 시스템을 개발하여 국내에서 GM 작물을 개발하는 연구자들이 활용할 수 있도록 기반을 조성하는 것이 매우 중요하다. 제초제저항성 잔디의 개발되어 실용화 전 단계에 이르렀는데, GM 잔디의 전주와 제주지역의 생육상의 비교평가를 통해 지역적응성 시험을 실시하였다. 또한 GM잔디 재배포장 주변의 환경모니터링을 실시하여 비의도적 환경방출의 가능성을 검토하였다.

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Development of transgenic alfalfa having increased biomass and reduced lignin content

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Alfalfa has widely been cultivated to be used as forage for livestock due to its high nutrient content. However, the digestibility and utilization of alfalfa in livestock industry is hampered by its lignin content. Lignin is a cell wall component along with cellulose and hemicellulose constituents that accumulates in the plant tissues, particularly in the stem. While a certain amount of lignin is essential for healthy plants to be stand upright, lignin is an indigestible component of plants and reduces the fiber digestibility of forages in the rumen of livestock. Therefore, forage producers and commodity purchasers desire alfalfa with lower lignin levels but without loss of nutritional components such as protein and fiber (also called as "high-quality alfalfa").

In this work, we intend to develop biotechnology-derived high-quality alfalfa which has reduced lignin and increased biomass using useful genes including *CBSX2* (Cystathionine- β -synthase Domain-Containing Protein 2) and novel promoters which were screened from our previous studies with *Arabidopsis thaliana*. Through intensive phenotype analysis, we demonstrated that *CBSX2*-overexpressed (*CBSX2*-Ox) *Arabidopsis* plants showed reduced lignin deposition in the stem as well as delayed senescence and abscissions that led elevated biomass production when compared to wild-type plants at the same growth stage. These results strongly indicate that the *CBSX2* gene is a useful source to substantially improve quality and yield traits of alfalfa. Reproducibility of these phenotypes is going to be re-evaluated with *CBSX2*-Ox alfalfa plants that are currently under construction.

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Chemical composition and nutritions properties of soybean cultivars cultivated in the different locations

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This study was to evaluate the nutritional profiles of 14 kinds of soybeans cultivated in the three locations which were Daegu, Suwon, and Jeonju of south Korea. All of these soybeans were cultivated by standard and conventional agricultural practice. Commercial varieties of soybeans were analyzed to compare the nutritional profiles according to the different environmental conditions. The pH of soil, annual rainfall, and weather temperature were investigated for the environment differences. The micronutrients of vitamins, minerals and fatty acids were investigated for the environmental effects. The contents of minerals were not different among three locations but the contents of amino acid and lipid were different significantly ($p < 0.05$) among three locations. Micronutrients were affected more by the environment conditions such as cultivated locations than kinds of varieties. The fatty acid profile showed that linoleic acid, (10.2~12.5% of total) was the most abundant fatty acids followed oleic acid, palmitic acid, linolenic acid and stearic acid. Analyses of mineral content indicated that the most abundant mineral was potassium, followed by magnesium, calcium, iron, zinc, sodium and manganese. These data could be used in the safety assessment of new plants developed by the biotechnology by comparing the substantial equivalence.

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Plasticity between PTI and ETI through Nonsense-mediated mRNA decay

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Nonsense mediated mRNA decay is an essential mRNA control process in eukaryotes that eliminates potentially harmful transcripts containing premature termination codons. Although splicing errors may generate aberrant transcripts carrying upstream ORFs, intron(s) in the 3' UTR or long 3' UTR, the natural transcripts may also become NMD targets by possessing the above NMD-triggering features. A subset of *Arabidopsis* Resistance genes' transcripts are reportedly stabilised during bacterial infection, which suggests decrease of the NMD efficiency by this event. However, whether or not the individual R transcripts are the NMD substrates, and molecular details on release of NMD by bacterial challenge remain at large. We showed that 81.2% and 65.1% of fully spliced natural *TIR-NBS-LRR (TNL)* and *CC-NBS-LRR (CNL)* transcripts, respectively, retain signatures of NMD regulation. Recognition of bacteria initiates the destruction of UPF1, UPF2 and UPF3 within 30 minutes post-infection via the independent ubiquitination of UPF1 and UPF3 and the 26S proteasome pathway, and subsequently, NMD-sensitive *TNL* and *CNL* transcript levels increase. Induction of UPF1/UPF3 ubiquitinations was delayed specifically in *mpk3* or *mpk6*. Our findings therefore demonstrate that NMD is the control tower through which pattern recognition receptors can fine-tune NLR transcript levels to reduce fitness costs and achieve effective immunity.

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화장품 소재 단백질 생산용 형질전환 콩의 인체위해성 및 잡초화 가능성 평가 방법 개발

박정호, 박지영, 엄민식, 김혜진, 김창기*

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콩은 단백질 함유량이 높기 때문에 단백질 화장품 소재 생산에 적합한 작물이다. 본 연구에 사용된 형질전환 콩의 경우 기존에 이용되어온 대장균 발현 방법에 비하여 화장품 소재 단백질 생산단가의 90% 이상 절감이 가능하며 콩 재배 농민들에게 기존 일반 콩 수매가보다 6배 이상의 가격으로 수매가 가능할 것으로 예상된다. 본 연구에서는 화장품 소재 단백질을 생산하는 형질전환 콩 2종류의 인체위해성 평가와 환경위해성 평가 중 잡초화 가능성 평가를 수행하였다. 형질전환 콩의 인체위해성 평가를 위해서 대장균에서 대체 생산을 위한 도입단백질의 대량 정제법을 개발하였다. 또한 대장균에서 생산된 대체 단백질과 형질전환 콩의 도입단백질과의 동질성 검정을 위하여 SDS-PAGE 분석, Western blot 분석 및 N-말단 분석을 진행하였다. 형질전환 콩의 환경위해성 평가 중 잡초화 가능성 검정을 위하여 토양에 매몰된 형질전환 콩 종자의 활력과 잡초와 경합하는 환경에서 지속성을 분석하였다. 본 연구를 통하여 비임상 단회투여독성검정을 위한 시료 생산법을 개발하였고 형질전환 콩에 도입된 단백질의 정제를 위하여 항체를 제작하고 항체결럼을 제작하는데 성공하였으며 이를 이용하여 10개 N-말단 아미노산 서열이 대장균에서 발현된 단백질 서열과 일치하는 것을 확인하였다. 토양에 매몰된 형질전환 콩과 모품종 콩 종자 모두 월동이 가능하지만 6개월 이내에 활력을 잃었다. 이번 연구의 결과는 새롭게 개발되는 고부가가치 형질전환작물의 위해성평가 방법 개발에 기여 할 것으로 사료된다.

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RNAi 기법을 이용한 응애 저항성 생명공학 배추의 개발

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점박이응애(*Tetranychus urticae*)는 약 3,800 개의 넓은 기주 작물 범위를 가지고 있는 잡식성 해충이며, 한국에서 중요한 가치를 지닌 채소 중 하나인 배추도 점박이응애에 의해 피해를 입는다. 또한 살응애제에 저항성을 갖는 점박이응애 개체의 증가로 이를 방제할 다른 방안의 필요성이 대두됨에 따라 본 연구는 식물 매개 RNA interference(RNAi) 기법을 적용하기 위해 수행되었다. 배추의 형질전환을 위한 RNAi vector는 점박이 응애에서 유래한 상보적인 *COPB2* 유전자 단편과 선발 마커로 사용 된 *bar* 유전자를 포함하였다. *Agrobacterium*을 이용한 형질 전환이 수행되었고 DNA 및 RNA 수준의 분석을 통해 생명공학 배추를 선발하였다. 점박이응애 50마리를 접종하여 생물 검정을 수행한 결과, 생명 공학 배추의 잎을 흡즙한 점박이응애는 낮은 생존율을 보이다 접종 10일 후에는 모두 사멸되는 것을 보아 RNAi 기법이 적절히 작동하여 생명공학 배추가 점박이응애에 저항성을 보이는 것으로 확인되었다. 또한 T-DNA 내부 PCR 분석을 통해 도입된 T-DNA의 내부 변형없이 안정적으로 도입되었음을 확인하였으며 T-DNA 삽입 지역의 분석을 통해 도입된 T-DNA가 intergenic 지역에 삽입된 것을 확인하였다. 이후 선발된 생명공학 배추는 뇌수분을 이용한 세대 진전을 하여 선발과 고정 단계를 진행하고 있다. 본 연구 결과 RNAi 기법을 이용한 점박이응애 저항성 생명공학 배추의 개발이 가능함을 입증하였다.

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The change of ABA responsiveness through hydrophobic environments in the VxG Φ L motif of PP2Cs in *Oryza sativa*

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The abscisic acid (ABA) signaling pathway is based on protein-protein interaction between clade A type 2C protein phosphatases (PP2CAs), ABA receptor (PYL/RCAR) and kinase protein (SnRKs) in plants. In stress, ABA trigger for PP2Cs to release stress/ABA-activated protein kinases by binding to ABA-bound receptors for activation. Thus, the interaction of PP2CA with PYL/RCAR is a signaling trigger to respond biotic/abiotic stress. Although the wedging tryptophan in PP2Cs is critical in the interaction with PYL/RCARs in *Arabidopsis* and rice, it remains elusive as to how other interface regions are involved in the interaction. Previously, we reported the identification of a conserved region on PP2Cs, termed the VxG Φ L motif, which modulates the interaction with PYL/RCARs through its second and fourth residues. In this study, the effects of the second and fourth residues on the interaction of OsPP2C50 with several OsPYL/RCAR proteins are investigated by systematic mutagenesis. ABA response strength can be finely tuned with the alteration of hydrophobic environments of the motif to tiny, modest and bulky residues. The fourth residue of the VxG Φ L motif seems to be a major determinant of the interaction between OsPP2C50 and OsPYL/RCAR3 by X-ray crystallography, HDX-MS, bio-layer interferometry (BLI) and phosphatase inhibition assay. Modulation of ABA signaling by mutations in the VxG Φ L motif is demonstrated using rice protoplast system and transgenic *Arabidopsis* plants. Taken together, the VxG Φ L motif of PP2Cs appears to modulate the affinity of PP2Cs with PYL/RCARs and thus is likely to alter the ABA signaling, leading to the differential sensitivity to ABA *in planta*.

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GM콩 재배와 교잡종에 의한 곤충상 영향평가 개발 및 지침서 작성

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형질전환 대두(비타민 A 강화콩 등)의 환경방출과 비의도적 환경방출에 의한 야생콩과의 교잡종이 곤충상에 미치는 영향평가 방법 개발한다. 생태계에 서식하는 곤충 군집은 구성하는 종마다 생물학적 및 생태학적 특성이 다르기 때문에 적절한 모니터링 방법을 사용하여야 군집 및 개체군의 변동을 해석할 수 있으며, 조사방법에 따른 모니터링 방법간 상호 효율성 평가한다. 또한, 형질전환 대두(비타민 A 강화콩 등) 재배에 따른 곤충상의 발생양상 변화 및 잠재해충의 발생 가능성 등 생물환경안전성 평가를 위한 형질전환 대두 및 야생콩과의 교잡종에서 해충과 천적 등 곤충 군집상에 대한 영향을 분석하기 위하여, 포장에 발생하는 주요 곤충과 거미류 등의 절지동물의 계절발생과 먹이그물을 고려하여 절지동물 군집구조, 생물다양성, 발생밀도 및 생태학적 기능군의 구조를 분석한다.

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GM콩과 근연종의 교잡종 개발 및 환경 모니터링 분석

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GM콩은 전체 GM작물 재배 중 50%(9,140만 ha)를 차지하여 가장 많이 재배되는 작물이며, 특히 우리나라는 야생콩의 지리적 원산지로서 자연생태계 확산과 이에 대한 안전관리 문제를 야기할 수 있다. GM콩의 환경위해성 평가와 안전관리를 위해서 GM콩로부터 야생콩으로 수직 유전자이동 가능성, 교잡종의 잡초화/침입 가능성, 종자의 특성, 타감작용 평가 기술을 연구 개발할 필요성이 있다. 체초제저항성 유전자를 포함한 기능성 물질생산 GM콩(비타민 A 강화콩 등)을 이용하여 LMO격리포장에서 개화기 일치 등 자연 교잡 조건을 확립하고 야생콩으로의 유전자 이동을 통한 교잡종을 개발하여 교잡종의 월동성, 휴면성, 생식생육 특성, 경합력 및 침입성 등 잡초화 가능성 항목 조사 설정 및 조사한다. 복수년차 이상의 기간 동안 교잡종의 생식, 성장 특성을 조사하기 위해 장기 영향 평가 포장을 조성하여 생태, 생식 등의 변화를 대조군과 비교하여 교잡종의 잡초화 가능성 평가 및 환경모니터링 분석 방법을 개발할 예정이다.

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화장품 소재 단백질 생산용 형질전환 콩의 농업환경 생물종 위해성 평가 기술 개발

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GM작물은 2016년 기준, 26개국 185.1백만 헥타르에서 재배중이며, 최초 상업화 대비 100배 이상 성장하였으며, 세계 총자시장의 35%를 차지하고 있다. 현재 전세계 재배되는 콩 중 82%가 형질전환 콩이며, 전체 재배된 GM작물 중 50%에 달하는 가장 많은 비중을 차지하고 있어 경제적·상업적 가치가 높은 작물이다. 현재 국내에서 상업적인 목적으로 재배·판매되고 있는 형질전환 콩은 없으나, 형질전환 콩의 환경위해성 평가와 안전관리를 위해서 주변 환경에 미치는 영향에 대한 조사, 분석하고 농업환경 생물종 위해성 평가 기술을 연구 개발할 필요성이 있다. 이를 위해 화장품 소재 단백질 생산용 형질전환 콩에 대한 농업 환경 생물종 선정 및 시료 생산하고 농업 환경 생물종 평가용 형질전환 콩과 비형질전환 콩 시료 생산하고 농업 환경 생물종 위해성 평가 방법 및 평가 기준 설정한다. TRX/EGF 단백질 생산 형질전환 콩에 대한 농업 환경 생물종의 영향 평가를 수행하고 비의도적인 환경 방출에 의한 형질전환 콩 도입 유전자 발현도 분석할 예정이다. 또한, 화장품 소재용 TRX/EGF 단백질 생산 형질전환 콩에 대한 농업 환경 생물종의 영향 평가 표준화 및 가이드 제시할 것이다.

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The potential targets for improving plant tolerance to drought stress using drought-responsive microRNAs

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Abiotic stresses are major constraints of agricultural productivity. Drought, the most serious stress, and its negative impacts are likely to increase worldwide. Recent studies have shown that abiotic stresses induce aberrant expression of many noncoding RNAs, including miRNAs, thus suggesting that miRNAs may be promising targets for genetically improved crop tolerance to abiotic stresses. In general, abiotic stress induces miRNAs to downregulate their target mRNAs, and their downregulation leads to accumulation and activation of positive regulators. This implies that miRNAs do not control directly plant growth and development but control indirectly plant development by mediating a miRNA-target gene network. Therefore, it is evident that endogenous miRNAs have been shown to work as developmental switches and to regulate drought-responsive genes under drought stress. Previously, we identified the rice noncoding RNAs (66 miRNAs and 98 lncRNAs), whose expressions were highly regulated by drought conditions, and whose transcript levels were negatively correlated with the putative target genes. For a further investigation of the biological functions of each miRNA, we generated 12 miRNA overexpressing and knockout lines using constitutive GOS2 promoter and CRISPR/Cas9, respectively. During cultivation, we found several phenotypes in the overexpression lines, including premature leaf senescence, increased number of tillers and grain yield along with the drought tolerance phenotype. The use of miRNA-overexpressing and knockouts and their targets will be a promising technique for determining the native functions of individual miRNAs in response to drought stresses. The identification of the specific positions of miRNAs underlying their regulatory networks represents a convincing research area to pursue in the future.

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Resistance of transgenic rice events (*rbcS:cry1Ac*) against three lepidopteran rice pests

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The transgenic rice expressing *cry1Ac* gene, which is linked to the rice *rbcS* promoter and its transit peptide sequence (*tp*), was highly resistant against all instars of *Cnaphalocrocis medinalis* (Guenetée) (Lepidoptera: Crambidae). In this study, we evaluated the larval mortality, behavior change, and field occurrence of three main rice pests, *C. medinalis*, *Naranga aenescens* (Moore) (Lepidoptera: Noctuidae), and *Parnara guttata* (Bremer & Grey) (Lepidoptera: Hesperidae) in T4 generations of three Bt rice events (*rbcS3:cry1Ac*; 608102, 608104 and 608107) and non-Bt rice. All of the three Bt rice events were resistant to *C. medinalis* which showed significantly higher mortality for all instars compared to non-Bt rice. The resistance of Bt rice events against the larvae decreased gradually as the larvae developed. However, the survived larvae which ingested Bt rice events died eventually without further development. The resistance of three Bt rice events was investigated in the pot test, which was conducted with 3rd instars of *C. medinalis*, *N. aenescens*, and *P. guttata*, showed mortalities of over 70%. In behavioral assay, *C. medinalis* fed on the Bt rice events showed feeding avoidance and less leaf rolling behavior compared to that of the larvae fed on non-Bt rice. A 2-yr field survey conducted with larvae of *C. medinalis* and *P. guttata* also showed that the three Bt rice events significantly had lower damaged on leaves compared to that of non-Bt rice. Overall, the three Bt rice events were highly resistant to the larvae of lepidopteran target rice pests.

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인텔 빅데이터를 기반으로 한 자연변이 벼 품종 활용기술 개발

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차세대바이오그린21사업과 포스트게놈다부처유전체사업을 통해 농생명 빅데이터 생산 및 관련 자료 축적이 급속히 증가했지만 이의 활용을 위한 연구는 여전히 제한적이다. 또한, 현재까지 농업형질이 개선된 우수한 형질전환 식물체가 여럿 제작되었음에도 불구하고 유전자 변형 생물에 대한 오해 및 우려가 높아 이를 실용화하기란 매우 어려운 실정이다. 따라서, 이를 극복하기 위해 사람이 인위적으로 변형한 형질전환 식물체가 아닌 자연적으로 변이가 일어난 벼 품종을 활용하여 유용 작물을 발굴할 필요가 있다. 우리는 차세대 염기서열 해독 기술을 활용하여 483 국내 재배벼 및 핵심계통에 대한 전장염기서열해독 자료를 기반으로 개별 벼 유전자 단위(Locus ID)로 reference 벼 품종인 Nipponbare에 대해 insertion/deletion (indel) 형성 여부를 확인할 수 있는 데이터베이스를 공주대학교 연구팀의 도움으로 구축하였다. 이를 토대로 기존에 보고된 논문 중 가뭄 스트레스에 저항성을 가지는 유전자 5개를 선별한 후, 5개 유전자 모두에서 indel 형성이 일어난 품종 5개 (Cheongdo-donggok-4, Chungdo Hwayang 12, Wase Gingbouzu, AI-CHIAO-HONG, GUAN-YIN-TSAN), indel 형성이 하나도 일어나지 않은 품종 5개 (Pyeongbuk 3, Golyeong-2, Orido, Jejubukjeju-2002-420, Jejubukjeju-2002-340)를 확보하였다. 그 다음 정말로 indel이 형성 또는 형성되지 않았는지 sequencing을 통해 다시 한 번 재확인할 예정이다. 이는 염분 스트레스에 저항성을 가지는 품종을 선별하는 과정에서도 동일하게 적용될 것이다. 현재 공동연구를 통해서 관련 품종이 전개되어 있으며, 돌연변이가 확인된 품종에 대해서 수확 후 가뭄 및 염분 스트레스 실험을 수행할 예정이다. 우리는 이 과제를 통해 빅데이터를 활용한 유용 품종을 탐색 및 확보하고, 이를 실용화 할 수 있는 토대를 만들고자 한다.

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농업애로사항 해결용 유용 생명공학 배추 선발을 위한 농업 형질의 실질적 동등성 분석

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배추의 농업애로사항 해결을 위한 분자 육종 방법에는 배추 자체의 형질 개선을 이용하여 재배 및 육종을 용이하게 하는 방법과 생물학적 및 비생물학적 스트레스에 대한 저항성을 부여하는 방법이 있다. 배추에서의 자가불화합성은 1대 잡종 종자를 유지하기 위한 모본 유지 시 뇌수분, CO₂ 처리 등을 사용하고 있어 인건비 및 탄소 배출 등의 문제가 있다. 또한 배추좀나방의 경우 식해량은 적으나 살충제에 대한 감수성이 낮아 살충 효과가 적어 큰 피해를 주고 있으며, 흡즙성 해충인 응애 또한 잎의 조직을 파괴하여 생육에 영향을 주게 된다. 그러므로 전통 육종 및 분자 육종의 유기적 조화를 통한 신품종 개발은 이러한 육종 효율 증진 및 배추 병해충 피해 억제에 도움이 될 것이다. 이에 따라, 본 연구에서는 분자 생물학적 방법으로 선발된 유용 생명공학 배추를 이용하여, 주요 목표 형질과 함께 농업형질의 실질적 동등성을 확인하고 선발을 통하여 유용 계통으로의 고정 여부를 판단하였다. 각 형질들은 국립종자원에서 공시한 작물별 특성 조사 요령에 맞추어 식물체의 초장, 바깥잎의 크기 및 모양 등과 같은 총 33가지의 특성들을 조사하였다. 이후 배추 형질전환에 사용된 대조군인 inbred line CT001과 생명공학 배추를 비교 분석하여 유용개체를 선발 및 계통화 여부를 결정하였다. 분석 결과 원예형질의 실질적 동등성은 확인되었으며, 해충에 대한 섭식 피해가 유의적으로 적은 계통들이 확인되었다. 이와 같은 연구 결과는 생명공학 배추의 형질 분석 및 고정 연구에 기반이 될 것이다.

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국내 개발 고유 유전자의 형질전환체 분석을 통한 글로벌 시장용 벼 이벤트 선발 및 육성

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국내에서의 GM작물개발은 유전자의 지적재산권 결여, 우량 형질전환 이벤트 부족, 소비자의 사회문화적 수준을 고려하지 않은 GM작물개발 등의 문제점으로 인하여 아직까지 실용화된 예가 없다. 따라서 GM작물의 개발초기부터, 품종화까지 모든 단계에 적용되는 체계적인 GM작물개발 프로토콜과 기술이 필요하다. 본 연구에서는 유전체연구를 통하여 유전자 기능을 검증한 후보들을 활용하여 환경저항성 관련 유용 유전자를 선발하였으며, 국내 고유로 개발된 벡터를 이용하여 *35S:BrTSR15*, *35S:BrTSR53*, *35S:ArCspA*, *35S:PsGPD* 벡터로 재구성하였다. *Agrobacterium*(LBA4404)을 이용하여 총 383개의 독립된 형질전환 벼 식물체를 제작하였으며, TaqMan real time-PCR방법으로 copy수를 분석하여, *35S:BrTSR15*는 29계통, *35S:BrTSR53*는 38계통, *35S:ArCspA*는 52계통, *35S:PsGPD*는 84계통의 one copy T-DNA삽입 식물체를 확보하였다. TaqMan copy number assay 방법을 이용하여 확보된 1 copy 삽입 식물체를 FSTs 분석방법을 이용하여 T-DNA 삽입위치를 분석하여 intergenic 식물체를 선별하였다. 1 copy/intergenic T-DNA 삽입 형질전환 벼 식물체를 세대진전하여 T1 세대에서 copy number 분석법과 배지에서 항생제 선별방법을 이용하여 homozygosity 계통을 27계통 선별하였다. 형질전환체의 발현유무를 확인하기 위해 T0의 재분화 식물체를 RT-PCR을 수행하였다. 대부분의 식물체들이 정상적으로 발현된 것을 확인하였다. 이벤트 개발을 위해 확보된 식물체는 계속적으로 세대진전을 하며 포장에서의 표현형검정을 할 예정이며 또한 각 유전자의 기능 검정을 위해 분자생물학·생리학적 분석을 수행 중에 있다.

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중국 지역적응 이벤트 개발 및 활용을 위한 GM작물 개발

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GM작물 개발에 활용할 플랫폼을 구축하기 위하여 사업단에서 추천하는 국내개발 유용유전자를 분양 받아 형질전환 시스템을 확립하고, 이들 유전자를 조기에 고정하여 이벤트를 개발하는 것을 목표로 한다. 또한 개발된 이벤트를 육종 프로그램을 활용하여 각 지역에 적합한 품종에의 도입을 목적으로 최적의 육종 프로그램을 개발하려 한다. 또한 국내 특히 보유 유전자 및 운반체를 중국에 제공하여, 중국 지역에 적합한 품종에 도입하여 세계 시장 진출의 교두보로 활용 하려 하고 있으며, 고정 품종 뿐 아니라 이벤트를 인디카 계열의 응성불임 계통에 교배를 통해 유전자를 이전하여 1대 잡종 품종을 개발하는 것을 목표로 한다. 내재해성 및 내충성, 내병성을 검정하기에 적합한 지역을 선정하여 후보 유전자의 기능을 검정하고 이들 우수 계통을 이벤트화하고 중국내 각 지역에 적합한 GM품종을 개발하고 이들 품종을 동남아 지역까지 확대해서 보급하려는 과제이다. 금년도 중국 해남도 세대촉진 시험단지에서 68교배조합을 작성하였으며, Bt벼 품종 계통 200개를 세대촉진하였다. PGMS 불임계통 16개와 품종비교시험 계통 8개를 종자 증식 완료 하였다. 작년 Bt 잡종강세 시험결과를 토대로 그 중 우수한 12조합을 대량 채종하여 현재 품종비교시험을 통한 생산성검정시험을 진행하고 있는 중이다. Bt134 GM 계통을 중간시험단계를 완료하고 현재 중국농업부에 환경방출시험 허가를 받아 환경방출 시험을 실시하고 있다.

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Establishing plant viruses as tools to bioengineer corn, soybean, barley and important vegetable crops

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Several CRISPR-Cas9 orthologues have been used for genome editing in plant or animal systems, etc. Recently, a small Cas9 orthologue derived from *Campylobacter jejuni* (CjCas9) has been shown to be functional for efficient genome editing in vivo in animals. Here we used a potyvirus viral vector to efficiently express CjCas9 proteins systemically in *Nicotiana benthamiana*, with confirmation of expression in the newly-formed upper leaves demonstrated by RT-PCR. The single-guide RNA (sgRNA) required for activity is packaged in the viral vector multiple cloning site, flanked by hammerhead ribozyme sequences at both sides, such that the sgRNA is able to precise self-cleavage at these specific site to release the mature sgRNA sequence. Furthermore, a Theophylline-dependent hammerhead ribozyme switch is also used to control the release of the sgRNA. Our work is targeted to production of genome edited seed from the plant viral-Cas9 infected crop, which is expected to be a more convenient, cost-effective, and high-efficiency genome editing method.

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Genome information mediating discovery of useful rice genes for enhanced nutrient use efficiencies and the functional identification.

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This study has a purpose to identify the root development promoting genes using system biology and advanced rice genetic resources and to confirm the enhancement of nutrient utilization efficiency. To do this, a large number of genes predominantly expressed in the root hair or root of rice were identified and analyzed, and seven genes involved in root hair development and revealed by knockout mutations or overexpression studies were selected. Among them, one of overexpression line enhanced tolerance in response to phosphate starvation, and phosphorus content of the transgenic rice plant were about 50% higher than those of the wild-type plant. Another strategy is the evaluation of root-preferred promoters. To investigate the applicability of root-preferred promoters, transgenic rice plants overexpressing *OsPT4* which is involved in phosphate transport were generated by transforming *root-preferred promoter::OsPT4* and *root hair-preferred promoter::OsPT4* into *Dongjin* cultivar. Later, we will test the possibilities for enhanced phosphate use efficiencies compared to those of *ubiquitin promoter::OsPT4* plant. In addition, we analyzed big data sequence information for 483 rice varieties and checked the genetic variations of known nutrient use efficiency relating genes. To confirm the variations of these genes among rice varieties, we selected 23 varieties and will analyze the variation patterns. After then, we will utilize the related varieties to confirm the possibility of application as a breeding material of discovered good agricultural traits through natural variation.

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Strategic approaches to the development of β -carotene-enriched transgenic rice as GMO Events

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As a proof-of-concept, the β -carotene biofortified rice, stPAC (stPsy-F_{2A}-PTp-stCrtI) rice, has been developed via bicistronic expression of rice codon-optimized two synthetic genes encoding phytoene synthase (PSY) and carotene desaturase (CRTI) using ribosomal pausing 2A sequence (F_{2A}) derived from mammalian virus. To develop this β -carotene enriched rice events being able to be commercialized, safety of transgenes were evaluated and vector components to minimize patent infringement and improve the efficiency of transgenes expression were reconstituted. By allergenicity test, any elements in recombinant proteins were not found to possess similarities to known allergens. Through intensive patent search, patent-free vector, endosperm-specific promoters and chloroplast targeting transit peptides (Tp) were found, leading vector replacement from pMJ103 into pPZP200 and selection of globulin (GB) promoter from other two endosperm-specific promoters, glutelin-type B and C promoters and PTp/R3Tp from R1Tp, as most efficient components on β -carotene production in rice endosperm. By comparison of ribosomal pausing activity among 2A sequences, T_{2A} derived from non-mammalian virus were selected to replace F_{2A} since T_{2A} induced complete ribosomal pausing compared to F_{2A}, only inducing ~80% ribosomal pausing. On the basis of these results, we generated *GB::stPTAC* (*GB::stPsy-T_{2A}-PTp-stCrtI*) and *GB::stPTARC* (*GB::stPsy-T_{2A}-R3Tp-stCrtI*) constructs and integrated them into rice genome. Through mass production of rice transformants, 325 stPTAC and 239 stPTARC plants were obtained and 90 and 68 plants were selected as 1 copy-insertion lines by TaqMan-PCR. 45 single T-DNA insertion in stPTAC plant was confirmed by further flanking PCR with leaf tissue at T₀ generation. Among them, 23 plant lines showed the intergenic gene insertion after confirmation of their flanking loci in either or both ends of right and left border on rice genome. The same analysis regarding flanking PCR and intergenic gene insertion in stPTARC plants are being carried out. Collectively, we obtained the final candidates satisfying the eligibility condition as GMO events with 7% efficiency from initial number of rice transgenic plants.

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Carotenoid metabolic engineering via the polycistronic expression using viral 2A sequences and codon-optimized carotenogenic genes in rice endosperm

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In our previous study, the β -carotene biofortified rice, PAC (Psy-F_{2A}-CrtI) rice, showing golden color phenotypes was developed via a bicistronic expression of two genes encoding synthetic phytoene synthase (PSY) and carotene desaturase (CRTI) involving a ribosomal pausing 2A peptide (F_{2A}) from foot and mouth disease virus (Ha *et al.*, 2010). In succeeding study, the more β -carotene-accumulated version of PAC rice, stPAC (stPsy-F_{2A}-stCrtI) rice were invented by replacing *Psy* and *CrtI* gene into codon-optimized synthetic *Psy* (*stPsy*) and *CrtI* (*stCrtI*) (Jeong *et al.*, 2017). To overcome the limit of a mammalian pathogenic viral origin, 2A peptide sequences from *Thosea asigna* virus (T_{2A}) and Infectious myonecrosis virus (I_{2A}) were chosen from non-mammalian viral origins considering the reported in vitro efficiency and examined in planta their efficiency in transgenic rice endosperms. As a result, two recombinant genes of stPTAC (*stPsy-T_{2A}-stCrtI*) and stPIAC (*stPsy-I_{2A2}-stCrtI*) were built to compare their efficiencies for β -carotene production. Both transgenic rice plants expressed golden color and accumulated β -carotene in rice endosperms. Expression analysis of transgenes showed higher expression of proteins in stPTAC than stPIAC line. Interestingly, none of stPTAC and stPIAC lines generated a large form of fusion protein, PSY-2A-CRTI, unlike stPAC line, supporting the better efficiency of both T_{2A} and I_{2A2} than F_{2A} to induce ribosomal pausing. Therewith, by linking two additional synthetic genes encoding β -carotene hydroxylase (BCH) and β -carotene ketolase (BKT), required for zeaxanthin and astaxanthin biosynthesis, into stPTAC, tri-, tri- and tetra-cistronic expression constructs, *stPsy-T_{2A}-stCrtI-I_{2A1}-stBch* as stPTAC-IABc, *stPsy-T_{2A}-stCrtI-I_{2A1}-stBkt* as stPTAC-IABk, and *stPsy-T_{2A}-stCrtI-I_{2A1}-stBch-I_{2A2}-stBkt* as stPTAC-IABc-IABk, were generated, and successfully produced zeaxanthin, astaxanthin and astaxanthin in rice endosperm, respectively. Especially, accumulated astaxanthin in stPTAC-IABk indicated that BCH is not indispensable and can be omitted for astaxanthin metabolic engineering. Immunoblot analysis exhibited co-expression of PSY and CRTI in stPTAC-IABc and stPTAC-IABk lines but only CRTI in stPTAC-IABc-IABk line.

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Epigenetic regulation-mediated drought tolerance in rice

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Epigenetic regulation has been implicated in the many aspects of plant development and stress responses. The underlying mechanisms of epigenetic regulation include DNA methylation, histone modification, and non-coding RNA-mediated regulation of gene expression. Of these, non-coding small RNAs, including microRNAs (miRNAs) and small interfering RNAs (siRNAs), play a crucial role in negative regulation of gene expression at both transcriptional and posttranscriptional levels. To study the epigenetic role of rice small RNAs, small RNAs were sequenced from drought stress-treated seedlings and panicles as well as from control tissues. Using a static clustering method, we identified siRNA loci that matched to a set of 21-24 nt siRNAs that was significantly up- or down-regulated by drought stresses. This result implies that stress-inducible or repressible siRNAs may contribute to epigenetic regulation of gene expression. We also examine the possible role of a miRNA in epigenetic regulation of environmental stress response. In rice, miR820 has been known to be down-regulated by drought stress. It targets OsDRM2, which is involved in de novo DNA methylation of CG and non-CG sequences in the rice genome through a RNA-dependent DNA methylation mechanism. To explore the function of miR820 during drought stress, transgenic rice plants over-expressing miR820 was generated. The transgenic plants exhibited drought-resistant phenotype compared with wild type plants. In addition, several transposable elements, including RIRE7, CACTA, and Tos17, were up-regulated in these transgenic plants. These results might be due to down-regulation of OsDRM2, which is responsible for the suppression of those transposable elements. Possible roles of this epigenetic regulation by miR820 and OsDRM2 as well as their agricultural impacts on drought stress resistance will be discussed.

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식물표현체 기술을 이용한 벼의 생육 및 건조 형질 분석

김년희, 김송림, 최인찬, 지현소, 이홍석, 이은경, 백정호, 양종목, 안은숙, 김경환*

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식물 표현체 연구는 영상 정보를 이용하여 다양한 작물 표현형을 비파괴적으로 분석하는 기술로 단자엽 모델식물인 벼를 이용하여 농업 형질 특성 조사에 활용하고자 하였다. 벼의 영상데이터를 획득하고 분석 알고리즘을 통해 관심영역 (region of interest, ROI)의 잎 면적 (leaf area, LA), 잎 폭 (leaf width, LW), 잎 색 (leaf color, LC), 영상 초장 (projected plant height, PPH), 볼록 선체 (convex hull, CVH), 무게 중심 (center of mass Y, COMY), 밀집도 (compactness, COMP), 이심률 (eccentricity, ECC)의 파라미터를 추출하여 형질 분석에 활용하였다. 실제로, 밀양23호와 기호벼의 재조합 유전 자식세대 (recombinant inbred line, RIL)를 이용 벼 초기 생장물 양적형질 분석에 사용하였다. 그 결과, 초기 생장물의 경우는 2주와 4주의 유묘기에서 잎 면적 (LA)과 영상 초장 (PPH)이 염색체 1번의 반왜성 기간 유전자 (semi-dwarf)인 *sd-1*과 염색체 12번의 유전자좌가 주요 양적형질로 조사되었다. 반면에, 영양 생장시기인 6주와 8주된 식물체들은 영상 추출 파라미터들의 분석을 통해 1번과 12번 염색체외에도, 2, 3, 7, 9, 11번 염색체에서 생장관련 양적형질이 탐색되었다. 아울러 *Phytochrome B* T-DNA 삽입 돌연변이체 (*osphyb*)를 이용하여 건조저항성 형질 분석 결과, 건조 후 회복 시 *osphyb*가 대조구보다 잎 면적, 잎 폭이 크고 식물의 수분 함량이 높아서 개체간 유의성 있는 차이가 있어 건조저항성 형질 분석시 활용가능 할 것으로 판단되었다. 표현체 기술은 다양한 품종 및 형질 특성 분석을 통해 유전자 기능 대량분석, 육종 활용, 자원의 선발 등에 폭넓게 적용될 것으로 기대된다.

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농업생명공학연구사업 성과확산을 위한 사업화 인프라 구축 및 성공사례 도출

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국가 R&D성과의 활용을 위한 기술 수요조사 및 연구개발비 투입 비율이 대학/연구소에 편중되어 있고, R&D 사업화를 위한 산업체의 참여는 저조한 실정으로 R&D 결과물의 사업화는 다양한 형태의 직·간접적 상호작용을 통해 비 유형화된 형태의 성과로 창출되고 있으나 이에 관련한 지식확산 활동 노력은 여전히 부족한 실태이다. 또한 기술이전사업화 과정 및 성과에 중요한 영향을 미치는 요인들을 사업화 환경으로 범주화 할 수 있는 기술 사업화 관련 정책 및 제도, 기술이전 사업화를 위한 인프라(기술평가, 기술금융, 기술거래중개 등)로 구분되며, 연구개발 사업단의 경우, 성과 확산을 위한 인프라의 구축이 필수적인 상황이다. 이에 본 과제에서는 농림식품산업의 기여 및 민간 생명공학작물 개발기업의 육성이라는 농림식품 R&D분야의 정책적 목표 달성 조기화를 위해 생명공학작물 R&D 분야에 기술 전사업화 역량을 집중하는 방안을 마련하고자 하였다. 본 과제 추진내용으로 농업생명공학연구단 1~2단계 기수행과제 및 3단계 과제 진단 및 분석을 진행하였으며, 3단계 과제를 대상으로 사업화 전략수립을 진행하고 있다. 수요기업 발굴, 기술자료집 제작, 기술설명회 개최 등으로 기술 마케팅을 지원하고 있으며, 수행과제기반(Tech-Push) 네트워크 구축 및 타겟기업 기반(Market Pull) 네트워크를 구축하여, 통합 교류회 운영 및 전문가 진단으로 워킹그룹을 운영하여 사업화 전략 수립 및 공유를 지원하고 있다. 또한 연구단 성과 홍보 및 우수사례 확산을 위한 기술가치평가, 맞춤형 비즈니스 모델 개발, 성과 및 기업 통합 DB구축에 대한 연구확산 프로세스를 개발하고자 한다. 본 과제를 통해 연구기관-기술사업화 전문회사 간의 기술사업화 관점에서의 기술 활용 극대화를 통한 성공모델 확보 및 기술 Value-chain 형성하였으며, 이전대상 기술의 기술성, 대상 기업의 재무건정성 등 경영안정성, 사업추진에 따른 비즈니스 모델의 사업성 등을 종합적으로 고려하여 성공적인 Business Model 확립하고자 한다. 또한 기술 실시기업 대상 상용화 현황 및 애로사항을 파악하고, 깎 중간연구 등의 지원을 통해 연구성과의 성공적인 사업화에 걸린 역할을 하고자 한다.

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Stable expression of brazzein protein with alternative sweetener in rice cell lines

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Brazzein is the smallest sweet protein and was isolated from the fruit pulp of *Pentadiplandra brazzeana* Baillon, native to tropical Africa. From ancient times, the indigenous people used this fruit in their diet to add sweetness to their daily food. Brazzein is 500 to 2000 times sweeter than sucrose on a weight basis and 9500 times sweeter on a molar basis. This unique property has led to increasing interest in this protein. However, it is expensive and difficult to produce brazzein other than in its native growing conditions which limits its availability for use as a food additive. In this study, we have studied high production yields of brazzein protein in transgenic rice cell lines. Brazzein gene was constructed by SWPA2 promoter which specific overexpressed in somatic cell of sweetpotato (Kim et al. 2003), and transformed via *Agrobacterium* methods. Total 160 cell lines introduced by Ti-plasmid vector were selected with growth speed. These cell lines were confirmed by PCR analysis and checked gene expression by RT-PCR and Western blot analysis. These results demonstrate that recombinant brazzein was efficiently expressed in rice cell lines, and that we will be development of pilot-scale system to product natural sweetener.

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Manipulation of plant autophagy Atg8 by pathogen effector PopP2

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Autophagy is involved in maintaining cellular homeostasis and regulates biotic/abiotic stresses in eukaryotes. Furthermore, autophagy contributes with both pro-death and pro-survival functions to specific pathogen infections. Several pathogens have evolved strategies to manipulate host autophagy pathways to suppress plant immunity. In this study, the plant autophagy-related gene 8 (Atg8) is colPed and acetylated by *Ralstonia solanacedarum* effector PopP2 which has an acetyltransferase activity. We further identify a putative Atg8 acetylation amino acid residue via a protein sequence analysis. PopP2 acetylates clade-specific Atg8 proteins but still is able to interact with other clade Atg8 proteins. Together, we demonstrate that autophagy Atg8 might be targeted by bacterial pathogen effector to manipulate host autophagy pathway. Regulation of Atg8 acetylation will provide new approaches in crop engineering.

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시데로포아를 대량생산하는 형질전환 양송이 구축

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식용버섯은 다양한 생리활성 작용과 독특한 풍미로 인하여, 소비가 증가하고 있는 건강식품이다. 특히, 양송이버섯은 세계적으로 가장 많이 생산되고 소비되는 대표적인 식용버섯으로 안전성이 입증된 유용한 생물자원이다. 본 연구에서는 양송이버섯에 철분의 흡수와 항생효과, 항암효과를 가진 시데로포아를 합성하는 유전자를 도입한 형질전환체를 제작하고, 이를 이용하여 시데로포아를 대량생산하는 물질생산공장으로 개발하고자 하였다. 이를 위하여 양송이버섯에서 시데로포아 생합성 유전자의 발현을 RT-PCR분석을 통하여 확인하였다. 그 결과 철분의 존재에 의하여 발현이 조절되는 HapX 와 SidA의 존재를 확인하였고, 이들의 대량 발현을 위하여 *Agrobacterium tumefaciens* mediated transformation (ATMT)를 이용한 형질전환체를 제작하였다. 형질전환용 벡터 DNA에 상기한 유전자를 삽입하고, 상시발현 promoter인 GPD promoter에 의하여 발현되게 하였다. pBGgHg-HapX 또는 pBGgHg-SidA를 양송이버섯과 새송이버섯 *gill*에 각 800개의 형질전환 시도를 통하여 10개 내외의 형질전환체를 확보하였다. 확보된 형질전환체의 유전자 서열과 발현분석을 통하여 HapX, SidA 유전자의 발현을 분석중이며, 이를 통하여 시데로포아 생산성을 검증할 계획이다.

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Development of image-based traits for model tomato(Micro-Tome)

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Massive genomic data of tomato has been generating after tomato genome sequence in 2012 and improvement of NGS technology. But most of phenotype data is still collected by using naked eye. Therefore, production speed of phenotype data is limited and it results in the lack of omics data for new cultivar development in agricultural industry of Korea. In order to improve such circumstance, there are needs for gathering phenotype data using image measurement which is possible to improve production speed. Thus development image-based traits for breeding are important for image measurement. In this study, we will develop image-based traits for image measurement through measuring whole growth period of tomato. Model tomato for the research was selected Micro-Tome which is under 90d for growth period and lower than 20cm height, suitable for image measurement. Development of traits process is as follows: 1) For candidate phenotype traits, gathering phenotype traits are guided based on International Union for the Protection of New Varieties of Plants(UPOV), interest of breeders, plant biology, plant anatomy, plant development and growth. 2) For categorizing candidate traits, indexing specific phenotype trait and it's related. 3) Getting morphological traits using image like plant height, leaf area, fruit size, density of shoots and setting condition for suitable image measurement for plant. 4) Comparing candidate traits and morphological traits, then find useful phenotype traits for breeding and image analysis. Through the development of image-based traits for model tomato, it will be used for phenotype data collection based on image measurement and numeric. In addition to the study, we expanded research area to normal tomato from model tomato for developing "Support system establishment on imaging modality for phenotype and selection of breeding tomatoes".

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Comparative study of antinutrient compounds in different Korean soybean varieties

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This study was conducted to evaluate the natural variability of total phenolics, phytic acid, and trypsin inhibitors in soybean varieties and to estimate whether the contents and distribution of these compounds are various among soybeans. 14 samples of commercials were cultivated in the three locations which were Daegu, Suwon, and Jeonju of south Korea. Total phenolics were estimated by using gas chromatography-time of flight mass spectrometry (GC/TOF MS) including tert-butyldimethylsilyl (TBDMS) derivatization. High linearity values of $r^2 > 0.99$ were obtained in the standard calibration curve. Total soluble phenolic acids (free and esterified forms) were characterized to determine the diversity among the phenolic acids. The profiles of 6 phenolic compounds were subjected to statistical analysis, including principal component analysis (PCA). 6 phenolic compounds from the commercial soybeans which were p-hydroxybenzoate, vanillate, syringate, coumarate, ferulate, and sinapate. These phenolic compounds were determined based on the retention time of the standards. PCA allowed for the visualisation of complex data and reveal that the varieties separated from the other PC 1 and PC 2. From this results, it could be concluded that the combined chemometric tools and statistical methods could be useful to the safety assessment for the new biotechnology organisms.

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Production of dammarenediol-II and protopanaxadiol in transgenic rice overexpressing *Panax ginseng* dammarenediol-II synthase gene

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Dammarenediol-II is biologically active tetracyclic triterpenoid, which is basic triterpene skeleton of ginsenoside saponin in *Panax* species. Here, we constructed the transgenic rice overexpressing *Panax ginseng* dammarenediol-II synthase gene (*PgDDS*) driven by rice endosperm-specific alpha-globulin promoter and confirmed the production of dammarenediol-II (DD) in rice grain by LC-MS analysis. Interestingly transgenic rice produced not only dammarenediol-II but also protopanaxadiol (ginseng sapogenin). In *Panax ginseng*, PPD is synthesized via the hydroxylation of DD by CYP716A47 enzyme. It has been known that PPD has a wide range of pharmacological activities. Production of DD and PPD was confirmed by comparison of retention times of total ion chromatogram and mass spectra of their peaks. Non-transgenic rice showed any signals for DD and PPD in rice grains. It is known that rice does not have CYP716 family genes which are lost by evolutionary event. It is interesting that transgenic rice can hydroxylate the DD into PPD, which might be resulted from the hydroxylation activity of unknown intrinsic CYP enzyme in rice. We isolated the putative CYP716B subfamily genes from rice and tested their possible role in hydroxylation activity of DD for the conversion to PPD.

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교배종 제초제내성 GM 잔디의 주변생태계에 미치는 영향평가

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한국잔디의 일종인 들잔디(*Zoysia japonica* Steud.)는 우리나라를 포함한 동아시아 지역과 대부분의 온대지역에 분포하고 있는 난지형 잔디 중의 하나이다. 잔디는 경관보호, 토양보호, 신변보호 등의 목적으로 이용되고 있으며, 도로, 주택, 공원, 스포츠 경기장 등으로 그 활용범위가 점차 확대되고 있다. 이와 더불어 잔디 관련 산업규모가 확대되고 있으며, 병해충저항성, 제초제저항성, 환경스트레스 내성, 왜성, 녹기 연장 등 다양한 특성을 가지는 신품종 잔디의 개발이 요구되고 있다. 잔디의 신품종 개발에는 주로 전통육종방법이 이용되어 왔으나, 전통육종을 통한 품종 개량은 오랜 시간이 걸릴 뿐만 아니라 개량 가능한 형질에도 한계가 있으므로, 최근에는 생명공학 기술을 이용한 신품종 개발 연구가 증가하고 있다. 본 연구팀은 선행연구를 통하여 제초제저항성 들잔디를 개발하였고, 최근에는 이 제초제저항성 들잔디를 부분으로 야생형 금잔디와 교배하여 제초제 저항성과 왜성 형질을 가지는 신품종 잔디를 선발하여 육성하였다. 신품종 잔디는 들잔디에 비해 초장 및 엽장이 짧은 왜성형질을 나타내었고, 엽폭이 좁은 세엽의 특성을 가지고 있었으며 부분의 특이인 제초제저항성도 가지고 있음을 확인하였다. 이와 같이 육성된 신품종 잔디는 외래 유전자가 도입된 GM 작물이므로 상용화를 위해서는 각종 환경위해성평가를 수행하여야 한다. 본 연구에서는 GM 작물의 환경위해성평가 항목 중 GM 잔디의 주변생태계에 미치는 영향에 대한 평가를 수행하고자 하였다. 현재까지 신품종 잔디의 집수정 내의 수서 미생물로의 수평적인 유전자전달 여부를 분석하였으며, 그 결과, 도입유전자의 수평적유전자전달은 일어나지 않은 것으로 확인되었다. 이와 더불어 신품종 잔디 추출물을 사용하여 제브라피쉬의 생육에 미치는 영향을 평가하고 있으며, 향후 이벤트 잔디의 곤충상에 미치는 영향, 토양 세균의 다양성에 미치는 영향 등 다양한 평가를 수행하여 신품종 잔디가 주변 생태계에 미치는 영향을 종합적으로 분석할 계획이다.

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교배종 제초제내성 GM 잔디의 육성 및 환경위해성평가

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들잔디(*Zoysia japonica* Steud.)는 난지형 잔디의 일종으로 우리나라를 포함한 동아시아 지역에 자생하고 있으며, 공원, 묘지, 경사면 녹화 등에 이용되어 왔다. 최근에는 잔디의 이용 범위가 스포츠 경기장, 골프장, 개인 주거지 등으로 점차 확대되고 있으며, 이에 따라 다양한 특성을 가지는 신품종 잔디의 개발이 요구되고 있다. 신품종 잔디에 요구되는 주요 형질로는 제초제 저항성, 환경스트레스 내성, 병해충 저항성, 왜성, 녹기 연장, 시각적 품질 개선 등이 있으며, 이들 형질의 대부분은 전통적 육종 방법으로 개발하기에는 한계가 있다. 본 연구에서는 제초제 저항성을 가지면서 초형, 질감, 밀도 등 시각적 품질이 개선된 신품종 잔디를 개발하기 위하여 선행연구에서 개발된 제초제 저항성 들잔디와 야생형 금잔디를 교배하여 신품종 잔디를 선발·육성하였다. 선발된 교배종 잔디는 제초제 저항성을 가지고 있으므로 잡초관리가 용이하고, 시각적 품질이 우수하기 때문에 경제성도 높을 것으로 기대되고 있다. 그러나 개발된 잔디는 생명공학기술이 활용된 GM 작물이므로 상용화를 위해서는 안전성심사에서 요구되는 각종 환경위해성평가가 반드시 수행되어야 한다. 따라서 본 연구에서는 국내의 GM 작물 개발자들이 활용할 수 있는 환경위해성평가 모델을 개발함과 동시에 신품종 잔디의 환경위해성평가 연구를 수행하고자 하였다. 신품종 잔디를 증식하여 농업적 특성 평가 구역, 유전자이동성 평가 구역, 잡초화가능성 평가 구역을 각각 조성하였고, 연구 계획에 따라 순차적으로 환경위해성평가를 수행할 계획이다. 현재까지 신품종 잔디의 초장, 엽장, 엽폭, 엽각도 등의 농업형질을 조사하였으며, 그 결과, 신품종 잔디는 초장, 엽장, 엽폭 등이 들잔디에 비해 작은 왜성 및 세엽 형질을 가지고 있었으며, 잔디의 질감도 들잔디에 비해 개선된 특성을 나타내었다. 본 연구를 통해 육성된 교배종 잔디는 잔디관리에 있어서 매우 중요한 요소들인 예초 및 잡초제거에 소요되는 비용 및 노동력의 절감에 기여할 수 있을 것이며, 우수한 시각적 품질은 소비자들이 선호하는 형질이므로 경제적 가치도 매우 높을 것으로 기대된다.

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GM콩과 교잡종간의 판별 성분 검출법 개발

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유전자변형(Genetically Modified, GM) 콩의 재배는 꾸준히 증가하여 2016년에 전세계에서 재배되는 콩 중 78%가 GM콩인 것으로 조사되었다. 이는 전체 재배된 GM작물 중 50%에 달하는 규모로, GM콩의 경제적·산업적 가치가 높음을 나타낸다. GM콩이 국내에 식품 및 농업용으로 수입승인되고 있어, 이의 비의도적 환경방출에 대한 조사 및 연구의 중요성이 커지고 있다. 때문에 본 연구에서는 GM콩과 야생콩과의 교잡에 의해 발생된 교잡콩의 대사체 분석을 통해 교잡종을 판별할 수 있는 검출법 개발을 목표로 하였다. 이를 위해, 기능성 물질 생성 증가를 목표로 개발된 비타민A 강화 GM콩과 야생콩을 대상으로 대사체 변화를 확인할 수 있는 분석 체계를 먼저 구축하고, 이후 얻게 될 교잡종에 이를 적용할 계획이다. GM콩의 목적 성분인 비타민A의 전구체인 카로티노이드를 분석하기 위해 HPLC를 이용하였다. 카로티노이드(carotenoids)는 자연계에 약 500여 종이 존재하며 이들 중 약 10%만이 레티놀(retinol)로 전환될 수 있는 것으로 알려져있다. 분석 결과, 비타민A 강화콩의 목적 성분인 베타-카로틴(beta-carotene)은 야생콩에서 상대적으로 미량 존재하였고, 관련된 주요 대사물질인 루테인(lutein)은 모품종(광안콩)>GM콩>야생콩 순서로 함량 차이가 있었다. 이러한 기능성 2차 대사물질의 생합성 경로를 추적하기 위해서는 1차 대사물질 프로파일링 연구가 필수적이다. 현재, GM작물의 목적 성분과 관련된 더 많은 주요 대사물질을 분석할 수 있는 체계를 확대 구축하고 있으며, 더불어 GC-TOFMS를 이용하여 친수성 1차 대사물질을 분석할 수 있는 체계를 콩에 맞춰 구축해나가고 있다. 대사체학을 이용한 포괄적인 대사물질 프로파일 데이터 확보는 기능성 강화 GM작물의 비의도적 환경방출로 인해 발생 가능한 교잡종의 대사변화를 연구하는데 중요한 역할을 할 수 있을 것이다.

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기능성 GM콩의 알레르기성 평가기술 개발

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생명공학기술의 급속한 발전에 따라 새로운 생명공학 작물이 지속적으로 개발되고 있다. 이와 함께 생명공학 작물의 비의도적이며 예기치 못한 영향 평가를 위해서 실질적 동등성 개념을 기본으로 한 안전성 평가가 이루어지고 있다. GM작물을 식품으로 이용할 경우 코덱스국제식품규격위원회(Codex Alimentarius Commission)의 규정 및 가이드라인에 따라 인체 건강 위해에 대한 안전성을 검증받도록 하고 있다. 특히 알레르기 유발성은 코덱스의 평가 방법에서도 별도의 항목을 둘 정도로 중요하게 여기고 있다. 알레르기 중 식품알레르기는 식품이나 식품첨가물을 섭취한 후 발생하는 이상 반응 중 면역 기전에 의해 발생하는 경우를 지칭하며, 대부분의 사람에게는 섭취하여도 문제가 되지 않는 성분이 일부 민감한 사람에게는 섭취 시 비정상적인 면역반응을 일으켜 큰 문제가 될 수도 있기에, GM작물에 도입된 새로운 단백질의 알레르기 유발성 평가는 필수적이다. 따라서 본 연구는 오메가-3 함량을 증대시킨 기능성 콩 형질전환체의 작물학적 가치 평가를 위해, 기존에 재배되고 있는 작물과의 영양성분 및 항영양소 비교 분석 뿐만 아니라 알레르기 유발 가능성 평가를 실시하고자 한다. 이를 위해서 이미 알려져 있는 알레르겐과의 아미노산 서열 상동성을 확인하고 인공소화액, 열 안정성 검정 등 물리화학적 특성시험법을 개발하여 GM콩 품종뿐 만 아니라 새로운 생명공학 작물의 알레르기 유발 가능성을 확인하고 나아가 GM작물 안전성 평가에 대한 자료를 제공할 수 있을 것으로 기대된다.

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Compositional analysis of hot pepper cultivars cultivated in the different locations and the natural variations by the environmental factors

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This study was to evaluate the nutritional profiles of 12 kinds of hot pepper fruits cultivated in the two locations which were Youngyang of Kyeongbuk and Imsil of Jeonbuk for two years. All of these peppers were cultivated by standard and conventional agricultural practice. Commercial varieties of hot peppers were analyzed to compare the nutritional profiles according to the different environmental conditions. The pH of soil, annual rainfall, and weather temperature were investigated for the environment differences. The micronutrients of vitamine, minerals and fatty acids were investigated for the environmental effects. The contents of minerals were not different between two locations but the amino acid contents were different significantly ($p < 0.05$) between two locations. Micronutrients were affected more by the environment conditions such as cultivated years and locations than kinds of varieties. The fatty acid profile showed that linoleic acid, palmitic acid, oleic acid, stearic acid and linolenic acid (0.2~0.5% of total) as the most abundant fatty acids followed lauric acid, arachidic acid, and behenic acid (0.02-0.1 % of total). Analyses of mineral content indicated that the most abundant mineral was potassium, followed by magnesium, calcium, iron, zinc, sodium and manganese. These data could be used in the safety assessment of new plants developed by the biotechnology by comparing the substantial equivalence.

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교배종 제초제내성 GM잔디의 분자생물 및 유전학적 특성평가

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들잔디(*Zoysia japonica*)를 포함한 난지형 조이시아(zoysiagrass) 잔디는 우리나라, 중국, 일본, 동남아시아, 호주 등지에 자생하고 있다. 현재 조이시아 잔디는 아시아 뿐만 아니라 미국, 유럽까지 전파되어 전 세계적으로 정원, 공원, 골프장, 야외 스포츠 공간 등에서 널리 이용되고 있으며 경제적 가치가 높은 산업성 농작물로 분류되고 있다. 잔디는 재배 혹은 잔디밭 조성 시에 잡초관리 비용이 매우 높으므로 제초제내성은 경제적 가치가 매우 높은 형질이다. 본 연구는 글루포시네이트 저항성 유전자변형 들잔디 JG21(*Z. japonica*)와 비변형 금잔디(*Z. matrella*)의 중간교잡을 통해 육성된 고품질 제초제내성 교배종 잔디 계통(JG21-MJ)의 LMO 안전성을 평가하기 위한 시험 연구이다. 당해 연도(2018년)에는 도입유전자 주변염기서열의 안정성 검정, T-DNA의 복제수 및 도입 특성 검정, T-DNA의 backnone DNA의 비의도적 DNA 도입 검정, 교배종 잔디(1세대)의 수분 및 종자 수확을 포함한다. 현재 연구를 위한 식물재료인 JG21의 모본 들잔디, JG21, 교배종 금잔디, 교배종 신품종 잔디 계통 등을 확인하고 관리하는 기본적인 일들을 수행하였다. 또한 차후 고품질 호모 계통 잔디의 선발, 복수세대에서의 도입유전자 안정성 평가 등을 위해 교잡1세대 식물의 자가수분 종자를 채종하였다. 교배종 잔디 내 도입 DNA가 삽입된 계승 상의 위치를 평가하기 위해 도입 DNA의 양쪽 주변염기서열의 특성을 분석하였다.

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글로벌화 가능 신규 재해내성과 수량성 증대 유전자 개발

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지구 환경변화로 인해 발생하는 다양한 환경 스트레스는 작물의 수확량 감소에 직접적인 원인으로 작용한다. 본 연구에서는 환경 스트레스에 내성이 있는 기능이 알려지지 않은 벼 유래의 유전자(*AK102606*)와 1, 2단계에서 검정된 배추(*Brasica rapa* sp.) 유래의 비타민 C 환원 유전자(*BrMDHAR*)의 기능 검정 및 생체 내 유전자의 특성을 심도 있게 규명하고 글로벌화 가능 신규 유용 유전자를 개발하고자 한다. 1차년도 (2018년) 개발목표 중 하나인 *AK102606*와 *BrMDHAR* 형질전환체의 GMO 포장지에서의 재해내성 및 수량성 분석을 위해 각 100-300 개체씩 이양하였다. 또한 GMO 포장지의 비점오염원 분석 및 날씨 모니터링을 위해 온도계를 설치하여 최대·최저기온을 측정하고, 관개수의 이온함량 측정을 진행 중이다. 추가적인 유전자 기능 검정을 위해 *AK102606*와 *BrMDHAR* 두 유전자를 콩에 도입시키기 위해 형질전환에 이용되는 벡터인 pENTR-topo vector로 클로닝을 완료하였다. 1차년도 남은 기간 동안 *AK102606* 벼 형질전환체의 전사체 기반 유전자 발현 및 대사체 물질 분석을 통해 환경 스트레스 내성 메커니즘에 대한 심층적인 분석을 진행할 계획이다.

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Production of recombinant brazzein proteins, a new type of alternative sweetener in transgenic rice

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Brazzein is the smallest sweet protein and was isolated from the fruit pulp of *Pentadiplandra brazzeana* Baillon, native to tropical Africa. From ancient times, the indigenous people used this fruit in their diet to add sweetness to their daily food. Brazzein is 500 to 2000 times sweeter than sucrose on a weight basis and 9500 times sweeter on a molar basis. This unique property has led to increasing interest in this protein. However, it is expensive and difficult to produce brazzein other than in its native growing conditions which limits its availability for use as a food additive. In this study, we report high production yields of, brazzein protein in transgenic rice plants. An ORF region encoding brazzein and driven by the 2 x CaMV 35S promoter was introduced into rice genome (*Oryza sativa* Japonica) via *Agrobacterium*-mediated transformation. After transformation, 17 regenerated plant lines were obtained and these transgene-containing plants were confirmed by PCR analysis. In addition, the selected plant lines were analyzed by Taqman PCR and results showed that 9 T0 lines were found to have a single copy out of 17 transgenic plants. Moreover, high and genetically stable expression of brazzein was confirmed by Western blot analysis. These results demonstrate that recombinant brazzein was efficiently expressed in transgenic rice plants, and that we have developed a new rice variety with a natural sweetener.

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의약소재 당대사 개선용 형질전환 벼 특성 및 효능평가

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거미 피브로인 단백질을 발현하는 당대사 개선용 형질전환 벼의 이벤트 육성과 제2형 당뇨치료효과의 검증자료 확보 및 제시하고자 본 연구를 수행하였다. 연구결과를 요약하면 거미피브로인 단백질은 항산화 작용, 간 기능 개선 작용, 인슐린 분비 촉진 작용, 혈중 콜레스테롤 상승 억제 작용, 신경계 질환 예방 및 개선 작용 등의 임상적 효과가 입증되어있다. 당대사 개선용 형질전환 벼를 대상으로 genotyping을 이용하여 유전자가 안정적으로 도입된 호모라인을 선발하였고, southern blot 분석을 실시하여 형질전환 벼에 도입된 유전자가 single copy로 존재하고 있음을 확인하였다. 또한, northern 및 western blot 분석을 실시하여 형질전환 벼에 도입된 유전자가 안정적으로 강하게 발현되는 것을 확인하였고, 목적단백질인 피브로인 단백질이 안정적으로 합성되는 것을 확인하였다. 선발된 형질전환 벼를 경북대학교 GM포장에 이양하여 바스타 처리를 통한 고정계통 선발, 농업형질 안정계통 및 우수계통 선발 및 검정교배에 의한 고정계통 제작을 통한 유전분석을 실시 중에 있다. Murine fibroblast cell line, NIH 3T3 cell을 대상으로 cytotoxicity, MTT assay 및 caspase-3 activity 분석하여 거미 실크 피브로인 단백질이 세포에 대한 독성이 없으며 및 세포사를 유도하지 않는 것으로 확인되었고, Murine macrophage cell line J774를 이용하여 macrophage stimulation 실험을 통해 거미 실크 피브로인 단백질이 proinflammatory mediator 및 cytokines의 생성을 유도하지 않는 것으로 확인되었다. 자연발생 제2형 당뇨병 모델쥐(BKS.Cg-m^{+/+}db mice)에 형질전환 벼를 급여 하여 당뇨관련 에너지대사과정 조사, 인슐린 신호전달과정 조사 및 당뇨관련 각 조직에서 병태생리 변화조사 실험을 진행 중에 있다. 이런 결과들로 볼 때 형질전환 벼를 의약 소재로 활용이 가능할 것으로 예상되어진다.

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PCR을 이용한 유전자변형 토마토 검출 방법 개발

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1994년 과육 연화 지연 특성을 주입한 토마토, FLAVR SAVR™가 상업용으로 최초 승인된 이래 현재까지 11개의 유전자변형(GM) 토마토가 상업용으로 승인을 받았다(2018년 6월 현재, ISAAA). 최근 외국에서 수입된 유채, 면화 종자에 GMO가 혼입되어 문제가 되고 있는 상황에서 GM 토마토의 유입에 대비하기 위해 GM 토마토를 검출하기 위한 시스템을 개발하고자 하였다. 1차적으로 토마토의 유전자 변형 여부를 검정하기 위한 universal marker 개발에는 cauliflower mosaic virus 35s (CaMV 35s) promoter, *Agrobacterium tumefaciens*의 nopaline synthase (nos) terminator, neomycinphosphotransferase (nptII)를 이용한 다중 pcr을 개발하였다. 또한 GMO로 판별된 토마토를 대상으로 이벤트를 판별하는 방법을 개발하였다. 여기에는 각 이벤트의 고유한 유전자인 1-aminocyclopropane-1-carboxylic acid (ACC) synthase, 1-aminocyclopropane-1-carboxylic acid deaminase (accd), S-adenosylmethionine hydrolase (SAM) gene, anti-sense ethylene-forming enzyme (anti-EFE), polygalacturonase (pg) gene, Cry1Ac, cucumber mosaic virus coat protein (CMVcp)를 목표 유전자로 이용하였다. 이벤트 선별용 검정에는 universal marker를 이용한 다중 pcr의 결과에 따라 사용되는 목표 유전자의 조합을 달리하였다.

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Development of α -linolenic acid-increased soybean by the overexpression of *PfFAD3-1* gene

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α -linolenic acid, an omega-3 fatty acid, is taken as health supplement. For economic reasons, α -linolenic acid is mainly extracted from fish. We have tried to transform soybean cultivated globally to produce competitive crops. *PfFAD3-1* gene, which is derived from *Physaria fendleri* called Lesquerella plant, strongly produces α -linolenic acid. *PfFAD3-1* gene was introduced into soybean by *Agrobacterium*-mediated transformation method. In transgenic plants (T₀), *PfFAD3-1* gene was identified by using PCR and Southern blot analysis of T-DNA. In addition, content of α -linolenic acid in the transformed seeds (T₁) was confirmed by gas-chromatography analysis, and α -linolenic acid content was measured 6-times higher than wild type soybean seeds. Agronomic characters including plant height, the number of nods per plant, branches per plant, pods per plant and total seed weight of 12 transgenic lines (T₁) with high α -linolenic acid content were investigated in the GMO field. As a result, the yield was increased in harvested T₂ seeds.

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Genome plasticity affects bacterial virulence in *Burkholderia glumae*.

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Burkholderia glumae is the causal agent of bacterial panicle blight and has a single LuxI-R type quorum sensing (QS) system. *N*-octanoyl homoserine lactone (C8-HSL) is biosynthesized by signal synthase, TofI, and is recognized by its cognate receptor, TofR. TofR complexes with C8-HSL to regulate production of toxoflavin, one of the major virulence factors of *B. glumae*. We collected 58 *B. glumae* isolates from diseased rice panicles, broken rice, and solanaceae crops. The differences in virulence of the isolates were determined, and its whole genome sequences were analyzed. Most isolates have similar genome structures of *B. glumae* BGR1 possessing two chromosomes and four plasmids. However, five of the isolates were significantly different from BGR1; two isolates had one big merged chromosome, and one isolate had significant gene rearrangement between two chromosomes. In the other two isolates, the genome structure of chromosome 1 was closely related to that of other *Burkholderia* species. Most of the strains isolated from broken rice did not produce toxoflavin. These toxoflavin-negative strains contained an IS element insertion in the promoter region of toxoflavin biosynthetic gene cluster. These results suggested that the *Burkholderia* species isolated from various inoculum have genome plasticity and it affects bacterial virulence.

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Establishing plant viruses as tools to bioengineer corn, soybean, barley and important vegetable crops

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Several CRISPR-Cas9 orthologues have been used for genome editing in plant or animal systems, etc. Recently, a small Cas9 orthologue derived from *Campylobacter jejuni* (CjCas9) has been shown to be functional for efficient genome editing in vivo in animals. Here we used a potyvirus viral vector to efficiently express CjCas9 proteins systemically in *Nicotiana benthamiana*, with confirmation of expression in the newly-formed upper leaves demonstrated by RT-PCR. The single-guide RNA (sgRNA) required for activity is packaged in the viral vector multiple cloning site, flanked by hammerhead ribozyme sequences at both sides, such that the sgRNA is able to precise self-cleavage at these specific site to release the mature sgRNA sequence. Furthermore, a Theophylline-dependent hammerhead ribozyme switch is also used to control the release of the sgRNA. Our work is targeted to production of genome edited seed from the plant viral-Cas9 infected crop, which is expected to be a more convenient, cost-effective, and high-efficiency genome editing method.

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국회의원의 GM기술 및 GMO에 대한 인식변화 추이

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일반적으로 소비자들은 식품 안전성 문제에 있어 매우 민감하게 반응하고 충분한 정보를 제공받지 못하거나 불확실한 정보를 제공하는 경우 소비자들의 식품안전에 대한 불안감은 커진다. 소비자들의 우려를 불식시키거나 위험 인지 수준을 낮추기 위해서는 정확한 정보가 중요하다. 국내에서의 유전자변형식품에 대한 사회적 인식은 부정적인 경향이 높다. 따라서 오피니언 리더 그룹의 정보전달 방법과 전달할 내용을 맞춤형으로 정보제공을 통해 오피니언 리더 그룹에 의한 GMO 인식이 왜곡되지 않도록 하고 올바른 GMO 인식을 확산시킬 필요가 있다. 본 조사에서는 19대 국회의원(2015년)~20대 국회의원(2017년)에 걸쳐 GMO에 대한 국회의원 인식도 조사를 실시했다. 주요 정책을 수립하는 국회의원은 오피니언 리더로서 국민여론형성에 매우 큰 영향을 미치고 있어 국회의원의 GMO 인식도 파악을 통해 정확한 정보제공을 하고 올바른 GMO 정책 수립을 위한 기초자료로 제공하고자 한다. 국회의원의 GMO에 대한 인식도는 2015년 42.4%, 2016년 37.9%, 2017년 46.9%로 50%에 미치지 못하고 있고 GMO에 대해 관심을 갖는 이유는 'GMO의 안전성여부(36.1%)와 국민의 불안감(25.3)이 높게 나타났다. GMO에 대한 지식정도는 평균 응답률이 2015년 54.5%, 2016년 52.5%, 2017년 53.5%로 매년 비슷한 응답을 보여 GMO에 대한 지속적인 정보전달이 필요한 것으로 나타났다. 국내 유전자변형기술에 대한 국회의원의 인식은 '식량위기를 극복할 수 있는 대안이 될 수 있다'는 응답이 2015년 23.6%, 2016년 21.6%, 2017년 28.5%로 식량확보 대안의 응답이 10명 중 3명이다. '환경파괴, 인체위해 등이 우려된다'는 응답은 2015년 32.5%, 2016년 40.5%, 2017년 29.8%로 2017년도에는 다소 감소한 경향을 보였다. GMO표시제 확대법안에 대해 찬성하는 국회의원의 의견은 2015년 93.1%로 높았으나 2016년 79.7%, 2017년 74.1%로 다소 감소하는 경향을 보였다. GMO표시제 확대 법안에 반대하는 이유는 '표시로 인해 소비자의 불안을 야기할 수 있다'와 'GMO 단백질이 남아있지 않는 경우는 검출이 불가능하다'였다. GMO 확대법안에 찬성하는 이유는 '소비자 알 권리 보장하기 위해서(82.7%)'이 높은 응답을 보였다. 우리나라의 GM작물 개발에 대해서 가장 많은 응답은 'GM작물 중 식용이 아닌 사료나 화훼, 의료용 등의 GM작물로만 국한해서 개발해야 한다'로 2015년 38.4%, 2016년 41.9%, 2017년 34.6%이고, 그 다음 'GM작물 개발은 자국의 농업환경을 바꿀 수 있고 식량을 안정적으로 확보할 수 있으므로 우리나라도 GM작물을 상업화시켜야 한다'로 응답률이 2015년 15.8%, 2016년 14.9%, 2017년 25.9%로 2017년이 2016년보다 11% 증가했다. GMO에 대한 의사소통 시 우선 대상으로는 대국민 정보제공의 응답률이 가장 높아 2015년 58.3%, 2016년 62.5%, 2017년 39.0%이고, 국회의원을 포함한 오피니언리더는 2015년 9.6%, 2016년 13.8%, 2017년 33.8%로 오피니언 리더를 대상으로 한 정보제공의 필요성이 점점 증가하는 것으로 나타났다. 필요정보로는 '식품으로서의 안전성에 대한 정보(61.3%)'와 'GM기술의 기대와 우려에 대한 정보(15.1%)'로 나타났다. 국회의원의 GMO 인식도는 50%이하로 여전히 낮은 것으로 나타나 지속적인 정보제공이 필요한 것으로 사료된다.

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농업생명공학에 대한 효율적 정보제공 프로그램 개발

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이용자 중심의 농업생명공학 정보제공 효율화 방안 도출과 생명공학 관련 오프라인 정보제공 분석을 통해 농업생명공학에 대한 효율적 정보제공 프로그램을 개발하고자 연구를 수행되었다. 온라인 농업생명공학 정보제공 효율화 방안 도출을 위한 이용자의 니즈(필요 정보)를 분석하기 위해 설문조사를 수행하였다. 농업생명공학 정보제공 실태에 대한 설문조사는 농업생명공학 연구자와 일반인(성인, 학생, 농업인)으로 대상을 구분하여 진행하였으며, 농업생명공관련 연구자 450명 및 중고등학생 400명을 대상으로 수행되었다. 현재 설문조사 결과를 분석 중에 있으며, 향후 연구자 200명 및 학생 400명에 대한 설문조사를 추가로 진행할 예정이다. 생명공학 관련 오프라인 정보제공 분석을 통한 효율적 정보제공 프로그램 개발을 위해 청소년직업박람회 학생 참석자 100명을 대상으로 DNA 분리체험 및 농업생명공학소개를 수행하였다. 향후 중·고생 및 대학생을 대상으로 한 농업생명공학 오프라인 교육을 추가적으로 4회 이상 수행할 계획이다. 또한 일반 성인 소비자를 대상으로 농업생명공학 교육을 실시하고 피드백을 통한 정보제공 프로그램 효율화 방안 도출도 수행할 계획이다.

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High expression of recombinant proteins in *Arabidopsis* protoplasts by using Gal4/UAS gene expression system and PTGS suppressor

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Various approaches have been attempted to achieve high production of recombinant proteins in plant tissues, such as strong promoter design, specific 5' untranslated region (UTR) insertion, utilization of virus RNA replication system and so on. In this study, we investigated Gal4/Upstream Activation Sequence (UAS) and post transcriptional gene silencing (PTGS) suppressor to utilize them synergistically for high production of recombinant proteins in plant tissues. Compared with the construct driven by the CaMV 35S promoter that is generally used for protein overexpression in plant tissues, coexpression of the Gal4-VP16 led to more than 2 times higher expression level increase of the target protein regulated by the UAS promoter in *Arabidopsis* protoplasts. However, Gal4-VP64m induced protein expression with only similar amount of the target protein driven by the 35S promoter, indicating that 4 repeats of VP16 minimal domain are not sufficient to increase protein expression significantly as reported in previous researches. The PTGS suppressor P38 coexpression also enhanced the target protein expression level effectively and combination with Gal4/UAS system accomplished much higher protein production, suggesting that the synergic effect of these independent approaches can be usefully applied for high production of recombinant proteins. Taken together these results, we concluded that each approach using Gal4/UAS system or PTGS suppressor is remarkably effective for high production of recombinant proteins in plant tissues and sophisticated utilization combining them can be the useful strategy to increase recombinant protein expression level even more dramatically.

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LegCompara: A bioinformatic module for comparative analysis of legume genomes

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Comparative genome analysis is a powerful approach to look into the genomic organizations among different, but evolutionary related, species, to predict function of certain genes of interest and to interpret evolutionary relationships between compared species. For such reasons, development of efficient and automated bioinformatic visualization tool is essential in this research field. To achieve this goal, we intended to construct an interactive and flexible bioinformatic interface for the comparative analysis focused on legume genomes, named 'LegCompara'. This platform consists mainly of two parts: a web-based user interface and corresponding relational databases. The database harbors a diverse array of genomic information (e.g., functional annotation, ortholog groups) for seven legumes (*M. truncatula*, *G. max*, *P. vulgaris*, *C. cajan*, *V. radiata*, *C. arifinum*) and two model plants (*A. thaliana*, *O. sativa*). This genome browser, unlike other traditional genome browsers, was designed for researchers to dynamically interact with user interface, so it can navigate multiple chromosomes of different or same species simultaneously, resulting in genome-wide and/or regional comparisons by depicting corresponding synteny with either blocks or lines between orthologous regions or genes. It is expected that LegCompara may provide researchers and breeders with useful resources for more efficient and user-friendly comparative genome analysis.

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LegExpress: A translational bioinformatic platform for transcriptome analysis of the legumes

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Genome-wide transcriptome analysis is one of the most powerful means to gain a broad and deep insight into the molecular mechanisms that underlie dynamic interactions among numerous genes in organisms. Although several bioinformatic platforms for gene expression profiling have been developed for individual species, platform for cross-species transcriptome analysis is not currently available. We employed the technical concept of translational genomics between different species and aimed to build the platform in user-friendly manner. This DB-linked platform, named LegExpress, harbors wide array of transcriptome data for three representative species with relatively the most comprehensive gene expression information, including *Glycine max*, *Medicago truncatula* and *Arabidopsis thaliana*. All these expression data were collected from publically available ArrayExpress(<http://www.ebi.ac.uk/arrayexpress/>)DB and composed mainly of Affymetrix GenChip data. Raw data were processed to select high-quality transcriptome data and normalized by the RMA standardization method. We developed a program for visualization of the data and organized the user interface according to suitable criteria, such as organs, developmental stages, time courses and different stimuli (e.g., hormones, biotic/abiotic stresses). It is anticipated that LegExpress may play a useful role for breeder/researcher-friendly transcriptome analysis platform and can be applied to design breeding programs through helping breeders discover trait-associated genes.

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작물 표현형 분석을 위한 IR 카메라의 정밀 자세 추정 방법

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작물의 3차원 표현체를 자동 추출하기 위해 다중 시점 영상을 활용하는 경우, 카메라의 자세 및 초점 거리등을 정밀하게 얻어내는 과정이 필요하다. 한국과학기술연구원에서 개발하고 있는 다중 시점 영상 취득 시스템은 정밀하게 제어 되는 회전 로봇 팔에 RGB 카메라, IR 카메라, 깊이 카메라 (depth camera) 등이 설치되어 있어 단 시간내에 단일 작물의 다중 시점 영상을 취득할 수 있는데, 특히 IR 카메라와 깊이 카메라의 경우 적외선 영상을 취득하여 활용한다. 본 연구에서는 chamber내에 설치된 로봇 팔과 그 위에 장착된 IR 카메라의 위치를 정밀하게 추정하는 방법을 개발하였다. 이를 위해 Chamber 벽면에 전방향으로 입사광을 반사하는 retro-reflective 재질의 marker를 배치하고 그 위치를 3차원 레이저로 미리 정밀하게 측정해 둔다. IR 카메라의 뒷 면에 배향된 조명에 의해 전반사 마커가 IR 영상에 취득되게 되며, 미리 측정해 둔 3차원 위치 정보와 영상 내에서 검지된 마커의 위치를 이용해서 카메라의 자세 및 변수를 측정한다. 이 과정은 제한된 화각을 가지는 카메라의 경우 정확히 자세를 추정하지 못하는 문제가 발생하므로, 본 연구에서는 이에 덧붙여 영상 취득시의 로봇 팔의 자세와 팔 끝단에 고정된 카메라의 자세 변동을 동시에 추정하여 더욱 정밀한 자세 추정을 얻을 수 있다. 이 때, 보통 1축의 회전을 가하는 로봇 운동의 특성을 고려한 전방 자세 최적화를 수행하여 노이즈에 강인하고 정확한 카메라 자세 추정이 가능하다. 다중 깊이 영상을 단일 모델로 정합하는 실험을 통해 IR 카메라의 자세 추정 정밀도는 재투영 오차를 기준으로 1 pixel 이내이며 3차원에서도 기존의 방법에 비해 정밀한 위치 정합 결과를 얻어 작물의 3차원 모델을 빠른 시간안에 얻을 수 있음을 보였다.

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Function of iron permeases of *Fusarium graminearum* in pathogenesis

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FgFtr1 and FgFtr2 are putative iron permease and FgFet1 and FgFet2 are putative ferroxidase of *Fusarium graminearum*. They have high homologies to iron permease, ScFtr1 and ferroxidase, ScFet3 of *Saccharomyces cerevisiae* respectively at the level of deduced amino acids. Interestingly, the genes encoding iron permease and ferroxidase were localized on the same chromosome in the manner of FgFtr1/FgFet1 and FgFtr2/FgFet2. The GFP-fused versions of FgFtr1 and FgFtr2 showed normal functions when compared with FgFtr1 and FgFtr2 in *S. cerevisiae* system, and the cellular localizations of FgFtr1 and FgFtr2 in *S. cerevisiae* depended on the expression of their putative ferroxidase partners, FgFet1 and FgFet2 respectively. Although FgFtr1 was found on the plasma membrane when FgFet1 and FgFtr1 were co-transformed in *S. cerevisiae*, most of the FgFtr1 was found in the vacuole when FgFet2 was co-expressed. Furthermore, FgFtr2 was found on the vacuolar membrane when FgFet2 was co-expressed and the vacuolar iron contents were increased when FgFtr2 was deleted. From the two-hybrid analysis, it was confirmed that FgFtr1 and FgFet1 interacts physically and same result was found between FgFtr2 and FgFet2. Iron-uptake activity also depended on the existence of the respective partner. Finally, the FgFtr1 and FgFtr2 were found on the plasma membrane and vacuole respectively in the *F. graminearum*. Taken together, these results strongly suggest that FgFtr1 and FgFtr2 in the *F. graminearum* encode the iron permeases of the plasma membrane and vacuole membrane, respectively, and require its specific ferroxidases to carry out normal function. Furthermore, this report suggests that the reductive iron uptake system is conserved from yeast to filamentous fungi.

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Characterization of a male sterile mutant line reveals that asymmetric microspore division is controlled by a MYB transcription factor in Arabidopsis

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Correct development of gametophytes is central for sexual reproduction in flowering plants. The male gametophyte consists of two sperm cells and a vegetative cell which are formed through a meiotic and two mitotic cell divisions under an elaborate genetic program. In order to further understand the genetic regulation underlying the male gametophytic development, we adopted a forward genetics approach and isolated a mutant line, AP28-23, which dehisces a high level of aborted pollen grains. Genetic analysis revealed that the mutant allele is transmitted normally through the female but rarely through the male. Developmental analysis further showed that mutant microspores develop normally to polarized microspore stage but fail to enter pollen mitosis I and gradually degenerate. Map-based cloning and complementation analysis showed that the mutant pollen phenotypes are caused by a 2-amino-acid deletion in the R2R3 domain of a MYB transcription factor family member. RT-PCR and promoter-GUS reporter analyses showed that this MYB family member is expressed in a male-specific manner. In addition, the MYB-RFP fusion protein driven by the native promoter is detected specifically in the nuclei at the microspore stages and no longer detected after pollen mitosis I. Taken together, we identified a microspore-specific R2R3 MYB transcription factor essential for microspore division which is a determinative step for the male gamete production in Arabidopsis.

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Identification of a gene critical for the germ cell migration after pollen mitosis I in Arabidopsis

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Flowering plants proliferate through double fertilization mediated by the male and female gametophytes. The male gametophyte consisting of two sperm cells as the male gametes and a vegetative cell to generate the pollen tube is formed through an elaborate genetic control. To expand our understanding on the genetic control during pollen development, we morphologically screened mature pollen grains from a mutagenized pool. As a result, we isolated a mutant line, AP26-09, displaying a range of abnormal pollen phenotypes at maturity, which include pollen grains with the germline cells remained against the pollen wall. Genetic analysis showed that the female transmission of the mutation is normal but the male transmission is highly reduced. Developmental analysis revealed that the callose surrounding the germ cell is abnormally accumulated and the germ cell detachment from the pollen wall is impaired. By a map-based cloning and complementation analysis we show the pollen defects in the AP26-09 mutant line arise from a genetic lesion in a *Domain of Unknown Function 707 (DUF707)* gene. Publicly available microarray data and our expression analysis show that the *DUF707* gene is broadly expressed in both somatic and male gametophytic cells. Importantly, promoter fusion and protein fusion experiments show that the *DUF707* is specifically expressed in the germ line cells during pollen development. Our results show that the function of this DUF707 member is required for the germ cell to migrate inward after pollen mitosis I by ensuring correct callose metabolism in the germ cell.

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*Taraxacum kok-saghyz*에서 메탄올의 옆면 살포에 의한 천연고무 생산량 변화

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천연고무는 교통기관, 항공, 의료 등 전 세계적으로 매우 다양한 산업에 이용되는 중요한 원자재중 하나이다. 그러나 이런 중요성에도 불구하고, 현재 천연고무 생산은 파라고무나무 (*Para rubber tree, Hevea brasiliensis*) 단 한 종에만 의존하고 있다. 따라서 천연고무를 생산할 수 있는 대체작물에 대한 연구가 필요하다.

러시안 민들레 (*Russain dandelion, Taraxacum kok-saghyz*, 이하 Tks)는 고무나무의 천연고무와 비슷한 수준의 품질을 가진 천연고무를 생산하는 식물로 알려져 있다. 다만 천연고무의 생산비용은 고무나무에 비해 부족하므로 이를 해결하기 위해 우리는 민들레 개체당 고무생산량을 증가시키는 방법을 찾아보았다.

식물의 바이오매스와 뿌리 발달에 대한 메탄올의 영향은 많은 사람들에 의해 상세히 연구되어 왔으며, 메탄올을 사용하여 작물의 수확량과 생산성을 증가시키는데 관한 몇 가지 보고가 있다. 그래서 우리는 민들레에 메탄올을 처리한 뒤, 고무 생산에 어떤 변화가 일어났는지 확인해보았다.

실험결과, 메탄올을 처리한 민들레와 처리하지 않은 민들레에는 육안으로 확인가능한 분명한 차이가 있었다. 또, 25, 50, 75%의 메탄올 처리 시 식물 개체당 고무함량 및 고무생산량이 25% 처리구에서 많이 증가하였고 75%에서는 감소, 50%에서는 중간 정도의 증가를 보였다. 25%메탄올을 이용하여 옆면 살포와 뿌리 살포를 비교하는 실험을 했을 때, 옆면 살포에서 더 큰 효과를 보였다. 주위 환경에 노출된 밭에서 실험을 했을 때도, 메탄올이 처리된 식물에서 더 많은 고무 생산량을 보였다.

실험의 결과들을 종합하여 생각했을 때, 메탄올은 식물조직 내부에 탄소공급을 증대시키고 증가된 탄소들은 식물체 내의 MVA 및 MEP 경로에 의해 고무 생합성을 촉진하는 것으로 보인다. 따라서 메탄올을 사용하면 생산량과 함량이 증가한다. 다만 고농도의 메탄올이 식물에 작용할 경우 반대의 작용을 하는 것으로 보인다.

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Development of humanized rice cell lines for recombinant protein production in plants

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Plant-based molecular farming has advantages in several ways including production cost and safety. However, differences in the N-glycosylation pattern between plant and human proteins act as barriers to the molecular farming using plants. α 1,3-Fucosyltransferase (*OsFucT*) is responsible for transferring α 1,3-linked fucose residues to the glycoprotein N-glycan in plants. *Osfuct* mutant displayed pleiotropic developmental defects such as impaired pollen development and shorter plant height. Transgenic rice expressing a human α 1,6-Fucosyltransferase (*HsFucT8*) in *Osfuct* mutant is being analyzed with their N-glycan pattern using LC/MS. For the systematic removal of plant-specific N-glycans, CRISPR/Cas9 vectors were constructed and *in vitro* cleavage activity of each targets using ribonucleoprotein(RNP) CRISPR/Cas9 were analysed. These studies would facilitate a further understanding of the function of genes mediating N-glycan modification in plants.

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Development of hybrid-synthetic promoters responding to abiotic stress

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Abiotic stresses such as drought, heat, cold and salinity negatively affect the growth and productivity of crop. In order to cope with abiotic stresses, it necessary to understand the molecular regulatory networks that allow organisms to respond to adverse environmental stresses. Synthetic promoters are commonly used as tools for high level protein production or pathway engineering due to altering upstream regulatory sequence such as transcription factor binding sites.

In this study, we screened 5 stress-inducible promoters that are expressed only under stress conditions, thereby founding 40 *cis*-element in stress-inducible promoters using bioinformatics tool. We also used hybrid-synthetic promoter engineering to construct tightly-controlled, stress-inducible promoters that only express in abiotic stress such as drought. This is achieved by combining *cis*-elements from the native promoters which are expressed only under abiotic stress. Overall, control of the transcriptional networks is an efficient and useful strategy to be resistant to stress without causing growth delays. Furthermore, this approach enabled us to provide as an enabling tool for future synthetic biology applications that seek to exploit stress-resistance within a plant.

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Comparative composition of genetically modified soybeans conferring herbicide tolerance and cosmeceutical protein production

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The development and cultivation of genetically modified organism (GMO) has been increased continuously over recent years. As cosmetic materials, genetically modified soybeans (GM soybean) event CT-1001 and CT-4025 were developed. These soybeans contain genes that encode epidermal growth factor (EGF) and thioredoxin (TRX) genes for reducing skin wrinkles and improving skin whitening function, respectively. In addition, the phosphinothricin-*N*-acetyltransferase gene was used as a selectable marker gene for glufosinate tolerance. However, commercialization of these GM soybeans requires the safety assessment. Forty-six key nutrients (proximates, amino acids, fatty acids, isoflavones, vitamins and anti-nutrients) were analyzed in GM soybeans (non-sprayed and sprayed with glufosinate) and non-transgenic soybeans because comparison of composition is an important consideration in the safety assessment of GMO. Soybeans were cultivated in 2017 at two representative regions (Ochang and Jeonju) located in the Republic of Korea. Statistical analysis was performed to assess compositional equivalence between the GM soybean and non-transgenic soybean. The univariate statistical analysis of the linear model showed that most of the analyzed components in the GM soybeans had non-significant differences compared with its non-transgenic soybean. In addition, most nutritional components of GM soybeans fell within the range of values reported for other commercial lines. These comparisons support the conclusion that CT-1001 and CT-4025 are compositionally equivalent to the non-transgenic soybeans.

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CHIP1 mediates chloroplast anchoring via protein-protein interaction with CHUP1

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Light influences the life of plants not only as an energy source for photosynthesis but also as an environmental signal. Chloroplast photorelocation movement is essential to optimize photosynthetic ability and/or to prevent photodamage under various light conditions. Chloroplasts accumulate at the cell surface under weak light conditions (accumulation response) and move to the anticlinal walls parallel to the direction of incident light under strong light conditions (avoidance response). Chloroplasts attach to the plasma membrane via chloroplast actin (cp-actin) filaments. During the movement, cp-actin filaments are reorganized dynamically according to light intensity and direction. CHLOROPLAST UNUSUAL POSITIONING1 (CHUP1) is a key player not only for chloroplast movement as an actin nucleator but also in chloroplast anchoring by unknown protein-protein interactions. To investigate the molecular mechanism underlying chloroplast anchoring, we carried out yeast two-hybrid assays and identified a CHUP1-INTERACTING PROTEIN 1 (CHIP1) that is a novel plant-specific gene found only in land plant. The interaction between CHUP1 and CHIP1 was further confirmed by *in vitro* and *in vivo* binding assays. Furthermore, CHIP1 was phosphorylated *in vitro* by phot2. Since *Arabidopsis* has the other two CHIP1-LIKE genes (CHIL1 and CHIL2), any significant phenotypic changes were not observed in the single and double mutants of CHIP1 family. In contrast, chloroplasts in the *chip* mutants cell aggregated as shown in *chup* and *kac* mutant cells in *Marchantia polymorpha* that has single copies of those genes. These data suggest that chloroplast anchoring is mediated via protein-protein interaction between CHUP1 and CHIP1.

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Molecular breeding of vegetable crops for optimization of photosynthetic ability in light-controlled plant cultivation system

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Light plays pivotal roles not only in plant growth and development as an important environmental signal but also as an energy source for photosynthesis. Chloroplasts change their intracellular positions to optimize photosynthetic efficiency and/or reduce photodamage in response to the intensity and position of light. Chloroplast movement is redundantly mediated by phototropins (phot1 and phot2). The *Arabidopsis phot2* mutant is susceptible to photodamage under strong light conditions in which the chloroplasts are accumulated at the cell surface. On the other hand, it is expected that the photosynthetic rate of *phot2* mutants could be optimized when light intensity is set at less than a certain critical value to induce photodamage. On the basis of the characteristics of the *phot2* mutant, molecular breeding of vegetable crops is challenged to increase plant productivity in the light-controlled plant cultivation systems of plant factory. We chose green leaf lettuce and butterhead lettuce, of which exhibit high chloroplast motility as *Arabidopsis* does. Two *PHOT1* and *PHOT2* genes were cloned using PCR, based on the genetic information of *Cicerbita plumieri*, both of which belong to the same plant family, Compositae. To make lettuce *phot2* mutants using CRISPR/Cas9 system, three single-guide RNAs (sgRNA) target sites were designed in exons near the beginning of ORFs and were cloned into the Cas9-sgRNA plasmids. Transgenic lettuce plants with antibiotic resistance were obtained using the *Agrobacterium*-mediated transformation procedure.

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Overexpression of auxin biosynthetic enzyme YUCCA6 enhances multiple abiotic stress tolerances in arabidopsis

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Phytohormone auxin (IAA) is involved in every aspect of plant growth and development and is synthesized from tryptophan. YUCCA (YUC) proteins consisting of 11 homologs in Arabidopsis constitute a family of flavin monooxygenases (FMOs) and participate in indole-3-pyruvic acid (IPA) pathway catalyzing the conversion of IPA to IAA. Previously we reported that Arabidopsis YUC6 exhibits thiol-reductase *in vitro* and the activity facilitates drought tolerance *in planta*. Here, we also examined whether overexpression of YUC6 confers other abiotic stress tolerance. First we found that Arabidopsis plants overexpressing YUC6 driven by 35S promoter (YUC6-OX) and activation tagging *yuc6-1D* mutant exhibit enhanced oxidative stress tolerance with controlled ROS accumulation, suggesting that YUC6 may involve in multiple abiotic stress responses via redox homeostasis. Second, *yuc6-1D* shows extreme tolerance to nickel-induced heavy metal toxicity. Third, *yuc6-1D* displays reduced ROS accumulation by cold stress compared to wild-type (WT) plants. To identify whether other phytohormones are also regulated by induced IAA levels through YUC6 overexpression, we analyzed major phytohormones induced by stress condition. While IAA levels increased in YUC6-OX compared to wild type, the levels of jasmonic acid (JA) and salicylic acid (SA) decreased in YUC6-OX plants but abscisic acid (ABA) levels did not change. It suggests that YUC6 overexpression may affect IAA levels only, and be sensitive to biotic stress responses. These data suggest that YUC6 mainly confer the tolerance to abiotic stresses via maintenance of ROS homeostasis. [Supported by a grant from the Next-Generation BioGreen 21 Program (PJ013671012018), Rural Development Administration, Republic of Korea]

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차세대바이오그린21 GM작물개발사업단의 제1단계('11~'14) 및 제2단계('15~'17)의 연구 성과와 사업단을 계승한 농업생명공학연구단의 연구 성과물 보존과 새로운 자원으로서의 가치 부여를 통한 성과의 확대 재생산을 위한 연구 사업을 추진하고 있다. 연구 성과물은 생명정보(유전자 염기서열 정보), 생명자원(유전자 클론, 플라스미드 벡터), 생물자원(종자, 영양체)으로 구분되며 이들 정보를 관리하고 보존하며 활용하는 것이 궁극적인 목적이다. 주요 연구 내용은 1) 기존 GM작물개발사업단 연구 성과물의 유지, 증식, 보존, 2) 미기탁 성과물의 기탁 활성화 및 연구단 신규 자원의 통합 관리, 3) 생명/생물 정보 및 자원의 데이터베이스 구축, 4) 생물자원의 증장기 보존 사업, 5) 생명/생물 정보 및 자원의 분양과 연구 소재로의 재활용 등 이다.

구체적 실현 방안으로 농업생명공학연구원 홈페이지를 통하여 기탁된 생명/생물 정보와 자원에 대한 연구 이력, 상세 정보, 관련 참고문헌, 연구결과 보고서를 DB화한 후 일반(회원) 공개하고 필요시 후속 연구에 대한 추가 정보를 제공한다. 생물자원의 증장기 보존은 국립농업유전자원센터와 업무협약 및 공조를 통하여 증장기 무상 보존할 예정이다. 자원(유전자 클론, 종자)의 분양 서비스는 연구단이 생물자원 개발자와 수요자를 연계하는 중개자의 역할을 수행하는 방법으로 진행할 것이다. 아울러 기탁된 자원의 활력을 증진하고 특성을 검정하기 위한 소규모의 연구사업도 병행할 계획이다. 이 연구 사업을 통하여 연구단 성과물의 공공 소재로의 활용을 촉진하여 관련 연구개발 사업의 연속성 유지에 기여하고자 한다.

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Seed starch improvement in legumes: recent advances and applicability

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Starch is primary insoluble polymeric carbohydrate consisting of glucose, amylopectin and amylose produced mainly by most of higher plants. It also an essential nutritional component of human as well animal diet, also has various food and non-food industrial applications. Legumes which are affordable source of proteins and has potential to produce the starch which has advantage as resistance starch over cereal starch and can be alternative source to meet the increasing world wide demand of starch for various applications. Here we review research in key areas. First, we assess the general mechanism of starch synthesis in heterologous organ of legume. Second, we discuss factors influencing of starch digestibility and chemical composition of major legumes. Third, we access the advances at genetic, transcriptomic and metabolomics level in legumes. Finally, we discuss the breeding and biotechnological approaches being used for the improvement in the seed starch content and nutrition quality in legume crops. This may leads to enhance the food and non-food industrial uses of legume starch and give economic benefit to farmer.

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Optimization of plant expression vector for tomato transformation

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Phosphinothricin (PPT) inhibits the synthesis of glutamate synthase and accumulates ammonium in plants and kills plants. The bar gene encodes phosphinothricin acetyltransferase (PAT) and confer resistance to PPT. Thus, the bar gene is used as a selection marker to make herbicide resistant plants. But some dicot plants such as tomato and tobacco, was sensitively affected by phosphinothricin and declined transformation efficiency. We have introduced with two approaches the bar selection system to solve the problems. First was increase bar gene expression level using strong promoter such as enhanced 35S promoter (double 35S), and increase translation efficiency using the modified GUBQ1 promoter (G1-3:tobaint) which was isolated from the gladiolas polyubiquitin gene and replacement 5' intron of the promoter with 5' intron of tobacco polyubiquitin gene. The other was targeting the PAT enzyme to chloroplast using the transit peptide of oxygen evolving protein/rubisco small subunit. This study was carried out by two methods, transient and transgenic plant. The transient was compared with bialaphos treated with leaves, and the transgenic plant was compared with the normal shoot and root expression on medium containing bialaphos. As a result, in tobacco, PAT expression level was highest when using chloroplast transit peptide of rubisco small subunit and transformation yield was best when using modified GUBQ1 promoter.

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The development of biotic stress resistance plant using Hot pepper NADPH-cytochrome P450 reductase 2 (CaCPR2)

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There are various P450s exist in plant and they need electron to do function. Plant NADPH-cytochrome P450 (CPR) is membrane protein that transfer the electron to various plant P450s. Two types of CPR genes (CaCPR1, CaCPR2) were isolated from hot pepper (*Capsicum annuum* L. cv. Bukang). Quantitative PCR analysis was used for determining CaCPRs mRNA expression levels in various hot pepper tissues. The CaCPR1 expression level was gradually increased during fruit ripening. In case of CaCPR2, however, mRNA was constitutively expressed in all tissues and expression level was lower than CaCPR1. Under the stress condition, both of CaCPR1 and CaCPR2 were increased. There are two types of CaCPR2 (CaCPR2-f, CaCPR2-d) result from alternative splicing and different mRNA expression patterns were observed. CaCPRs were heterologously expressed in *Escherichia coli* to investigate the enzymatic properties. The enzymatic properties of CaCPRs were determined by characteristic absorption spectrum and catalytic activities measurement, which were assessed using protein and chemical substrates including P450, cytochrome c, ferricyanide and MTT. These results reveal that although the CaCPR2-f is not a major CPR in most tissues in hot pepper, but it could plays important role under the stress condition.

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Functional characterization of SIP450-72 gene from tomato through in vivo and in vitro

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The Cytochrome P450 proteins are the most abundant in number of members at plant comparing the other organisms. As many researches previously reported, plant P450s are necessary for the catalysis of many major reactions, typically in production of primary and secondary metabolites. The functions of these P450s normally involve the biochemical synthesis pathways included of terpenoids, fatty acids, lipids, as well biosynthesis of plant hormones. Especially, the many products which were metabolized by P450s are extremely important for chemical defense mechanism, and those things are their outstanding and noticeable role. Tomato plants also contain numerous CYP genes in their genome, however most of them have unknown function. To study their function, a P450 in CYP736A subfamily, CYP736A72 gene, isolated from tomato (*Solanum lycopersicum* cv. Micro-Tom) was selected. To discover the enzyme character of CYP736A72, this gene was heterologously expressed in *E. coli*, and the protein obtained after induction was used for analytical assays. The initial results show that this enzyme has 7-ethoxycoumarin *O*-deethylation activity. To identify the function of CYP736A72 in plant, the transgenic lines of tomato and tobacco (*Nicotiana tabacum* cv. Xanthi-NC) which over-expressed CYP736A72 gene were developed and observed.

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차세대바이오그린21 사업 시스템합성농생명공학사업단

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The comparison of two base-editors for precise nucleotide substitution in plants

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Cas9 proteins fused with cytidine deaminase can induce C to T nucleotide substitutions at a specific site when directed by guide RNAs. We examined the substitution activity and the substitution range of two base-editing systems: APOBEC1-nCas9 and nCas9-PmCDA1 to each other in the protoplasts of *Nicotiana tabacum* and *Brassica napus*. We then converted the specific amino acid in the *acetolactate synthase* gene of *N. tabacum* to generate herbicide-resistant plants. This study provides guidelines on which a base editor to use and how to adjust the length of a guide RNA for nucleotide substitutions at the desired genomic position in plants.

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Manipulation of inflorescence architecture for tomato productivity

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Inflorescence architecture highly influence flower production and crop yields. The inflorescence variations is determined by subtle changes of molecular programs during meristem maturation at the floral transitional stage. Here we introduce two most recent achievements for manipulation of inflorescence architecture especially for improving tomato productivity. First, we achieved a remarkable continuum of inflorescence variants by crossing natural and engineered alleles of inflorescence branching regulators with enhancing dosage sensitivity of the regulators. *s/+* and *j2^{TE} ej2^w/+* successfully allowed breeding of higher yielding genotypes. Second, CRISPR/Cas9 genome editing of S promoter resulted in diverse cis-regulatory alleles that provide beneficial variations in inflorescence branches. Six distinct promoter alleles (S^{CR-pro}) are revealed a range of inflorescence branching which would lead to breeding process for improving tomato productivity. Therefore, our approaches allow two methods for induction of inflorescence variations and immediate selection for fine-tuning of yield productivity.

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**차세대바이오그린21 사업
농생물게놈활용연구사업단**
유전체육종 활성화를 위한 빅데이터 플랫폼 소개

일시 2018년 7월 13일(금)
장소 제주 라마다플라자 호텔



- 유전체육종 활성화를 위한 빅데이터 플랫폼 소개 -

시간	발표
09:00~09:25	Development of molecular marker tools for genomics based crop improvement (식량작물(벼,콩) 유전체 정보 이용 분자표지 포털소개) - 유의수 박사 (DNAcare)
09:25~09:50	A comparative synteny analysis tool for target-gene SNP marker discovery: connecting genomics data to breeding in Solanaceae (원예작물(가지과) 유전체육종 지원 포털 소개) - 조성환 대표이사 ((주)씨더스)
09:50~10:15	TGIL: An integrative bioinformatic platform for genomics-assisted breeding (두과작물 다중오믹스 분석 플랫폼 소개) - 최홍규 교수 (동아대학교)
10:15~10:40	Genomic prediction and development of omics open source platform in Legume (유전체기반 오픈소스플랫폼 개발 및 공유) - 김남신 박사 (한국생명공학연구원)

식량작물 유전체 정보이용 분자표지 포털

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(주)DNACARE, 서울시 서초구 강남대로 43길 17

작물 유전체 연구의 주요목표 중 하나는 대량의 유전체 정보에서 획득되어진 고밀도 마커와 다중 오믹스 정보의 통합 해석의 결과를 육종 프로그램 내에 적용하여 목표형질 선발의 효율성을 강화할 수 있는 형질연관 마커의 개발 및 관련 유전자의 기능적 동정에 있다. 따라서 표준유전체 정보가 완성된 이후 국내외적으로 벼, 콩, 옥수수 등의 주요식량 작물들은 유전체재분석 또는 GBS 방법을 활용한 유전변이 확보가 가속되고 있으며 또한 다양한 형질데이터를 확보하기 위하여 다중 오믹스 정보(전사체, 표현체, 대사체, 단백질체, 이온체 등)의 데이터 생산에 주력하고 있다. 이 두 종류의 데이터는 형질연관분석을 통하여 다양하고 복잡한 양적형질의 동정에 활용되며 유전체기반 분자육종을 활성화하여 종자개발에 효율성을 증대 시킬 것으로 여겨진다. 데이터베이스 구축, 분석 도구 개발, 가시화 및 정보의 연동 등이 유전체, 다중 오믹스 정보를 육종에 효율적으로 활용하기 위해 반드시 필요한 요소이지만 현재까지 각 과제별 수행 결과물 중심으로 만들어져 정보 업데이트, 표준화, 연동, 공유 등이 매우 취약한 상황이다. 향후 데이터를 생산, 해석하고 이를 분자육종에 효율적으로 적용하기 위해서 사용자 중심의 효율적인 정보분석 플랫폼의 개발이 반드시 필요하다. 이 노력의 일환으로 본 과제는 사용자 편의성이 설계된 웹 인터페이스 기반 유전변이 분석, 마커설계, 집단유전체 분석 및 결과 가시화, 형질연관분석 및 결과 가시화, 오믹스데이터 연동 SNP 브라우저의 개발을 통해 작물육종에 적극 활용될 수 있는 오픈소스플랫폼 개발을 목표로 하고 있다. 본 발표를 통해서 인터페이스에 포함될 분자마커개발 파이프라인, 형질연관 분석 및 시각화 툴 등 과제 수행을 통해서 구축될 도구들을 소개하며 앞으로의 방향을 소개하려 한다. 이런 노력을 통해서 다양한 유전체/오믹스 정보를 분자마커 개발, QTL 탐지, 후보 유전자 동정 등 분자육종에 효율적으로 활용할 수 있게 하며, 분자육종의 선진화에 기여하고자 한다.

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A comparative synteny analysis tool for target-gene SNP marker discovery: connecting genomics data to breeding in Solanaceae

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It is necessary for molecular breeders to overcome the difficulties in applying abundant genomic information to crop breeding. Candidate orthologs would be discovered more efficiently in less-studied crops if the information gained from studies of related crops were used. We developed a comparative analysis tool and web-based genome viewer to identify orthologous genes based synteny as well as sequence similarity between tomato, pepper and potato. The tool has a step-by-step interface with multiple viewing levels to support the easy and accurate exploration of functional orthologs. Furthermore, it provides access to single nucleotide-polymorphism markers from the massive genetic resource pool in order to accelerate the development of molecular markers for candidate orthologs in the Solanaceae. This tool provides a bridge between genome data and breeding by supporting effective marker development, data utilization and communication. Database URL: <http://tgsol.seeders.co.kr/scomp/>

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TGIL: An integrative bioinformatic platform for genomics-assisted breeding

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Innovation and advancement of NGS technology, in recent years, have played a key role in acceleration of genomic data production and fast accumulation of related omics information. Literally, It is certain that biology is moving towards ‘big data era’ of omes. Such big data should be useful for molecular breeding and will open a new venue for omics-driven breeding programs. Towards this direction, we are developing and constructing a integrative bioinformatic platform for legume genomics-assisted breeding (named as TGIL: translational genomics interface for the legumes, <http://tgil.donga.ac.kr>). To build up the platform, a wide array of genome data, including seven fully sequenced legume species (*G. max*, *M. truncatula*, *L. japonicus*, *P. vulgaris*, *C. arietinum*, *Cajanus cajan* and *V. radiata*) and two non-legume models (*A. thaliana* and *O. sativa*), were employed as the fundamental information resources. The platform consists of three major modules, i.e., databases, analytical module and user interface. Including basic genome DB, the database contains gene functional information, orthologous gene DB, transcriptome DB and gene network DB. Analysis platform is equipped with interactive comparative genome analysis module and CSGM (cross-species 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’.

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두과작물 유전체예측 및 오믹스 오픈소스플랫폼 개발 및 활용

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유전체 기반 콩 연구는 816점의 재배종, 야생종 핵심집단의 제작, NAM 집단 및 표현체 작성 등 다양한 오믹스를 중심으로 활발히 진행되고 있으며 특히 유전체 연구는 고밀도 SNP-array 및 NGS 데이터를 통하여 전장 유전체 수준에서 GWAS 및 집단유전체 등 다양한 오믹스 분석 방법을 적용하고 있다. 핵심집단 및 NAM 집단의 유전자형-표현형 정보를 활용하여 상가효과를 갖는 마커를 바탕으로 개화기, 지방함량, 단백질함량, 백립중에 대하여 유전체예측 기법으로 예측을 수행하고 있다. 최근에는 인공지능 기법을 통해 예측율을 향상시키는 노력을 진행하고 있다. 신규 핵심집단 알고리즘에 의해 선발된 핵심집단을 바탕으로 전장유전체 데이터를 생산하였고 이를 활용하여 수천만개 이상의 방대한 량의 SNP, INDEL 등의 마커를 발굴하였고 잠재적으로 이를 활용하여 집단유전체 분석기법을 도입하여 재배화 유전자의 발굴, 품종간의 근연관계 등의 유추 등의 오믹스 기반 연구를 수행하고 있다. 또한 전장유전체 데이터는 반수체 정보를 제공해줄 수 있는 리소스로서 동위내에 존재하는 일배체형 정보는 기존 마커의 동위마커의 검색 및 활용에 사용될 수가 있다. 이러한 모든 리소스는 콩 연구의 활성화를 위하여 현재 k-crop.kr 오픈소스플랫폼을 개발하고 있으며, 다른 작물을 포함하여 내년부터 본격적인 서비스를 시작할 예정이다.

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Golden Seed Project

- 채소종자사업단 / 원예종자사업단 / 식량종자사업단 -

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장소 제주 라마다플라자 호텔



최근 농업연구 동향 및 엘지화학의 ag-biotechnology에 대한 비전

성동렬

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세계 인구는 계속 증가하여 2050년이면 97억명이 된다는 보고가 있다. 산업화로 인한 경작지 감소, 집약적인 농업의 발달로 인한 농업용수 감소, 지구 온난화로 인한 환경의 변화, 농업종사자의 고령화를 고려해보면, 계속 증가하는 인류를 위해 식량을 공급하는 일은 매우 도전적인 일이 되리라 예측된다. 새로운 품종개발 및 농업 생산성을 높일 수 있는 기술개발이 병행되어야 증가하는 인구에 맞춰 식량증산을 이뤄나갈 수 있을 것이다. 다행히, 농업 산업 전반에서 다양한 기술적 혁신이 이루어지고 있어서 당면한 인구증가에 따른 식량증산의 문제를 어느 정도 해결할 수 있으리라 기대된다. 기대되는 기술 혁신을 짚어보면, 컴퓨터를 이용한 산술 및 예측 연산의 발달로 인한 인공 지능 혹은 기계학습 분야의 발달, 화학적 염기분석에서 NGS(Next Generation Sequencing) technology를 기반으로 하는 유전자 염기서열 분석의 획기적인 전환, CRISPR/CAS9으로 본격적으로 시작된 유전자 편집 기술등은 다양한 품종 개발을 가능케 할뿐 아니라 앞당길 수 있으리라 예상된다. 이러한 최신 기술 동향을 엘지화학의 그린바이오 산업에 관한 비전과 연계시켜 고찰해보고자 한다.

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Surfing the web of plant innate immunity: from recognition to engineering

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Plants are exposed to a wide variety of potential pathogens and have developed a plethora of strategies aimed at protection. Pathogen effectors are injected into host cells where they target components of the host immune system to suppress immunity. Plants, in turn, evolved a defense response using resistance proteins to monitor pathogen effectors. If not properly regulated, immune responses have the potential to be deleterious to the host. For the ultimate goal of engineering durable resistance in crop plants, it is therefore necessary to improve our knowledge of the fundamental principles of plant immune system regulation as well as of resistance protein activation. Our research focuses on developing a novel method to engineer disease resistance in plants that takes advantage of the Arabidopsis resistance gene RPS5, which encodes a CNL resistance protein. RPS5 is normally activated by the proteolytic cleavage of a second host protein, PBS1, by the pathogen-secreted protease AvrPphB. RPS5 senses a conformational change in PBS1 that results from cleavage. Replacement of the AvrPphB-cleavage site within PBS1 with the recognition sequence for AvrRpt2, a different bacterial effector, and with the cleavage site for the NIa protease of Turnip Mosaic Virus activates RPS5 in the presence of the corresponding protease. Significantly, transgenic Arabidopsis expressing PBS1TuMV accumulates less virus. These data suggest that the AvrPphB cleavage site within PBS1 can be substituted with cleavage sites for other pathogen proteases, which will then enable RPS5 to confer disease resistance to new pathogens. The future research aims to understand the molecular mechanisms of plant immune activation and regulation. Ultimately, we plan to translate this foundational knowledge to crops with the goal of engineering durable and broad-spectrum resistance.

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Enrichment of *Brassica* Vegetables' genepool for secondary metabolites and disease resistance through wide-hybridization

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Interspecies hybridization is the tool to introduce target traits from one species to another. The family Brassicaceae has two related taxa, *Brassica oleracea* and *B. rapa* of important vegetable crops. Due to close genetic relationship, interspecies crosses between them facilitate to transfer beneficial agronomic traits, like glucosinolates (GLS) and β -carotene of secondary metabolites and the resistance genes/QTLs of clubroot disease; the devastating one for Brassica vegetables. Cabbage and Chinese cabbage suppose to have GLS and β -carotene (orange colour leaves), respectively. However, no orange colour in cabbage yet to report, aside with the present status of GLS content (ca. 200 μ mol/g) even not satisfactory. In addition, seven CR (clubroot resistance) loci so far reported yet in *B. rapa* are tried to transfer in cabbage for conferring satisfactory resistance. Therefore, our objectives are to develop cabbage cultivars with orange colour (β -carotene), enhanced GLS status and improved clubroot resistance. Three different interspecies breeding schemes are ongoing; i) high GLS cabbage cultivar, SCNU36 (ca. 200 μ mol/g GLS) was crossed with the twiggy turnip (*B. fruticulosa*; ca. 2880 μ mol/g GLS in leaf), ii) a cross was made between orange Chinese cabbage hybrid cultivar β -flash (OR mutant) with cabbage cultivar ASC-82 (white leaves), and iii) clubroot resistance Chinese cabbage lines LCR36 and LCR38 were crossed with two cabbage lines (ASC-82 and Plimio). Embryos were rescued after 20 days of hybridization and placed on MS medium, F1 embryos were confirmed by PCR with A-, F- and C-genome specific markers. The interspecies hybrids were treated with 0.2% colchicine as root-dip method. Amphidiploid plantlets were selected by flow cytometry. BC1F1 and BC2F1 were retrieved by crossing back to SCNU36, ASC-82, and Plimio lines with their amphidiploid F1s. Desired BC2F1 plantlets were selected using HPLC of GLS, PCR amplification of *OR* and *CR* allele specific markers, and bioassay for clubroot resistance. Significance changes in GLS profile, pale orange, and clubroot resistance phenotypes of cabbage were detected. We believe that BC2F1 progeny given new types of cabbage lines with enriched secondary metabolites and clubroot resistance.

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Bioinformatics applications in horticultural crops using conventional tools and methodologies for crop improvement

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Molecular markers are valuable tools for breeders to accelerate crop improvement. Specifically, High throughput sequencing technologies facilitate the discovery of large-scale variations that have led to direction of next generation plant breeding. Already, a number of bioinformatics methodologies have been developed for molecular markers identification using high-throughput sequencing data. Also, utilizing these technologies, several plants genome sequences and discovery of genetic variations were increased rapidly much faster and cheaper. In this regard, we have customized existing bioinformatics methods/pipelines and successfully implemented in horticultural marker development with aid of sequencing and also public resources. Large number of horticultural samples were collected and sequenced using different sequencing methods (Restriction-site associated DNA sequencing (RAD-seq)), Genotyping by Sequencing (GBS-seq), Whole genome re-sequencing (WGR)) with specific objectives associated with various diseases. Further, unique bioinformatics pipeline was implemented to handle these large datasets to identify genetic variants such as single nucleotide polymorphisms (SNPs) and insertion and deletions (InDels) in large scale. Thus, the identified potential genetic variants along with available public resources have been correlated together to find out casual genes associated variants, construction of QTL, genetic map, and assisted to marker assisted backcrossing (MABC). In addition, we have developed a simple PCR based pathovar and race specific detection marker for black rot disease and clubroot diseases in *Brassica* species through whole genome re-alignment methodologies. (This research was supported by the Golden Seed Project, Grant no. 213007-05-1-CG100).

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중앙아시아 씨감자시장 진출을 위한 기반조성 성과

서상기

농업회사법인 흥익바이오(주), 경기도 평택시 팽성읍 안정로 89

중앙아시아는 건조한 사막성 대륙성기후로 대부분은 수목이 잘 자라지 못하는 스텝지역인데 천산산맥을 중심으로 해발 1,500m ~ 2,000m의 고원지대에서 감자의 주산지가 형성되어 있다. 겨울철에 많이 내린 눈이 고온 건조한 여름 내내 작물재배에 필요한 물을 공급함으로써 품질이 우수한 감자를 생산하는데 좋은 조건을 가지고 있다고 볼 수 있다. 이 지역의 감자 재배면적은 약 41만ha로 생산량은 약 900만톤에 이르고 있다. 그 중 재배면적으로 볼 때 카자흐스탄이 약 44%를 차지하고 있으며 우즈베키스탄과 키르기스스탄이 각각 20% 정도를 재배하고 있다. 구소련시절 중앙아시아에서는 씨감자의 생산과 유통체계가 잘 갖추어져 있었으나 독립 후 농업체계, 특히 씨감자의 보급체계가 무너졌으며, 중요한 식량작물임에도 불구하고 아직도 씨감자의 대부분은 네델란드나 독일에 의존하고 있는 실정이다. GSP를 통해 2014년부터 이 지역에서의 씨감자 사업을 위한 시장조사, 지역적응성시험을 통한 우수품종 선발, 현지 파트너 물색 등을 실시해 왔다. 2017년도에는 현지법인 'SK Seeds'를 설립하였으며 금년도 알마티인근에 씨감자 생산농장을 확보하여 본격적인 생산에 들어가 있다. 중앙아시아는 적합한 품종개발과 씨감자 생산 및 유통체계를 확보한다면 중앙아시아 자체는 물론, 전 세계감자재배면적의 각 30%와 10%를 차지하는 중국과 러시아가 있어 시장의 확장성이 용이하다고 볼 수 있다.

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배가 반수체(Doubled Haploid) 기술에 의한 국내 옥수수 육종체계 변화

류시환*, 최재근, 박종열, 남궁민, 박기진, 최준근

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옥수수 계통육종은 우량 교잡종을 육성하기 위한 필수단계로서, 99% 이상의 순도를 가진 계통을 육종하기 위해서는 전통적인 방법에 의해 7회 이상의 인공교배(selfing)를 실시하여야 한다. 많은 노동력과 시간이 소요되는 전통육종의 이러한 단점을 보완하고자 최근 선진국을 중심으로 배가반수체(Doubled Haploid) 방법에 의한 계통육종 방법이 실용화되고 있다. 배가반수체 방법에 의하면 2~3작기에 순도 100%의 계통을 육성할 수 있다. 선진기술인 배가반수체 기술을 도입하여 국내의 옥수수 계통육종에 활용하고자 강원도농업기술원 옥수수연구소에서는 국제옥수수·밀연구소(CIMMYT)와 협력하여 배가반수체 기술 이용에 필수적인 반수체 유기체(Inducer)의 사용 권리를 확보하였고, 2014년부터 이 기술을 국내 환경에 맞게 정착시켜오고 있다. 국내에서의 옥수수 육종은 1년에 1작기가 일반적이고, 교배시기의 잦은 경우는 화분량이 적은 배가 식물체의 교배에 부적합하므로 시설하우스를 설치하여 안정성을 향상시켰다. 국내에 적합한 배가반수체 기술은 유기체와의 교배를 통한 반수체 유기 및 종자선별, 염색체 배가 및 인공교배를 통한 계통 육성, 그리고 육성 계통의 특성평가 및 종자증식 등 3단계로 이루어진다. 찰옥수수 및 종실용 옥수수 집단의 반수체 유기율은 각각 5.4~7.4%와 5.7~9.4%였다. 2016년과 2017년 6집단으로부터 총 431계통을 육성하였다. 육성된 계통의 표현형적 특성평가를 실시하여 적응성, 도복, 내병성 등이 우수한 종실용 DHF1 및 찰옥수수 DHW1을 선발하여 국내 최초로 배가반수체 기술에 의해 육성된 계통을 국립종자원에 출원하였다. 육성된 계통은 기존의 엘리트 계통과의 교배를 통해 조합능력 및 생산력검정을 수행하고 있으며, 배가반수체 기술의 국내도입 및 성공적인 정착으로 향후 옥수수 계통 및 교잡종 육성의 효율성이 크게 향상될 것으로 기대된다.

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산림분야발표
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Progress and challenges of tree breeding in South Korea

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In Korea, people traditionally thought that forests were nature and there was no owner of the forest until Joseon dynasty (1932-1910). The depletion of forests started to deplete because of the conception. Furthermore, Korean forests had been destroyed much during Japanese colonial ruling (1910-1945) and the Korean War (1950-1953). During the Japanese occupation, a large area of forest was destroyed by over-cutting. In addition, the Korean War lasted for three years. After that, many people went to the forests and cut the trees without any permit from the authority. Thus, almost all mountains except remote areas were denuded. Forest Genetics Research Institute was established in 1956. First, the Institute has done much of hybrid breeding such as hybrid pines (*Pinus regitaeda*) and hybrid poplars (*Populus alba* x *P. glandulosa*). Second, introduction breeding has been done. During the Japanese occupation, which was the first phase of introduction, a total of 376 species was introduced from 30 foreign countries and tested adaptation ability at 388 different sites. In the second phase, 415 species from 38 countries were introduced again and eight species were selected and released. In the third phase (1996-present), continuous adaptation test and selection have been doing. Third, plus trees have been selected from wild forests since 1959 and used for establishing seed orchards. Lastly, special purpose tree breeding program has been doing and developed many new varieties of fruits. Recently, molecular breeding and genomics are being applied into conventional works. In my presentation, major achievement and prospect from tree breeding works will be stated and the trend and prospect will also be discussed.

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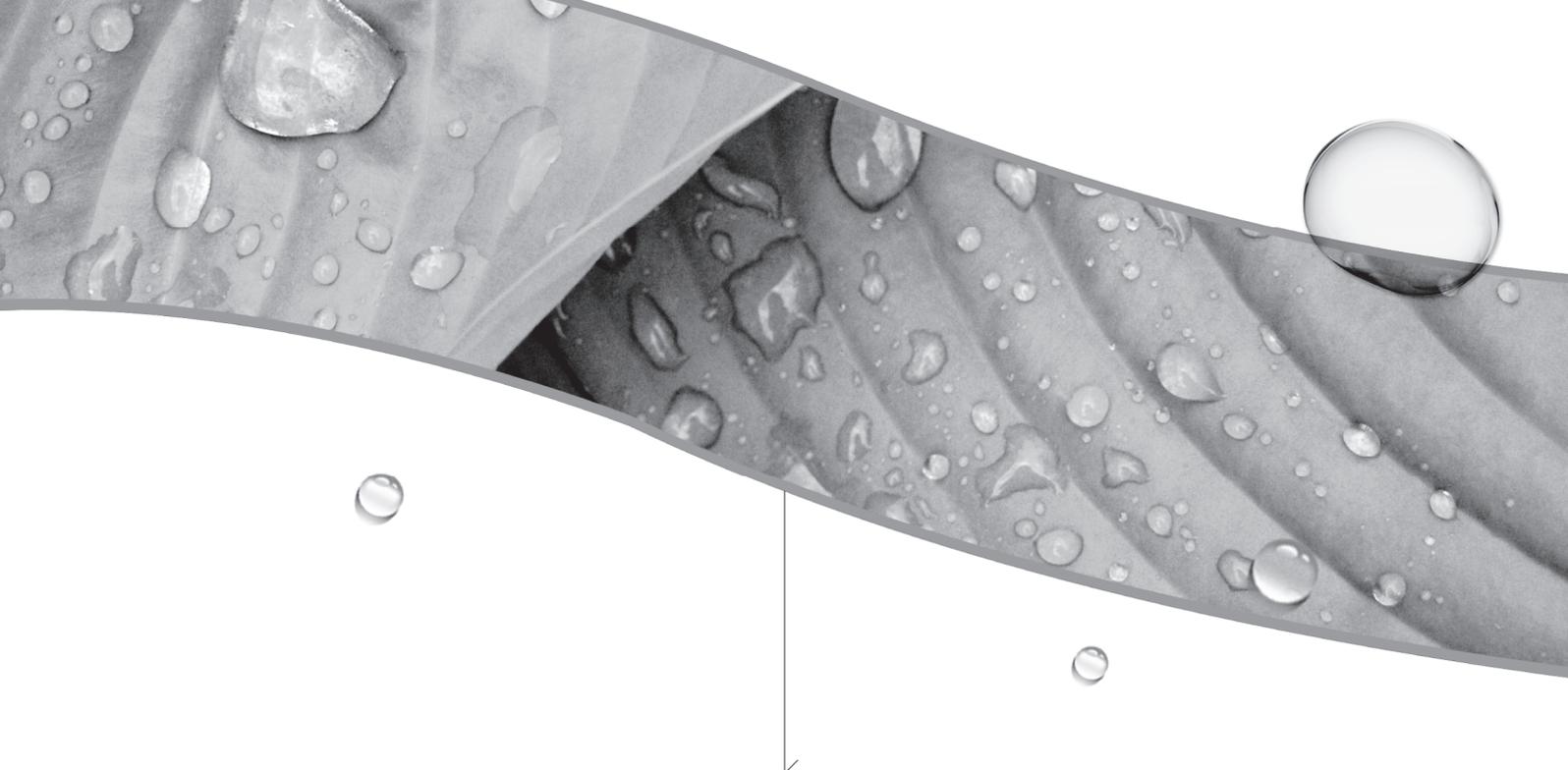
Discovery of trait-associated omic-markers in Korean chestnut species

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The aims of this study were 1) to investigate the molecular mechanisms of metabolic-transcriptional regulations in both nut weight (NW) and its sugar contents during entire nut developmental stages, and 2) to select NW-associated RNA-based SNP markers for Korean chestnut trees (*Castanea crenata*). Omic-datasets were first obtained by metabolic and transcriptomic profiling using two representative genotypes (large vs small nut-bearing individual). Both datasets were analyzed by integrative correlation analysis and further confirmed significant negative correlation between nut weight and sugar contents at Stage III using test accessions (n=30). We also performed RNA sequencing of 42 training accessions. We identified 397,059 high quality SNPs and revealed their transcriptome-wide distribution. Both association and machine learning (ML) studies using 8 different marker sets further showed a clear differentiation between large and small nut-bearing groups. Finally we validated a marker set (21 SNPs, $p < 10^{-5}$) with Sanger sequencing, showing that the prediction accuracy by ML matrix ranged 0.70~0.78. Our findings suggest that variation determined using the RNA-seq technology might become an established tool to address future chestnut productivity issues.

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2. 한국육종학회상 연구상

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- 논문제목 Identification of Heterosis QTLs for Yield and Yield-Related Traits in Indica-Japonica Recombinant Inbred Lines of Rice (*Oryza sativa* L.) (PBB.2017.5.4.371)
- 수상자 손황배 (국립식량과학원 고령지농업연구소)
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한국육종학회 연구윤리교육

“올바른 연구윤리의 이해”

▶ 연구자의 연구윤리 준수의 중요성

“연구윤리가 제대로 확립되었을 때 비로소 연구의 진실성이 확보된다. 진실성이 결여된 연구를 통해서도 진리에 도달할 수 없고, 인류 사회 발전에 기여할 수도 없다. 진리를 추구하는 연구자는 누구보다도 스스로 연구윤리를 엄격히 준수해야 한다.……연구윤리를 훼손하는 행위는 학문공동체의 성장 동력을 파괴할 뿐 아니라 국가의 위신과 장래까지도 훼손할 수 있기 때문이다”

- 출처: 연구윤리확립추진위원회, “연구윤리 확립을 위한 권고문”(2007. 4)

■ 연구윤리 위반 유형의 특성

1. 표절

가. 출처를 표시하지 않은 경우

- 유형1: 타인의 저작물에 있는 독창적인 아이디어나 사고 구조(생각의 프레임)를 출처를 밝히지 않고 자신의 것인 것처럼 활용하는 경우
- 유형2: 일반적 지식이 아닌 타인의 독창적인 개념(용어), 어휘(구), 문장, 단락, 그림, 표, 사진, 데이터 등을 출처를 밝히지 않고 활용한 경우
- 유형3: 타인이 쓴 글을 그대로 쓰지 않고 저자가 말바꿔쓰기(paraphrasing) 또는 요약(summarizing)했지만, 출처를 표시하지 않은 경우

나. 출처를 표시했지만 부적절하게 표시한 경우

- 유형1: 활용한 타인의 저작물에 대해 출처를 표시했지만 직접 인용하면서도 인용부호 (“ ”)없이 그대로 사용한 경우
- 유형 2: 2차 문헌 표절, 저자가 외국인이 쓴 1차 문헌을 직접 보고 그대로 번역하거나 말바꿔쓰기 또는 요약을 하지 않고 2차 문헌에 인용된 내용을 그대로 쓸 때, 재인용 표시를 해야 함에도 직접 원문을 본 것처럼 1차 문헌을 출처표시 한 경우
- 유형 3: 인용된 부분에 출처를 표시했지만 본인의 것이라고 인정할 수 없을 정도로 너무 많은 아이디어나 어구 및 문장을 가져온 경우

2. 중복게재

- 유형1 : 출처표시를 하지 않은 중복게재 (자신의 이전 저작물의 일부나 상당 부분이 이후의 저작물에서 활용되고 있지만 출처를 표시하지 않아, 마치 새로운 것을 처음 발표하는 것으로 오해케 하는 경우)
- 유형 2: 출처 표시가 정확하지 않은 중복게재 (자신의 이전 저작물을 여기저기서 가져와 활용하면서도 어느 일부만 출처를 표시하고 나머지 부분은 표시하지 않는 경우)

3. 부당한 저자 표시

- 유형1 : 저자로서 정당한 자격을 갖춘 사람에게 저자 자격을 부여하지 않거나, 저자로서 정당한 자격을 갖추지 못한 사람에게 저자 자격을 부여한 경우
- 유형2 : 연구 내용 중 일부를 연구자가 아닌 다른 사람에게 2차 용역을 주고 그 결과를 최종 보고서에 포함시킬 때, 저자 표시를 적절하게 하지 않은 경우

4. 기타 작성 시 유의해야 할 사항

- 유형1 : 본문에서 활용한 저작물에 대한 출처의 누락 혹은 부정확한 표기

- 출처: 경제·인문사회연구회, “연구윤리사례집” (2012. 07)



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