

2017 한국육종학회 · 차세대BG21사업단 · GSP사업단 공동심포지엄

식물육종과 생명공학의 현재와 미래도전

Current and Future Challenges in Plant
Breeding and Biotechnology

- 일 시 : 2017년 7월 5일(수)~7월 7일(금)
- 장 소 : 대구 엑스코



- 주 최 : 사단법인 한국육종학회
- 공동주관 : 차세대BG21사업단 (농생물게놈활용연구사업단, GM작물개발사업단, 식물분자유종사업단),
GSP사업단 (채소종자사업단, 원예종자사업단, 식량종자사업단), 서울대학교 식물유전체육종연구소,
동아대학교 농업생명과학연구소, (사)경북세계농업포럼
- 후 원 : 농촌진흥청, 한국농식품생명과학협회, 국립종자원, 경북대학교 농업과학기술연구소
한국과학기술단체총연합회, 대구컨벤션관광뷰로 **dcvb** 대구컨벤션뷰로
Daegu Convention & Visitors Bureau



한국육종학회

2017한국육종학회 - 차세대BG21사업단 - GSP사업단 공동심포지엄 일정

식물육종과 생명공학의 현재와 미래도전
Current and Future Challenges in Plant Breeding and Biotechnology

I 2017년 7월 5일 (수) I

19:00~20:00	이사회 및 조직위원회의
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I 2017년 7월 6일 (목) I

09:00~09:50	등록 및 포스터 부착
10:00~10:20	개회식 개회사 - 박순기 (조직위원장, 경북대학교) 환영사 - 정영수 (회장, 동아대학교) 축 사 - 오병석 (국립종자원 원장)

<< 1부 Plenary Session >>

	▶ 좌장: 고희중 (서울대학교)
10:20~11:00	Genome editing in rice and maize - Dr. Bing Yang (Iowa State Univ, USA)
11:00~11:40	A genomic roadmap for breeding of tastier vegetables - Dr. Sanwen Huang (AGI, China)
11:40~13:30	중 식
	▶ 좌장: 박수철 (국립농업과학원)
13:30~14:10	Targeted soybean breeding for maximum yield potential in different latitudes - Dr. Kristin Bilyeu (USDA-ARS, USA)
14:10~14:50	Functions and applications of innate immune receptors in plants - 손기훈 (포항공과대학교)
14:50~15:30	Food allergies, celiac disease and wheat sensitivities: biotechnology strategies to reduce the immunogenic potential of wheat flour - Dr. Altenbach Susan (USDA-ARS, USA)



<< 2부 한국육종학회 분과발표 >>

분과발표-1: Genes and Molecular Breeding

▶ 좌장: 강권규 (한경대학교)

15:40~16:10	<ul style="list-style-type: none"> ▶ Improvement of indica rice varieties using molecular breeding at the International Rice Research Institute (IRRI), Philippines – 김성률 (IRRI 필리핀)
16:10~16:30	<ul style="list-style-type: none"> ▶ The <i>OsRFS</i> encoding a CHD3/Mi-2 chromatin remodeling factor is involved in multiple developmental processes and ROS scavenging in rice – 강기운 (서울대학교)
16:30~16:50	<ul style="list-style-type: none"> ▶ Controlling flowering time by genetic and environmental factors in rice – 최희백 (경희대학교)
16:50~17:10	<ul style="list-style-type: none"> ▶ An integrated “multi-omics” approach to investigate the ethylene and abscisic acid signaling in <i>Glycine max</i> leaves – Ravi Gupta (부산대학교)
17:10~17:30	<ul style="list-style-type: none"> ▶ Plastidic phosphoglucomutase and ADP-glucose pyrophosphorylase isoforms are essential for successful fertilization in rice – 이상규 (경희대학교)
17:30~17:50	<ul style="list-style-type: none"> ▶ Development of the phenome and genome database for breeding – 이근표 (국립농업과학원)

분과발표-2: Phenotypes and Agronomic Traits

▶ 좌장: 권택윤 (국립농업과학원)

15:40~16:05	<ul style="list-style-type: none"> ▶ Genome editing mediated trait development to improve the efficiency of biorefinery from lignocellulosic biomass – 정제형 (한국과학기술연구원 강릉분원)
16:05~16:30	<ul style="list-style-type: none"> ▶ Rice RING E3 ligases: their roles in abiotic stress – 장철성 (강원대학교)
16:30~16:55	<ul style="list-style-type: none"> ▶ High-throughput phenotyping of plant using image analysis – 김경환 (국립농업과학원)
16:55~17:20	<ul style="list-style-type: none"> ▶ Isolation and Identification of a novel Sg-9 gene responsible for DDMP saponins biosynthesis in soybean – 송종태 (경북대학교)
17:20~17:40	<ul style="list-style-type: none"> ▶ Genetic fine mapping and characterization of the <i>sy-2</i> locus, responsible for low temperature sensitivity in pepper – Dr. Venkatesh Jelli (서울대학교)

<< 2부 한국육종학회 분과발표 >>

분과발표-3: New Breeding Technology & Related Industry

▶ 좌장: 양태진 (서울대학교)

15:40~16:10	▶ DIY CRISPR for plant genome editing - 김상규 (서울대학교 IBS)
16:10~16:30	▶ CRISPR system-mediated soybean genome editing - 김혜란 (서울대학교 IBS)
16:30~16:50	▶ TGsol: Open Innovation Platform 구축을 통한 정보공유 및 새로운 육종의 도전 - 조성환 (씨더스)
16:50~17:10	▶ 유전체기반 작물 육종을 위한 통합 생물정보분석 시스템 - 유익수 (파이젠)
17:10~17:30	▶ Workflow solutions for current challenges in agricultural biotechnology - 정미영 (LGC Genomics)
17:30~17:50	▶ Microfluidic genotyping system - 정윤재 (Fluidigm)

분과발표-4: Commercial Breeding and Seed Industry

▶ 좌장: 노일섭 (순천대학교)

15:40~16:00	▶ 종자산업 육성을 위한 정책방향 - 최근진 (농축산식품부 종자생명산업과장)
16:00~16:20	▶ 동남아시아 단옥수수 개발 및 종자시장 리뷰 - 강항구 (농우바이오 해외영업본부 본부장)
16:20~16:40	▶ 인도 고추종자 시장동향과 상품개발전략 - 박형준 (솔라눔네트웍스 대표)
16:40~17:00	▶ 글로벌 양배추 종자시장 분석 및 품종육성 전략 - 유재흥 (조은종묘 차장)
17:00~17:20	▶ 글로벌 시장의 토마토 육종전략 - 김명권 (토마토생명과학연구소 대표)
17:20~17:40	▶ 종자산업진흥센터의 첨단분자유종 분석시스템 소개 및 활용 - 조영일 (농업기술실용화재단 종자산업진흥센터)



구두발표-1: Oral Presentation of Young Breeders

▶ 좌장: 이주경 (강원대학교)

15:40~17:40	▶ Efficient FISH analysis method using synthetic oligomers for conserved high copy repeat blocks - Nomar Espinosa Waminal (서울대학교)
	▶ 파프리카 유전자적 웅성불임 유전자 <i>ms1</i> 의 후보 유전자 탐색 - 정규미 (전북대학교)
	▶ Identification of <i>SRK</i> -homologous gene family and its use in development of a reliable haplotyping system for the <i>S</i> locus determining self-incompatibility in radish (<i>Raphanus sativus</i> L.) - 김동선 (전남대학교)
	▶ Characterization of complete chloroplast genome of <i>Peucedanum japonicum</i> and its application for genetic diversity analysis - 조호준 (서울대학교)
	▶ Overexpression of <i>YUCCA6</i> gene enhanced drought tolerance in transgenic soybean - 박진술 (동아대학교)
	▶ Transcriptome profiling of differentially expressed genes associated with secondary growth in radish (<i>Raphanus sativus</i> L.) - 최고 (서울대학교)
	▶ Engineering rice with lower grain arsenic - 송원용 (포항공과대학교)
17:40~18:00	한국육종학회 정기총회 & 학회상 시상
18:00~18:30	포스터발표
18:30~	간담회

I 2017년 7월 7일 (금) I

<< 3부 Concurrent session >>

▶ Concurrent session-1: 식물분자육종사업단 & GM작물개발사업단

▶ 좌장: 고희중 (서울대학교), 박수철 (국립농업과학원)

09:00~09:50	▶ SP-LL-37, human antimicrobial peptide, enhances disease resistance in transgenic rice - 강권규 (한경대학교)
09:50~10:40	▶ Optimization of crop productivity in tomato by manipulating genetic variations in florigen related genes - 박순주 (원광대학교)

▶ Concurrent session-2: 농생물게놈활용연구사업단

주요작물의 GWAS 분석을 통한 후보유전자 선별과 기능연구 콘서트

▶ 좌장: 문중경 (국립식량과학원)

09:00~09:25	▶ 벼의 오믹스 정보육종: 새로운 시도와 경험 - 박용진 (공주대학교)
09:25~09:50	▶ SNP 분석을 통한 유전자형에 따른 재배콩 및 야생콩 핵심집단 구축 - 최만수 (국립식량과학원)
09:50~10:15	▶ 고추 핵심집단을 이용한 주요농업형질의 게놈전체연관분석 - 권진경 (서울대학교)
10:15~10:40	▶ 콩에서 NAM 집단 개발과 GWAS 분석결과 활용 - 강성택 (단국대학교)

▶ Concurrent session-3: Golden Seed Project

▶ 좌장: 임용표 (충남대학교)

09:00~09:25	▶ 하늘초 품종 육성 - 박용주 (바이오통육종연구소)
09:25~09:50	▶ 고추 나출 소포자 배양을 이용한 정상 자엽배 생산 및 반수체와 배가반수체의 배수성 검증 - 박은준 (국립원예특작과학원)
09:50~10:15	▶ 아시아 시장 공략을 위한 오리엔탈 백합 품종 개발 - 최강준 (강원도농업기술원)
10:15~10:40	▶ 원예작물의 분자마커 개발 및 통합 지원체계 구축 - 박종인 (순천대학교)

▶ 좌장: 노일섭 (순천대학교)

10:40~11:00

Coffee Break



<< 3부 Concurrent session >>

구두발표-2: Oral Presentation of Young Breeders

▶ 좌장: 조영찬 (국립식량과학원)

09:00~10:40	<ul style="list-style-type: none"> ▶ Enhanced thermo-tolerance in <i>Arabidopsis thaliana</i> through over-expression of CBF1 gene – Rupesh Tayade (경북대학교)
	<ul style="list-style-type: none"> ▶ Complex genome structure of <i>Panax ginseng</i> revealed by ten BAC clone sequences obtained by 3rd generation SMRT sequencing platform using pooled DNA – 장우중 (서울대학교)
	<ul style="list-style-type: none"> ▶ 벼의 중배축 신장과 토종출아율의 관계 – 이현숙 (충남대학교)
	<ul style="list-style-type: none"> ▶ Soybean transgenic plants with <i>AtKDA1</i> gene showed morphological change in plant height – 김혜정 (동아대학교) ▶ 자포니카 벼 입형 다양화 육종소재 개발 및 적용 – 박현수 (국립식량과학원)

구두발표-3: Oral Presentation of Young Breeders

▶ 좌장: 임기병 (경북대학교)

09:00~10:40	<ul style="list-style-type: none"> ▶ <i>Mutator</i> based transposon display: genetic tool for evolutionary and crop improvement studies in maize – Rahul Vasudeo Ramekar (강원대학교)
	<ul style="list-style-type: none"> ▶ Chloroplast genome, nuclear ribosomal genes and polymorphic SSR markers derived from two whole genome sequence of <i>Euonymus hamiltonianus</i> individuals – 이준기 (서울대학교)
	<ul style="list-style-type: none"> ▶ Development of high tryptophan japonica rice with good eating and grain quality – Franz Marielle Nogoy (충북대학교)
	<ul style="list-style-type: none"> ▶ Candidate gene analysis of plant height and antioxidant using NILs – 전윤아 (충남대학교) ▶ Mapping by exome sequencing in wheat: a tall mutant case study – 모영준 (국립식량과학원)

10:40~11:00

Coffee Break

<< 4부 Plenary Session >>

▶ 좌장: 서용원 (고려대학교)

11:00~11:40	▶ Seeds market and biotechnology development in China – David Yeh (Bayer CropScience Ltd., China)
11:40~12:20	▶ Crop breeding by genome-editing – 김주곤 (서울대학교)
12:20~13:30	시상식 및 폐회식



2017 Annual Symposium of Korean Society of Breeding Science

Date and Place : July 5 - July 7, 2017 & EXCO, Daegu

1st day [July 5, 2017]

19:00~20:00	General meeting of organizing committee
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2nd day [July 6, 2017]

09:00~09:50	Registration
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10:00~10:20	Opening Ceremony
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10:00~10:20	Opening Address
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10:00~10:20	– Dr. Soon-Ki Park (Organizer, Kyungpook National Univ. Korea)
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10:00~10:20	Welcome Address
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10:00~10:20	– Dr. Young-soo Chung (President of KSBS, Dong-A Univ. Korea)
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10:00~10:20	Congratulatory Address
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10:00~10:20	– Dr. Byeong Seok Oh (Korea Seed & Variety Service, Korea)
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<< Plenary Session >>

► Chair: Prof. Hee-Jong Koh (Seoul National University)

10:20~11:00	Genome editing in rice and maize – Dr. Bing Yang (Iowa State Univ, USA)
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11:00~11:40	A genomic roadmap for breeding of tastier vegetables – Dr. Sanwen Huang (AGI, China)
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11:40~13:00	Lunch & Poster
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► Chair: Soo-Chul Park (National Acad. Agri. Sci.)

13:30~14:10	Targeted soybean breeding for maximum yield potential in different latitudes – Dr. Kristin Bilyeu (USDA-ARS, USA)
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14:10~14:50	Functions and applications of innate immune receptors in plants – Dr. Kee Hoon Sohn (POSTECH, Korea)
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14:50~15:30	Food allergies, celiac disease and wheat sensitivities: biotechnology strategies to reduce the immunogenic potential of wheat flour – Dr. Altenbach Susan (USDA-ARS, USA)
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<< Oral Presentation >>

15:40~17:40	Session 1: Genes and Molecular Breeding Session 2: Phenotypes and Agronomic Traits Session 3: New Breeding Technology & Related Industry Session 4: Commercial Breeding and Seed Industry Session 5: Oral Presentation of Young Breeders
17:40~18:00	General Meeting
18:30~	Banquet

3rd day [July 7, 2017]

<< Concurrent Session >>

09:00~10:40	– The National Center for GM Crops & Plant Molecular Breeding Center – – The Agricultural Genome Center – – Golden Seed Project (Vegetable, Horticulture, Cereal) Session: Oral Presentation of Young Breeders
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<< Plenary Session >>

► Chair: Yong-Won Seo (Koera University)

11:00~11:40	► Seeds market and biotechnology development in China – David Yeh (Bayer CropScience Ltd., China)
11:40~12:20	► Crop breeding by genome-editing – Dr. Ju-Kon Kim (Seoul National Univ. Korea)
12:20~13:00	Awards Ceremony & Closing Remark



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한국육종학회 분과발표

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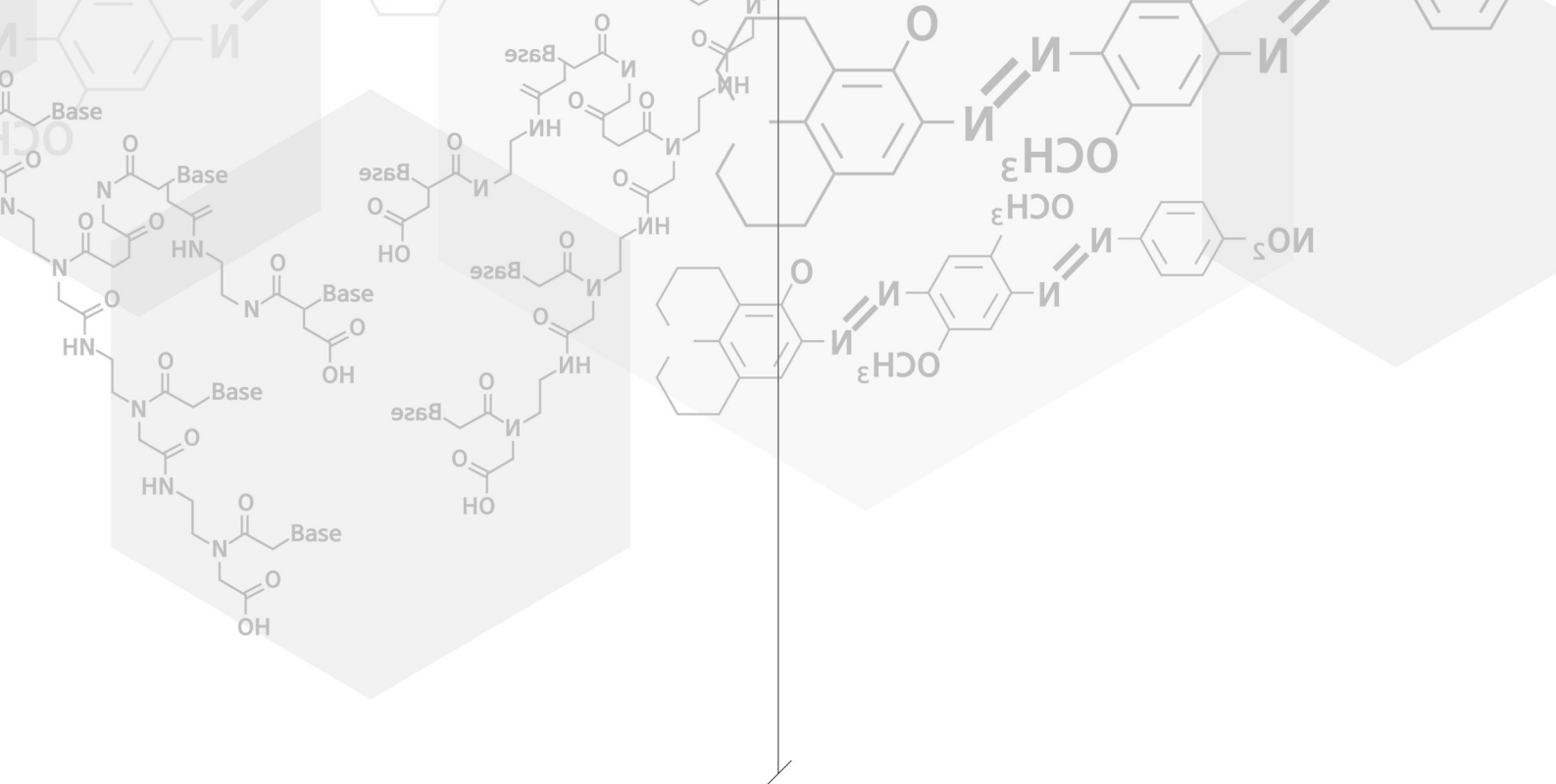
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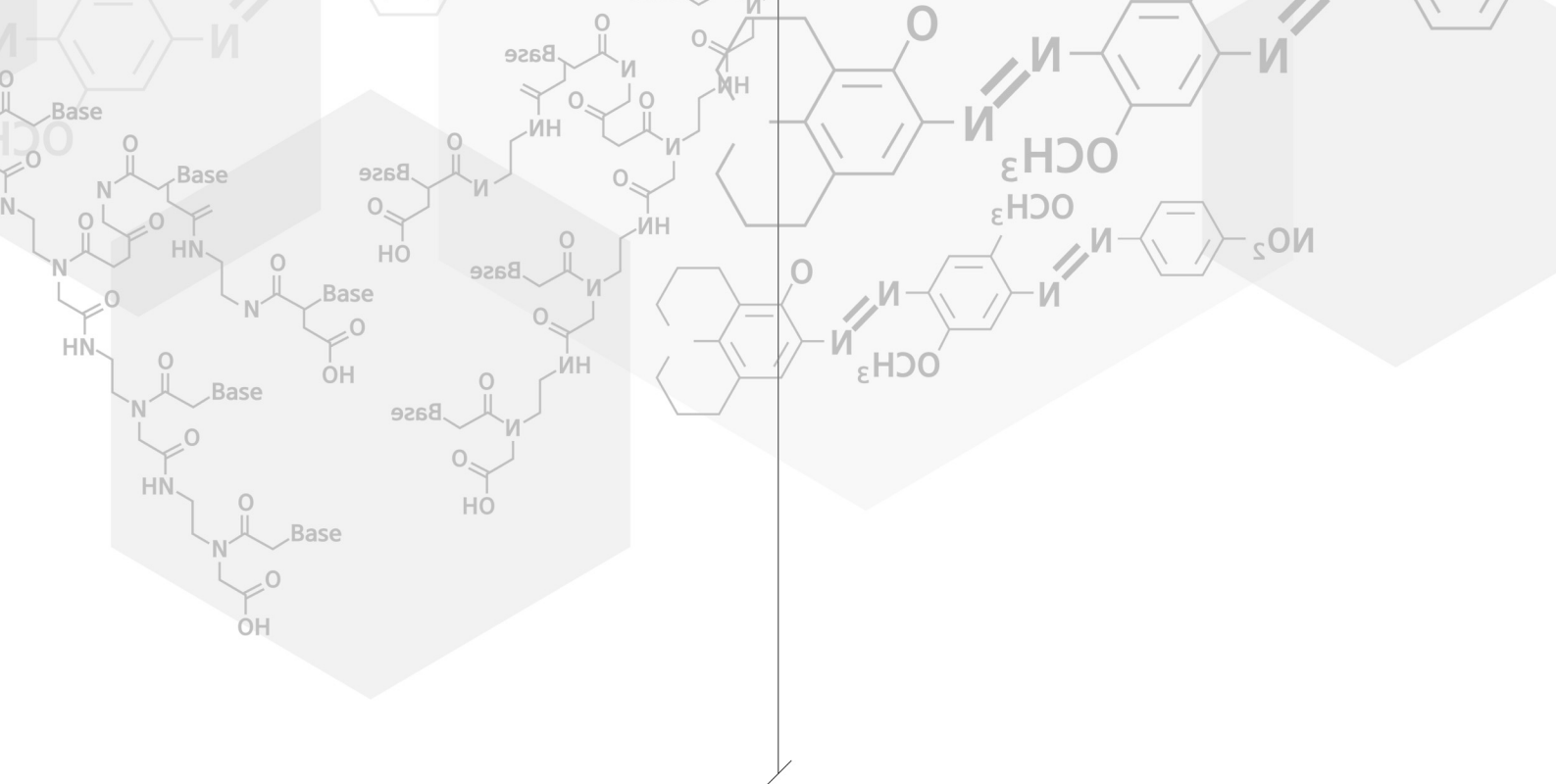


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Plenary Session





Plenary Session



Genome editing in rice and maize

Bing Yang

Department of Genetics, Development and Cell Biology

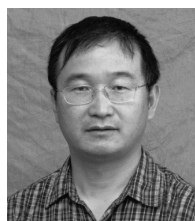
Iowa State University

Ames, IA 50011, USA

Engineered nucleases represent a group of potent enzymes to induce DNA double strand breaks (DSBs) and subsequently precise genetic alteration in target genomes. Modified CRISPR (clustered regularly interspaced short palindromic repeats) systems, comprising Cas9 nucleases and single guide RNAs (sgRNAs), and TALENs (TAL effector nucleases) have emerged as potent biotechnological tools for both basic and applied research. The most promising utilization of both Cas9/sgRNA and TALENs is for targeted genome editing, precise genetic alterations within any genome of interest, as demonstrated in a plethora of organisms including several crop plants. My presentation describes development and application of these two technologies to generate heritable genome modifications in rice and maize. TALENs were employed to generate stable, heritable mutations in dozens of rice genes and maize *glossy2* gene. The frequency of mutagenesis varied from species and constructs targeting different genes. The highest rate in rice reached about 65% of transgenic lines carry desired mutations, while construct targeting the maize *glossy2* gene produced mutant lines from the maize genotype Hi-II at a frequency of about 10%. Phenotypic changes associated with mutated genes were observed in some mutant lines in rice and maize. We also modified the Cas9/sgRNA system suitable for targeted gene mutagenesis in rice and maize, respectively. The two systems have been successfully applied to rice and maize for targeted mutagenesis of many genes. Transgenic lines of T0 generation carrying site-specific mutations were produced at frequency as high as 100% in rice and 80% in maize. Our results demonstrate that TALENs and Cas9/sgRNA are effective toolboxes for genome editing in rice and maize, empowering the discovery of gene function and the trait improvement.

Corresponding Author: E-mail: byang@iastate.edu

Dr. Bing Yang



Associate Professor
Department of Genetics, Development and Cell Biology
Iowa State University
Ames, IA 50011
USA
515-294-2968
byang@iastate.edu

Research interests

- Genome editing technology development and application in plants, -TALENs, CRISPR;
- Microbe/host plant interaction, - basic understanding of molecular mechanism underlying plant disease susceptibility and resistance mediated through bacterial type III effectors;
- Engineering plant disease resistance through genome editing

Education

2000. May	Ph.D. in Plant Pathology	Kansas State University
1989. June	M.S. in Agriculture	Southwest Forestry University, Chin
1986. June	B.S. in Agriculture	Southwest Forestry University, China

Professional experiences(starting with the most recent one)

2003-	Associate Professor	Iowa State University
2007-2013	Assistant Professor	Iowa State University
2004-2006	Research Assist. Prof.	Kansas State University
2000-2004	Postdoc Res. Associate	Kansas State University
1995-2000	Graduate Res. Assistant	Kansas State University
1989-1995	Research Assistant	Kunming Institute of Zoology, CAS

Selected publications

- Si Nian Char, Anjanasree K. Neelakandan, Hartinio Nahampun, Bronwyn Frame, Marcy Main, Martin H. Spalding, Philip W. Becraft, Blake C. Meyers, Virginia Walbot, *Kan Wang, *Bing Yang 2016. An *Agrobacterium*-delivered CRISPR/Cas9 system for high-frequency targeted mutagenesis in maize. *Plant Biotechnology Journal* 15(2):257-268.
- Si Nian Char, Erica Unger-Wallace, Bronwyn Frame, Sarah A. Briggs, Marcy Main, Martin H. Spalding, Erik Vollbrecht, Kan Wang and *Bing Yang 2015 Heritable site-specific gene mutagenesis using TALENs in maize. *Plant Biotechnology Journal* 13(7):1002-1010.
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A genomic roadmap for breeding of tastier vegetables

Sanwen Huang

Agricultural Genomics Institute, Chinese Academy of Agricultural Sciences, China

The majority crop today is domesticated from their wild ancestors. Cucurbits were domesticated from their wild ancestors that had extremely bitter fruits. Cucurbitacins are triterpenoids that confer a bitter taste in cucurbits such as cucumber, melon, watermelon, squash, and pumpkin. With genomics and biochemistry, we identified nine cucumber genes in the pathway for biosynthesis of cucurbitacin C and elucidated four catalytic steps. We discovered transcription factors Bl (Bitter leaf) and Bt (Bitter fruit) that regulate this pathway in leaves and fruits, respectively. Traces in genomic signatures indicated that selection imposed on Bt during domestication led to derivation of nonbitter cucurbits from their bitter ancestors. Tomato serves as an important resource of vitamins, minerals and other nutrients in daily diet, however, the modern commercial tomato suffers from the deterioration in flavor. To understand and ultimately correct this deficiency, we quantified flavor associated chemicals in 398 modern, heirloom, and wild accessions. A subset of these accessions was evaluated in consumer panels, identifying the chemicals that made the most important contributions to flavor and consumer liking. We found that modern commercial varieties contain significantly lower amounts of many of these important flavor chemicals than older varieties. Whole-genome sequencing and a genome-wide association study permitted identification of genetic loci that affect most of the target flavor chemicals, including sugars, acids, and volatiles. Together, these results provide an understanding of the flavor deficiencies in modern commercial varieties and the information necessary for the recovery of good flavor through molecular breeding.

Corresponding Author: E-mail: huangsanwen@caas.cn

Dr. Sanwen Huang



Principal Investigator
Deputy Director General
Agricultural Genomics Institute,
Chinese Academy of Agricultural Sciences (CAAS)
Shenzhen 518124, China
Phone: 86-10-82109512
E-mail: huangsanwen@caas.cn

Research interests

- Decoding vegetable genomes of cucumber, potato, tomato, etc.
- Developing variation maps of vegetables
- Uncovering the genetic basis of important biological processes

Education

2000.9-2005.1	Ph.D. in Plant Breeding	Wageningen University
1993.9-1996.7	M.S. in Plant Science	China Agricultural University
1989.9-1993.7	B.S. in Horticulture	China Agricultural University

Professional experiences(*starting with the most recent one*)

2014.10-	Principal Investigator	Agricultural Genomics Institute, Chinese Academy of Agricultural Sciences (CAAS)
2005.2-	Principal Investigator	Institute of Vegetables and Flowers, CAAS
1996.7-2000.9	Research Associate	Institute of Vegetables and Flowers, CAAS

Selected publications

- Denise Tieman, Guangtao Zhu, ..., Matias Kirst, **Sanwen Huang**, Harry Klee. (2017) A chemical genetic roadmap to improved tomato flavor. **Science**, 355:391-394 (Corresponding authors).
- Yuan Zhou, Yongshuo Ma, Jianguo Zeng, Lixin Duan, Xiaofen Xue, ..., Yi Shang, **Sanwen Huang** (2016) Convergence and divergence of bitterness biosynthesis and regulation in Cucurbitaceae. **Nature Plants**, 16183:1-8 (Corresponding authors).
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Targeted soybean breeding for maximum yield potential in different latitudes

Kristin Bilyeu

Plant Genetics Research Unit, Agricultural Research Service-USDA, Columbia, Missouri USA

Achieving appropriate maturity in a target environment is essential to maximizing crop yield potential. In soybean [*Glycine max* (L.) Merr.], the time to maturity is largely dependent on developmental response to dark periods. Once the critical photoperiod is reached, flowering is initiated and reproductive development proceeds. Therefore, soybean adaptation has been attributed to genetic changes and natural or artificial selection to optimize plant development in specific, narrow ranges of latitude. In the United States (US), these regions have been classified into maturity groups (MG). Growing soybean lines not adapted to a particular environment typically results in poor growth and significant yield reductions. The objective of this study was to develop a molecular model for soybean maturity based on the alleles underlying the major maturity loci: *E1*, *E2*, and *E3*. We examined allelic variation and diversity of the *E* maturity genes in a large collection of landraces, North American ancestors, Chinese cultivars, North American cultivars or expired Plant Variety Protection lines, and private-company lines. The *E* gene status of accessions in the USDA Soybean Germplasm Collection with SoySNP50K Beadchip data was also predicted. We determined the *E* allelic combinations needed to adapt soybean to different MGs in the US and discovered a strong signal of selection for *E* genotypes released in the US. The *E* gene maturity model proposed will enable plant breeders to more effectively transfer traits into different MGs and increase the overall efficiency of targeted breeding for specific MGs.

Corresponding Author: E-mail: kristin.bilyeu@ars.usda.gov

Dr. Bilyeu, Kristin D.



Research Molecular Biologist
Plant Genetics Research Unit
Agricultural Research Service-USDA
110 Waters Hall
University of Missouri
Columbia, Missouri USA 65211
Phone: +1 573-884-2234
E-mail: Kristin.bilyeu@ars.usda.gov

Research interests

- Molecular-genetic analysis and characterization of soybean seed composition traits to improve oil and meal functionality
- Optimizing allele combinations to maximize soybean yield potential in different environments
- Development of high oleic acid and low linolenic acid soybean germplasm
- Increasing palatability, nutrition, and functionality of soy foods

Education

1997. Dec.	Ph.D. in Cell and Molecular Biology	Baylor College of Medicine.
1991. May	B.S. in Biochemistry	University of Missouri.

Professional experiences *(starting with the most recent one)*

2015-	GS-15	USDA/ARS
2010-2015	GS-14	USDA/ARS
2006-2010	GS-13	USDA/ARS
2003-2006	GS-12	USDA/ARS
1997-2003	Postdoctoral fellow	USDA/ARS and University of Missouri

Selected publications

- Langewisch T, Lenis J, Jiang G-L, Wang D, Pantalone V, **Bilyeu K** (2017) The development and use of a molecular model for soybean maturity groups. *BMC Plant Biology* 17 (1):91
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Functions and applications of innate immune receptors in plants

Kee Hoon Sohn

Dept. of Life Sciences, Postech, Republic of Korea

Plant innate immunity relies on two layers of pathogen detection. Cell surface-localized pattern recognition receptors detect pathogen-associated molecular patterns (PAMPs) of invading microorganisms and activate PAMP-triggered immunity (PTI). Successful pathogens must circumvent PTI to colonize plants, and many bacterial pathogens use type III secretion (T3S) to deliver effectors that suppress PTI into plant cells. Effectors can be detected directly or indirectly by plant disease resistance (R) proteins, which then activate effector-triggered immunity (ETI) generally together with a hypersensitive response (HR) of the infected tissue. Plant pathogenic bacteria, *Pseudomonas syringae* and *Erwinia amylovora*, translocate a type III secretion-dependent effector protein, AvrRpt2, in host plant cells. AvrRpt2 is a cysteine protease and cleaves its host target protein RIN4. AvrRpt2-directed cleavage of RIN4 is recognized by CC-NB-LRR type immune receptors RPS2 and MR5 in *Arabidopsis* and *Malus*, respectively. Interestingly, RPS2 and MR5, although both recognize AvrRpt2, do not share significant sequence homology. We found that RPS2 but not MR5 shows autoactivity as shown by a rapid programmed cell death when transiently overexpressed in *Nicotiana benthamiana* leaf cells. Thus, we hypothesized that the mechanisms by which RPS2 and MR5 are activated by AvrRpt2-directed cleavage of RIN4 differ from each other. Further mechanistic details of AvrRpt2-triggered activation of MR5 will be presented.

Corresponding Author: E-mail: khsohn@postech.ac.kr

Dr. Sohn, Kee Hoon



Assistant Professor
Department of Life Sciences, Postech,
77 Cheongam-ro, Nam-gu, Pohang, 37673, Republic of Korea
Phone: 82-54-279-2357
E-mail: khsohn@postech.ac.kr

Research interests

- Molecular mechanisms of plant disease resistance and susceptibility
- Engineering and deployment of plant immune receptors to develop disease resistant crops

Education

2009	Ph.D. in Biological Science	University of East Anglia/The Sainsbury Laboratory (UK)
2003	M.S. in Plant Pathology	Korea University
2001	B.S. in Agricultural Biology	Korea University

Professional experiences(*starting with the most recent one*)

2015-present	Assistant Professor	Postech
2015-present	Adjunct Associate Professor	Massey University (NZ)
2013-2015	Lecturer/Bioprotection Research Fellow	Massey University (NZ)
2009-2013	Senior Research Associate	The Sainsbury Laboratory (UK)

Selected publications

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Food allergies, celiac disease and wheat sensitivities: biotechnology strategies to reduce the immunogenic potential of wheat flour

Susan B. Altenbach

USDA-ARS Western Regional Research Center, USA

Many proteins that contribute to the unique viscoelastic properties of wheat flour also trigger human health problems including food allergies, celiac disease and other wheat sensitivities. To determine whether it is possible to reduce the immunogenic potential of wheat flour without impacting its functional properties, RNA interference was used to silence two complex groups of gluten protein genes in transgenic wheat. The omega-5 gliadins trigger the serious food allergy wheat-dependent exercise-induced anaphylaxis (WDEIA) while the omega-1,2 gliadins contain immunodominant epitopes for celiac disease. Transgenic lines were selected in which all target proteins were significantly reduced in flour with few changes in other flour proteins. End-use quality was assessed in omega-5 gliadin suppressed lines using mixing and baking studies and the allergenic potential of the flour was evaluated by 2-dimensional immunoblot analysis using sera from a collection of WDEIA patients. The data demonstrate that elimination of omega-5 gliadins results in flour with decreased allergenic potential and improved end-use quality. Similar analyses are being conducted with omega-1,2 gliadin suppressed lines. While RNA interference proved to be an effective strategy to reduce the immunogenic potential of wheat flour, the resultant plants are transgenic and unlikely to reach the marketplace because of consumer acceptance issues. Future studies will employ genome editing to develop wheat with reduced immunogenic potential that can be rapidly deployed in breeding programs.

Corresponding Author: E-mail: susan.altenbach@ars.usda.gov

Dr. Altenbach, Susan B.



Research Biologist
USDA-ARS Western Regional Research Center
800 Buchanan Street
Albany, California 94710 USA
Phone: 001-1-510-559-5614
E-mail: susan.altenbach@ars.usda.gov

Research interests

- Molecular basis of wheat end-use quality and immunogenic potential
- Proteomic analysis of the effects of environment on wheat flour protein composition and end-use quality
- Biotechnology approaches to improve end-use quality and reduce immunogenic potential of wheat flour

Education

1983	Ph.D. in Biology	University of California, San Diego
1977	B.S. in Zoology	University of Wisconsin, Madison

Professional experiences

1992-present	Research Biologist	USDA-ARS Western Regional Research Center, Albany, CA, USA.
1987-1991	Senior Scientist	The Plant Cell Research Institute, Inc., Dublin, CA, USA.
1983-1986	Postdoc & Staff Scientist	ARCO Plant Cell Research Institute, Dublin, CA, USA.

Selected publications

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Seeds market and biotechnology development in China

David Yeh

Head of Market Acceptance APAC and Seeds Greater China

China is the second largest seed market in the world with a market value of \$7.5bn (ex-company price). Agriculture modernization remains high priority for China and seed industry development plays a key role in agriculture supply-side structural reform. Since 2015, China has revised its Seed Law and released a series of implementation regulations to promote the reform of marketization and support domestic industry development. The Chinese government is working to create favorable environment for innovation in the seed sector by strengthening IPR and encouraging the private sector to be more involved in variety breeding.

Biotechnology development has been written into China National Strategy. China will pursue the commercialization of GM corn to address market demand and food security and will continue to enhance GMO administration, stewardship and public education. Currently, several crops are in R&D process such as herbicide tolerant (HT) /disease resistant (DR)/insect resistant (IR) rice, IR/HT corn, salinity tolerant (ST)/HT/DR soybean, DR/HT OSR, HT/drought tolerant (DT) wheat and DT/HT/DR cotton, etc.

Corresponding Author: E-mail: David.yeh@bayer.com

Mr. David Yeh



Head
Market Acceptance APAC & Seeds Greater China,
Bayer CropScience (China) Co., Ltd.
Bayer Center, No. 27,
Dongsanhuan North Road, Chaoyang District, China
Phone: +86-10-6589-3455
E-mail: David.yeh@bayer.com

Education

2015.	MBA degree	Vlerick Leuven Gent Management school/ Peking University joint program
2002.	M.S. Biological Systems Engineering and Biotechnology & Certification of Business	Texas A&M University

Professional experiences

2015 -	Head of Market Acceptance APAC	Bayer CropScience China
2012 -	Head of Seeds Greater China	Bayer CropScience China
2007-2014	GMO regulatory & market acceptance for S. East Asia	Bayer CropScience China
2002-2007	China Registration Manager	Bayer CropScience China

Crop breeding by genome-editing

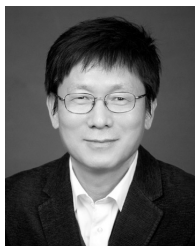
Ju-Kon Kim

Graduate School of International Agricultural Technology, Seoul National University

Genome-editing is going to generate new crop varieties with desirable traits that can satisfy the various demands for global agriculture. As one of the new plant breeding techniques, genome-editing allows plant breeding without introducing a transgene, and this has led to new challenges for the regulation and social acceptance of genome-edited crops. This modern technology can produce novel plants that are similar or identical to those generated by conventional breeding techniques, thus creating indistinct boundaries with regards to genetically modified organism (GMO) regulations. Therefore an appropriate regulatory response is required towards the social acceptance of genome-edited crops. In this symposium, I review the recent development of genome-editing of crops and propose a concept of appropriate regulatory models by unraveling the indistinct boundaries.

Corresponding Author: E-mail: jukon@snu.ac.kr

김주곤 교수



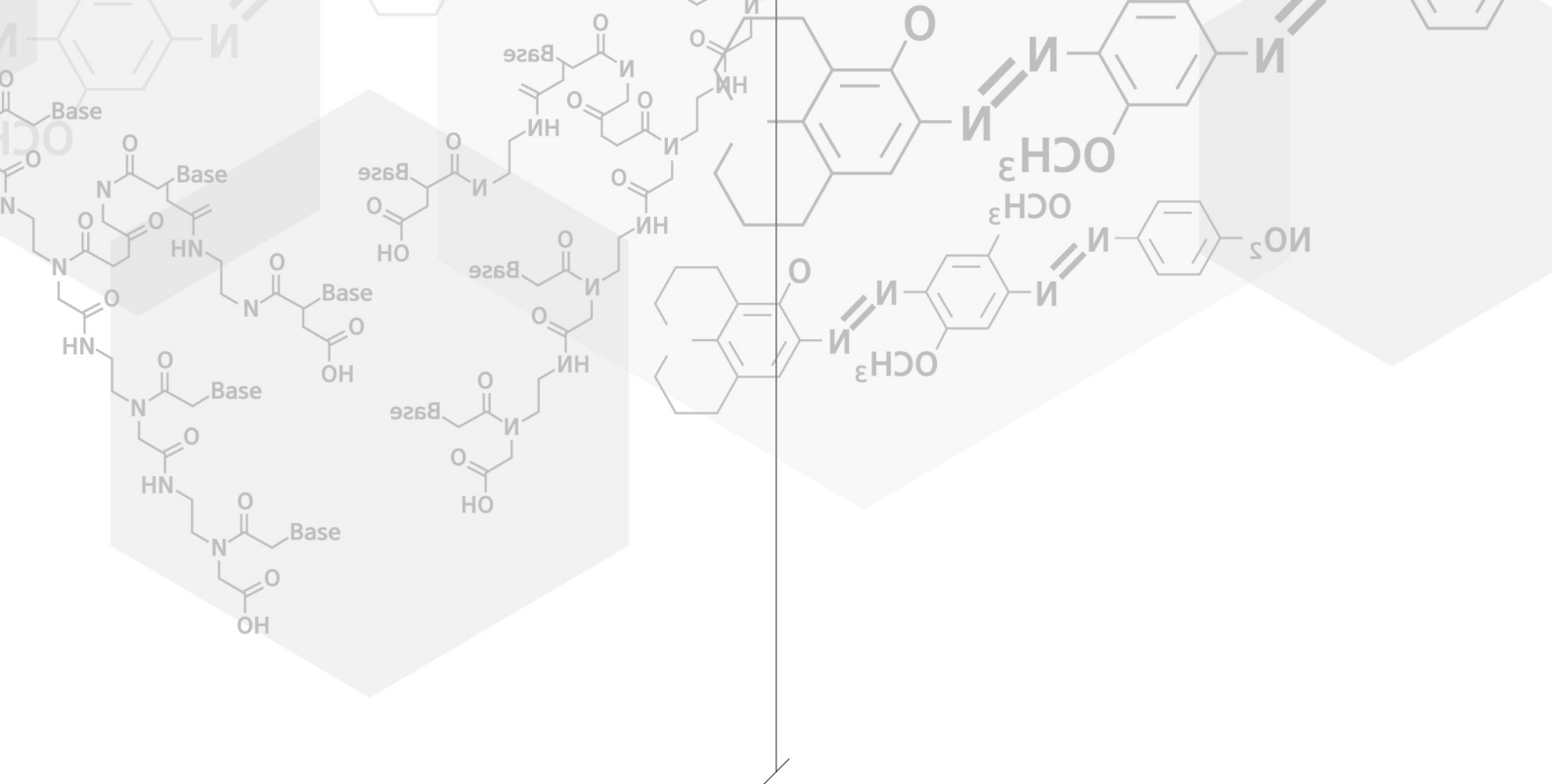
서울대학교 국제농업기술대학원 교수/학과장
종자생명과학연구소장
강원도 평창군 대화면 평창대로 1447
033-339-5826
jukon@snu.ac.kr

교육 및 연구경력

1977-1981	서울대학교 농화학과 학사
1981-1983	한국과학기술원 (KAIST) 생물공학과 석사
1987-1992	미국 코넬대학교 식물분자생물학 박사
1996-2013	명지대학교 생명과학정보학부 조교수/부교수/교수
2006-2008	한국분자세포생물학회, 편집위원
2007-2013	한국응용생명화학회 간사장, 부편집위원장, 편집위원장
2010-2013	한국연구재단 RB (Review Board, 전문위원)
2014-2015	한국응용생명화학회장
2008-현재	한국식물생명공학회 부회장, 편집위원
2011-현재	차세대바이오그린21사업/전문가위원회 위원장
2013-현재	서울대학교 국제농업기술대학원 교수/학과장 종자생명과학연구소장
2017-현재	한국과학기술단체총연합회 부회장/학술진흥위원회 농수산분과 위원장

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한국육종학회 분과발표



Improvement of indica rice varieties using molecular breeding at the International Rice Research Institute (IRRI), Philippines

Sung-Ryul Kim, Joie Ramos, Sherry Lou Hechanova, G.D. Prahalada, Jeom-Sig Lee and Kshirod K. Jena

Breeding Platform, International Rice Research Institute (IRRI), Philippines

Rice (*Oryza sativa* L.) is one of the major crops and feed more than half of the world's population. Especially people in most of Asian countries have been eating rice as a staple food, and in current situation rice consumption is rapidly growing in African countries. The International Rice Research Institute (IRRI) has been doing important roles in overall rice sciences including finding/sharing new valuable traits of rice, breeding/distribution of new rice varieties, sharing genetic resources, gender research and training of rice scientists/breeders to reduce poverty and to secure stable rice production, especially in South East and South Asian countries expanding to East African countries, since foundation of IRRI in 1960. In the presentation, the current breeding target traits/genes of IRRI with molecular breeding strategy will be briefly introduced. The presentation will be more focused on marker-assisted breeding of rice yield-enhancing genes such as *Gn1a* and *OsSPL14* for improvement of indica rice cultivars and revealing of optimal alleles combinations of five major heading genes (*Hd1*, *Hd2/OsPRR37*, *Hd3a*, *Hd4/Ghd7* and *Hd5/DTH8*) for the adaption of Korean varieties in the tropical regions. Furthermore utilization of high-throughput and high-density SNP genotyping system, whole genome sequencing, and CRISPR/Cas9 genome editing techniques for molecular breeding will be discussed.

Corresponding Author: s.r.kim@irri.org

The *OsRFS* encoding a CHD3/Mi-2 chromatin remodeling factor is involved in multiple developmental processes and ROS scavenging in rice

Kiyeon Kang, Sung-Hwan Cho and Nam-Chon Paek*

Department of Plant Science, Plant Genomics and Breeding Institute, Research Institute of Agriculture and Life Sciences, Seoul National University, Seoul, 08826, Republic of Korea

As an important agronomic trait, rice leaf rolling has attracted much attention from plant biologists and breeders because moderate leaf rolling increases photosynthetic competence and hence raises grain yield. However, the relevant molecular mechanism remains unclear. *Rolled fine striped* (*RFS*), a key gene controlling rice leaf rolling, chloroplast development and ROS scavenging, was isolated and characterized. Map-based cloning revealed that *rfs-1* mutant harbors CHR4/Mi-2 chromatin remodeling factor belonged to the SNF2-ATP-dependent chromatin remodeling family. The *rfs-2* T-DNA insertion mutants under different genetic background mimicked the *rfs-1* phenotype, exhibiting extremely incurved leaves phenotype due to defective development of vascular cells on the adaxial side. *RFS* was expressed in various tissues and accumulated mainly in the vascular cells throughout leaf development. Furthermore, *RFS* deficiency resulted in cell death phenotype, that was caused by generating more ROS in *rfs-2* mutants compared with wild-type. Quantitative PCR experiments showed that expression of five ROS-scavenging genes (*CATC*, *APX8*, putative copper/zinc superoxide dismutase, putative superoxide dismutase and *Prx IIE2*) was decreased in the *rfs-2* mutant. Further analysis by western-blot and chromatin immunoprecipitation (ChIP) demonstrated that *RFS* had reduced levels of H3K9me2, H3K4me3 and H3K27me3 at five ROS-scavenging genes. Loss-of-function in *RFS* also led to developmental defect including pollen development, grain filling and root development. Our results suggest that *RFS* is involved in development processes and play an important role in ROS scavenging to modulate ROS homeostasis.

*Corresponding Author: E-mail: ncpaek@snu.ac.kr

Controlling flowering time by genetic and environmental factors in rice

Jinhuan Wei^{1*}, Heebak Choi^{1*}, Ping Jin^{1*}, Yunfei Wu¹, Jinmi Yoon¹, Yang-Seok Lee², Taiyong Quan³, Gynheung An¹

¹Graduate School of Biotechnology, Kyung Hee University, Yongin 446-701

²School of Life Sciences, Gibbet Hill Campus, The University of Warwick, Coventry, CV4 7AL, UK

³The Key Laboratory of Plant Cell Engineering and Germplasm Innovation, Ministry of Education, College of Life Science, Shandong University, Jinan 250100, People's Republic of China

Yield and quality traits are tightly related to flowering time. Most high-yield rice cultivars flower late, whereas high-quality cultivars flower early. Shortening flowering time without quantity reduction or delaying flowering time with maintaining seed quality are in demand. In this study we elucidated genetic and environmental factors that control flowering time. First, we analyzed the effects of SD treatment on flowering time. Second, we examined the effect of exogenous sucrose on controlling flowering time. Third, we performed a screening of T-DNA tagging lines to find a promising genetic factors. Screening T-DNA tagging population resulted in identification of two early flowering mutant lines where expression levels of *Roc4* gene were significantly enhanced. The early flowering phenotypes were observed in LD conditions but not SD conditions, similar to *ghd7*. Further experimental results lead our conclusion to the identification of *Roc4* as flowering time inducer contributed to control flowering time in rice and it showed potentials for improving quantity traits through modulating *Ghd7* expression.

***Corresponding Author:** E-mail: genean@khu.ac.kr (G. An)

An integrated “multi-omics” approach to investigate the ethylene and abscisic acid signaling in *Glycine max* leaves

Ravi Gupta¹, Cheol Woo Min¹, Ramesha H. Jayaramaiah¹, Sun Tae Kim^{1*}

¹Department of Plant Bioscience, Pusan National University, Miryang Campus, Republic of Korea

Phytohormones are the chemical messengers that regulate plethora of biological processes throughout the life cycle of a plant. Although several components related to the biosynthesis and signaling of these phytohormones have been identified, a deep understanding of downstream targets is missing, especially at the protein and metabolite levels. Therefore, here we used an integrated physiological, proteomics and metabolomics approach to investigate the ethylene, ABA and combined ABA+ethylene signaling in soybean leaves. A protamine sulfate precipitation (PSP) method was employed to enrich the low-abundance proteins followed by their identification and quantification using label-free quantitative proteomics. This approach allowed the identification of 5171 unique proteins and 1182 differentially modulated in one or more treatments. Moreover, phosphoproteome analysis led to the identification of 716 class 1 phosphorylation sites (localization probability ≥ 0.75 , score difference ≥ 5) belonging to 532 unique phosphoproteins. In particular, increased phosphorylation of MPK3/6 was observed after ethylene treatment while ABA resulted in dephosphorylation of these MPKs. Functional annotation of the identified proteins showed an increased abundance of proteins related to the flavonoid and isoflavonoids biosynthesis in response to ethylene treatment and a shift in the fatty acid metabolism upon ABA treatment. HPLC analysis showed an accumulation of isoflavones (Genistin, Daidzein, and Genistein) upon ethylene treatment, validating the proteomics results. Further, metabolome analysis using LC-MS/MS confirmed the accumulation of flavonoids and isoflavonoids in response to ethylene treatment and accumulation of lipids in response to ABA treatment. Taken together, our results showed potential cross-talks between ethylene and MPK-signaling and ABA and lipid signaling pathways.

***Corresponding Author:** E-mail: stkim71@pusan.ac.kr

Plastidic phosphoglucomutase and ADP-glucose pyrophosphorylase isoforms are essential for successful fertilization in rice

Sang-Kyu Lee*, June-Seob Eom, Seok-Hyun Choi, Dae-Woo Lee and Jong-Seong Jeon

Graduate School of Biotechnology & Crop Biotech Institute, Kyung Hee University, Yongin 17104, Korea

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.

*Corresponding Author: E-mail: jjjeon@khu.ac.kr

Development of the phenome and genome database for breeding

Keunpyo Lee^{*1}, Junkyoung Choe², Younghoon Park³, Jin-Hee Lim⁴, Byung-Chun In⁴, Sung-Chur Sim⁴

¹Genomics Division, National Institute of Agricultural Sciences, Jeonju, Korea

²SEEDERS Inc., Daejeon, Korea,

³Department of Horticultural Bioscience, Pusan National University, Miryang, Korea

⁴Department of Bioresources Engineering, Sejong University, Seoul, Korea

Advance of next generation sequencing (NGS) techniques and bioinformatics has led to dramatic increase of genome data in crop species. The linkage between genotype and phenotype is essential to develop molecular tools, which can accelerate to improve agronomically important traits in breeding programs. In the present study, we developed a prototype of the 'Phenome and Genome Database for Breeding (PGDB)' using the tomato data. The PGDB provides not only high-quality phenotypic data, but also SNP markers for traits of interest. For the phenotypic data, we selected traits based on Plant Ontology System, UPOV test guideline, and comments from breeders and used a collection of 314 accessions representing contemporary varieties, vintage varieties, and wild species. The SNP genotypes of tomato varieties were produced using the SolCAP array consisting of 7,720 genome-wide SNPs and the publicly available resequencing data. With these phenotypic and genotypic data, this web-based database provides multiple options to find molecular markers associated with traits of interest. Thus, the PGDB is a useful breeder's toolbox to facilitate cultivar improvement in tomato breeding programs and could be further extended for other crops.

*Corresponding Author: E-mail: kplee@korea.kr

Genome editing mediated trait development to improve the efficiency of bio-refinery from lignocellulosic biomass

Je Hyeong Jung^{1*}, Ja Kyong Ko², Sun-Mi Lee²

¹Center for Natural Products Convergence Research, Korea Institute of Science and Technology (KIST), Gangneung 25451, Republic of Korea

²Clean Energy Research Center, Korea Institute of Science and Technology (KIST), Seoul 02792, Republic of Korea

Lignocellulosic biomass has been considered one of the most promising alternatives to fossil resources for the production of fuels and fine chemicals. However, bio-refinery from biomass into bio-based products remains suboptimal primary due to the recalcitrant nature of biomass. Plant cell walls of lignocellulosic biomass are highly heterogeneous, composed of various polysaccharides and aromatic compounds in the form of (hemi)cellulose and lignin. Simple sugars recovered from (hemi)cellulose are utilized as the main substrate for bioconversion, while lignin prevents the efficient hydrolysis of (hemi)cellulose into fermentable sugars by forming a physical barrier and non-productively adsorbing hydrolyzing enzymes. In this respect, reduced lignin content and/or altered lignin structure have been desirable traits for the biomass feedstock, and modifying lignin biosynthetic pathway has been a straightforward strategy to improve the bioconversion efficiency. Genome editing technologies enables rapid introduction of desired traits by precise sequence modification and controlled incorporation of fine-tuned gene units. Here, we reports targeted mutagenesis of one of the lignin biosynthetic genes, caffeic acid *O*-methyltransferase (*COMT*) in sugarcane and barley through TALEN and CRISPR/Cas9, respectively. Targeted mutation of *COMT* resulting in reduced lignin content led to a substantial increase in fermentable sugars and bio-ethanol yields. In addition, a strong synergism in elevating ethanol productivity was created by the combination of utilizing lignin reduced biomass and deploying engineered yeast strain co-fermenting both xylose and glucose.

*Corresponding Author: E-mail: jhjung@kist.re.kr

Rice RING E3 ligases : their roles in abiotic stresses

Cheol seong Jang

Plant Genomics Lab. Department of Applied Plant Sciences, Kangwon National University, Chuncheon 200-713, Korea

As sessile organisms, plants are constantly exposed to adverse environmental stresses, such as high salinity, water deficit, and temperature fluctuation. Therefore, plants have evolved mechanisms that allow them to adapt and survive in various adverse environmental conditions. The proteins harboring RING finger motif(s) have been shown to mediate protein–protein interactions that are relevant to a variety of cellular processes including abiotic stress adaptation. To elucidate the evolutionary dynamics of the rice RING finger protein family, a total of 488 potential RING finger protein genes were retrieved via *in silico* analysis from the rice genome and then divided into groups on the basis of the presence of zinc-coordinating Cys and/or His residues in their RING domains. In this study, molecular dissection of four was performed by examining their E3 ubiquitin ligase activity and subcellular localization, and determining their substrate proteins. First, *OsHCII* was specifically induced by heat and cold stress treatments, and its subcellular localization was shown to be mainly associated with the Golgi apparatus and changed rapidly and extensively moving along the cytoskeleton. Thus, *OsHCII* may have accumulated in the nucleus under high temperatures. In addition, heterogeneous overexpression of *OsHCII* in *Arabidopsis* highly increased the survival rate through acquired thermotolerance. Secondly, *OsCTR1* was highly expressed under dehydration and defense related phytohormones, and its encoded protein was localized in both the chloroplasts and the cytosol. Two chloroplast-localized proteins (*OsCP12* and *OsRPI1*) interacted with *OsCTR1* in the cytosol, and ubiquitination by *OsCTR1* led to protein degradation via the Ub 26S proteasome. The *Oryza sativa* RING finger protein with microtubule-targeting domain 1 (*OsRMT1*) is a functional RING E3 ligase likely involved in a salt mechanism. Functional characterization revealed that *OsRMT1* undergoes homodimer formation and subsequently autoubiquitination-mediated protein degradation under normal conditions. The other protein *OsSAD1* was highly induced in response to high salinity, dehydration treatment, and ABA stresses. For the results of Yeast-Two hybridization, *in vivo* protein degradation assay supports that *OsSAD1* interacts with 3 substrates namely *OsSNAC2*, *OsGRAS44*, and *OsPIRIN1*, and mediates proteolysis of these 3 substrates via the 26S proteasome pathway. In conclusion, these comprehensive studies provide insight into the biological function of OsRFPs, which may be useful in understanding how rice plants adapt to unfavorable environmental stresses.

Corresponding Author: Tel. +82 33-250-6416, E-mail: csjang@kangwon.ac.kr

High-throughput phenotyping of plant using image analysis

Inchan Choi, Hyeonso Ji, JeongHo Baek, Song Lim Kim, Taek-Ryoun Kwon, Kyung-Hwan Kim*

Genetic Engineering Division, The National Institute of Agricultural Sciences, RDA, Jeonju, Republic of Korea

Considerable progress has been made in plant genotyping with the establishment of next generation sequencing methods. However phenotyping is a limiting factor in crop development, which makes it difficult to develop accurate and large scale genetics and breeding. Recently, plant phenomics has emerged as a new research area through high-throughput analysis of plant traits such as plant structure, water contents, physiological status etc. using image analysis. RDA has been setting a high-throughput crop phenotyping (HTCP) facility with RGB, IR, and NIR image analysis instruments. In addition, robotic XYZ phenotyping systems with RGB, 3D-Laser, and fluorescence cameras are being installed. The crop plant phenotyping facility consists of an environmental control greenhouse, image acquisition devices, conveyor, watering system, DB and data management programs. As the first trial to utilize the HTCP system in real study, we are analyzing key characteristics of rice plants such as height, leaf area, and leaf color etc. using RGB images. Besides, the color of the soybean seeds and the flower shape of the *Phalaenopsis* were analyzed with the image technology. This facility shall continue to be utilized for analysis of various target traits of rice plants such as abiotic stress tolerances and yield components in the future.

***Corresponding Author:** E-mail: biopiakim@korea.kr

Isolation and identification of a novel *Sg-9* gene responsible for DDMP saponin biosynthesis in soybean

Jong Tae Song

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

We recently isolated the DDMP-deficient saponin mutants in soybean [*Glycine max* (L.) Merr.]. In soybean, two groups of saponins, group A and DDMP saponins were reported till now. 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 has more beneficial to human health than group A saponins when consumed as regular diet. However, DDMP saponin biosynthesis and associated genes did not come to limelight yet. Therefore, we utilized two EMS mutant lines (PE2248 and PE2371) with DDMP-deficient saponins 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. 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 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. Sequence analysis of *Sg-9* gene revealed a single nucleotide polymorphism in PE2248 (G626A) and PE2371 (C137T) mutant lines. In addition, we verified the mutant alleles by complementation analysis between two mutants.

Corresponding Author: E-mail: jtsong68@knu.ac.kr

Genetic fine mapping and characterization of the *sy-2* locus, responsible for low temperature sensitivity in pepper

Jelli Venkatesh¹, Li Liu¹, Min-Young Kang¹, Jin-Kyung Kwon¹, Yeong Deuk Jo¹, Jin-Ho Kang¹, Sota Koeda², Munetaka Hosokawa², Sandra Goritschnig³, Byoung-Cheorl Kang^{1*}

¹Department of Plant Science and Plant Genomics and Breeding Institute, Seoul National University, Seoul 151-921, Korea

²Department of Agronomy and Horticultural Science, Graduate School of Agriculture, Kyoto University, Sakyo-ku, Kyoto, 606-8502, Japan.

³Keygene N.V., P.O. Box 216, 6700 AE, Wageningen, The Netherlands.

Capiscum chinense 'sy-2' is a low temperature-sensitive natural pepper mutant. The low temperature-sensitivity of the 'sy-2' is controlled by a single recessive gene, *sy-2* located on pepper chromosome 1. In the present study, the *sy-2* locus was fine mapped using F₂ mapping populations developed from across between *C. chinense*'sy-2' and 'No.3341'. Based on genetic linkage analysis and genomic information of pepper, the *sy-2* gene was delimited to an interval of 138.8-kb region flanked by SNP 5-5 and SNP 3-8 markers. Two putative F-box genes, *ORF10* and *ORF20* were identified as candidates for low temperature sensitivity from the *sy-2* target region based on the relative gene expression analysis. The 'sy-2' plants under low temperature exposure (20°C) had a lower expression level of these F-box genes than wild-type plants, even under 28°C growth temperature. Virus induced gene silencing (VIGS) of *ORF10/ORF20* genes in wild type pepper, 'No.3341' resulted in plants with abnormal leaves similar to as that of 'sy-2' mutant pepper under low temperature. Silencing of *ORF10/ORF20* homologs in *Nicotiana benthamiana* has also resulted in the development of similar mutant phenotype. Protein-protein interaction studies suggest that ORF10 and ORF20 are part of Skp, Cullin, F-box (SCF) complex proteins, which plays important roles in proteasome-mediated degradation of proteins. Taken together, these results suggest that the *sy-2* candidate F-box proteins, as a component SCF complex protein could play an important role in plant growth and development under low temperature conditions. Further functional characterization of these F-box genes would offer new insights into the molecular and physiological mechanisms of low temperature sensitivity in pepper.

*Corresponding Author: E-mail: bk54@snu.ac.kr

DIY CRISPR for plant genome editing

Sang-Tae Kim, Hyeran Kim, Je Wook Woo, Hee-Jung Sim, Jae-Young Yun, Hyo-min Ahn, Jahee Ryu, Min Kyung Choi, youjin Shin, Beum-Chang Kang, Suji Bae, Sunyoung Moon, Jin-Soo Kim, Sang-Gyu Kim*

Plant Research Team, Center for Genome Engineering, Institute for Basic Science, Korea

Genome editing tools have been developed to manipulate genomic DNA in animals and plants. In particular, the recent genome editing tool, CRISPR/Cas9, allows us to induce targeted mutagenesis with high efficiency and low cost. As the PCR (polymerase chain reaction) has revolutionized molecular biology, the CRISPR system will become a key and basic technique to answer many biological questions. In addition, the CRISPR system will be widely used in applied science, such as gene therapy, drug development, and livestock and crop breeding. In this talk, I will talk about how to do gene editing with CRISPR/Cas9 system for plant genome editing. Especially, I will suggest a basic guide line for the beginner: how to design a guide RNA, how to check a mutation frequency, and how to deliver Cas9-guide RNA into a plant cell. Finally, I will talk about the new CRISPR system, base-editor for targeted nucleotide substitutions.

*Corresponding Author: sgkim@ibs.re.kr

CRISPR system-mediated soybean genome editing

Hyeran Kim

Research Fellow, Center for Genome Engineering, Institute for Basic Science

Genome editing has been recently democratized by the development of RNA-guided endonucleases (RGENs) repurposed from the type II CRISPR/Cas9 prokaryotic adaptive immune system. CRISPR/Cas9 and CRISPR/Cpf1 system have been rapidly implemented for plant genome editing and crop breeding. Crop improvement is essential to attaining world food security and enhancing nutrition for human beings. Both conventional breeding and modern molecular breeding have contributed to increased crop production and quality. However, the time and resources for breeding practices have been limited. It takes a long time to bring a novel improved crop to the market, and the genetic sources from wild species cannot be always available for crops of our interests. Genome editing-mediated molecular breeding can overcome those limitations of time and resource by facilitating the specific editing of plant genomes. We successfully set up versatile CRISPR/Cas9 and CRISPR/Cpf1 systems for plant research and crop breeding. In this seminar, RGENs (Cas9 and Cpf1)-mediated soybean genome editing and our recent studies will be shared and discussed.

Corresponding Author: E-mail: ranny@ibs.re.kr / ranny96@gmail.com

TGsol: Open Innovation Platform 구축을 통한 정보공유 및 새로운 육종의 도전

조성환*, 이봉우, 김지은, 최준경, 김웅범, 오재은, 이정희

대전광역시 유성구 테크노1로 11-3, (주)씨더스

신품종 육성은 다양한 분야의 지식과 경험이 한데 어우러져 만들어지는 총체적인 산물로 생각할 수 있다. 최근 유전체 정보를 포함하여 다양한 오믹스 데이터와 생물정보학 기술이 크게 발전하면서 혁신적인 육종 시대를 앞당기고 있다. 그럼에도 불구하고 데이터가 지니는 다양성, 복잡도, 대용량의 크기 등으로 인해 독립된 각자의 팀에 의해 실용적 활용에 한계가 발생하고 있다. 심지어는 절망을 경험하기도 한다. 따라서 데이터를 생산하거나 확보하는 차원에서 그치는 것이 아니라, 어떻게 데이터로부터 얻은 정보를 효율적으로 활용하여 우리가 원하는 신품종을 개량해 갈 수 있을지 고민하게 되었다. 그 중 하나의 시도는 오믹스 정보 및 분석 기술, 아이디어 등을 함께 공유하고, 공동의 문제를 함께 풀어갈 수 있는 오픈 플랫폼을 구축하는 것이다. TGsol은 가지과 작물(토마토, 고추, 감자)의 유전체 육종을 구현하도록 돕는 것을 목적으로 농생명게놈활용연구사업단의 지원을 받아 2012년부터 구축하여 공개해 왔다. 지난 수년간 표준유전체와 250여 계통의 토마토 유전자원 **resequencing** 결과 및 고추 RIL **resequencing** 결과를 이용하여 수백만의 **genome-wide SNP**와 다양한 정보를 확보하였다. 또한 모든 정보는 사용자가 검색하여 이용할 수 있도록 제공하고 있으며, 육종활동에 필요하다고 판단되는 다양한 툴을 개발해 왔다. 그러나 수많은 데이터 확보에도 불구하고 데이터베이스의 활용이라는 측면에서 한계를 느끼게 되었다. 만들어 놓은 정보를 검색하여 제공하는 수준으로는 해외 선진 연구팀 혹은 산업체와 경쟁이 어렵다는 것을 인식하였다. 이제는 많은 전문가의 참여를 통해 상호 간의 이해의 폭을 넓혀 실질적인 활용사례를 만들고, 문제점을 해결해 나갈 수 있는 통로를 확보하는 것이 절실하게 필요하다는 것을 배우게 되었다. 이를 위해서는 사용이 편리한 플랫폼을 만드는 것뿐만 아니라 서로의 정보를 공유하는 것이 서로에게 도움이 된다는 것을 이해하고 실천하는 것이 필요하다. 이를 위해서 TGsol 웹사이트 내에 의견을 공유할 수 있는 공간을 만들어 가면서 다양한 의견교류가 정보기반의 육종을 앞당기기를 기대해본다. (TGsol web site: <http://tgsol.seeders.co.kr>)

***주최자:** Tel. 042-710-4035, E-mail: shjo@seeders.co.kr

유전체기반 작물 육종을 위한 통합 생물정보분석 시스템

유익수*, 최범순, 김남훈, 이현오, 박미소, 이승욱

(주)파이젠, 경기도 성남시 분당구 성남대로 331번길 13

차세대 유전체 염기서열분석 및 생물정보학의 비약적 발전은 많은 유전체정보를 신속하고 효율적이며 저비용으로 생산, 해석할 수 있는 방법을 제공하였고, 이를 바탕으로 표준유전체 해독 및 유전체 또는 작물 고유의 특성을 통합적인 해석을 통해 이해하기 위한 많은 사업들이 진행되고 있다. 또한 resequencing/GBS와 같이 응용된 NGS기술을 이용하여 주요작물의 유전 변이를 대량 확보하고 이를 분자유육종에 이용하고자 하는 유전체 기반 분자유육종이 대두되고 있다. 최근 국제미작연구소 (IRRI)와 중국 BGI에서 진행한 “rice 3k project”는 95개국에서 수집된 재래/재배벼 3,000점을 4-60x 정도로 resequencing을 하여 대량의 유전변이를 수집하였고 이를 표현형과의 연관분석을 통해 다양하고 복잡한 양적형질의 동정에 활용할 계획이다. 이런 추세는 농업 전분야로 확대되어 대량의 유전체 데이터의 생산 및 분석이 이루어지고 있어 효율적 생물정보분석시스템의 개발이 향후 데이터를 생산, 해석하고 이를 분자유육종에 효율적으로 적용하는데 반드시 필요한 분야로 여겨진다. 분자유육종의 효율성을 가속화하기 위해서 본 유전체기반 분자유육종 시스템구축 과제는 다양한 유전체 분석 도구들의 개발로 효율적인 유전체 정보의 활용과 분석이 될 수 있도록 하는 시스템을 구축하고자 한다. 주요 내용으로는 1) 다양한 유전체정보 (유전체, 전사체, SNP정보, 분자마커 정보, 표현형 정보 등)를 수집하여 통합 유전체 데이터베이스를 운영하고, 2) NGS기반의 SNP genotyping에 필요한 효율적 파이프라인을 구축하고, 3) 유전체정보와 변이정보를 연동하여 visualization 할 수 있는 브라우저와 분자마커 개발에 필요한 도구의 개발이다. 본 발표를 통해서 비교유전체 도구, 분자마커개발 파이프라인 및 시각화 툴 등 과제 수행에서 구축된 도구들을 소개하며 앞으로의 방향을 소개하려 한다. 이런 노력을 통해서 다양한 유전체 정보를 분자마커 개발, QTL 탐지, 후보 유전자 동정 등 분자유육종에 효율적으로 활용할 수 있게 하며, 분자유육종의 선진화에 기여하고자 한다.

*주저자: Tel. 031-716-0041, E-mail: yeisooyu@phyzen.com

Workflow solutions for current challenges in agricultural biotechnology

Lincoln Ong

APAC commercial director, LGC-Genomics

본 세션에서는 LGC그룹이 보유하고 있는 첨단 대규모 육종지원 시스템을 소개하고 대규모 분자유육종에 효율적으로 활용할 수 있는 다양한 지원 시스템을 소개하고자 합니다. LGC그룹은 영국 런던에 본사를 둔 글로벌 라이프사이언스 회사로서 1842년 회사 창립을 시작으로 올해 175년의 장대한 역사를 지닌 그룹입니다. LGC그룹은 실험실 서비스, 측정과 계측관련 표준 및 기준 물질, 유전체 및 분석시험 분야에 있어 글로벌 리더로서 전 세계 22개 국가에 제품 공급 및 서비스를 하고 있으며, 글로벌 시장에 발맞춰 전 세계 거점 지역내 9곳의 제조라인과 3곳의 특화된 서비스 연구소가 있습니다.

- LGC그룹내 Genomics 비즈니스 유닛은 리서치, 진단 및 적용 분야에 있어 토털 유전체 솔루션을 제공하는 글로벌 리더입니다.
- LGC 제품군은 end-point PCR 및 qPCR분야에 있어 최상의 시약, 특화된 기기와 고객니즈에 맞춘 서비스를 제공하는 토털 포트폴리오입니다. 시약으로는 전 세계적으로 사용되는 KASP, BHQ® 프로브등이 있으며 장비로는 Array Tape을 기반으로 한 전 자동 최신 시스템인 Nexar®, DNA extraction을 위한 최적의 기기인Oktopure™ 및 Genotyping의 장비군인 SNPlane과 더불어 PCR 플랫폼과 liquid handling이 통합 운영되는 IntelliQube®등이 있습니다. 이와 더불어Genotyping, DNA extraction, Array, GBS(Genotyping by Sequencing), Sanger sequencing과 NGS등, LGC의 혁신적인 기술과 서비스를 통해 고객의 니즈에 맞는 프로젝트 서비스와 랩 서비스가 제공되고 있습니다.
- 보다 자세한 LGC 그룹에 대한 내용은 웹사이트(www.lgcgroup.com)또는 국내 LGC genomics담당자인 정미영 이사(michelle.jeong@lgcgroup.com)에게 연락주시기 바랍니다. 감사합니다.

Microfluidic genotyping system

정윤재, MS.Eng., MBA

Korea Business Manager, Fluidigm Corporation

This presentation describes how to perform genotyping of low-concentration DNA with the Juno™ Genotyping IFC (integrated fluidic circuit) on the Juno™ system.

This is possible through advanced microfluidics technology that integrates preamplification and genotyping reactions of up to 96 samples and 96 genotyping assays in a single workflow on an IFC.

The IFC produces 9,216 genotypes in less than three hours using a simple workflow with minimal hands-on time. Samples are loaded into individual inlets of the Juno 96.96 Genotyping IFC, then distributed across multiple reaction chambers in nanoliter-volume aliquots. With high-quality samples, detecting the specific targets requires thermal cycling for preamplification and PCR for genotyping on the instrument. After genotyping is performed on the Juno system, the IFC is scanned on the EP1™ system or the Biomark™ HD system to collect genotyping data for later analysis.

Corresponding Author: E-mail: Ken.jung@fluidigm.com

종자산업 육성을 위한 정책방향

최근진, 오동진, 양미희, 김태영, 김진욱

농림축산식품부 종자생명산업과

종자산업은 농업에 있어서 가장 기본이 되는 자산이며 생명산업 및 ICT 등과 융합하여 미래의 고부가가치 산업으로서 가능성이 높은 산업이다. 따라서 다국적기업들이 종자산업에 참여하여 시장을 점유해가고 있는 형편이며 특히 국제적으로는 듀폰의 다우 인수, 캄차이나의 신젠타 인수, 바이엘의 몬산토 인수와 국내적으로는 LG화학의 동부팜한농, 농협농우인수 등의 변화가 있었다. 우리는 이러한 대내외 환경변화에 적극 대처하고 국내 종자기업이 세계시장에서 경쟁력을 갖출 수 있도록 새로운 육성정책을 발굴하고 지원할 필요성이 있다고 할 것이다. 이를 위해 그동안 정부는 민간육종연구단지의 조성, 방사선육종센터의 설립 그리고 GSP사업을 추진해오고 있다. 그러나 세계종자시장의 급격한 증가 및 변화에도 불구하고 국내종자시장의 규모는 거의 증가가 없는 상태이다. 이는 파종기술의 기계화 및 정밀화, 종자시장의 포화, 경지면적 감소 등의 원인이 있는 것으로 볼 수 있다. 따라서 정부는 종자산업의 발전을 위해 세계종자시장의 점유율을 확대하고 글로벌 및 우수종자기업을 육성하기 위해 종자산업의 시장규모를 확대하고 종자산업 기초향상 및 기반구축, 시장주도형 신품종개발, 우수종자 공급, 유통질서 확립 및 종자기업의 경쟁력향상을 추진할 계획이다. 또한 종자산업의 세계화를 위해서는 수출시장의 다변화 및 새로운 수출시장의 개척에 목표를 두고 수출전용품종의 육성, 품질관리강화, 신수요의 창출, 국제협력의 확대를 추진해 나갈 계획이다.

교신저자: Tel. 044-201-2471, E-mail: kjchoi1001@korea.kr

동남아시아 단옥수수 개발 및 종자시장 리뷰

강항구

농우바이오 해외사업본부 본부장

Sweet Corn 동남아 지역 개발에 있어서 필수적인 고온 및 우기 잘 자랄 수 있는 특성을 가진 품종 개발(Tropical Type)이 매우 중요하다. 2016년 인도 및 인도네시아에서 시험포 사업을 여러 차례 실시하여 매우 긍정적인 결과를 얻었다. 인도에서는 1품종이 상업화 되었으며 1조합이 매우 유망한 조합으로 선발되었다. 인도네시아에서는 3조합이 선발되어 2017년도에 확대 시험 할 예정이다. 인도 및 인도네시아 선발 조합들이 같은 조합들은 없었다. 인도네시아 기후 조건이 인도보다 열악하므로 인도네시아 조합들은 초세 및 내병성 부분에서 인도 요구 특성보다 훨씬 강한 특성을 지닌 방향으로 육성을 해야 할 것이다.

동남아 지역 Sweet Corn 시장은 아직까지 큰 시장이 형성된 것은 아니나 지속적으로 시장 규모가 증가 추세에 있으므로 향후 시장성은 매우 크다고 예측되며, 해외법인 국가(인도, 인도네시아 및 중국 남부)를 중심으로 적극적으로 우선 개발 계획을 가지고 있으며 그 외 국가들도 점차적으로 개발을 확대할 계획이다.

인도 고추종자 시장동향과 상품개발전략

박형준

솔라눔네트웍스 대표

종자 시장은 품종의 기술적인 경쟁력이 가장 중요한 Product Driven Market이다. 특히 품종들의 유전적 특성의 차별화를 만들어 내기 힘든 상황에서는 Management Competition 또한 품종 개발 성공의 중요한 한 축이다. 기술적인 차별화의 중요한 부분들을 활발히 육성하는 것이 전체 종자사업의 중요한 한 chain이다. 즉 종자산업에서는 육성 이외의 여러 다른 축들이 존재하므로, 품종 육성을 통한 유전적 품종의 차별화 뿐 만 아니라 supply chain의 또 다른 기능들을 통해서 차별화하는 것도 종자산업의 중요한 부분이다. 인도 고추 종자시장은 현재 수확량만 가지고 차별화 되는 1단계를 넘어 인도 고유의 품종적 요구도와 내병성을 겸비한 3단계로 발전한 시장으로 급속히 이동하고 있으므로, 전체적인 supply chain에서의 차별화를 만들어 내지 않으면 시장에서 성공하기 힘들다.

교신저자: E-mail: paul0525@naver.com

글로벌 양배추 종자시장 분석 및 품종육성 전략

유재홍^{1*}, 이종훈¹, 안경구¹

¹충북 괴산군 청안면 문방리 농업회사법인 조은종묘(주)

세계 양배추 재배 면적은 약 200만 ha (FAO 2010년 자료)로 채소용 배추와 재배 면적으로는 가장 넓은 재배면적의 작물로 전세계으로 널리 재배 및 섭취되고 있으며, 전세계 종자 소요량은 500여톤, 시장규모는 판매가격 기준으로 1억 7천만불 (약 1900억원)이상으로 추정된다. 전체 양배추 재배면적 중 3분의 2에 해당하는 지역이 아시아이며 중국 인도의 재배면적이 100만 ha 이상으로 추정되고, 유럽은 약 42만 ha로 약 20% 내외로 추정된다. 양배추 주요 생산 및 소비지역인 유럽과 아시아지역의 양대 시장 규모는 각각 약 7천3백만불, 6천9백만불로 전체의 80% 이상을 차지하는 것으로 추정된다. 재배 면적이 제일 큰 아시아 시장은 여러 국내회사들의 노력으로 일본 및 해외 거대기업들과 각축을 벌일 수 있는 수준으로 발전을 해왔으나 고부가가치 시장으로 금액적인 시장규모는 가장 큰 유럽 지역은 네덜란드 및 일본 회사들에 비해 국내 회사들의 진출이 미미한 상황이다. 글로벌 양배추 시장에서 해외 기업들과 경쟁할 수 있도록 시들음병, 검은썩음병, 뿌리혹병등 주요 내병성 품종 및 저장성을 높이는 내열구성 품종 육성 연구를 통해 유럽시장으로의 진출과 아시아 및 세계 여러 시장에도 수출을 증대시키고 있다. 또한 종자 및 농업 관련 무역회의 참석을 통한 품종 홍보 활동 강화 및 국가별 핵심 거래처를 확보, 해외 현지 지역 잡지를 통한 지속적인 홍보와 자체 브랜드 판매 비율을 확대함으로써 브랜드력을 강화하는 활동등 수출 시장 확대를 위한 마케팅 전략 강화 활동도 병행하고 있다.

*주저자: Tel. 043-836-3514, E-mail: andy.yoo@joeunseeds.com

글로벌 시장의 토마토 육종전략

김명권

충북 청주시 청원구 오창읍 중부로 590, 토마토연구소

토마토는 세계적으로 과채류(fruit vegetable) 중에서 가장 재배면적이 많으며 글로벌 채소 종자 시장에서 중요한 위치를 차지하고 있다. 각 나라마다 재배환경, 소비형태에 따라 다양한 토마토 품종들이 재배되고 있다. 이에 품종육종도 지역별, 재배형태별, 이용방법에 맞추어 품종을 육성하고 있으며, 크게 protected cultivation and open field cultivation, fresh usage and processing usage로 나눌 수 있다. 육종형질적인 면에서 보면 생육특성, 과품질, 내병성 요소로, 생육특성은 유한형 무한형, 저온신장성 고온신장성, 내건성 내습성, 초세, 엽형, 절간, 화방발달 등이고, 과품질은 착과비대 균일성, 색상의 선명도, 어깨색, 경도, 열과저항성, 저장성, 당도, 식미, 성분함량 등이며, 내병성은 토마토황화잎말림바이러스(TYLCV), 토마토모자이크바이러스(ToMV), 토마토반점위조바이러스(TSWV), 시들음병(Fusarium), 반신위조병(Verticillium), 근부위조병(Fusarium radices), 역병(Phytophthora), 겹둥근무늬병(Alternaria), 잎곰팡이병(Cladosporium), 선충(Nematode), 갈색근부병(Pyrenochaeta), 흰가루병(Powdery mildew), 풋마름병(Bacterial wilt), 점무늬병(Stemphylium), 세균성반점병(Xanthomonas) 등이 있다. 여러 특성과 형질들을 Target 시장에 맞추어 육종하여야 하며, 현지 적응성시험으로 정확한 평가와 조직적인 홍보 마케팅 활동, 대농민 고객 컨설팅이 병행되어야만 성공적인 품종을 개발할 수 있다.

교신저자: Tel. 043-235-3368, E-mail: mkkim207@naver.com

종자산업진흥센터의 첨단분자유종 분석시스템 소개 및 활용

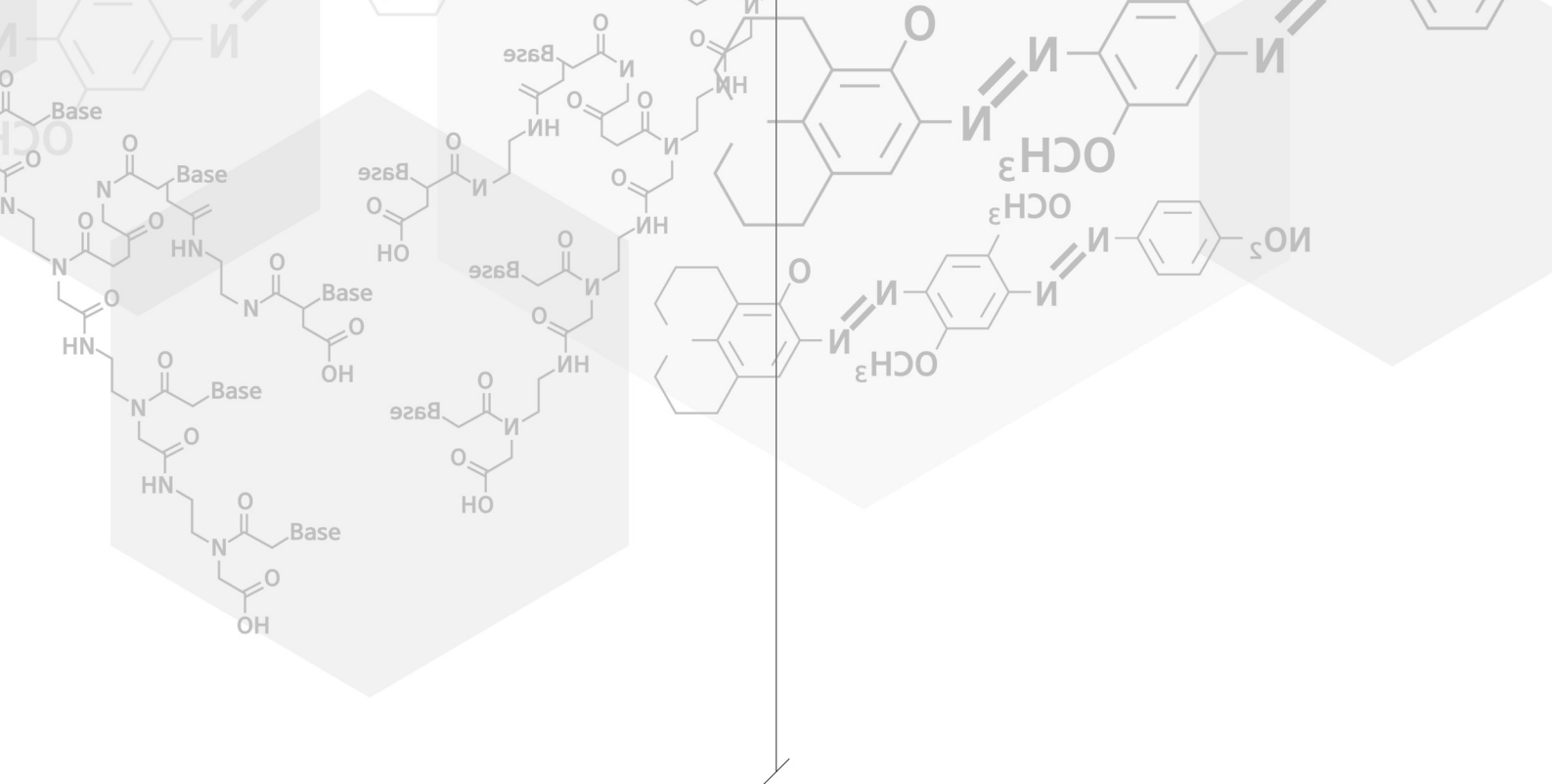
조영일

전라북도 김제시 백산면 씨앗길 232, 농업기술실용화재단 종자산업진흥센터

최근 종자산업은 바이오 에너지, 식품, 의약, 신소재 등 미래 성장유망 산업의 원천이 되는 기반산업으로 부각되고 있으며, 종자관련 기술이 첨단 BT, IT기술과 융합하면서 새로운 고부가가치 산업으로 급성장하고 있다. 이러한 세계적 흐름에 부응하여 정부는 종자산업을 미래 신성장동력산업으로 육성하기 위한 종자산업 육성정책의 일환으로 육종 R&D 인프라 구축 및 지원사업인 “종자산업진흥센터(민간육종연구단지)”를 2016년 10월 전라북도 김제시 백산면에 조성하였다. 종자산업진흥센터는 민간 종자기업의 우수 신품종 개발과 수출을 확대할 수 있도록 지원하는 서비스 전문기관으로 민간육종연구단지 내 위치하여 분자표지 및 기능성 분석서비스 등 첨단 육종기술 지원서비스 제공하고, 국제종자박람회 개최 등 종자산업 육성 지원과 산업전문인력 양성교육 및 안정적 공급, 민간육종연구단지 운영·관리 등의 업무를 수행한다.

종자산업진흥센터는 민간 종자기업의 육종 R&D를 글로벌 수준의 차세대 분자유종체제로 전환하고, 글로벌 시장 경쟁력 향상을 위해 몬산토, 신젠타 등 다국적 종자기업이 사용하고 있는 첨단 분석장비(주요 장비 7종)를 도입하여 분자표지 분석 및 기능성 성분 분석 등 맞춤형 육종기술 지원서비스를 제공하고 있다. 종자산업진흥센터의 분자표지 분석서비스는 대용량 자동화 DNA 추출장치, 대용량 유전자 분석장치 등 첨단 분석시스템 3종을 국내 최초로 도입하였고, 고추, 배추, 벼 등 9개 작물을 대상으로 확보된 병저항성 및 특성검정, 종자순도검정, 품종판별, 여교배 선발(MAB : Marker-assisted backcross)용 분자표지 등 약 2,770여개를 이용하여 종자기업이 우수 계통의 조기 선발과 품종의 특성을 신속·저렴하게 검정할 수 있도록 분석서비스를 제공하고 있다. 또한 고기능성 계통 선발과 고품질의 품종 개발 지원을 위해 국내 종자기업을 대상으로 사전 수요조사를 통해 선정된 서비스 요구도가 높았던 카로티노이드, 깎사이시노이드 등 7가지 기능성 성분에 대해서도 분석서비스를 제공하고 있다. 향후 종자산업진흥센터는 수요에 따라 식물 종자분야뿐만 아니라 축산, 수산 분야로도 단계적으로 서비스 항목 및 영역을 확대해 나갈 예정이다.

교신저자: E-mail: breedy01@efact.or.kr



한국육종학회 구두발표



Efficient FISH analysis method using synthetic oligomers for conserved high copy repeat blocks

Nomar Espinosa Waminal^{1,2}, Remnyl Joyce Pellerin¹, Sung-Min Youn¹, Tae-Jin Yang^{2*} and Hyun Hee Kim^{1*}

¹Chromosome Research Institute, Department of Life Science, Sahmyook University, Seoul, 01795, Republic of Korea

²Department of Plant Science, Plant Genomics and Breeding Institute, and Research Institute of Agriculture and Life Sciences, College of Agriculture and Life Sciences, Seoul National University, Seoul, 08826, Korea

Fluorescence *in situ* hybridization (FISH) is a highly efficient molecular cytogenetic tool to visualize distribution of DNA elements in a genome. Conventional FISH procedure involves preparation of fluorescence-labeled probes that is time-consuming and requires technical experience. To improve this process, we designed oligodeoxynucleotide (ODN) probes for three commonly used targets, 5S, 45S rDNA, and telomere repeats. We designed twelve, four, and one ODN probes for 45S rDNA and 5S rDNA, and telomere tandem arrays, respectively. The rDNA probes has universal utility for plants including gymnosperms and angiosperms, animals, and fungi and telomere probe can be utilized for most of plants harboring *Arabidopsis*-type, (TTTAGGG)_n, telomere array. Use of different fluorochromes conjugated to the 5' end of each ODN probes permitted the simultaneous visualization of the genomic loci of the three target sequences which are commonly the most distinct feature of a chromosome complement. Utilization of pre-labelled ODN probes reduced efforts and time for FISH analysis. It greatly reduced the FISH hybridization time from ~16h at 37°C for conventional FISH to as short as 5 min at room temperature. The ODN probes can be ideal for routine FISH analysis even for species without preliminary chromosomal data. The method is efficient, reliable, and rapid in simultaneously detecting several target repeats, and is particularly useful in rapid chromosomal analysis of crop collections in breeding studies.

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***Corresponding Author:** Tae-Jin Yang: Tel. 02-880-4547, E-mail: tjyang@snu.ac.kr

Hyun Hee Kim: Tel. 02-3399-1715, E-mail: kimhh@syu.ac.kr

파프리카 유전자적 웅성불임 유전자 *ms₁*의 후보 유전자 탐색

정규미, 금보라, 이준대*

전라북도 전주시 덕진구 전북대학교 농업생명과학대학 원예학과

파프리카의 경제적인 일대 잡종 종자를 생산하기 위해 노동력과 비용을 절감할 수 있는 유전자적 웅성불임(genic male sterility, GMS) 시스템을 사용하고 있다. 기 개발된 PmsM1-CAPS 분자표지는 유전자적 웅성불임 유전자인 *ms₁*으로부터 약 2-3 cM 떨어진 곳에 위치해 있기 때문에 제한적으로 사용되었다. 따라서 본 연구에서는 파프리카 1,118 개체 F₂ 분리집단을 사용하여 *ms₁* 유전자좌 고밀도 유전자 지도를 작성하였으며, NGS 분석을 통해 얻은 SNP 정보를 이용해 *ms₁* 유전자좌에 아주 가깝게 연관된 12개의 HRM 분자표지를 개발하였다. 또한 이 분자표지를 이용하여 재조합이 일어나지 않은 869.9 kb 구간을 설정할 수 있었고, 그 곳의 염기서열을 FGENESH 웹 프로그램을 이용하여 분석한 결과, 11개의 open reading frames(ORF)이 존재함을 확인하였다. 그 중 가장 강력한 후보 유전자는 CA05g06780으로 *Arabidopsis* MALE STERILITY 1 (*MS1*) 유전자와 아주 높은 상동성(homology)을 보이고 있었는데, *Arabidopsis*에서 *MS1* 유전자는 plant homeodomain(PHD)-type 전사 인자로서 화분(pollen)과 융단조직(tapetum)의 발달을 조절하는 기능을 가지고 있다고 보고되었다. 따라서 가임(male-fertile, MF)과 불임(male-sterile, MS) 파프리카의 CA05g06780 유전자를 염기서열 분석한 결과, 불임 유전자에서 1 bp의 결실(deletion)이 발견되었다. 이 결실은 2번째 엑손(exon) 내에서 발생하였는데, 이는 3번째 엑손에서 premature stop codon을 야기시켜 가임 단백질(664개의 아미노산)보다 훨씬 짧은 단백질(197개의 아미노산)을 만들도록 영향을 미치는 것이었다. 이러한 정보를 바탕으로 1 bp InDel을 구분할 수 있는 luna probe HRM 분자표지를 개발하여 다양한 파프리카 재료에 테스트한 결과 마커형과 표현형이 완벽히 일치함을 확인하였다.

***교신저자:** Tel. 82-62-530-2061, E-mail: ajfall@jbnu.ac.kr

Identification of *SRK*-homologous gene family and its use in development of a reliable haplotyping system for the *S* locus determining self-incompatibility in radish (*Raphanus sativus* L.)

Dong-Seon Kim^{1*}, Juyeon Jung², Yeon-Ok Choi², Sunggil Kim^{1*}

¹Department of Plant Biotechnology, Biotechnology Research Institute, Chonnam National University, Gwangju 500-757, Korea

²Vegetable Breeding Institute, Farm Hannong Co., Ltd., Ansung 456-933, Korea

Eleven *SRK*-homologous genes were identified from two draft genome sequences of radish (*Raphanus sativus* L.). The phylogenetic tree of the *SRK* and its homologs showed that all homologs were more closely related to the class II *SRK* genes compared with class I *SRK*s. Three homologs were shown to be tightly linked to the *S* locus. To develop efficient and reliable *S* locus haplotyping system, partial sequences of the tightly linked *SP6* and *SRK* genes were isolated from 35 diverse breeding lines showing differential self-incompatibility responses. A total of 24 *SP6* and 29 *SRK* alleles were isolated. 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. Among 35 breeding lines, 14 have combinations of the unique *SLL2* and *SP6* alleles, but the others shared a common allele of either *SLL2* or *SP6* genes. Except for two breeding lines which contained the same *SLL2*, *SRK*, and *SP6* alleles, all breeding lines were shown to harbor unique haplotypes consisting of the *SLL2*, *SRK*, and *SP6* alleles. When 57 additional diverse breeding lines were analyzed by this new *S* locus haplotyping system, haplotypes of all breeding lines were clearly identified. In addition, four novel haplotypes containing the same *SRK* allele but different *SP6* alleles were identified.

*Corresponding Author: Tel. 82-62-530-2061, E-mail: dronion@jnu.ac.kr

Characterization of complete chloroplast genome of *Peucedanum japonicum* and its application for genetic diversity analysis.

Ho Jun Joh¹, Junki Lee¹, Sae Hyun Lee¹, Hyun-Oh Lee², Sang-Choon Lee¹, Tae-Jin Yang^{1,3*}

¹Department of Plant Science, Plant Genomics and Breeding Institute, and Research Institute of Agriculture and Life Sciences, College of Agriculture and Life Sciences, Seoul National University, Seoul 08826, Korea

²Phyzen Genomics Institute, 605, Baekgoong Plaza1, Seongnam-si, Gyeonggi-do, 13558, Republic of Korea

³Crop Biotechnology Institute/GreenBio Science and Technology, Seoul National University, Pyeongchang 25354, Korea

Peucedanum japonicum, a perennial herbal plant species belonging to the Apiaceae family, is distributed around coastal regions in Korea, Japan and Taiwan. In Korea, the leaves and roots are utilized as edible vegetables and oriental medicine named Sik-Bang-Poong, respectively. However, like most medicinal plants, very few genomic studies have been performed for this plant species. In this study, we have collected wild accessions from Jeju, Wan-do and Geumo-do and then characterized complete chloroplast (cp) genomes and 45S nuclear ribosomal DNA sequences by *de novo* assembly using next generation sequencing data of whole genome. Comparative analysis identified size and structural variations among cp genomes of *P. japonicum* accessions. In particular, two types of inverted repeats (IRs), short IR and long IR, were identified, which were correlated with sequence polymorphisms in other regions of cp genomes. Taken together, sequences and polymorphisms identified in this study will be valuable genetic resources that can be applied for molecular breeding of *P. japonicum*.

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*Corresponding Author: Tel. 02-880-4547, E-mail: tjyang@snu.ac.kr

Overexpression of *YUCCA6* gene enhanced drought tolerance in transgenic soybean

Jin Sol Park¹, Hye Jeong Kim¹, Hyun Suk Cho¹, Jae Seong Kim¹, Wan Woo Yeom¹, Jae Yong Han¹, Dae-Jin Yun², Young Soo Chung^{1*}

¹Dept. of Molecular Genetics, College of Natural Resources and Life Science, Dong-A University, Busan 49315, Republic of Korea

²Dept. of Biomedical Science and Engineering, KonKuk University, Seoul 05029, Republic of Korea

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.

***Corresponding Author:** Tel. 051-200-5683, E-mail: chungys@dau.ac.kr

Transcriptome profiling of differentially expressed genes associated with secondary growth in radish (*Raphanus sativus* L.)

Goh Choe*, Yogesh Gupta, Ana Cecilia Aliaga Fandino, Ji-Young Lee

School of Biological Sciences, Seoul National University, Seoul Korea

The Root system has two important functions for plants, providing mechanical support to the aerial parts of the plant by anchoring the plant body to the ground; and absorbing nutrients and water from the soil to distribute them throughout the plant. To better adapt to the environment, some plant species evolved to fortify these functions by increasing the root girth through secondary growth. The secondary growth has its importance in biomass accumulation as well. Many plants utilize roots as storage organs of carbohydrates produced during photosynthesis. The demands for plant biomass is increasing rapidly in the food market as well as energy industry. A continuous breeding effort aiming at improving biomass production is required. Radish, which specializes on the biomass allocation to roots with vigorous radial growth characteristics, can be a good candidate for the breeding purposes and for understanding secondary growth in plants. Although the molecular mechanisms underlying these events are still elusive, it is known that secondary growth originates at the vascular cambium which is located between the xylem and phloem. Vascular cambium divides periclinally to provide additional cell layers which will be differentiated into secondary xylem and phloem cells to the inside and outside respectively, contributing secondary growth capability. To identify important regulators facilitating root secondary growth, we collected laser-dissected tissue samples including cambium, cortex, and parenchyma from radish inbred lines showing contrasting secondary growth, and generated RNA-seq data. Novel transcripts were identified from *de novo* transcriptome assembly. Differentially expressed genes in cambium were isolated and analyzed.

***Corresponding Author:** E-mail: gohchoe@snu.ac.kr

Engineering rice with lower grain arsenic

Fenglin Deng¹, Naoki Yamaji², Jian Feng Ma², Enrico Martinoia³, Youngsook Lee¹, Won-Yong Song^{1*}

¹Department of Integrative Bioscience and Biotechnology, Pohang University of Science and Technology, Pohang 790-784, Korea

²Institute of Plant Science and Resources, Okayama University, Kurashiki, Japan

³Institute of Plant Biology, University Zurich, Zurich, Switzerland

Rice is a staple food for billions of people in Asia, and its consumption is increasing in Europe and the USA, because it is regarded as a healthy, gluten-free alternative source of carbohydrates. However, the As content of rice poses a serious problem. As is a poison, and chronic exposure, even in low doses, can cause skin problems, bladder disease, and cancer. Particularly alarming are baby foods based on rice, which were considered to be nutritious and safe, but in fact contain relatively high amounts of As and can cause diseases and developmental problems in children. Reducing the As content in rice grains is therefore a very important issue for human health. To establish an effective technology for reducing As in rice grains, we devised a strategy to store As in the root and other vegetative organs of the plant, thereby inhibiting As from moving into the rice grain. This idea builds on results from our ongoing long-term research into the transport of toxic heavy metals and metalloids in plants. In the present work, we report the successful engineering of rice lines with reduced As in brown rice grains, using a tissue-specific promoter to drive the expression of genes encoding As transporters to sequester As into the vacuole. The engineered rice plants have lower levels of root-to-shoot and internode-to-grain As translocation, resulting in a 70% reduction in As accumulation in the brown rice grain. This work provides an innovative approach for reducing human exposure to As by making rice a safer source of calories and nutrition.

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

Enhanced thermo-tolerance in *Arabidopsis thaliana* through over-expression of CBF1 gene

Rupesh Tayade^{1*}, Tien Dung Nguyen, Lee Dasom¹, Sung Aeong Oh, Soon Ki Park^{*}

School of Applied Biosciences, Kyungpook National University, Korea

Adaptation of plants to global warming temperature is a challenging task. Current scenario is that heat stress and drought is becoming emerging abiotic stress causing serious threat to global food security. Enhancing the high temperature tolerance of crop species can facilitate the adaption of plant to ever changing environment and increase the yield. In *Arabidopsis thaliana* the C-repeat binding factor (CBF) transcription factor is involved in responses to low temperature and water deficit. In several plant species, over-expression of CBF genes leads to enhanced low temperature tolerance and growth inhibition. In the current study we generated transgenic *Arabidopsis* plants and observed the increased survival rate at heat stress condition (42°C, 4h:30min) and, the delayed leaf senescence and flowering time compared to wild-type plant. In addition, it also observed the increased seed size. This result indicates that CBF1 gene may incorporate stress signals into developmental program for better adaptive growth under unfavorable conditions.

***Corresponding Author:** Tel. +82-53-950-7751, E-mail: psk@knu.ac.kr

Complex genome structure of *Panax ginseng* revealed by ten BAC clone sequences obtained by 3rd generation SMRT sequencing platform using pooled DNA

Woojong Jang¹, Nam-Hoon Kim², Junki Lee¹, Nomar Espinosa Waminal¹, Sang-Choon Lee¹, Murukarthick Jayakodi¹, Hong-il Choi³, Jee Young Park¹, Yeeun Jang¹ and Tae-Jin Yang^{1*}

¹Department of Plant Science, Plant Genomics and Breeding Institute, and Research Institute of Agriculture and Life Sciences, College of Agriculture and Life Sciences, Seoul National University, Seoul, Korea

²Phyzen Genomics Institute, Seongnam, Korea

³Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongseup, Korea

Korean ginseng (*Panax ginseng* C. A. Meyer) which has excellent pharmacological effects has been used as a valuable medicinal plant for a long time. In spite of its usefulness however, there has not been sufficient genetic information until now. Especially, its complex genome structure has not been elucidated. To understand its genome structure, we obtained ten random ginseng bacterial artificial chromosome (BAC) clone sequences through single-molecule real-time (SMRT) sequencing of a pooled DNA of the ten BAC clones. The ten assembled sequences corresponding to total 1,163,364 bp were obtained. Out of the ten BAC clones, nine were immaculately assembled in complete without any gap. The microcosm of ginseng genome were revealed that the 89.7% was composed of various repeat elements which have complex insertion patterns through careful sequence analysis. Especially, the large fraction of sequences were occupied by *Ty3/Gypsy* family long terminal repeat retrotransposons (LTR-RTs) as 46.9%. Six novel LTR-RTs were characterized the structure and their insertion time. Fluorescence *in situ* hybridization (FISH) analysis demonstrated that *PgDel2* and *PgDel5* elements had a subgenome-biased distribution. In remaining 10.3% of non-repeat regions of the 1,163 kb, only eleven protein-coding genes were identified. Collectively, our analysis reveals that ginseng genome has very complex genome structure with abundant repeats and rare gene frequency. The knowledge generated through this study provides various resources for understanding of ginseng genome and its breeding.

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*Corresponding Author: Tel. 02-880-4557, E-mail: tjyang@snu.ac.kr

벼의 중배축 신장과 토중출아율의 관계

이현숙¹, 전윤아¹, 강주원^{1,2}, 안상낙^{1*}

¹대전광역시 유성구 대학로99 충남대학교 농업생명과학대학 식물자원학과

²경남 밀양시 점필재로 20 국립식량과학원 남부작물부

벼 재배에 있어서 노동력 부족과 임금 상승 등의 이유로 벼 직파재배가 점점 늘어나는 추세에 있다. 이들 직파재배에서 유식물체 토중출아율은 잡초와의 경쟁력을 높이는 중요한 요인 중 하나이다. 벼 유식물체의 토중출아율은 초엽과 중배축 신장성이 관련한다고 알려져 있다. 본 연구에서는 재배벼(*Oryza sativa* L.) Nipponbare와 Kasalath 교배 집단을 이용하여 중배축과 초엽의 양적형질 유전자좌 (QTLs) 분석을 실시하고 토중출아율과의 관계를 조사하였다. Nipponbare와 Kasalath의 98개 여교배 집단을 이용하여 토중 5cm 파종 조건에서 중배축 신장 관련 QTLs은 염색체 1, 3, 6에서, 초엽 신장 관련 QTLs은 염색체 3, 5에서 탐지되었다. 이들 QTLs에 의한 중배축 또는 초엽 신장성 신장 조절이 토중출아율에 미치는 영향을 알아보기 위하여 염색체 단편 치환 변이군(chromosome segment substitution lines, CSSL)을 이용하여 실험하였다. Nipponbare와 Kasalath 유래 54개 CSSLs을 토중 5cm 파종 후 14일 동안 토중출아율과 중배축, 초엽 신장성을 조사하고 상관분석을 실시한 결과 중배축과 출아율 사이에는 높은 정의 상관관계 ($r > 0.6$)를 보였으며 초엽과는 유의적인 상관관계를 보이지 않았다. 이들 54 CSSLs 계통 중에서 중배축 QTL, *qMel-1*, *qMel-3*을 각각 또는 모두 포함하는 3 계통, CSSL-6 (*qMel-1*), CSSL-15 (*qMel-3*), CSSL-5 (*qMel-1* + *qMel-3*)을 선발하여 토양 깊이별 출아율과 중배축, 초엽의 길이를 조사하였다. 토양 깊이는 3cm, 5cm, 7cm, 10cm 깊이별로 종자를 파종하고 출아율을 관찰한 결과 7cm, 10cm의 깊이에서 중배축 신장성이 가장 좋은 CSSL-5가 Nipponbare나 다른 계통들에 비하여 가장 빠른 출아율을 보였다. 본 연구에서는 중배축 신장 조절을 조절하는 QTLs을 염색체 1번과 3번에서 탐지하였고 CSSLs 계통을 이용하여 중배축과 토중 출아율의 상관관계가 있음을 확인하였다.

*주저자: Tel. 042-821-7038, E-mail: ahnsn@cnu.ac.kr

Soybean transgenic plants with *AtKDA1* gene showed morphological change in plant height

Hye Jeong Kim¹, Hyun Suk Cho¹, Jae Seong Kim¹, Jin Sol Park¹, Wan Woo Yeom¹, Jae Yong Han¹, Jeong-Il Kim², Young Soo Chung^{1*}

¹Dept. of Molecular Genetics, College of Natural Resources and Life Science, Dong-A University, Busan 49315, Republic of Korea

²Dept. of Biotechnology, Chonnam National University, Gwangju 61186, Republic of Korea

Plants use light as a source of both energy and information about their environment. Among photoreceptors, cryptochromes are blue-light receptors that regulate multiple light responses including hypocotyl growth, flowering, circadian clock and gene expression in plants and animals. Transgenic soybean plants overexpressing *AtKDA1* were produced by *Agrobacterium*-mediated transformation using the modified half-seed method. The integration of the transgene was confirmed from the genomic DNA of transformed soybean plants using PCR, and the copy number was determined by Southern blotting using leaf samples from T₂ seedlings. To examine the effect of *AtKDA1* expression on plant height and its yield in transgenic plants, we compared their growth characteristics to those of non-transgenic (NT) plants. The chosen three transgenic seedlings (#9, #10 and #15) exhibited longer hypocotyls than NT seedlings. Agronomic traits including plant height, the number of nodes per plant, branches per plant, pods per plant and total seed weight were also investigated in GMO field. In phenotypic analysis, *AtKDA1* transgenic plants showed longer plant heights than NT plants.

*Corresponding Author: E-mail: chungys@dau.ac.kr

자포니카 벼 입형 다양화 육종소재 개발 및 적용

박현수*, 백만기, 남정권, 신운철, 김춘송, 이진미, 박슬기, 조영찬, 김보경

전라북도 완주군 이서면 혁신로 181 농촌진흥청 국립식량과학원

벼 낱알의 크기와 형태는 쌀의 품질과 소비자 선호도에 중요한 역할을 한다. 우리나라에서 육성된 대부분의 자포니카 벼 품종은 현미장폭비 1.50-2.00의 단원형이고, 현미천립중 22.0g 내외의 중소립 특성을 나타낸다. 본 연구는 우리나라 자포니카 벼 품종의 협소한 입형 특성을 다양화하기 위해 벼 낱알 크기와 형태가 다양화된 육종소재를 개발하기 위해 수행되었다. 입형 특성을 다양화하기 위해 국내립 자포니카 유전자원 'Jizi1560'(현미천립중 48.1g)과 'Jizi1581'(38.0g)을 우리나라 자포니카 초다수 품종인 '드래찬'(24.7g)과 '보람찬'(22.9g)에 각각 인공교배한 후 약배양을 수행하였다. 4조합에서 360개 약배양 계통을 육성하였고, 이중 열악형질 수반 계통을 제외한 290계통에 대해서 입형 및 농업형질 특성을 조사하였다. 이를 통해 농업형질이 양호하고 입형 특성이 다양화된 91계통의 '입형 다양화 육종소재'를 선발하였다. '입형 다양화 육종소재'는 현미장폭비 1.53-2.83, 현미천립중 18.6-41.5g의 다양한 낱알 형태 및 크기를 보유하였다. 입형 관련 주동 유전자인 *GW2*, *GS3*, *SW5*의 유전자형을 분석한 결과 '드래찬'과 '보람찬'은 *GW2GS3sw5*, '대립벼1호'는 *gw2GS3sw5*, 'Jizi1581'은 *gw2gs3SW5*, 'Jizi1560'은 *gw2gs3sw5*의 대립유전자형을 가지고 있었다. '입형 다양화 육종소재'는 세 개 유전자로 작성 가능한 8개 조합 모두가 확인되었으며, 유전자형 분석을 통해 입형 관련 유전자가 입형 및 주요 농업형질 특성에 미치는 영향을 구명하였다. 중원형 입형 특성의 'DGS77'(현미장폭비 2.07)는 '전주598호'로 명명되어 지역적응성시험에 공시되었고, 대립 특성을 가지고 있는 'DGS8'(현미천립중 40.4g), 'DGS59'(41.5g; *gw2gs3sw5*) 등은 제분효율 증진을 위한 대립형 쌀가루 품종 개발의 교배모본으로 활용되고 있다. 장원형 특성의 'DGS79'(현미장폭비 2.78)와 'DGS83'(2.83; *GW2gs3SW5*)은 자포니카 장원형 품종 개발의 교배모본으로 활용되어 DGS79/보람찬 조합으로부터 유망한 'HR30971-B-B-30-1-1' 계통을 육성하여 생산력 검정시험 중이다. 본 계통을 활용하여 입형 및 내병성에 관련된 분자표지를 활용한 MAS 육종체계로 조생, 복합내병성의 장원형 고품질 품종을 개발하여 쌀수출 산업에 활용할 예정이다.

*주저자: Tel. 063-238-5216, E-mail: mayoe@korea.kr

Mutator based transposon display: Genetic Tool for Evolutionary and crop improvement studies in maize

Rahul Vasudeo Ramekar¹, Neha Samir Roy², Youn Sung Kim³, Kyong Cheul Park^{4*} and Ju Kyong Lee^{1*}

¹Department of Applied Plant Sciences, Kangwon National University, Chuncheon 24341, South Korea

²Department of Molecular Biosciences, Kangwon National University, Chuncheon 24341, South Korea

³Nong-Hyup Seed, Anseong 17558, South Korea

⁴Department of Agriculture and Life Industry, Kangwon National University, Chuncheon 24341, South Korea

Transposable elements (TEs) account up to 85% of maize genome and has a significant implication in crop improvement and evolutionary analysis. *Mutator* (*Mu*) transposons superfamily, a class of DNA transposons, is the most complex and active element in maize genome suggesting a special role in plant evolution. They can be traced in plants, 60-70 million years ago since the ancestor of maize and rice diverged. *Mu* element transposition associates preferentially into or near genic regions causing high mutation rate. These elements can capture host genome sequences contributing to new gene structure. In the present study, we have designed, a set of *Mu*-specific primers based on terminal invert repeats and utilized a modified transposon insertion display method (*Mu*-TD) for genotyping. Based on this approach we 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 strong evidence of recent activity of *Mu* element in both the species. *Mu*-TD analysis suggests the presence of high polymorphic insertion among the species and subspecies indicating the utility of the method in studying genetic variations and species relationship regarding repetitive elements. Further, we analyzed 80 maize RIL population; *Mu*-TD generated an average of 60% *Mu* anchored polymorphic fragments where element insertion appeared to be segregating in significantly high number. The amplification profile was highly reproducible exhibiting the utility of *Mu* elements as a new set of transposon display (TD) markers useful for developing the high-density genetic map.

*Corresponding Author: Tel. +82-33-250-7770, kyongcheul.park@kangwon.ac.kr

Tel. +82-33-250-6415, jukyonglee@kangwon.ac.kr

Chloroplast genome, nuclear ribosomal genes and polymorphic SSR markers derived from two whole genome sequence of *Euonymus hamiltonianus* individuals

Junki Lee¹, Shin-Jae Kang¹, Ho Jun Joh¹, Nam-Hoon Kim², Sang-Choon Lee¹, Woojong Jang¹, Hyun-Seung Park¹, Jee Young Park¹, Tae-Jin Yang^{1,3*}

¹Department of Plant Science, Plant Genomics and Breeding Institute, and Research Institute of Agriculture and Life Sciences, College of Agriculture and Life Sciences, Seoul National University, Seoul, Korea

²Phyzen Genomics Institute, Seongnam 13558, Korea

³Crop Biotechnology Institute/GreenBio Science and Technology, Seoul National University, Pyeongchang, Republic of Korea

Whole genome sequencing (WGS) technologies provide large amount of sequence data. WGS-based molecular markers also have been used in plant research including breeding, barcoding and authentication. Although large number of molecular markers have been developed and actively applied, the development of marker was still limited in non-model plants due to their insufficient genetic resources. Therefore, a simple and universal approach is required to develop molecular markers. In this study, an efficient protocol for assembly complete chloroplast (cp) genome, nuclear ribosomal DNA (nrDNA), and polymorphic simple sequence repeat (pSSR) which are important to understand genetic diversity and evolution in plant, was designed using the low amount of WGS data. We analyzed cp genome, nrDNA, and pSSR of *Euonymus hamiltonianus*, a medicinal and ornamental plant. Using 950 Mb of two WGS data of *E. hamiltonianus* individuals obtained by MiSeq platform, 157,360-bp complete cp genome, 5,824-bp nrDNA, and 162 pSSR candidate contigs were identified in *E. hamiltonianus*. In addition, this protocol was applied to *Peucedanum japonicum* individuals for pSSR identification. Taken together, the protocol designed in this study will help to understand fundamental nature of non-model plants.

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*Corresponding Author: E-mail: tjyang@snu.ac.kr

Development of high tryptophan japonica rice with good eating and grain quality

Franz Marielle Nogoy¹, Hye-Jung Lee¹, Marjohn Nino¹, Dal-A Yu¹, Me-Sun Kim¹, Sothea Ouk¹, Yu-Jin Jung², Kwon-Kyoo Kang², Yong-Gu Cho^{1*}

¹Department of Crop Science, Chungbuk National University, Cheongju 28644, Korea

²Department of Horticulture, Hankyong National University, Ansong 17579, Korea

Tryptophan is one of the essential amino acids needed by human bodies and can only be obtained by eating meat, eggs, milk etc. In this study, we harnessed the potential of rice to deliver tryptophan in human diet. Several EMS-mutated rice lines with 30 times higher tryptophan content than their wildtype in rice grains were generated. We characterized the eating and grain quality of these high tryptophan rice lines and found out that they have low eating and grain quality. To improve the rice eating and grain quality, we performed crosses with two elite Korean varieties (Samgwangbyeon and Hopumbyeon). A total of four single cross combinations were forwarded in later generation until we get a stable line with high tryptophan, and good eating and grain quality. Among each population, we performed significant tests for several values on palatability, final viscosity, and amylose to select the best line in each cross combination. In addition, we have also utilized two mutant high tryptophan lines and four breeding lines as wildtypes in transforming CRISPR/Cas9 vectors to regulate the expression of four starch synthesis related genes. Results of this study will enable us to understand the function and correlation of these genes in regulating the amylose content of Japonica rice.

*Corresponding Author: ygcho@cbnu.ac.kr

Candidate gene analysis of plant height and antioxidant using NILs

Yun-A Jeon¹, Dong-Min Kim², Hyun-Sook Lee¹, Sun Ha Kim¹, Sang-Nag Ahn^{1*}

¹Department of Agronomy, College of Agriculture and Life Sciences, Chungnam National University, Daejeon 34134, Republic of Korea

²Seed Testing and Research Center, Korea Seed and Variety Service, Gimcheon 39660, Republic of Korea

A high-resolution physical map targeting a cluster of yield-related QTLs on the long arm of rice chromosome 9 was constructed across a 37.4kb region containing the six predicted genes including probable ascorbate peroxidase (*OsApx*). To analysis of candidate genes, a BC₄F₆ near isogenic lines (NILs) derived from a cross between the *Oryza sativa* Hwaseong and *O. rufipogon* were further evaluated and compared to Hwaseong for nine agronomic traits. Significant difference in plant height was observed between Hwaseong and NILs due to an increase in internodes, particularly in the 1st and 4th internode, than Hwaseong. To investigate the antioxidant activity in Hwaseong and NILs, the 3,3-diaminobenzidine (DAB) staining and 2,2-diphenyl-1-picrylhydrazyl (DPPH) assay were both conducted. The DAB staining was also performed to understand whether or not *OsApx* gene is important in scavenging H₂O₂ in rice. Based on DAB staining, dark-brown color was barely detected in NILs than Hwaseong. Also, the DPPH scavenging ability of NILs showed higher value than Hwaseong. Hence, these results suggested that the internode elongation and antioxidant activity might possibly be controlled by *OsApx* gene.

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*Corresponding Author: Tel. 042-821-7038, E-mail: ahnsn@cnu.ac.kr

Mapping by exome sequencing in wheat: a tall mutant case study

Youngjun Mo^{1,4*}, Hans Vasquez-Gross¹, Luis Alejandro de Haro², Tyson Howell¹, Stephen Pearce³, Jorge Dubcovsky^{1,5}

¹Department of Plant Sciences, University of California, Davis, CA 95616 USA

²Instituto de Biotecnología, CICVyA, INTA, Buenos Aires, Argentina

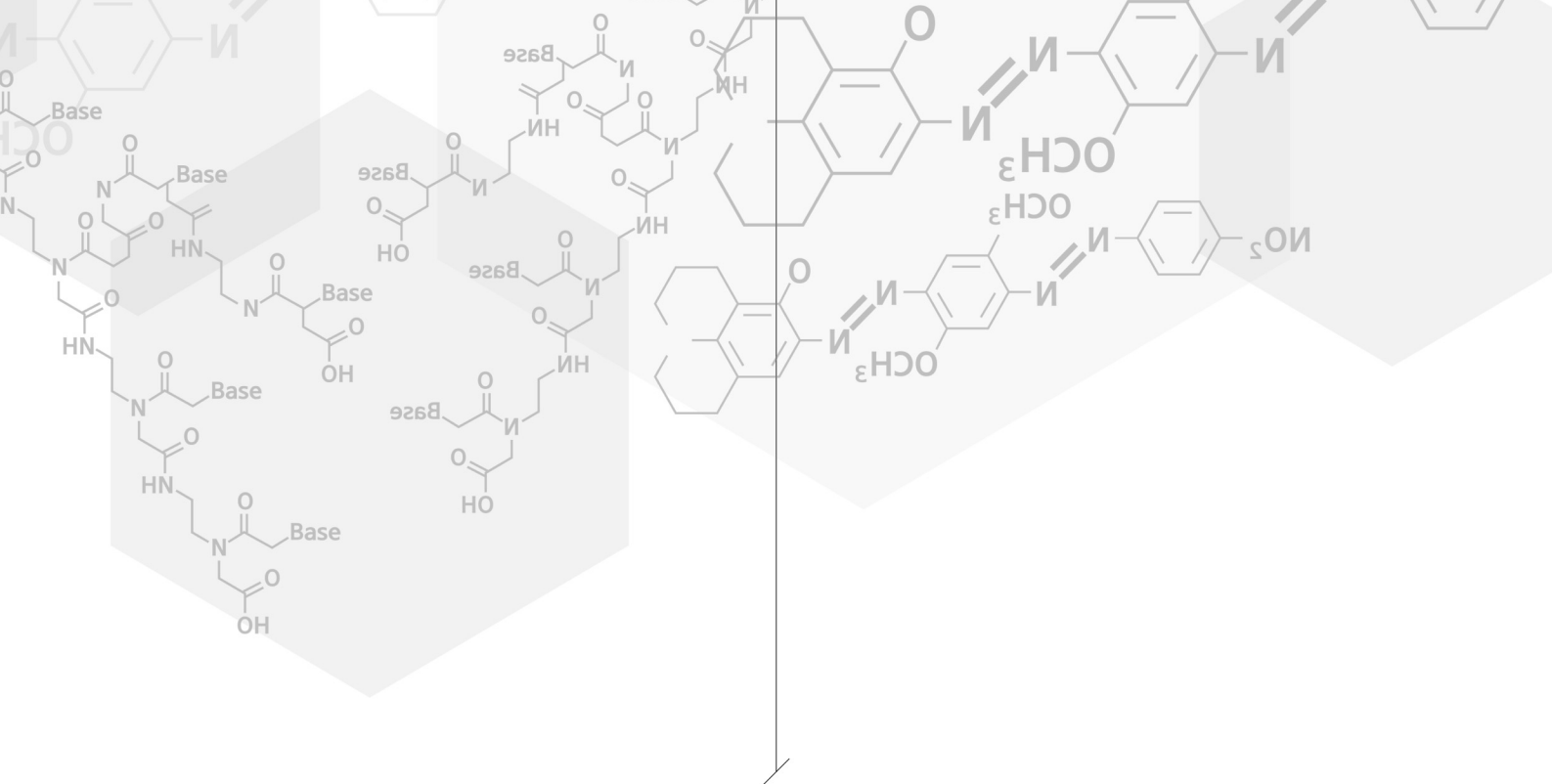
³Department of Soil and Crop Sciences, Colorado State University, Fort Collins, CO 80523, USA

⁴National Institute of Crop Science, Rural Development Administration, Wanju 55365, Korea

⁵Howard Hughes Medical Institute, Chevy Chase, MD 20815, USA

Despite recent advances in high-throughput sequencing technologies, mapping by whole genome sequencing is still not economically feasible in species with large, complex genomes, such as wheat. We used exome capture to reduce genome complexity and tested a rapid mapping strategy in tetraploid wheat to identify a causal mutation responsible for an increased height phenotype. A mutant progeny population segregating for the mutant phenotype was used for mapping, bypassing the two generations of crossing and self-pollination required for generating an F₂ mapping population. We barcoded individual genomic libraries prior to multiplexed exome capture and sequencing to retain genotype information of each mapping individual. Analysis on induced mutations segregating in the mapping population identified a strong candidate region potentially harboring the causal mutation. Coverage analysis conducted in this region identified 1.9 Mb deletion on chromosome 4BS as the most likely causal variant. Our study provides a rapid mapping approach to identify candidate causal mutations in crop species with large polyploid genome such as wheat.

***Corresponding Author:** Tel. +1-530-204-8510, E-mail: yjmo@ucdavis.edu



한국육종학회 포스터발표



Molecular cloning, expression and characterization of a squalene synthase gene from grain amaranth (*Amaranthus cruentus* L.)

Young-Jun Park^{1*}, Kazuhiro Nemoto², Kenichi Matsushima², Han-Yong Um¹, Jung-Hoon Choi¹, Chan-sung Oh¹ and Tomotaro Nishikawa³

¹Rural Research Institute, Korea Rural Community Corporation, 870 Hae-an-ro Sangnok-gu, Ansan-si, Gyeonggi-do, 15634, Republic of Korea

²Graduate School of Agriculture, Shinshu University, 8304 Minami-minowa, Kami-ina, Nagano 399-4598, Japan

³Ministry of Agriculture, Forestry and Fisheries, 1-2-1 Kasumigaseki Chiyodaku, Tokyo 100-8950, Japan

A gene encoding squalene synthase from grain amaranth was cloned and characterized. The full-length cDNA was 1805-bp long and contained a 1248-bp open reading frame encoding a protein of 416 amino acids with a molecular mass of 47.6 kDa. Southern blot analysis revealed that the *A. cruentus* genome contained a single copy of the gene. Comparison of the cDNA and genomic sequences indicated that the amaranth *SQS* gene had 12 introns and 13 exons. All of the exons contributed to the coding sequence. The predicted amino acid sequence of the *SQS* cDNA shared high homology with those of *SQS*s from several other plants. It contained conserved six domains that are believed to represent crucial regions of the active site. We conducted qRT-PCR analyses to examine the expression pattern of the *SQS* gene in seeds at different developmental stages and in several tissues. The amaranth *SQS* gene was expressed late in seed development and played a role in the perisperm, and mainly expressed in stem and root tissues.

*Corresponding Author: Tel. 031-400-1888, E-mail: ramses11@ekr.or.kr

Gene pyramiding of *Sub1A* and *Pup1* in rice

Na-Hyun Shin¹, Joong Hyoun Chin^{2*} and Soo-Cheul Yoo^{1,3*}

¹Department of Plant Life & Environmental Science, Hankyong National University, Anseong, 456-749, Korea

²Graduate School of Integrated Bioindustry, Sejong University, Seoul, 05006, Korea

³Institute of Ecological Phytochemistry, Hankyong National University, Anseong, 456-749, Korea

Rice is one of the major staple food in Asia, covering around half of the world population. More than 40% of rice cultivation area are subject to abiotic stresses such as drought, submergence and phosphate deficiency. Pyramiding useful genes into elite variety is a promising strategy to develop tolerance varieties to multiple abiotic stresses. However, some genes are not functionally compatible when they are introgressed into the same elite variety. Here, we tested the functional compatibility of *Sub1* and *Pup1*, major QTLs for tolerance to submergence and phosphate (P)-deficiency conditions, respectively. Phenotypic analysis revealed that IR64-*Sub1 Pup1* (SP1) plants harboring both *Sub1* and *Pup1* QTLs showed significant tolerance to submerged conditions, similarly in IR64-*Sub1* (Sub1) plant, while SP1 plants failed to tolerate to P-deficiency conditions; only IR64-*Pup1* (Pup1) showed strong P-deficiency tolerance phenotype. In submerged conditions, the expression levels of *Sub1A* and *PISTOL1*, major genes for *Sub1* and *Pup1* QTLs, respectively, were not significantly different in between Pup1 and SP1 plants. On the other hand, the expression of both *Sub1A* and *PISTOL1* was significantly downregulated in P-deficiency conditions, suggesting that *Sub1* and *Pup1* repressed gene expression each other in P-deficiency conditions. These results suggest *Pup1* does not compromise the *Sub1* function in submerged conditions while *Sub1* suppresses the function of *Pup1*, possibly by regulating transcript level of *Pup1*. In conclusion, *Sub1* and *Pup1* are functionally compatible in terms of submergence tolerance but not in P-deficiency conditions. Further analysis need to be performed to elucidate how *Sub1* suppresses the function of *Pup1* in P-deficiency conditions.

*Corresponding Author: E-mail: scyoo@hknu.ac.kr

국내개발 풀 사료작물 신품종 육성 현황 및 종자수출 확산

지희정^{1*}, 황태영¹, 이기원¹

¹충남 천안시 서북구 성환읍 신방1길 114 국립축산과학원 초지사료과

현재 우리나라에서 풀사료 작물로는 이탈리아 라이그라스가 70% 이상을 차지하고 있으며 종자공급량은 약 5천톤 정도로 상당히 큰 비중을 차지하고 있다. 또한 이탈리아 라이그라스는 지중해 연안이 원산지라 추위에 약하지만 당도가 높아 가축 기호성 및 사료가치가 좋은 것으로 나타나 수입종자 대부분은 추위에 약해 월동전 이나 월동후 이른봄 날씨가 풀리면서 식물체와뿌리가 말라서 많이 동사하여 수량감소의 원인이 되어 주로 남부지방을 중심으로 재배해왔다. 따라서 국립축산과학원에서는 지역별 재배시기별 맞춤형 품종으로 총 13품종을 육성하였다. 이들 품종은 논에서 수확시기가 빨라 이모작 재배에 알맞은 극조생종인 그린팜 등 3품종과 5월 상순에 수확할 수 있는 조생종인 코그린 등 3품종, 봄 재배에 알맞은 중생종인 코윈마스터가 있으며 밭에서 여러 차례 수확이 가능한 만생종인 화산101호 등 6품종을 육성하여 보급하고 있다. 이로써 재배지가 대전이남에서 중북부지방으로 확대하게 되었다. 또한 우리 품종에 대하여 해외에 홍보를 강화하기 위하여 2013년부터 미국 오레곤주 등 11개소에서 국외적응성 검정시험을 실시하여 우리품종의 우수성이 입증되었다. 따라서 종자수입국에서 수출국으로 변모할 수 있는 계기로 2016년에는 국외기술이전을 그린팜 등 2품종에 대하여 2016년부터 5년간 835톤 미국 수출계약을 체결하였다. 더불어 우리 품종을 유럽시장에 판매하기 위한 수출기반 조성책으로 2016년도에 EU에 그린팜을 품종보호출원을 실시하여 금년부터 현지 적응성 재배 시험중에 있다. 또한 미국에 그린팜 품종을 품종보호출원을 추진하여 2016년 2월에 국내 최초로 풀 사료작물인 그린팜을 미국시장에 품종 등록 하였다. 풀사료 종자 중에서 중요한 종자품질에 대한 국제적인 인증을 얻기 위해서 국제보종종자인증협회(AOSCA)에 품종등록을 추진하여 현재 그린팜 등 4품종에 대해서도 품질인증등록을 마쳤다. 또한 최근에 육성한 그린팜 2호에 대해서도 2016년도부터 국외 적응성 재배시험을 추진하고 있으며 국외 품종등록과 종자수출 계약을 지속적으로 할 계획이며 우리나라의 남부지방에서 현재보다 수량이 10%이상 증수할 수 있는 초다수성 신품종 개발에 매진하고 있다.

*주저자: Tel. 041-580-6749, E-mail: cornhc@korea.kr

PCR 기반 단일 염기 다형성 마커를 이용한 하례조생 품종 선발 및 다중 중합 효소 연쇄 반응에 의한 신속한 품종 판별

진성범¹, 박재호¹, 박석만¹, 김민주¹, 김호방², 윤수현^{1*}

¹농촌진흥청 국립원예특작과학원 감귤연구소

²㈜바이오메딕 생명과학연구소

제주도내 주로 재배되고 있는 대부분의 온주밀감 품종들은 모계의 유전형질을 동일하게 갖고 있는 주심배 와 가지변이 등에 의하여 육성되었기 때문에 묘목 상태로 농가에 공급된 품종들에 대하여 형태학적으로 품종을 판별하는 것은 어렵다. 따라서, 본 연구는 제주도내 재배되고 있는 온주밀감 품종 중 하례조생 품종만을 판별할 수 있는 마커개발을 목적으로 수행하였다. 하례조생 품종에 특이적인 SNP(single nucleotide polymorphism) 마커 6조합과 negative control 1조합을 이용하여 총 8품종 (하례조생 원목, 궁천조생, 흥진조생, 유라조생, 궁본조생, 상야조생, 미택온주, 일남 1호)의 온주밀감 중 하례조생 품종만을 선발하기 위하여 PCR를 수행하였다. 그 결과 하례조생 품종만 특이적으로 증폭되는 SNP 마커 2 조합(P1: HL-SNP-SCAF_2-23997586-F, HL-SNP-SCAF_2-23997586-R; P5: HL-SNP-SCAF_9-30793978-F, HL-SNP-SCAF_9-30793978-R)을 선발하였고, P1(165bp)과 P5(526bp)의 PCR증폭산물은 1회의 Multiplex PCR반응을 통하여 동시에 얻었다. 또한, 주심배실생 품종(하례조생)의 SNP 지역은 모체인 품종(입간조생)과 유전적으로 변이가 있음을 확인하였고, 온주밀감 17품종을 재배하는 농가에서 하례조생 품종의 판별은 Multiplex PCR로 확인 할 수 있었다. 따라서 이 SNP 마커를 이용한 Multiplex PCR방법은 하례조생 품종을 농가에 공급함에 있어서 시간적인 단축과 경제적인 경비를 절감할 수 있을 것으로 기대된다.

*주저자: Tel. 064-730-4106, E-mail: yunsh04@korea.kr

국내 재래종 밀 과발현 Bx7 고분자 글루테닌 서브유닛 분석

조성우, 김재덕, 강택규, 백연경, 박철수*

전북대학교 농업생명과학대학 작물생명과학과

좋은 제빵 적성을 위해 *Glu-B1a1* (과발현 Bx7; Bx7^{OE} + By8) 대립유전자는 매우 중요한 역할을 한다. 이 대립유전자는 핵산표지인자를 이용하여 국내 재래종 밀에서 발견되었다. 이 대립유전자의 x-형 유전자에 의해 암호화 된 글루테닌 서브유닛인 Bx7 의 과발현을 확인하기 위하여 분자수준의 분석을 수행하였다. 국내 재래종 밀 (IT166460)의 SDS-PAGE결과는 유전적으로 Bx7^{OE} 지니고 있는 Glenlea(Canadian western red spring wheat)와 유사한 단백질 발현 양상을 보였다. 이차원 전기영동 (two-dimensional electrophoresis)을 이용한 분석 결과 역시 IT166460에서 Glenlea처럼 Bx7^{OE}를 확인하였다. 고분자 글루테닌 서브유닛들 (HMW-GSs)에서 Bx7의 비율을 확인하기 위하여 RP-HPLC를 수행하였다. IT166460의 Bx7의 비율은 $56.2 \pm 0.2\%$ 로써 CS (Chinese Spring, $34.8 \pm 1.0\%$)과 Glenlea ($46.3 \pm 1.8\%$)보다 높은 것으로 확인되었다. 유전자 중복 (gene duplication)과 프로모터 영역의 43 bp indel (insertion and deletion)은 Bx7^{OE}의 원인이다. IT166460은 두 요인 모두가 충족되는 것을 분석을 통하여 확인하였다. Bx7^{OE}를 지닌 대부분의 밀 계통들은 주로 미국에 분포하고 있다. 따라서 국내 밀 육종 프로그램에 있어 과발현 Bx7 고분자 글루테닌 서브유닛을 지닌 국내 재래종 밀 (IT166460)은 제빵 적성 향상을 위한 유전자원으로써 중요한 역할을 할 것으로 생각된다.

*교신저자: Tel. 063-270-2533, E-mail: pc89@jbnu.ac.kr

Glu-D1 유전좌위상의 새로운 y-형 고분자 글루테닌 서브유닛 특성

조성우, 김재덕, 강택규, 백연경, 박철수*

전북대학교 농업생명과학대학 작물생명과학과

Glu-D1 유전좌위상에서 Glu-1Dy12.K 명명된 새로운 y-형 고분자 글루테닌 서브유닛이 금강과 CS (Chinese Spring)과의 교배 조합 (F₉)에서 확인되었다. Glu-1Dy12.K의 특징으로 SDS-PAGE에서 기존의 Glu-Dy12보다 빠른 전기영동이동도와 낮은 분자량이 확인되었다. 이차원 전기영동을 바탕으로 한 질량분석에서 Glu-1Dy12.K는 ID: P08488 (GLT3 WHEAT)인 ‘Glutenin, high molecular weight subunit 12’과 높은 유사성이 이차원 전기영동을 바탕으로 한 질량분석을 통하여 확인되었다. Glu-1Dy12.K를 암호화하는 유전자 *Glu-1Dy12.K*는 652아미노산에 상응하는 1962 염기서열로 이루어져 있는 것을 클로닝을 바탕으로 염기서열 분석을 통하여 확인하였다. *Glu-1Dy12.K*은 높은 유사성을 보이는 *Glu-1Dy10* (GI: 164457872 in NCBI)과 6 bp와 18bp에 상응하는 두 곳의 indels (insertion and deletion)와 21 SNPs (single nucleotide polymorphisms)가 다른 것을 확인하였으며, *Glu-1Dy12* (GI: 1036031968)와는 한 곳의 indel과 3 SNPs가 다른 것을 확인하였다. Glu-1Dy12.K에서만 ‘AACAGGACAAGGGCAACA’ 에 상응하는 예측된 ‘TGQGQQ’인 펩타이드 서열이 결실된 것을 확인하였다.

*교신저자: Tel. 063-270-2533, E-mail: pc89@jbnu.ac.kr

Identification of IDD7 and IDD14 mutants in *Arabidopsis thaliana*

Le Thi Dung, Hyun Uk Kim*

Department of Bioindustry and Bioresource Engineering, Plant Engineering Research Institute, Sejong University, Seoul 05006 Republic of Korea

The *Arabidopsis* genome contains 16 Indeterminate Domain (IDD) transcription factors. They have divided into two groups with the arrangement of zinc finger motifs at N-terminus and several motifs at C-terminus. In this study, to elucidate the role of IDD7 and IDD11 in plants, identification the mutants and generation of overexpressed plants for *IDD7* and *IDD11* genes is required. Here we report that IDD7 and IDD11 have a distinct motifs arrangement at C-terminus and have not yet characterized their biological functions. Analyzed amino acid sequence showed two transcription factors have high identical. Loss-of-function of these IDD genes exhibits significantly development with the seedling and seed size are larger than wild-type plants, while double mutants *idd7-1* and *idd11-1* showed smaller growth. Overexpression of IDD11 plants showed the weak development what belong phenotype inhibitor. Analyzed fatty acid concentration in seeds showed that having a significantly increase in *idd7-1* and *idd11-1* mutant seeds than their wild-type. Our results provide useful information to detect the function of IDD7 and IDD11 transcription factors in *Arabidopsis thaliana*.

*Corresponding Author: Tel. 02-3408-4318, E-mail: hukim64@sejong.ac.kr

LegExpress: A bioinformatic platform for transcriptome analysis in legume genomes

Joo-Seok Park¹, Chaeyoung Lee², Jin-Hyun Kim², Yoram Choi¹, Min-Gyun Jeong¹ and Hong-Kyu Choi^{3*}

¹Department of Applied Bioscience, Dong-A University, Busan, Republic of Korea

²Department of Medical Bioscience, Dong-A University, Busan, Republic of Korea

³Department of Molecular Genetics, Dong-A University, Busan, Republic of Korea

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. To develop such a bioinformatics system, 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.

*Corresponding Author: Tel. 051-200-7508, E-mail: hkchoi@dau.ac.kr

LegCompara: A bioinformatic platform for interactive comparative genome analysis in legumes

Jin-Hyun Kim¹, Chaeyoung Lee¹, Joo-Seok Park², Yoram Choi², Min-Gyun Jeong² and Hong-Kyu Choi^{3*}

¹Department of Medical Bioscience, Dong-A University, Busan, Republic of Korea

²Department of Applied Bioscience, Dong-A University, Busan, Republic of Korea

³Department of Molecular Genetics, Dong-A University, Busan, Republic of Korea

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. arretinum*) and two model plants (*A. thaliana*, *O. sativa*). This genome browser was developed by employing the JavaScript and SVG (Scalable Vector Graphics)-based programs. As a result, we could significantly reduce server's workload, gain rapid response, and enhance graphic visibilities of the interface. This system, unlike other traditional genome browsers, was designed for researchers to dynamically interact with user interface, so it can navigate multiple chromosomes of different or same species simultaneously, resulting in genome-wide and/or regional comparisons by depicting corresponding syntenies with either blocks or lines between orthologous regions or genes. Instant transition of micro-to-macro synteny analyses are also possible by zooming in/out from individual gene to full chromosome scale. It is expected that LegCompara may provide researchers and breeders with useful resources for more efficient and user-friendly comparative genome analysis.

***Corresponding Author:** Tel. 051-200-7508, E-mail: hkchoi@dau.ac.kr

Alternative splicing events of drought-related genes under drought stress in maize

Kitae Song¹, Hyochul Kim¹, Kyung-Hee Kim¹, Jun-Cheol Moon², Jae Yoon Kim³, Byung-Moo Lee^{1*}

¹Department of Life Science, Dongguk University-Seoul, Seoul 04620, Republic of Korea

²Agriculture and Life Sciences Research Institute, Kangwon National University, Chuncheon, 24341, Republic of Korea

³Department of Plant Resources, College of Industrial Science, Kongju National University, Yesan 32439, Republic of Korea

Drought stress is an important factor determining yield, growth and seed quality in maize. We have analyzed drought related genes and their alternative splicing which can make change tolerance using RNA-sequencing and bioinformatics tools. We identified a total of 723 genes and 235 transcripts whose expression was changed by drought in maize. The genes and isoforms were classified by blast, and we also found a multitude of possibilities to estimate correlation between drought and gene function. Furthermore, we identified several drought responsive transcript factors containing zinc finger and NAC domains. The transcript factors are frequently involved in gene expression, included gene regulation and alternative splicing. Overall, our results provide a genome-wide analysis of differentially expressed genes (DEGs), novel transcripts, and alternative splicing under drought stress. Further characterization of the drought-responsive transcripts and their expression patterns identified in this study has potential to advance our understanding of drought tolerance in maize.

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***Corresponding Author:** Tel. 031-961-5130, E-mail: bmlee@dongguk.edu

Development of Japonica advanced backcross lines having bacterial blight resistant genes from a cross between japonica and indica

Woo-Jae Kim*, Jae-Beom Chun, Hyun-Su Park, Hyun-Soon Kim, Kyung-Ho Kang, Ji-Ung Jeong, Jae-Kwon Ko

National Institute of Crop Science, RDA, Wanju, Republic of Korea 565-851

This study was carried out to develop rice variety integrated with rice bacterial blight resistance gene. Advanced Backcross Lines (ABLs) 5 that contains *Xa1*, *Xa3*, *xa5*, and *Xa21*, was developed from backcross 2 times between Japonica cultivar Hopum having bacterial blight resistant *Xa3* gene and Indica cultivar VND95-20 having *Xa1*, *xa5*, and *Xa21* gene and disease resistance bioassay and marker-assisted selection. Advanced Backcross Lines (ABLs) 21 that contains *Xa3* and *Xa21*, was developed from backcross 2 times between Japonica cultivar Hanggeumnuri having bacterial blight resistant *Xa3* gene and Indica variety IRBB21 having *Xa21* gene and disease resistance bioassay and marker-assisted selection. Reaction of ABL5-1 and ABL21-1 against 18 isolates in K3a race showed stable durable resistance reaction and lesion length shorter than the donor parents. Analysis of variance conducted for confirm uniformity in pathogenicity of isolates and repeat values of lesion length to each isolates were not significant at $p=0.05$. In result of cluster analysis, HB4032 isolate showed very high pathogenicity among 18 isolates.

***Corresponding Author:** Tel. 063-238-5235, E-mail: suwonman@gmail.com

Study in search for the heritable force driving phenotypic variation in soybean seed size

Sampathkumar Palaniswamy¹, Jagadeesh Sundaramoorthy¹, Gyu Tae Park¹, Jeong-Dong Lee¹, Hak Soo Seo², Jong Tae Song^{1*}

¹School of Applied Biosciences, Kyungpook National University, Daegu, Republic of Korea

²Department of Plant Bioscience, Seoul National University, Seoul, Republic of Korea

From the time when agriculture began, food grains undergo various selections and breeding for size as well as for other attribute. These phenotypic characters are governed by the genetic makeup. Soybean [*Glycine max* (L.) Merr] is one of the major agricultural crop mostly used for food and oil. 100 seed weight is the common method to measure the seed size of soybean. For accuracy, measurements like seed length, seed width, seed thickness and seed volume are also added. With the development of molecular biology techniques, marker assisted breeding and advanced genetic sciences it is possible to uncover the genetic makeup involved in the seed size. Over three decades many Quantitative Trait loci (QTLs) are identified for improving this trait. But still the allelic genes responsible for larger seed size and smaller seed size are unknown. In search of genetic resource involved in this trait, we developed an Ethyl methanesulfonate (EMS) mutant line PE887 with smaller seed size. In addition segregating population was developed by breeding cross between PE887 and Pungsannamul. Further genetic linkage mapping will be carried out to find gene(s) involved in the determination of seed size.

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

Identification of the gene responsible for high and low inorganic phosphorus in soybean

Thi Hai Yen Nong¹, Jagadeesh Sundaramoorthy¹, Gyu Tae Park¹, Jeong-Dong Lee¹, Hak Soo Seo², Jong Tae Song^{1*}

¹School of Applied Biosciences, Kyungpook National University, Daegu, Republic of Korea

²Department of Plant Bioscience, Seoul National University, Seoul, Republic of Korea

Phosphorus (P) is a nutrient essential for growth of plants that is available in composition of the nucleic acids, ATP, coenzyme. Phytic acid (myo-inositol-1,2,3,4,5,6-hexakisphosphate) is the main storage form of phosphorus in yeast, mammalian and almost economically important crops. In soybean [*Glycine max* (L.) Merr] seeds, phytic acid is found in the form of phytate salt mixtures with multivalent cations, proteins, Ins P and starch that prevent their assimilation through the digestive system. Thus, a large amount of phosphorus in the form of phytate undigested monogastric animals and excreted into environment. The objective of the present study is to identify soybean mutants with high available P. Inorganic P was content in 1,266 ethyl methanesulfonate (EMS) M₄ lines from the cultivar Pungsannamul. As the result of our study, we isolated four EMS lines (PE379, PE432, PE2205 and PE2503) with high inorganic P (1.21-1.56 g kg⁻¹) and six EMS lines (PE718, PE828, PE1466, PE1552, PE3378 and PE3386) with low inorganic P (0.38-0.60g kg⁻¹)(compare with control line Pungsannamul: 0.90 g kg⁻¹). In present, we are selected homozygous of HIP mutant line (PE432). In the future, we will continue selection of homozygous LIP mutants and carried out breeding cross between mutant lines and wild controls lines in order to find the gene(s) responsible for the low and high inorganic P phenotypes.

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

Identification of SNP markers in boysenberry using genotyping-by-sequencing

Juhyun Im¹, Woon Ji Kim¹, Sang Hun Kim¹, Seung Cheol Oh², Lan Cho², Si-Yong Kang³, Sung-Hwan Jo⁴, Bo-Keun Ha^{1*}

¹Division of Plant Biotechnology, Chonnam National University, Gwangju, 61186, Korea

²Bioplus Co., Wanju, 55310, Korea

³Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongeup, 56212, Korea

⁴Seeders Inc., Daejeon, 34015, Korea

Boysenberry is one of the genus *Rubus* and derived from a cross between Loganberry and a trailing blackberry. Recently, several new boysenberry and blackberry genotypes were developed from mutation breeding technology. In this study, we evaluated genetic diversity among 10 boysenberry genotypes and 6 blackberry genotypes using SNP markers. These SNP markers were identified by genotyping-by-sequencing (GBS) technology. GBS libraries were constructed using 16 different barcodes and the restriction enzyme *ApeKI* (GCWGC). SOAPdenovo2 produced the highest number of contigs at a k-mer length of 31 and the assembled contigs were used as references. We identified a total of 23,529 polymorphic SNPs and 464 InDel among 16 boysenberry and blackberry genotypes. After filtering SNPs with missing rates < 30%, 1,504 SNPs were used to built a phylogenetic tree among 16 genotypes. In addition, we identified 24 SNP marker set discriminating 16 boysenberry and blackberry genotypes. This SNP marker set will allow for the rapid identification of *Rubus* germplasm.

***Corresponding Author:** Tel. 062-530-2055, E-mail: bkha@jnu.ac.kr

Identification and characterization of new high stearic acid soybean mutant induced by gamma-ray irradiation

Sang Hun Kim¹, Juhyun Im¹, Woon Ji Kim¹, Ryuli Gang¹, Si-Yong Kang², Bo-Keun Ha^{1*}

¹Division of Plant Biotechnology, Chonnam National University, Gwangju, 61186, Korea

²Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongeup, 56212, Korea

Soybean [*Glycine max* (L.) Marr.] seeds are the most valuable sources of vegetable oil. However, the partially hydrogenated soybean oil desirable for solid fat baking applications creates *trans* fats associated with negative health effects on blood lipids. The chemical hydrogenation can be reduced by increasing stearic acid content that is a saturated fatty acid and neutral effect on cholesterol level. This study identified new mutant genotype containing ~17% stearic acid. This mutant genotype was developed from gamma irradiation treatment with original cultivar, Ilmi containing ~3% stearic acid. The mutant contained a three base pair deletion in the 1st exon of stearoyl-acyl-carrier protein desaturase (SACPD-C) gene. The deletion of three bases resulted in a protein that is missing one amino acid. This mutation could affect the function of SACPD-C gene and elevate seed stearic acid levels.

*Corresponding Author: Tel. 062-530-2055, E-mail: bkha@jnu.ac.kr

Human *Bone Morphogenetic Protein-2* (hBMP-2) 유전자가 도입된 벼 형질전환체 개발

이주영, 김용호*

충남 아산시 순천향대학교 의료생명공학과

뼈형성 단백질(Bone morphogenetic protein, BMP)은 세포조절인자로 현재까지 최소 20종류가 보고되었다. 본 연구에서는 인간 BMP-2 유전자를 일미벼에 형질전환하고 도입 유전자의 발현수준을 전사체와 단백질 수준에서 확인하였다. hBMP-2 유전자를 pPZP200 vector를 사용하여 *Agrobacterium*을 매개로 벼 캘러스에 도입시킨 형질전환체에서 total RNA를 추출하여 cDNA를 합성한 뒤 Quantitative real time-PCR(qRT-PCR)을 수행하였다. 벼의 내재유전자로 사용된 *actin*과 도입 유전자인 hBMP-2의 비특이적인 증폭 여부를 확인하기 위해 melt curve를 분석한 결과 대조구인 일미벼를 제외한 나머지 시료에서 melting temperature가 83°C로 모두 일정하게 나타났다. 전사체의 상대적인 mRNA량은 기준량 대비 1.9~3.7배가 발현됨을 확인하였으며, 또한 western blot analysis를 통하여 형질전환체에는 도입유전자에 의한 단백질이 형성되었음을 확인하였다.

*주저자: Tel. 041-530-1281, E-mail: yohokim@sch.ac.kr

Molecular studies of mutations induced by proton beam irradiation in soybean using genotyping-by-sequencing (GBS)

Woon Ji Kim¹, Juhyun Im¹, Sanghun Kim¹, Bo-Keun Ha^{1*}

¹Division of Plant Biotechnology, Chonnam National University, Gwangju, 61186, Republic of Korea

Ionization radiation causes DNA single strand breaks (SSB), double strand breaks (DBS), damage or loss of bases, and intramolecular / intermolecular crosslinking. Since there is no report on the mutation rate according to the proton beam irradiation in soybean, the present study investigates the genetic variation in the soybean chromosome induced by the proton beam irradiation. Total of 22 plants including each 10 M₂ plants induced from 118Gy and 239Gy of proton beam, respectively, and 2 wild-type plants (Deapungkong) were sequenced using GBS technology. Total of 7,453 SNPs were observed in proton beam irradiated M₂ plants. Of these, 3,569 SNPs were observed in the genic regions. Among 5,829 union SNPs, transition and transversion were 47% and 53%, respectively. The highest substitution ratio was for transversion A / T with 37%. Most SNPs (82%) were distributed in one gene, while the rest (12%) had 2 to 5 SNPs per gene. The SNPs induced by proton beam were uniformly distributed in most of the chromosomes. This study will establish a framework for constructing a pool of mutant genetic resources using the proton beam.

***Corresponding Author:** Tel. 062-530-2055, E-mail: bkha@jnu.ac.kr

A genome-wide association study of amino acids in core collection of wild soybean (*Glycine soja*)

Woon Ji Kim¹, Juhyun Im¹, Sanghun Kim¹, Ju Seok Lee², Sungtaeg Kang³, Soon-Chun Jeong⁴, Jung-Kyung Moon⁵, Bo-Keun Ha^{1*}

¹Division of Plant Biotechnology, Chonnam National University, Gwangju, 61186, Republic of Korea

²Department of Plant Science, Seoul National University, Seoul, 08826, Republic of Korea

³Department of Crop Science & Biotechnology, Dankook University, Cheonan, 31116, Republic of Korea

⁴Bio-Evaluation Center, Korea Research Institute of Bioscience and Biotechnology, Cheongju, 28116, Republic of Korea

⁵National Institute of Agricultural Sciences, Rural Development Administration, Wanju, 55365, Republic of Korea

In this study, we conducted a genome-wide association study (GWAS) between genetic variation and amino acid contents in core collection of wild soybean. The 203 accessions were used for analyzing amino acids with an amino acid auto-analyzer (S433-H, SYKAM). The total amino acid contents of 203 accessions ranged from 32,896 to 53,251 (mg/100g). The content of cystine was 222.79 ~ 756.63(mg/100g) and the content of methionine was 339.12 ~ 734.81(mg/100g). The correlation between cystine and methionine was $r = 0.293^{**}$, and the 17 amino acids showed highly significant and positive correlation with each other. By GWAS with 130K SNP genotyping data, AX-90330677 SNP marker showed significant association with three amino acids such as glutamic, leucine, and phenylalanine. The AX-90330677 was located in 47,702,857 bp of chromosome 9. Four genes, Glyma.09g257300, Glyma.09g258000, Glyma.09g249100, and Glyma.09g250700, associated with amino acids were identified near the genetic region of AX-90330677. Our results will help us to understand the genetic basis of amino acid biosynthesis in soybean seeds.

***Corresponding Author:** Tel. 062-530-2055, E-mail: bkha@jnu.ac.kr

종자가 크고 쓰러짐과 협개열성에 강한 녹자엽 검정콩 ‘태청’

서정현¹*, 강범규¹, 김현태¹, 신상욱¹, 김홍식¹, 백인열¹, 한원영¹, 윤홍태², 이병원², 고종민³, 곽도연¹

¹경남 밀양시 점필재로20 국립식량과학원 남부작물부

²경기도 수원시 수인로126 국립식량과학원 중부작물부

³전북 완주군 이서면 혁신로181 국립식량과학원

검정콩은 맛이 좋고 무름성이 좋아 예로부터 밥밑용으로 사용되어 왔으며 최근에는 종피에 들어있는 기능성 물질에 대한 관심이 높고 연구가 활발하다. 이러한 검정콩은 건강 기능성 식품으로서 소비가 증가하고 시장가격이 높게 형성되어 농업인들의 수요가 늘고 있지만 도복, 탈립 등 재배행질이 불리하여 이에 대한 개량이 필요하다. 소비자들은 검정콩의 자엽색이 푸른 것을 선호하며 용도 확대를 위하여 다양한 크기의 품종개발이 요구된다. ‘태청’은 대립이면서 녹자엽인 검정콩 육성을 목표로 하여 ‘YS1593(밀양136호×단파흑대두)’을 모본으로, ‘청자2호’를 부본으로 2005년에 인공교배 하였으며 계통육종법에 의해 ‘YS1764-2B-7-1-5-3-1-1’이 선발되었다. ‘12~’13년도에 실시한 생산력검정시험에서는 극대립 녹자엽 계통으로 유망시되어 ‘밀양278호’의 계통명을 부여하고 ‘14~’16년 3년 간 7개소에서 지역적응시험을 실시하였다. ‘태청’은 유한신육형으로서 엽형이 난형, 꽃색이 자색, 모용색이 갈색, 종실은 구형으로 검은색 종피에 자엽색이 녹색인 고유특성을 가지고 있다. 성숙기는 10월20일로 청자3호보다 3일 늦으며 100립중은 44.5g으로 청자3호에 비하여 10g 더 무겁다. 지역적응시험에서 ‘태청’의 내도복성은 청자3호와 비슷한 수준으로 강하였고, 협개열성은 청자3호보다 강하였다. ‘태청’의 수량은 지역적응시험 7개소 평균 240kg/10a로 청자3호(254kg/10a)의 94% 수준이었다. 이처럼 ‘태청’은 알이 굵으면서도 도복과 탈립에 강하여 재배특성이 좋고 우수한 외관품질을 가지고 있으므로 콩초콜릿 등 가공용(제과용) 및 밥밑용 콩으로서 널리 사용될 것으로 기대된다.

*주저자: Tel. 053-663-1111, E-mail: next0501@korea.kr

Genetic diversity analysis in *Perilla* crop from northern areas of china based on SSR molecular markers

Shi Jun Ma, Kyu Jin Sa, Tak-Ki Hong, Ju Kyong Lee*

Department of Applied Plant Sciences, College of Agriculture and Life Sciences, Kangwon National University, Chuncheon, 200-701, Korea

In this study, 21 simple sequence repeat (SSR) markers were used to evaluate the genetic diversity and population structure among 77 *Perilla* accessions from high-latitude and middle-latitude areas of China. 95 alleles were identified with an average of 4.52 alleles per locus. The average polymorphic information content (PIC) and genetic diversity (GD) values were 0.346 and 0.372, respectively. The level of genetic diversity and PIC value for cultivated accessions of var. *frutescens* from middle-latitude areas were higher than accessions from high-latitude areas. Based on the dendrogram of unweighted pair group method with arithmetic mean (UPGMA), all accessions were classified into four major groups with a genetic similarity of 46%. All accessions of cultivated var. *frutescens* were clearly discriminated from the cultivated var. *crispa*. Furthermore, most accessions of cultivated var. *frutescens* collected in high-latitude and middle-latitude areas were clearly distinguished depending on their geographical location. However, the geographical locations of several accessions of cultivated var. *frutescens* have no relation with their positions in the UPGMA dendrogram and population structure. This result implies that the diffusion of accessions of cultivated *Perilla* crop in the northern areas of China might be through multiple routes. On the population structure analysis, 77 *Perilla* accessions were divided into Group I, Group II, and an admixed group based on a membership probability threshold of 0.8. Finally, the findings in this study will provide useful theoretical knowledge for further study on the population structure and genetic diversity of *Perilla* and benefit for *Perilla* crop breeding and germplasm conservation.

*Corresponding Author: Tel. 033-250-6415, E-mail: jukyonglee@kangwon.ac.kr

Bulk segregant analysis (BSA) for drought stress in maize inbred lines using SSR markers

Muhammad Qudrat Ullah Farooqi, Shi Jun Ma, Kyu Jin Sa, Ju Kyong Lee*

Department of Applied Plant Sciences, College of Agriculture and Life Sciences, Kangwon National University, Chuncheon, 200-701, Korea

In this study, maize inbred lines were used to evaluate performance under drought stress. Based on germination ability, 24 lines were screened out with tolerance or susceptibility to drought stress. Genetic diversity, relationship, and population structure were evaluated by using 100 SSR molecular markers linked with drought tolerance in maize. A total of 465 alleles were identified with an average of 4.65 alleles per locus using bulk segregant analysis (BSA). Out of them, 199 were specific alleles with tolerance and 35 were susceptible to drought, while the remaining 231 were shared between the two types. The major allele frequency varied from 0.39 to 0.61 with an average of 0.47. The gene diversity (GD) and polymorphic information content (PIC) average values from all lines were 0.64 and 0.59, respectively. Based on UPGMA analysis, four main cluster groups were identified as most of the drought tolerant lines were clearly discriminated from drought susceptible lines with 33% genetic similarity. On population structure analysis, 24 inbred lines with tolerance and susceptibility were divided into 3 groups. In addition to BSA, a total of 88 SSR's were identified as specific to tolerance and 29 SSR markers were specific to susceptible lines. Among these, bnlgl627, umc1946, dupssr30b, bnlgl1812, and dupssr24 SSR markers had great potential for the improvement of drought resistance in maize. Our results were in good agreement with previous studies for drought tolerance using SSR molecular marker and will be useful for further maize breeding studies.

*Corresponding Author: Tel. 033-250-6415, E-mail: jukyonglee@kangwon.ac.kr

Construction of a Linkage map and mapping of QTLs related to agronomic traits in maize with help of Mutator based transposon markers and simple sequence repeat markers

Rahul Vasudeo Ramekar¹, Kyong-Cheul Park², Kyu Jin Sa¹, Ju Kyong Lee^{1*}

¹Department of Applied Plant Sciences, College of Agriculture and Life Sciences, Kangwon National University, Chuncheon, 200-701, Korea

²Department of Agriculture and Life Industry, Kangwon National University, Chuncheon 200-701, Korea

Genetic Linkage map can provide a deeper understanding of random markers distribution along the chromosome which can be employed for a range of plant breeding objectives. Transposons constitute a large fraction of eukaryotic genome and can have a high impact on overall genome structure. We have designed a set of *Mutator* (Mu) specific primers based on terminal invert repeats and utilized a modified transposon insertion display method (MU-TD) for genotyping. Here we describe the chromosomal distribution of Mu markers added to a linkage map of maize using anchored SSR markers. The mapping population included 80 F_{7,8} RILs derived from cross between dent corns and waxy corn, evaluated for ten grain yield and kernel quality related traits over 2 year period. The TD analysis produce a high profile of the polymorphism between the parental lines with 20 Mu- specific primers. Number of polymorphic bands ranged from 5 to 33. The linkage map included 258 Mu-anchored fragments along with 614 SSR markers distributed along 10 chromosomes and covered a span of 6102.92 cm. The integration of Mu loci extended the map in several telomeric regions and reduced several gaps present in previous map. A total of 22 QTLs were confirmed in 2011 and 2012 for various traits which included total of 18 Mu loci. This work represents an important step forward in genomics and marker assisted breeding in maize.

*Corresponding Author: Tel. 033-250-6415, E-mail: jukyonglee@kangwon.ac.kr

Understanding genetic differentiation and association mapping of agronomic traits in waxy and common maize based on mutator transposon display

Rahul Vasudeo Ramekar¹, Kyong-Cheul Park², Kyu Jin Sa¹, Ju Kyong Lee^{1*}

¹Department of Applied Plant Sciences, College of Agriculture and Life Sciences, Kangwon National University, Chuncheon, 200-701, Korea

²Department of Agriculture and Life Industry, Kangwon National University, Chuncheon 200-701, Korea

In Gangwon Agricultural Research and Extension services at the Maize experiment station a large collection of maize inbred lines (waxy and common) of diverse origins, both from local farmers and other countries are assembled. Waxy maize has originated from cultivated flint maize and most recently underwent divergence from common maize. Thus understanding genetic variation and differentiation in this elite lines is fundamental for selection, by which progress in plant breeding can be achieved. Transposable elements (TEs) account up to 85% of the maize genome, creates a large and stable insertions in the genome generating variations which reflect selection acts during evolution and plays a significant role in genome organization, yet they have not been used in population genetics and association analysis. We recently developed a set of *Mutator* specific primers based on terminal invert repeats and utilized a modified transposon insertion display method (MU-TD) for genotyping. Using this method we studied genetic diversity and population structure of 40 waxy and 40 common maize. Also to explore the contribution of *mutator* TEs to phenotypic variation, we undertook association analysis in the same maize line phenotype by ten economical important traits. The results revealed substantial genetic diversity in the studied panel, and that genetic variation in waxy maize was lower compared to common maize. Principle co-ordinate analysis, neighbor-joining cluster analysis, and STRUCTURE analysis supported the presence of two genetically distinct groups. Analysis of molecular variance revealed significant genetic differentiation within the population than among the population describing genetic variation mainly resides within the population. We also found a highly significant association between seven *mutator* loci with four different traits. These results will be useful for marker-assisted selection in maize breeding program to help breeders choose parental lines and markers for crossing as well as in understanding the role of transposons in creating diversity and shaping the evolution in maize.

*Corresponding Author: Tel. 033-250-6415, E-mail: jukyonglee@kangwon.ac.kr

완전미울 높고 속색 좋은 중생종 벼 ‘상보’ 육성

박노봉^{1*}, 남민희¹, 김상열², 여운상², 이지윤², 권오덕¹, 박동수², 이종희³, 조준현², 송유천², 오성환⁴

¹경북 영덕군 병곡면 원황길 44 농촌진흥청 국립식량과학원 영덕출장소

²경남 밀양시 내이동 점필재로 20 국립식량과학원 남부작물부

³전북 전주시 완산구 농생명로 300 농촌진흥청 연구정책국

⁴전북 전주시 완산구 농생명로 300 농촌진흥청 기획조정관실

국립식량과학원 영덕출장소에서는 최근의 이상기상에 따른 병해충 증가에 대응하기 위해 밥맛과 재배 안정성이 뛰어난 고품질 벼 품종을 육성하고자 노력한 결과, 우리나라 중부 및 영남 평야지와 동해안 냉조풍지에 알맞은 고품질 중생종 벼 ‘상보’를 개발하였다. 모본으로 재배 안전성이 뛰어난 ‘영덕32호(삼덕벼)’를, 부분으로는 도정율이 우수한 ‘남평벼’를 2002년 하계에 인공교배하여 2003년 하계에 32개체의 F₁ 식물체를 양성, YR24256의 교배번호를 부여하였다. 2004년 하계포장에 전개한 F₂ 집단을 포장과 실내 선발하여 2005년 하계에 F₃ 세대 142계통을 육성하였다. 이후 F₄~F₈ 세대를 계통육종법으로 전개하면서 예비선발 시험을 실시하여 미질특성이 우수하고 병해와 재해에 안정적인 계통을 선발하였다. 2011년 생산력검정 예비시험, 2012~2013년 생산력검정 본시험을 실시한 후 중생이면서 우량계통인 YR24256-142-5-3-1-1-2을 선발하여 ‘영덕59호’로 명명하였다. 2013년부터 3년간 지역적응시험을 실시한 결과, 복합내병성이면서 특히 속색이 양호한 것으로 평가되어 2015년 12월 농작물직무육성신품종선정위원회에서 ‘상보’로 명명하게 되었다. ‘상보’는 보통기 재배 시 출수기는 8월 9일로 중생종이며, 간장은 77cm로 약간 큰 반직립 초형이다. 탈립은 잘되지 않고 이삭추출은 양호하며 까락이 거의 없다. ‘화성벼’ 보다 수당립수는 19개 더 많으며, 현미천립중도 24.1g으로 더 무겁다. 쌀알이 맑고 투명하며, 도정특성과 밥맛도 ‘화성벼’ 보다 우수하다. 또한 불시출수는 안되는 편이고, 위조현상에 강하고 성숙기 엽노화가 느린 편이며, 내병성은 ‘화성벼’ 보다 약한 중약 정도이다. 잎도열병에 중정도의 저항성을 보였고, 줄무늬잎마름병, 흰잎마름병(K₁, K₂, K₃)에는 강하나 오갈병, 검은줄오갈병에는 약하고, 벼멸구 등 충해에는 감수성이다. 쌀 수량은 지역적응시험 보통기 재배 9개소에서 6.21MT/ha로 ‘화성벼’ 보다 11% 증수 되었으며 이모작 적응성도 높아 적응지역인 중부 및 영남평야지, 남부중산간지, 동남부해안지에 보급하게 되었다.

*주저자: Tel. 054-732-0385, E-mail: parknb@korea.kr

Effect of sound wave on the expression of ethylene biosynthesis-related genes through regulation of transcription factors RIN and HB-1

Mi Jeong Jeong*, Joo Yeol Kim*, Soo In Lee and Jin A Kim

Rural Development Administration (RDA), National Institute of Agricultural Sciences (NAS), Jeonju 54874, Korea Republic of

We previously reported that sound wave treatment (1 kHz) delays fruit ripening in tomato (*Solanum lycopersicum*), affecting the expression of ethylene biosynthesis-related genes encoding 1-aminocyclopropane 1-carboxylic acid (ACC) synthases (ACS) and ACC oxidases (ACO). In this study, we investigated the activity of the transcription factors RIN and HB-1, which function in the ethylene biosynthetic pathway, in response to sound treatment. To investigate whether RIN and HB-1 directly activate the transcription of ACS and ACO, we performed transcriptional activation analysis in *Arabidopsis thaliana* leaf protoplasts, transiently expressing RIN or HB-1 and using reporter constructs with promoters of the tomato ACS and ACO genes. Activation of the endogenous AtACS and AtACO genes was also measured by qPCR. The RIN- and HB-1-induced expression of these genes decreased, but the HB-1-induced expression of some genes increased after sound treatment. To confirm these results, we performed transient assays in *Nicotiana tabacum*, which produced results similar to those observed in *Arabidopsis*. The major ethylene biosynthesis-related genes harbor a CArG-box as a RIN-binding motif. These findings indicate that RIN and HB-1 affect the expression of ethylene biosynthesis-related genes in response to sound treatment, and they suggest that RIN may regulate the ethylene biosynthesis-related genes by binding to their CArG-boxes.

*These authors contributed equally to this work.

Author E-mail: center1097@korea.kr

Phylogenetic analysis of 246 Korean rice varieties using core sets of microsatellite markers

Yong-Sam Kwon¹, Norvie L. Manigbas², Do-Hon Kim¹ and Gihwan Yi^{3*}

¹Department of Genetic Engineering, College of Natural Resources and Life Science, Dong-A University, Saha-Gu, Pusan, 604-714, Korea;

²Plant Breeding and Biotechnology Division, Philippine Rice Research Institute, Science City of Munoz, Nueva Ecija, Philippines;

³Institute of Agricultural Science and Technology, Kyungpook National University, 80 Daehakro 41566, Korea.

Phylogeny of 246 Korean rice varieties from 3 breeding institutes were evaluated using 26 SSR primers. Two hundred ninety alleles were detected on 11 chromosomes. The number of alleles detected per locus ranged 7-16, with an average of 11.15 alleles per locus. The highest frequency of allele occurrence was 22.1% on chromosome 6 and the lowest frequency was 1.7% on chromosome 11. The polymorphic information content (PIC) values ranged 0.523–0.879 with an average of 0.731. Higher PIC values suggests that primer sets could be used in identifying Korean rice varieties. Genetic similarity analysis revealed two major groups. Group 1 included most of the *japonica* varieties, and Group 2 included predominantly the *tongil* type rice which is a hybrid of *indica* and *japonica*. Cluster analysis showed that there were no distinct clusters among breeding institutes however, some varieties from the same breeding institute occurred in the same sub-cluster. Rice varieties released by the Department of Rice and Winter Cereal Crop exhibited the greatest genetic differences, whereas those of the National Institute of Crop Science exhibited the lowest among the breeding institutes. The phylogenetic data suggests that genetic diversity of varieties released by National Institute of Crop Science was greater than that of Department of Rice and Winter Cereal Crop and the Department of Functional Crop. Genetic diversity of special purpose rice such as aromatic, pigmented, waxy, and super yield was greater than rice grown for premium quality. Phylogenetic analyses provide a reference data in determining parents to cross for genetic improvement.

*Corresponding Author: Tel. 053-950-8538, E-mail: gihwan@knu.ac.kr

Selection of highly informative SNP markers for Sesame (*Sesamum indicum*) cultivar identification

Jin-Kee Jung*, Eun-Jo Sim, Seul-Ki Lim, Dong-Min Kim and Seung-In Yi

Seed Testing & Research Center, Korea Seed & Variety Service, Gimcheon, 39660, Korea

The construction of a DNA database for identify the Sesame(*Sesamum indicum*) has been made possible by the development of novel single nucleotide polymorphism(SNP) markers. For the development of novel SNP marker, out of 123 varieties, 71 varieties (38 application for protection of new varieties of plants and 33 registration for production and import) that are registered at the Korea Seed & Variety Service for Plant Variety Protection (PVP) and 52 imported varieties were used in this study. Finally 48 SNP(include 7 InDel) loci derived from EST region were tested for develop SNP marker for varieties identification. Finally, 27 SNP markers based on EST were developed for identification of 127 Sesame (*Sesamum indicum*) and constructed of a DNA database. Totally 119 varieties (67 Korean cultivar and 52 imported cultivar include China, Ethiopia, India, Sudan and Uzbekistan) were identified using these markers except 4 Korean varieties (Alibaba/Superstar, Yeolyeora/Supertaegang). Average polymorphism information content (Shannon's information index) was 0.553, ranging from 0.317 to 0.687. And we selected highly informative 12 SNP markers and construed multiplex systems for effective application to Sesame variety identification for Korean cultivars. These highly informative SNP markers will useful for variety identification related to seed dispute and distinctness, uniformity and stability (DUS) test and origin identification for Sesame.

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*Corresponding Author: Tel 054-912-0230, E-mail: jinkeejung@korea.kr

Genome-wide identification and characterization of cold stress tolerance and early flowering in rice using next generation sequencing technology

Songhwa Chae^{§1}, Joung Sug Kim¹, Kyong Mi Jun², Sang-Bok Lee³ and Yeon-Ki Kim^{1*}

¹Division of Bioscience and Bioinformatics, Myongji University, 116, Myongji-ro, Cheoin-gu, Yongin-si, Gyeonggi-do, 17058, Republic of Korea

²GreenGene Biotech Inc., 116, Myongji-ro, Cheoin-gu, Yongin-si, Gyeonggi-do, 17058, Republic of Korea

³Chuncheon substation, National Institute of Crop Science, 251, Chungyel-ro, Chuncheon-si, Gangwon-do 24219, Republic of Korea

Rice (*Oryza sativa*) has evolved under a tropical climate and expanded its growth area into temperate zones through the domestication by human. Accordingly flowering and cold resistance are main agronomic traits to guarantee for stable crop production in the area. Efforts to find quantitative trait loci related to these traits have intensified with the next generation sequencing technology. We have developed 400 recombinant isogenic lines (RILs) using Jinbuolbye (JBO) as a female and Samgwang (SG) as a male. JBO is cold stress tolerance and heading at Jul. 12 while SG is cold sensitive and heading at Aug. 15. SG has a high seed quality and been commercialized in Korea. These RILs have currently iterated over 6 generations and the traits related to panicle development and cold resistance been documented. Around 12 gb (40 x genome) have been sequenced for parents and 2 RILs, respectively to provide saturated markers based on single nucleotide polymorphisms (SNPs). The phylogenic relation has been analyzed with snphylo showing the relationship between parental and 2 RILs. Mutations in genic and intergenic regions are further analyzed with SnpEff. Around 590,000 variants are detected among the lines across the chromosomes. The significance of the SNPs related to agronomic traits are discussed.

*Corresponding Author: kim750a11@gmail.com

Transcriptomic profiling of pear plant defense responses against *Venturia nashicola* infection

Il-Sheob Shin^{1,3*}, Jaean Chun² and Yoon-Kyeong Kim¹

¹Pear Research Institute, National Institute of Horticultural & Herbal Science, RDA, Naju 58216, Korea

²Fruit Research Division, National Institute of Horticultural & Herbal Science, RDA, Wanju 55365, Korea

³The World Vegetable Center, Tainan 74151, Taiwan

The molecular understanding of pears against scab caused by *Venturia nashicola*, a most detrimental fungal disease to pear fruit production worldwide, is very limited. Comparing resistant line '93-3-98' [93DB, interspecific hybrid between 'Danbae' (*Pyrus pyrifolia* × *P. ussuriensis*) and 'Bartlett' (*P. communis*)] with susceptible cultivar 'Sweet Skin' (SS, *P. pyrifolia*) according to seven time points of 0, 0.5, 1, 2, 3, 4, 8 days post inoculation (DPI), transcriptomes derived from infected and mock-inoculated young leaves were obtained through Illumina sequencing and analyzed to evaluate the tolerant response and to mine candidate genes of pear to the scab pathogen. Analysis of the mapped reads showed that the infection of *V. nashicola* led to significant differential expression of 17,827 transcripts with more than 3-fold change in the seven pairs of libraries, of which 9,672 (54%) are up- and 8,155 (46%) are down-regulated. These included mainly receptor (NB-ARC domains-containing, CC-NBS-LRR, TIR-NBS-LRR, seven transmembrane MLO family protein) and transcription factor (ethylene responsive element binding, WRKY DNA-binding protein) related gene. To identify transcripts specifically expressed in response to *V. nashicola*, RT-PCRs were conducted and compare to the expression patterns of genotypes with a range of highly resistant to highly susceptible symptom. An arsenal of defense response of highly resistant pear accessions derived from European pear was probably supposed no sooner had *V. nashicola* infected its host than host genes related to disease suppression like Polyketide cyclase/dehydrase and lipid transport protein, WRKY family transcription factor, lectin protein kinase, cystein-rich RLK, calcium-dependent phospholipid-binding copine protein were greatly boosted and eradicated cascade reaction induced by pathogen attack within 48 hours. Moreover transcripts activating defense response to *V. nashicola* were assumed to be triggered by stronger and faster signaling of ethylene and/or jasmonic acid as a stimulus for defense priming to pear plant. This study provides the first transcriptional profile by RNA-seq of the host plant during scab disease and insights into the response of tolerant pear plants to *V. nashicola*.

*Corresponding Author: E-mail: il-sheob.shin@worldveg.org

QTL Detection for Durable Resistance to Blast in a *Japonica* Variety, Palgong

Man-Kee Baek¹, Jong-Min Jeong¹, Hyun-Su Park¹, Soon-Wook Kwon², Woo-Jae Kim¹, Jeong-Kwon Nam¹, Seul-Gi Park¹, Choon-Song Kim¹, You-Chun Song¹, Bo-Kyeong Kim¹, Young-Chan Cho^{1*}

¹National Institute of Crop Science, RDA, 181 Hyeuksin-Ro, Iseo-myeon, Wanju 55365, Republic of Korea

²Department of Plant Bioscience, College of Natural Resources and Life Science, Pusan National University, Milyang 627-706, Republic of Korea

Rice blast caused by the fungal pathogen *Magnaporthe oryzae* is a destructing disease of rice that poses serious threats to the world's food security. The use of blast resistant variety of rice is known as the most effective and economical method of controlling this disease. The resistance genes are rapidly been overcome by the new pathogens to be differentiate race. The quantitative trait loci (QTL) is stable against different pathogenic races of the rice blast fungus; hence, the use of QTL is one of the most promising measures for blast control. This study is to identify QTL related to durable resistance in a *japonica* variety, Palgong that has showed resistance to blast since 1987. Palgong was crossed with a susceptible *japonica* variety Ilpum and F1 was backcrossed with Palgong. A BIL population was developed from the resultant BC1F1 plants by the single-seed descent method. A BIL population was genotyped by Illumina array analysis 768 SNP of *japonica* rice genetic background (Nagasaki et al. 2010). 216 SNPs except for SNPs of monomorphic and over 10% of missing data were constructed to linkage map and analyzed to QTL for the data of blast nursery screening. In CIM analysis, the putative QTLs were over 2.52 of an average LOD in $P < 0.05$ and over 3.80 of an average LOD in $P < 0.01$, respectively. There were detected 16 putative QTLs explaining 1.2-56.7% of phenotype variation on chromosomes 2, 4, 7, 11 and 12. The major QTLs were qPbn2.1, qPbn2.3, qPbn4.1, qPbn4.2, qPbn7.2, qPbn11.1, qPbn11.2 explaining 15.7-56.7% of phenotype variation.

*Corresponding Author: Tel. +82-63-238-5211, E-mail: yccho@korea.kr

중산간지 적응 복합내병성 고품질 조생종 벼 신품종 “성산”

김정주^{1*}, 신운철², 김우재³, 박현수³, 강위금¹, 남정권³, 백만기³, 조영찬³, 김보경³, 김대식¹

¹경상북도 상주시 화서면 중화로 2161 국립식량과학원 상주출장소

²전라북도 완주군 이서면 혁신로 181 국립식량과학원 기획조정과

³전라북도 완주군 이서면 혁신로 181 국립식량과학원 작물육종과

조생종 벼 품종은 주로 중산간 지역에서 재배되어 왔으나 평야지에서도 추석전 햅쌀 조기출하를 목적으로 조기재배 면적이 증가하고 있다. 따라서 조생종 벼 재배면적을 늘림으로써 쌀 출하시기 조절 및 노동력 분산 효과를 기대할 수 있다. 중산간지 적응 복합내병성 고품질 조생종 벼 신품종 “성산”은 2008/2009년 동계에 복합내병성 조생 계통인 운봉42호와 중산간지 적응 도열병 저항성 계통인 상주40호 (IT242653)를 인공교배하여 교잡육종법으로 육성되었다. 인공교배 후 분리세대인 F₂ 집단에서 초형 및 이삭특성을 고려하여 포장선발하고 F₃이후부터는 계통으로 전개하여 주요 병해충 및 미질 특성을 고려하여 선발하였다. 그 중 조생종이면서 복합내병성인 계통으로 선발된 HR28493-55-B-1은 2013~2014년 동안 생산력검정시험에서 초형이 우수하고 복합내병성이면서 수량성이 양호하여 “상주51호”로 계통명을 부여하였다. “상주51호”는 2014~2016년 3년간 지역적응시험을 수행한 결과, 복합내병성을 갖추고 밥맛이 양호한 계통으로 농촌진흥청 농작물 직무육성신품종 선정심의회를 거쳐 “성산”으로 명명되었다. 주요특성을 요약하면 다음과 같다. 중산간지 보통기 보비재배에서 “성산”의 평균 출수기는 7월 27일로 오대벼보다 3일 늦고, 등숙비율은 88.2%로 오대벼보다 높으며 현미천립중은 20.2g으로 중소립종이다. “성산”은 도열병, 줄무늬잎마름병, 흰잎마름병(K1~K3)에 강하지만, 기타 바이러스병 및 해충에는 약하다. “성산”의 쌀알은 맑고 투명하며 백미완전립률 및 완전미 도정수율이 각각 92.0 및 68.3%로 오대벼보다 높다. 중산간지에서 보통기 보비재배에서 “성산”의 쌀수량은 5.52MT/ha로 오대벼보다 5% 증수하였다. “성산”의 적응지역은 남부중산간지, 북부평야지 및 중산간지, 남부고냉지, 동해안 북부해안지이다.

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***주저자:** Tel. 054-533-0465, E-mail: jjkim74@korea.kr

Characterization of breeding materials with diverse grain size and shape in *japonica* rice

Hyun-Su Park^{*}, Man-Kee Baek, Jeong-Kwon Nam, Woon-Chul Shin, Choon-Song Kim, Gun-Mi Lee, Seul-Gi Park, Young-Chan Cho, Bo-Kyeong Kim

Crop Breeding Division, National Institute of Crop Science, RDA, Wanju 55365, Korea

We developed the Breeding Materials with Diverse Grain Size and Shape in *japonica* rice (BM_DGS). To characterize BM_DGS, we analyzed allele types for three grain size-related genes, *GW2*, *GS3*, and *SW5*. The alleles of *GW2*, *GS3*, and *SW5* showed two types, wild type or loss-of-function mutant type. Deuraechan and Boramchan had wild types of *GW2* and *GS3* and mutant type of *SW5*, *GW2GS3sw5*. Daeripbyeo 1, Korean large grain cultivar, had wild type of *GS3* and mutant types of *GW2* and *SW5*, *gw2GS3sw5*. Jizi1581, extremely large grain *japonica* germplasm, had wild type of *SW5* and mutant types of *GW2* and *GS3*, *gw2gs3SW5*, and the other extremely large grain germplasm, Jizi1560, had mutant types of all three genes, *gw2gs3sw5*. In BM_DGS, eight allele combinations, all possible combinations using three genes, were confirmed. We evaluated the effect of genes on phenotypic variation of grain-related and agronomic traits. The genes mostly affecting grain length (GL), grain width (GW), grain thickness (GT), and 1,000-grain weight (TGW) were *GS3*, *GW2*, *GW2*, and *GW2*, respectively. The loss-of-function mutant allele type, *gw2*, *gs3*, and *sw5*, had an effect on increasing grain size. Among allele combinations, *gw2gs3gw5* exhibited the largest and heaviest grain while *GW2GS3SW5* was the smallest and lightest grain. *GW2gs3SW5* resulted in the highest ratio of length to width (RLW) by long and slender grain. The BM_DGS carrying *gw2* showed lower panicle number (PN), ratio of ripened grain (RRG), and yield than those of wild type. The BM_DGS carrying *gs3* showed earlier heading and lower RRG and yield. The BM_DGS carrying *sw5* exhibited much PN but lower number of spikelets per panicle (NS) while had no effect on RRG and yield. The results of this study could be useful to elucidate the relationship between grain size-related genes and grain-related and agronomic traits of BM_DGS. Also, the BM_DGS are being utilized in the breeding programs to diversify the grain size and shape of *japonica* rice.

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

장경 다수성 소립 나물용 콩 ‘아람’

강범규^{1*}, 김현태¹, 서정현¹, 신상욱¹, 김홍식¹, 윤홍태², 이영훈³, 오은영¹, 정찬식³, 오인석², 곽도연¹

¹경남 밀양시 점필재로20 국립식량과학원 남부작물부

²경기도 수원시 수인로126 국립식량과학원 중부작물부

³전북 완주군 이서면 혁신로181 국립식량과학원

제주지역은 국내 나물용 콩 생산량의 80% 이상을 차지하는 나물콩 주산지이다. 이 지역은 소립콩을 생산하기에는 적합하지만 토성과 지리적 위치 및 기후에 의해 경장과 꼬투리가 달리는 높이(협고)가 낮아져 기계화 수확에 적합하지 않다. 이에 경장과 협고가 높으면서도 도복에 강하고, 콩나물 재배특성이 우수한 나물용 콩 품종 ‘아람’을 개발하였다. ‘아람’은 ‘보석’을 모본으로 ‘Camp’를 부분으로 2007년 인공교배하여 ‘08~’09년 F₁ 및 F₂ 세대를 집단으로 전개하고 개체 선발하였다. ‘10년에는 아시아채소연구개발 센터(AVRDC)에서 F₃~F₄ 세대추진을 거쳐 ‘11년 F₅세대에서 계통선발하고 ‘12~’13년 생산력검정시험을 수행하였다. 경장이 크고 소립이며 도복에 강한 특성으로 ‘밀양283호’의 계통명을 부여하고 ‘14~’16년 3년간 제주 등 4지역에서 지역적응시험을 수행하였다. ‘아람’은 유한신육형이며 화색은 자색, 모용색은 회색, 엽형은 삼각형의 특성을 지니고 있다. 종실은 황색 종피, 담갈색 제색, 구형이며 백립중은 9.9g으로 ‘풍산나물콩’ 대비 1g 가볍다. 생육특성은 성숙기가 10월 15일로 ‘풍산나물콩’ 대비 7일 늦은 만숙종이며, 경장은 65cm, 협고는 13cm로 ‘풍산나물콩’ 대비 각각 11cm, 2cm 높다. ‘아람’은 불마름병과 SMV 모두 강하였고, 내도복성은 2배 밀식재배 조건에서 ‘풍산나물콩’ 대비 강하였다. ‘아람’의 발아율은 96%로 ‘풍산나물콩’ 대비 2% 높았고, 콩나물 수율은 598%로 ‘풍산나물콩’과 비슷하였다. 수량성은 적응지역 평균 359kg/10a로 ‘풍산나물콩’ 대비 11% 증수되고, 특히 제주(318kg/10a)에서는 20% 증수되었다.

*주저자: Tel. 053-663-1120, E-mail: hellobk01@korea.kr

장경 다절 내탈립 단기성 작부체계용 콩 ‘장울’

강범규^{1*}, 김현태¹, 서정현¹, 신상욱¹, 김홍식¹, 최만수², 윤홍태³, 고종민², 백인열¹, 한원영¹, 이영훈², 이병원³, 오기원¹, 김현영², 곽도연¹

¹경남 밀양시 점필재로20 국립식량과학원 남부작물부

²전북 완주군 이서면 혁신로181 국립식량과학원

³경기 수원시 수인로126 국립식량과학원 중부작물부

콩은 동계작물과의 이모작 작부체계를 구성하기 위해서는 생육기간이 90~100일 정도로 짧아야 한다. 그러나 짧은 생육기간으로 수량이 감소하고, 그동안 개발된 조숙성 품종들은 탈립성이 높아 적기에 수확하지 못할 경우 손실량이 많았다. ‘장울’은 표준품종인 ‘새울콩’보다 경장이 크고 마디수가 많아 수량이 높고 탈립성이 개선된 품종이다. 장울은 ‘SS86001’을 모본으로 ‘수원192호’를 부분으로 2001년 인공교배하여 조합번호 SS01402를 부여하고 F₁~F₂ 세대를 집단으로 전개 후 선발하였다. F₃ 세대부터 계통육종법으로 선발하고 ‘09~’10년 생산력검정시험을 수행하였으며 ‘밀양235호’의 계통명을 부여한 후 ‘11~’13년 3년간 5개 지역에서 지역적응시험을 실시하였다. ‘장울’은 유한신육형이며 엽형이 난형이고 화색은 백색, 모용색은 회색인 질적특성을 가지고 있다. 지역적응시험 수행 결과 경장이 64cm, 마디수가 14개로 ‘새울콩’ 대비 각각 19cm 길고, 3개 많았다. 종실은 구형이며 제색과 종피는 황색이나 백립중이 18.9g으로 중립종의 특성을 지니고 있다. 생육일수는 지역에 따라 88~104일이며 ‘새울콩’과 유사하였다. 불마름병과 콩모자이크바이러스(SMV)는 ‘새울콩’보다 강하였다. 성숙협을 40℃ 48시간 처리 후 협개열성을 조사한 결과 개열협 비율이 0%로서 탈립에 강하였다. 수량성은 전국 평균 212kg/10a로 ‘새울콩’ 대비 9% 증수되었다.

*주저자: Tel. 053-663-1120, E-mail: hellobk01@korea.kr

울릉도 고유종인 섬말나리의 유전적변이

최유현¹, 김형태¹, 임기병^{1,2*}

¹대구광역시 북구 산격동 경북대학교 농업생명과학대학 원예학과

²대구광역시 경북대학교 농업과학기술연구소

울릉도는 Neogene 에서 Quaternary에 있었던 화산활동으로 만들어진 화산섬으로 풍화와 침식작용으로 인해 해안의 해식에, 깊은 계곡 등 울릉도만이 지니는 독특한 지형이 형성되었다. 이 후 도입 식물 및 섬 내부에서 종 분화 과정으로 생성된 자생종을 포함하여 약 550여종이 현재 서식하는 것으로 알려져 있다. *L. hansonii* (섬말나리)는 section *Martagon* 속하는 울릉도 자생종으로서 3열의 윤생하는 잎과 크고 노란 꽃으로 다른 lily들과 비교해 독특한 특징을 가지고 있어 상품성이 높을 것으로 여겨지나 현재까지 연구는 주로 계통학적 연구에 제한되어 왔다. 따라서 향후 *L. hansonii* 를 상업적으로 이용하기 위하여 다양한 연구가 필요하다. 울릉도 나리령과 나리분지에서 채집한 *L. hansonii* 를 재료로 하여 집단 간 및 집단 내의 유전학적 변이를 관찰하고자 Fluorescent In situ Hybridization (FISH) 방법을 이용, 세포 내 염색체의 45S ribosomal DNA와 5S ribosomal DNA의 개수, 위치를 확인하였다. 이전 연구에서는 section *Martagon* 에 속하는 *L. distichum* (말나리)과 *L. tsingtauense* (하늘말나리), *L. martagon* (서양 말나리)은 염색체 내 45S와 5S rDNA의 개수가 각각 8개, 2개로 개체간 동일하게 나타난다고 확인되었다. 그러나 *L. hansonii*의 경우 나리령에서 집단 내 45S rDNA가 14-16개로 다양하게 나타났으며 5S rDNA는 2개씩 동일하게 나타났다. 나리분지에서는 45S rDNA가 14개, 16개로 관찰되었으며 5S rDNA는 2개로 나리령과 동일하게 관찰되었다. 결과적으로 section *Martagon* 에 속하는 *Lillium*들의 5S rDNA는 2개로 변함이 없으며 오직 *L. hansonii*에서만 45S rDNA 개수의 차이를 확인 할 수 있었다. 본 연구 결과는 섬에 서식하는 자생종이 본토에 서식하는 근연종 보다 유전적 다양성이 작다는 일반적인 결과와 상반된다. 이는 섬말나리 종 형성 시기 혹은 이후 섬말나리가 울릉도 전역에 군집을 확장하는 과정에서 유전적으로 차이가 있으나 형태적으로 유사하며 생식적 격리가 없는 집단의 이주 (migration) 가 있었을 것으로 여겨진다.

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***교신저자:** E-mail: kblim@knu.ac.kr

Soybean transgenic plants with *AtKDA1* gene showed morphological change in plant height

Hye Jeong Kim¹, Hyun Suk Cho¹, Jae Seong Kim¹, Jin Sol Park¹, Wan Woo Yeom¹, Jae Yong Han¹, Jeong-Il Kim², Young Soo Chung^{1*}

¹Dept. of Molecular Genetics, College of Natural Resources and Life Science, Dong-A University, Busan 49315, Republic of Korea

²Dept. of Biotechnology, Chonnam National University, Gwangju 61186, Republic of Korea

Plants use light as a source of both energy and information about their environment. Among photoreceptors, cryptochromes are blue-light receptors that regulate multiple light responses including hypocotyl growth, flowering, circadian clock and gene expression in plants and animals. Transgenic soybean plants overexpressing *AtKDA1* were produced by *Agrobacterium*-mediated transformation using the modified half-seed method. The integration of the transgene was confirmed from the genomic DNA of transformed soybean plants using PCR, and the copy number was determined by Southern blotting using leaf samples from T₂ seedlings. To examine the effect of *AtKDA1* expression on plant height and its yield in transgenic plants, we compared their growth characteristics to those of non-transgenic (NT) plants. The chosen three transgenic seedlings (#9, #10 and #15) exhibited longer hypocotyls than NT seedlings. Agronomic traits including plant height, the number of nodes per plant, branches per plant, pods per plant and total seed weight were also investigated in GMO field. In phenotypic analysis, *AtKDA1* transgenic plants showed longer plant heights than NT plants.

***Corresponding Author:** Tel. 051-200-5683, E-mail: chungys@dau.ac.kr

Overexpression of *YUCCA6* gene enhanced drought tolerance in transgenic soybean

Jin Sol Park¹, Hye Jeong Kim¹, Hyun Suk Cho¹, Jae Seong Kim¹, Wan Woo Yeom¹, Jae Yong Han¹, Dae-Jin Yun², Young Soo Chung^{1*}

¹Dept. of Molecular Genetics, College of Natural Resources and Life Science, Dong-A University, Busan 49315, Republic of Korea

²Dept. of Biomedical Science and Engineering, KonKuk University, Seoul 05029, Republic of Korea

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.

***Corresponding Author:** Tel. 051-200-5683, E-mail: chungys@dau.ac.kr

QTL identification for seed storability in rice

Dong-Min Kim^{1*}, Eun-Jo Shim¹, Seung-Eun Park¹, Shin-Sook Park¹, Gyu-Chan Shim², Seung-In Yi¹

¹Seed testing & research center, Korea seed & variety service, Gimcheon, Republic of Korea

²Department of Agronomy, Chungnam National University, Daejeon, Korea

Rice seed storability is an important characteristic of seed quality. Presently, little is known about the genetic and physiological mechanisms controlling rice seed storability. In this study, a molecular linkage map consisting of 133 SSR markers was employed to identify QTL associated with seed storability. 96 introgression lines derived from a cross between Hwaseung as the recurrent parent and *Oryza rufipogon* as a donor parent and parents were evaluated for traits including seed vigour (SV) and germination percentage (GP) under the artificial aging. A total of nine QTLs were detected on chromosome 3, 4, 6, 9 and 10 and the phenotypic variance explained by each QTL ranged from 14.0 to 58.9%. The *O. rufipogon* allele contributed the positive effect at these nine QTL loci. These results provide important information for understanding the genetic mechanisms on rice seed storability, and will be useful for breeding new rice varieties with high seed storability.

***Corresponding Author:** Tel. 054-912-0222, E-mail: acekdm@korea.kr

Human drug niclosamide can be used to inhibit *Xanthomonas oryzae*-induced rice leaf blight

Jun Soo Kwak^{1*}, Won Joo Shin¹, Beom Seok Choi¹, Hak Soo Seo¹

¹Department of Plant Science, Seoul National University, Seoul 151-921, Korea

Bacterial leaf blight is one of the major diseases in rice and affects yields. Thus, various methods have been applied to protect rice from this disease. Here, we show systemic translocation of the human drug niclosamide (5-chloro--(2-chloro-4-nitrophenyl)-2-hydroxybenzamide) in rice and its long-term effect on prevention of rice leaf blight. The development of pv-induced rice leaf blight was effectively inhibited in untreated systemic leaves as in niclosamide-treated leaves, although its effect gradually decreased in a time-dependent manner. Time-course examination after niclosamide treatment showed that the niclosamide level was highest after 3 h in non-treated distal leaves, suggesting fast systemic movement of niclosamide from the treated local site to untreated distal regions. Our data indicate that niclosamide controls rice leaf blight by its rapid systemic movement and that its effect is maintained for a long time.

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***Corresponding Author:** Tel. 02-880-4558, E-mail: seohs@snu.ac.kr

Seed germination is controlled by sumoylation in *Arabidopsis*

Sang Woo Park^{1*}, Woo Sub Kim¹, Hak Soo Seo¹

¹Department of Plant Science, Seoul National University, Seoul 151-921, Korea

Seed germination is an important stage in the lifecycle of a plant because it determines subsequent vegetative growth and reproduction. Here, we show that the E3 SUMO ligase AtSIZ1 regulates seed dormancy and germination. The germination rates of the *siz1* mutants were less than 50%, even after a short period of ripening. However, their germination rates increased to wild-type levels after cold stratification or long periods of ripening. In addition, exogenous gibberellin (GA) application improved the germination rates of the *siz1* mutants to the wild-type level. In transgenic plants, suppression of *AtSIZ1* caused rapid post-translational decay of SLEEPY1 (SLY1), a positive regulator of GA signaling, during germination, and inducible *AtSIZ1* overexpression led to increased SLY1 levels. In addition, overexpressing wild-type SLY1 in transgenic *sly1* mutants increased their germination ratios to wild-type levels, whereas the germination ratio of transgenic *sly1* mutants overexpressing mSLY1 was similar to that of *sly1*. The germination ratios of *siz1* mutant seeds in immature developing siliques were much lower than those of the wild type. Moreover, *SLY1* and *DELAY OF GERMINATION 1 (DOG1)* transcript levels were reduced in the *siz1* mutants, while the transcript levels of *DELLA* and *ABSCISIC ACID INSENSITIVE 3 (ABI3)* were higher than those of the wild type. Taken together, these results indicate that the reduced germination of the *siz1* mutants results from impaired GA signaling due to low SLY1 levels and activity, as well as hyperdormancy due to high levels of expression of dormancy-related genes including *DOG1*.

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***Corresponding Author:** Tel. 02-880-4558, E-mail: seohs@snu.ac.kr

AtSIZ1-mediated Abiotic stresses are regulated by E3 ubiquitin ligase activity of COP1.

Joo Yong Kim^{1*}, Kyu Ho Lee¹, Hak Soo Seo¹

¹Department of Plant Science, Seoul National University, Seoul 151-921, Korea

Ubiquitination and sumoylation are essential post-translational modifications that regulate growth and development processes in plants, including control of hormone signaling mechanisms and responses to stress. This study showed that COP1 (Constitutive photomorphogenic 1) regulated the activity of Arabidopsis E3 SUMO (Small ubiquitin-related modifier) ligase AtSIZ1 through its E3 ubiquitin ligase activity. Yeast two hybrid analysis demonstrated that COP1 and AtSIZ1 directly interacted with one another, and subcellular localization assays indicated that COP1 and AtSIZ1 co-localized in nuclear bodies. Analysis of ubiquitination showed that AtSIZ1 was polyubiquitinated by COP1. The AtSIZ1 level was higher in *cop1-4* mutants than in wild-type seedlings under light or dark conditions, and overexpression of a dominant-negative (DN)-COP1 mutant led to a substantial increase in AtSIZ1 accumulation. In addition, under drought, cold, and high salt conditions, SUMO-conjugate levels were elevated in DN-COP1-overexpressing plants and *cop1-4* mutant plants compared to wild-type plants. Taken together, our results indicate that COP1 controls responses to abiotic stress by modulation of AtSIZ1 levels and activity.

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***Corresponding Author:** Tel. 02-880-4558, E-mail: seohs@snu.ac.kr

Isolation and characterization of putative F-box proteins in wheat

Min Jeong Hong¹, Dae Yeon Kim², Joon-Woo Ahn¹, Sang Hoon Kim¹, Hong-Il Choi¹, Si-Yong Kang¹, Yong Weon Seo², Jin-Beak Kim^{1*}

¹Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, 29 Geumgu, Jeongeup 580-185, Republic of Korea

²Division of Biotechnology, Korea University, Seongbuk-Gu, Seoul 136-713, Republic of Korea

F-box protein is components of the SCF (Skp1-Cullin-F-box protein) E3 ubiquitin ligase complex which binds specific proteins destined for ubiquitination and degradation. F-box proteins are known to play a critical role in the regulation of various development processes in plants. However, detailed functions of F-box proteins in wheat remain unknown. In order to collect F-box gene family through genome-wide survey, the draft genome sequence of wheat (IWGSC Reference Sequence v1.0 assembly) was used. About 950 F-box protein genes have been identified in the wheat genome. We used Illumina Hiseq 2000 sequencing platform for expression analysis of F-box protein genes according to expression level at wheat developmental stages. We obtained the full length sequences of 3 F-box protein genes (*TaFBX1*: Traes_2AS_3ADE97AEF, *TaFBX2*: Traes_7AL_001F061F8, and *TaFBX3*: Traes_1BL_80A1C84CE), which contains a putative F-box domain and leucine-rich repeats (LRR). The *TaFBX* genes were differentially expressed in wheat tissues and respond to grain developmental stages. To determine the subcellular localization of wheat F-box proteins, we examined the sub-cellular localization of TaFBX-GFP fusion proteins in a transient assay using tobacco (*Nicotiana benthamiana*). Our data demonstrated that GFP-tagged TaFBXs were targeted to the plasma membrane and nucleus. Using the yeast two-hybrid screen, we identified TaFBXs-interacting proteins in a wheat library. And also, we performed yeast two-hybrid assay to investigate protein-protein interaction between TaFBX proteins and various wheat SKP-like proteins. Our study of putative F-box proteins will aid on understanding the functions of F-box proteins in wheat.

***Corresponding Author:** Tel. 063-570-3313, E-mail: jbkim74@kaeri.re.kr

다수성 분홍색 스탠다드 절화용 거베라 ‘Pinkie Girl’ 품종 육성

박종택*, 정재아, 박상근, 김미선

농촌진흥청 국립원예특작과학원 화훼과

거베라 ‘Pinkie Girl’은 2008년 수원 국립원예특작과학원에서 분홍색 반겹꽃 ‘Free Zone’과 살구색 ‘Atilia’를 인공교배하여 실생계통을 양성하고, 실생계통으로 부터 선발한 연분홍색 ‘09B3-76’을 부분으로 사용하고, 진분홍색 ‘Lila’를 모본으로 2011년 인공교배하였다. 인공교배로 획득한 종자로부터 실생 계통을 양성하여, 화색이 선명하고 화폭이 큰 분홍색의 스탠다드 반겹꽃 ‘원교 12B3-58’을 개체선발하였다. 선발된 개체에 대하여 2012년 조직배양으로 개체를 증식한 후 2012년부터 2014년까지 12차 생육특성검정을 수행하고, 2015년에 ‘원교 B3-58호’로 계통명을 부여하여 3차 특성검정, 안정성·균일성에 대한 연차별 재현성 및 기호도 평가를 수행한 결과, 화색 및 화형에 대한 기호도가 우수하고, 연간채화량이 많은 다수성 품종으로 그 우수성이 인정되어, 2015년 농촌진흥청 직무육성품종심의회의를 거쳐 ‘Pinkie Girl’로 명명되고 직무육성품종으로 등록되었다.

‘Pinkie Girl’의 생육 및 개화특성은 화색과 화형이 유사한 ‘Chavez’를 대조품종으로 하여 조사하였다. ‘Pinkie Girl’의 설상화는 RHS color chart RP65C의 분홍색 반겹꽃으로, 대조품종의 R38D보다 선명한 분홍색으로 갈색의 화반과 어우러진다. ‘Pinkie Girl’의 화경과 내화경이 각각 12.0 ± 0.2 cm, 5.7 ± 0.3 cm으로 대조품종의 11.3 ± 0.2 cm, 5.4 ± 0.3 cm보다 큰 대륜계 품종이며, 내부설상화 가장자리가 규칙적이다. 화반 직경은 3.0 ± 0.2 cm로 대조품종의 4.0 ± 0.1 cm보다 작다. 외부설상화의 길이와 폭은 5.4 ± 0.3 cm, 1.2 ± 0.1 cm로 넓은 도란형이다. 잎의 길이와 폭은 46.2 ± 2 cm와 15.4 ± 1 cm이며 결각은 보통수준이다. 절화장은 68.8 ± 4.1 cm로 길며, 절화수명은 평균 12.9 ± 1.5 일로 대조품종 9.0 ± 0.3 일 보다 길었다. 또한 연간채화량이 54.0 ± 3.5 (본/주)로 다수성 품종이다.

*교신저자: Tel. 063-238-6813 jongtaek@korea.kr

Identification of QTLs for tolerance to hypoxia during germination in rice

Suk-Man Kim^{1,2}, Kyeong-Ho Kang³, Jong-Min Jeong³, Russell Reinke¹

¹Plant Breeding, Genetics, and Biotechnology Division, International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines

²C/o IRRI-Korea Office, National Institute of Crop Science, Rural Development Administration, Jeollabuk-do 55365, Republic of Korea

³National Institute of Crop Science, Rural Development Administration, Jeollabuk-do 55365, Republic of Korea

Direct seeding of rice is increasingly being adopted by rice farmers to establish their crops as a means of saving labor and reducing costs. However, the method often results in a poor environment for germination as excessive water levels after seeding can cause poor seedling establishment and a concomitant reduction in yield potential, especially in submergence prone areas. In this study we discovered QTLs associated with tolerance of anaerobic germination in new genetic accessions using genotypic data derived from the Illumina 6K SNP chip. The mapping population developed for QTL analysis comprised a total of 285 F₂ plants derived from across between an AG tolerant *indica* variety Tai Nguyen (TN) and a susceptible variety Anda. Using 872 SNPs showing polymorphism between the parents, a genetic linkage map was constructed with a mean of 67 markers harbored within each chromosome with a total length of 1,448.45cM and an average interval length of 1.7cM. A total of three QTLs associated with AG tolerance were identified in the population, qAG1a and qAG1b on chromosome 1 and qAG8 on chromosome8 using composite interval mapping (CIM). The percent of variance explained by these QTLs ranged from 5.49 to 14.14 %. The lines with three QTLs (*qAG1b+qAG1a+qAG8*) demonstrated approximately 50% survival rate under anaerobic conditions

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

High temperatures induce diploid pollen and male sterility in *Arabidopsis*

Tien Dung Nguyen, Sung Aeong Oh, Soon Ki Park

School of Applied Biosciences, Kyungpook National University, Korea

Plants are frequently exposed to environment including adverse changes such as temperature stresses. Global climate changes have been being a big challenge for crops, of which, high temperature stresses are known to be more serious in plants occasionally leading male sterility at many the disruption of pollen development leading male sterility. In this study, we demonstrate that a high temperature stress caused completely male sterility due to inhibition of pollen development from microspore stage. High temperature affected plants to decrease length of stamens containing no viable pollen, but not on female organs, indicating that male reproductive organs were more sensitive to heat stress than female. Interestingly we observed that sizes of heat-induced pollen were enlarged to similar level with those from 4X plants. In addition, using marker lines, we found that two set of 8 chromosomes were produced in heat-induced pollen grains. These results strongly indicate that high temperature stress not only causes male sterility, also could induce polyploidy pollen in *Arabidopsis*.

Corresponding Author: +82-53-950-7751, E-mail: psk@knu.ac.kr

Identification and molecular characterization of DDMP saponin biosynthesis gene in soybean

Jagadeesh Sundaramoorthy¹, Gyu Tae Park¹, Seokhyung Lee¹, Jeong-Dong Lee¹, Hak Soo Seo², Jong Tae Song^{1*}

¹School of Applied Biosciences, Kyungpook National University, Daegu, Republic of Korea

²Department of Plant Bioscience, Seoul National University, Seoul, Republic of Korea

Saponins are a group of secondary metabolites available in soybean [*Glycine max* (L.) Merr.]. Soybean saponins are classified as group A and DDMP saponins. Group A saponins are undesirable component of food products due to its bitterness and astringency. In contrast, DDMP saponins and their derivatives are not possessing bitterness and astringency and beneficial to human health when consumed as regular diet. We recently isolated two EMS mutant lines (PE2248 and PE2371) with DDMP-deficient saponins. The objective of the present study is 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. Segregation analysis showed that the both the mutant phenotype is controlled by 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. Complementation between two mutations by crossing of PE2248 and PE2371 exhibited that the mutation sites lie on the same gene. Further, *Sg-9* gene characterization will be carried out by cloning and overexpression studies.

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

Identification and evaluation of abiotic stress tolerant genes in *Arabidopsis thaliana* and develop transgenic rice for heat stress tolerance

Rupesh Tayade^{1*}, Tien Dung Nguyen, Lee Dasom¹, Sung Aeong Oh¹, Ki Hong Jung², Soon Ki Park^{*}

¹School of Applied Biosciences, Kyungpook National University, Korea

²Graduate School of Biotechnology & Crop Biotech Institute, Kyung Hee University, Korea

Abiotic stress such as heat and drought are predominating in the current environment scenario. In recent decades global warming is major concern as increasing environment temperature is an alarming threat to crop production worldwide. Recently several genes that confer tolerance to environmental stress have been reported. However, the intensities of tolerance vary significantly depending on cultivars, growing conditions, and mechanisms. In this study, we investigated the profiles of abiotic stress tolerant genes, six-candidate genes of *NDPK2*, *AtGolS1*, *PRE1*, *YUCCA6*, *AtHSP101* and *CBF1* from *Arabidopsis Thaliana* and constructed twenty four vectors combined with four promoters driving constitutive and pollen/anther specific expression, *UBQ14*, *TDF1*, *RMP1* and *OsLPS1*. We conducted *Agrobacterium*-mediated transformation to generate transgenic *Arabidopsis* plants and rice as heterologous system. In T₂ generation, *Arabidopsis* transgenic plants will be evaluated further for heat stress at seedling, flowering and other developmental stages traits whereas rice T₀ plants will be evaluated in the field condition for heat stress tolerance. The comparative evaluation may give the border understanding of selected genes and find out more efficient gene for heat stress tolerance and its applicability to other crops.

*Corresponding Author: Tel. +82-53-950-7751, E-mail: psk@knu.ac.kr

Identification of genetic basis causing a cytokinesis defect in *Arabidopsis* mutant phenotype by map-based cloning

Saima Akhter, Ha Thi Lieu, Rupesh Tayade, Sung Aeong Oh, Soon Ki Park

School of Applied Biosciences, Kyungpook National University, Korea

Pollen development can be considered as model system not only for the analysis of important processes in plant reproduction but also for learning diverse biological aspects. Gametophytic cytokinesis is necessary for the development and function of male and female gametophytes. In this study we report here that a gametophytic mutant line isolated in activation-tagging pool. Pollen developmental analysis revealed that the asymmetric mitotic division in microspore is compromised by the mutation, leads to the repositioning of the cell plate and partial or complete failure of cytokinesis. Transmission analysis showed that defects in both gametophytes, but severe defects observed in male gametophytes and leads to the production of divided or twin celled pollen. Map-based cloning was used to identify the gene causing mutant pollen phenotype. Mapping population was generated through reciprocal crossing of mutant plant with different ecotype plant and genetic analysis of F₂ plants were carried out. To define chromosomal region causing the mutation we conducted PCR-based analysis of approximately 800 F₂ plants using SSLP markers and narrowed down the region up to 445Kb in chromosome 1. In conclusion the region we narrowed down can serve as candidate for further fine mapping of responsible gene.

Corresponding Author: Tel. +82-53-950-7751, E-mail: psk@knu.ac.kr

무의 background selection용 SNP 개발

김진희*, 이은수, 안윤균, 김도선, 홍종필, Abinaya Manivannan, 최승국

농촌진흥청 국립원예특작과학원 채소과

SNP(single nucleotide polymorphisms)는 마커의 빈도수가 풍부하여 개발이 비교적 용이하고 비용이 저렴하며, 무엇보다 최근에 다양한 high-throughput 분석 기술로 SNP 분석의 자동화가 가능한 장점이 있어, 육종 조합에 적용이 가능한 마커세트를 확립할 수 있다. 무는 배추와 함께 우리나라 2대 채소로 1인당 소비량은 19.6kg(2012년 기준) 포함되는 등 경제적으로 주요한 작물이며 김치의 부재료로 사용되는 등 그 이용 범위가 매우 넓다. 국내 무가 세계적인 경쟁력을 갖추기 위해서는 분자표지를 이용한 분자 육종 시스템 구축이 요구된다. 이러한 무의 분자표지 기반 육종 과정을 효율적으로 하기 위해 본 연구에서는 육종에서 주로 활용되는 형질들을 파악하여 대표 육성 계통 35개를 선정한 후 Illumina Hiseq 4000을 통해 전사체 염기서열 분석을 진행했다. 계통 선정에는 추대성, 비대양상, 근장, 엽형, 근색, 육색, 형태 등의 형질을 고려했고, 조합이 달라져도 여교배 등의 육종 과정에 적용될 수 있도록 선정하였다. 계통별 평균 염기서열은 5,869,258,936 bp(58,509,167 reads)이며, GC 함량은 48%, Q30 값은 97%이다. 전사체 염기서열의 비교를 통하여 다양한 무 계통들의 SNP를 분석했으며 다수의 SNP를 확보했다. 선발한 327개의 SNP는 품종 분류, 분자마커를 이용한 여교배, 형질 마커 개발, 유전지도 작성 등 다양한 목적에 따라 Fluidigm을 이용한 SNP 분자마커 세트로 개발할 예정이며 가까운 미래에 이러한 SNP 마커 풀을 이용해 다양한 육종 프로그램에 대응할 수 있을 것으로 기대한다.

***교신저자:** Tel. 063-238-6672, E-mail: sayzinni@korea.kr

Molecular genetic mapping of *Chili veinal mottle virus* (ChiVMV) resistance genes in pepper

Joung-Ho Lee¹, Jeong-Tak An¹, Koeun Han¹, Seula Choi¹, Muhammad Irfan Siddique¹ and Byoung-Cheorl Kang^{1*}

¹Department of Plant Science, Plant Genomics & Breeding Institute, and Research Institute of Agriculture and Life Sciences, Seoul National University, Korea

Chili veinal mottle virus (ChiVMV) is the notorious virus affecting the severe loss of pepper production in Asia and Africa. To map the positions of ChiVMV resistance genes, F₂ mapping populations were constructed by crossing each resistance accession, *Capsicum annuum*, 'CV3', 'CV4', and 'CV8' with susceptible *C. annuum*, 'Jeju'. In the 'CV3' and 'CV8' mapping populations, resistance genes were inherited by a single dominant manner and located on the short arm of pepper chromosome 6. The ChiVMV resistance marker reported in the previous study was co-segregated with these genes. Through allelism test of resistance genes from 'CV3' and 'CV8', it was revealed that the resistance gene in each line was originated from the same locus, and we named this gene, *Cvr1* (ChiVMV resistance 1) locus. We developed several SNP markers linked to *Cvr1* using pepper genome information and pepper bacterial artificial chromosome (BAC) sequences. By contrast, the inheritance mode of ChiVMV resistance in CV4 was different from those of CV3 or CV8. The inheritance study showed that two independent complementary genes involved in ChiVMV resistance in CV4. To map the resistance genes in CV4, SNP-based linkage map was constructed by genotyping-by-sequencing (GBS) method. The result of this study will accelerate the ChiVMV resistance research and breeding resistance cultivar to ChiVMV in pepper.

***Corresponding Author:** Tel. 02)880-4563, E-mail: bk54@snu.ac.kr

Evaluation of phenotypic variants and identification of non-pungent mutants among EMS-treated M₂ populations

Muhammad Irfan Siddique¹, Koeun Han¹, and Byoung-Cheorl Kang^{1*}

¹Department of Plant Science, Plant Genomics and Breeding Institute, and Vegetable Breeding Research Center, College of Agriculture and Life Sciences, Seoul National University, Seoul 151-921, Republic of Korea

Plant breeding needs genetic variation of economical traits to develop new, high-yielding and improved cultivars. EMS-induces mutation has been practiced to cause mutations at loci regulating economically important traits and/or to knock out the genes to elucidate their functions. The present study was under taken to induce mutations in a *Capsicum annuum* “Micro-Pep”. Micro-Pep is a small, pungent pepper generally used as ornamental purpose. The accession is convenient to use in mutation study and molecular research due to its compact growth habit, and small size. The seeds were treated with 1.3% of mutagen to induce mutation and 30% less germination percentage was observed in EMS treated seeds in comparison to control seeds. A total of 6,620 M₁ plants were grown under greenhouse condition and 3996 M₂ mutant lines were harvested. Among these mutants 700 lines were evaluated for novel traits. The mutants were observed with various phenotypic variants such as plant growth, habit, leaves color and shapes, flower and fruits morphology. These Micro-pep mutant collections will serve as platform for TILLING by sequencing to accelerate functional genomics research in pepper. In parallel to this, mutants were screened for non-pungent mutants using Gibbs reagent method. In a result, 1 putative non-pungent mutant was identified. These mutant phenotypes and non-pungent mutant s will be valuable genetic resources for identification of functional genes and molecular breeding of pepper.

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

QTL mapping for inward rolling of leaf blade in rice using RIL population

Su Jang, Hyekyung Son, Taejun Kim, Jinwoo Lee and Hee-Jong Koh^{*}

Department of Plant Science, Research Institute of Agriculture and Life Science, and Plant Genomics and Breeding Institute, Seoul National University, Seoul, 151-921, Korea.

Degree of leaf rolling is one of the important traits that determines plant architecture. Moderate leaf rolling can contribute to improve photosynthetic efficiency not only at individual level but also at population level by increasing erectness of upper leaf. Furthermore, this morphological trait is closely related to planting density, ventilation, and drought resistance. In this study, RILs from cross between Tong-il type variety M23 and japonica variety T887 were used to identify QTL controlling leaf rolling. this population was phenotyped for rolling index of flag leaf (FLRI) and upper second leaf (SLRI) for two years. Total six QTLs for FLRI and SLRI on chromosome 1, 2, and 9 were identified using composite interval mapping. One stable QTL located on chromosome 9 showed consistent effects for FLRI and SLRI in both years, explaining 10.6-10.9% and 13.3-13.6% of phenotypic variation. Two QTL on chromosome 2 that were detected in almost the same region were also associated with both traits, implying that two leaf rolling traits could be controlled by same genetic mechanism. The result of QTL analysis would contribute to understanding genetic basis for leaf rolling and these QTLs identified in this study can be used in rice breeding program to improve plant architecture.

*Corresponding Author: Tel. 02-880-4551, E-mail: heejkoh@snu.ac.kr

Fine-mapping and characterization of a new light dependent incomplement dominant lesion mimic mutant in rice (*Oryza sativa* L.)

Zhuo Jin, Jin seok Moon, Somyung Lee and Hee-Jong Koh*

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

Rice (*Oryza sativa* L.) is one of the most important food crops. There have been tremendous efforts to increase rice productivity via genetic improvement based on understanding of developmental mechanisms associated with grain yield. To date many lesion mimic mutants have been identified in rice and these mutants are important to understand the mechanism of the programmed cell death and disease resistance. In this study we identified a new light-dependent lesion-mimic mutant in rice, through a chemical mutagenesis on Koshihikari with Ethyl methanesulfonate (EMS). The mutant displayed a lesion-mimic phenotype in the absence of pathogen attack and also early senescence phenotype. Lesions appeared on the leaves of the mutant at early stage, and at flowering stage lesions were dispersed over the entire leaf surface. After flowering the mutant showed a significant decrease in chlorophyll content, and high concentrations of reactive oxygen species (ROS). Genetic analysis revealed that spot leaf was caused by incomplete dominant mutation. Using bulked segregant analysis method and sequence-tagged site (STS) markers, the gene that cause lesion-mimic and early senescence phenotype, was located at chromosome 5 within a physical region of 2Mb. The MutMap method is being applied for cloning the gene by a whole-genome resequencing of pooled DNAs from a segregating population.

*Corresponding Author: Tel. 02-880-4551, E-mail: heejkoh@snu.ac.kr

The evolution of tomato mitochondrial genomes and intracellular gene transfer in tomato

Hyoung Tae Kim* and Je Min Lee

Department of Horticultural Science, Kyungpook National University, Daegu, Korea

Three complete mitochondrial genomes (chondrome) (two in *Solanum lycopersicum* and one in *S. pennellii*) were newly assembled and the intra- and interspecific variations of chondrome were analyzed. The lengths of three chondrome sequences were 423,596 ~ 446,257 bp. Although there were numbers of rearrangement between chondromes of *S. lycopersicum* and *S. pennellii*, over 97% of chondrome sequences were very similar with each other. In terms of intracellular gene transfer (IGT) between organelle genomes, 9,598 bp (2,558 bp in large single copy, 32 bp in small single copy, and 7,008 bp in inverted repeat) of plastome sequences were found in three chondromes in common. Among mitochondrial plastid DNAs (MTPTs) in tomato, five MTPTs were exclusively detected in chondrome of *S. pennellii*. These five MTPTs seems to be deleted in the chondrome of *S. lycopersicum* because three and five of them were found in chondromes of *Nicotiana* and *Capsicum*, respectively. In addition, Numbers of nuclear copies of mitochondrial DNAs (NUMTs) and nuclear copies of plastid DNAs (NUPTs) were found in nuclear genomes of *S. lycopersicum* and *S. pennellii*. Hotspots of NUMTs and NUPTs were found as well. Among IGTs between nuclear genome and chondrome, three of them were recently occurred from nuclear genome to chondrome in *S. pennellii* but most of them are likely to be transferred from organelle genomes to nuclear genome. As a result, our results support that endosymbiotic gene transfers have frequently occurred recently in tomato genomes.

*Corresponding Author: rladbgs@gmail.com

수량성 및 튀김유풀이 높은 팝콘용 옥수수 신품종 ‘오륜2호’

최재근^{1*}, 박종열¹, 장은하², 류시환¹, 서영호¹, 박기진¹, 남궁민¹, 윤석원¹, 용우식¹, 최준근¹

¹강원도 홍천군 두촌면 장남길 26 강원도농업기술원 옥수수연구소

²강원도 춘천시 충열로 83 강원도농업기술원 원예연구과

옥수수연구소에서 팝콘용 튀김옥수수 연구를 1997년부터 시작하여 현재 오륜팝콘, 지팝콘을 개발하여 국내 재배농가에 보급하고 있다. 현재 국산품종을 이용한 팝콘은 국내산을 선호하는 소비자층을 중심으로 소비가 되며 원료공급을 위한 친환경재배단지가 조성되어 있다. 소비자가 손쉽게 접할 수 있게 팝콘으로 튀긴 가공 상품으로 개발되어 완제품으로 공급되고 있으며 또한 농촌체험활동 및 가정에서 간식대용으로 즉석에서 튀겨 먹는 용으로 알곡으로만 포장되어 소비자에게 공급되고 있다. 영화관에서 주로 소비되는 국내 팝콘시장은 연간 3천억 이상의 규모로 형성되어 있으나 대부분 수입산 알곡을 이용하고 있다. 앞으로 국내에서 개발한 품종으로 수입산을 대체하기 위하여 2012년에 강원도옥수수연구소에서 “오륜”품종을 개발하여 전국에 20ha의 재배단지를 형성하여 국내시장에 보급되고 있다. 본 연구는 오륜품종보다 수량성 및 튀김유풀이 높은 품종을 개발하고자 수행하였다. “오륜2호”는 튀김용 모집단에서 분리된 GP5를 모본, GP3를 부본으로 하여 개발하였으며, 수량성은 “오륜” 대비 9%증수한 497kg/10a로 수량이 높으며, 도복지수는 2로 “오륜”의 3보다 낮아 내재해성도 강하며, 100립중은 15.7g으로 “오륜” 16.2g보다 소립인 특성을 갖고 있다. 튀김유풀은 알곡 수분이 11.0~12.0%일 때 “오륜2호”가 27배로 “오륜”의 25배 보다 높아 가공용으로도 적합한 특성을 가지고 있어 앞으로 농가에 보급하여 재배단지를 확대하면 수입산을 대체할 품종으로 기대한다.

*주저자: Tel. 033-248-6921, E-mail: jaekeun@korea.kr

RNA sequencing and gene network analysis in rice irradiated with gamma-rays and ion-beams

Hong-Il Choi¹, Sung Min Han¹, Sun-Goo Hwang², Cheol Seong Jang², Soon-Jae Kwon, Joon-Woo Ahn, Yeong Deuk Jo, Sang Hoon Kim, Si-Yong Kang¹ and Jin-Baek Kim^{1*}

¹Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongeup 56212, Republic of Korea.

²Plant Genomics Lab, Department of Applied Plant Sciences, Kangwon National University, Chuncheon, 24341, Republic of Korea.

Exposure to ionizing radiation has been regarded as a kind of abiotic stresses that can change the expression of genes in living organisms. This study aimed on investigating the variations in gene expressions induced by two different types of irradiations with different doses, which were low linear energy transfer (LET) gamma rays and high LET ion-beams on rice. RNA sequencing was carried out using the Illumina HiSeq-2500 platform. More than 90% of the RNA-seq reads were mapped to the rice reference genome sequence (IRGSP-1.0). A total of 247 differentially expressed genes (DEGs) were identified by comparison of the gene expression levels between the wildtype and the irradiated individuals. The 247 DEGs were divided into five modules and 27 intra-modular hub genes were found using the weighted correlation network analysis (WGCNA) method. The METurquoise module had the most number of genes with 75 related to carbohydrate and small molecule metabolic processes. The co-expression network reconstructed using ARACNE (algorithm for reconstruction of accurate cellular networks) showed specific up- or down-regulation of the genes in each module according to the types and doses of radiation. This study will contribute to understanding the gene expression responses to ionizing irradiation.

*Corresponding Author: Tel. 063-570-3313, E-mail: jbkim74@kaeri.re.kr

바이오매스가 높고 복합내병충성을 보유한 만생 내도복 사료용 벼 품종 ‘청우’

안역근¹, 이상복¹, 이점호², 장재기³, 원용재¹, 이정희¹, 정국현¹, 하운구¹, 정웅기¹, 김명기¹, 정종민¹, 서정필², 양창인¹

¹국립식량과학원, ²농촌진흥청, ³국립원예특작과학원

2016년 국내 쌀 생산량은 420만톤, 일인당 쌀 소비량이 61.9kg로 생산량은 감소하지 않으면서 소비는 지속적으로 줄어들고 있어 구조적으로 쌀의 공급 과잉 현상이 심화되고 있다. 사료용 벼는 논의 형상과 기능을 유지하면서 이러한 수급불균형을 해결할 수 있는 좋은 대안임에도 불구하고 현 시점에서는 밥쌀용 벼와 비교하여 소득이 낮아 정부의 보조금 없이는 농가현장에서 재배를 기피하는 경향이 있다. 이에 수량성(바이오매스) 향상 등을 통한 경제적 가치를 올릴 필요가 있다. 이번에 육성한 사료용 벼 ‘청우’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 조사로 생산이 가능할 뿐만 아니라 농업경영비도 절감 할 수 있다. 또한 ‘청우’의 지상부 건물수량은 중부평야, 영남평야 및 호남평야지 4개소에서 3년간 시험한 결과 평균 20.6톤/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 일반 사료작물과 비교하여 떨어지지 않아 사료적 가치가 높다고 판단된다. 이처럼 복합내병충성, 높은 지상부 건물수량 및 가소화양분을 보유한 ‘청우’는 재배 확대 시 쌀 생산조절을 통한 수급조절에 기여할 것으로 기대된다.

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***주저자:** Tel. 031-695-4027, E-mail: okahn@korea.kr

이미다졸리논계 제초제 저항성 사료용 벼 계통 선발 및 MutMap 집단 육성

안역근^{*}, 홍하철, 정국현, 원용재, 현웅조

경기도 수원시 권선구 수인로 126 농촌진흥청 국립식량과학원 중부작물부 중부작물과

사료용 벼는 논의 형상과 기능을 유지하면서 쌀 수급불균형을 해결할 수 있는 좋은 대안임에도 불구하고 현 시점에서는 밥쌀용 벼와 비교하여 소득이 낮아(소득차이: 177,090원/10a, KREI, 2011) 정부의 보조금 없이는 농가현장에서 재배를 기피하는 경향이 있다. 이에 이양재배에 비해 생산비 10%, 노동력 22.8% 절감되는 직파재배가 필수적인데 직파재배는 잡초발생과 관리가 큰 문제점으로 되어 있다. 이를 해결하기 위해 화학돌연변이를 통한 이미다졸리논계 제초제 저항성 사료용 벼를 선발하였다. 사료용 벼 중 수량성과 내병충성이 좋은 ‘영우’ 종자를 EMS(ethyl methane sulphonate) 처리하여 돌연변이를 유도하고 자가수분으로 M₁을 양성한 후 M₂세대 6,000개체를 포장에 이양하여 최고분얼기에 Imazaquin(제품명: 톤업)을 400ml(유효성분 20%)/10a를 처리하여 정상적인 생육을 보이는 저항성 개체 4개체를 선발하였다. 현재 돌연변이 된 부위 탐색을 목적으로 MutMap(a method based on whole-genome resequencing of pooled DNA from a segregating population) 방법 적용을 위해 저항성 개체에 ‘영우’ wild type을 여교배하여 분석 집단을 창출하였다. 차후 whole-genome resequencing 후 reference sequence와 비교(SNP index=1)를 통해 변이 부위를 확인하고 이미다졸리논계 제초제 저항성 사료용 벼 개발 및 육종에 이용할 계획이다.

사사: 본 연구는 농촌진흥청 연구사업(세부과제명: 사료용 벼 유용 형질 도입 계통 생산력 검정 시험, 세부과제번호: PJ012552022017)의 지원에 의해 이루어진 것임.

***주저자:** Tel. 031-695-4027, E-mail: okahn@korea.kr

Construction and application of functional gene modules to regulatory pathways in rice

Woo-Jong Hong[§], Anil Kumar Nalini Chandran[§], Jong-Seong Jeon^{*} and Ki-Hong Jung^{*}

Graduate School of Biotechnology and Crop Biotech Institute, Kyung Hee University, Yongin 17104, Republic of Korea

Signal transduction and transcriptional regulation pathways are key elements in the control of diverse physiological responses and agronomic traits in plants. The regulatory roles of more than 1,000 known genes have been functionally characterized in rice, a model crop plant, and many of them are associated with transcriptional regulation and signal transduction pathways. In this study, we collected and analyzed 417 known genes associated with regulatory pathways, about 40% of the known genes, using the regulation overview installed in the MapMan toolkit. Connecting novel genes to current knowledge about regulatory pathways can elucidate their molecular functions and inspire ideas for further applications. We have summarized the functions of known regulatory genes in the areas of transcriptional regulation, epigenetic regulation, protein modification, protein degradation, signaling and hormone metabolism, also we have emphasized the unique features of several gene families in these classes, including MADS box families, which are strongly associated with the regulation of floral organ identity and flowering time. In addition, our construction of functional modules in four agronomic categories, morphological, physiological, biotic stress and abiotic stress, suggests a basic framework for expanding current knowledge about regulatory pathways to enhance agronomic traits in rice. We also provide a quick illustration of the positive and negative regulatory relationships of the target gene to manipulate agronomic trait by using genome-wide transcriptome data of knockout or overexpression mutations of genes of interest in each functional module.

***Corresponding Author:** E-mail: khjung2010@khu.ac.kr (K.-H. Jung), jjeon@khu.ac.kr (J.-S. Jeon)

[§]These authors contributed equally.

Quadratic code system for genetic identification of rice cultivars using InDel markers specific to dense variation blocks

Hyangmi Park^{1*}, Yongjae Won¹, Kukhyun Jung¹, Hyun Ungio¹, Hacheol Hong¹, Yulho Kim²

¹Central Area Crop Breeding Division, NICS, Suwon 16429, Republic of Korea

²Highland Agriculture Research Institute, NICS, Pyeongchang, 25342, Republic of Korea

Sequence diversity was accumulated through evolution and breeding process. We developed quadratic code system based on insertion/deletion(InDel) markers, each of which is specific to a dense variation block (dVB) with non-random recombination due to many variations. Firstly, 2,351 VBs were mined by analyzing of 40 Korean cultivars and published genome sequences of rice(*Oryza sativa* L. spp japonica) for transferability to dVB-specific InDel markers. Secondly, 12,174 putative InDels in the dVB regions were identified for the development of rice barcode system. A set of 595 PCR-based novel InDel markers was designed in order to widen the genetic basis for national rice breeding programs. Among them, 112 dVB-specific InDels from all rice cultivars were selected by gel electrophoresis, which were converted as 2D barcode types according to comparing amplicon polymorphisms in the eight cultivars to the reference cultivar. Finally, the polymorphism of the markers were assessed in 284 rice cultivars, and the rice barcode system that allows a clear distinction among rice cultivars is also detailed. In addition, the changing of the dVBs in a chromosomal level can be quickly identified by investigating the reshuffling pattern of the rice cultivars with 44 marker sets. These results could provide significant information not only for the crop identification but also for breeding of varieties with minimal screening by using a small number of the selected InDel markers.

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***Corresponding Author:** Tel. 031-695-4032, E-mail: parkhm2002@korea.kr

Quantitative trait loci(QTLs) for gummy stem blight resistance using Bi-parental populations in watermelon

Eun Su Lee*, JinHee Kim, Yul-Kyun Ahn, Jong Pil Hong, Abinaya Manivannan, Tae Sung Park, Minkyung Kim and Do-Sun Kim

Vegetable Research Division, National Institute of Horticultural and Herbal Science, RDA, 100, Nongsaeangmyeong-ro, Iseo-myeon, Wanju-gun, Jeollabuk-do, Korea

Watermelon (*Citrullus lanatus*) is an important vegetable crop in the world and contains various health promoting compounds including many antioxidants such as lycopene and beta-carotene. Gummy stem blight (*Didymella bryoniae* (Auersw.)) is one of the most destructive diseases and causes crown blight, defoliation and fruit rot, resulting in severe production loss in watermelon. Single nucleotide polymorphisms (SNPs), important molecular markers for genetic studies are frequent sequence variation in the plant genome. We selected 113 SNP markers using Fluidigm SNP genotyping analysis from two watermelon lines, one susceptible('920533') and the other resistant('PI189225') to gummy stem blight. We surveyed phenotypes of disease resistance regarding pathogenic fungus (KACC 40937) inoculating F₂ population whose number is 94 samples. Phenotypes consist of 3 types. (1 type : not infection, 2 type : infection, 3 type : severe infection) Genotypes of F₂ samples are identified by utilizing Fluidigm SNP genotyping analysis and were scored as 'A(P₁ homozygous)', 'H(heterozygous)' and 'B(P₂ homozygous)'. We calculated genetic distance from SNP markers using Carthagen ver. 1.3 program and genetic linkage map was constructed using F₂ population derived from '920533' × 'PI189225'. We performed QTLs(quantitative traits loci) using genotype and phenotype data related to resistance index of gummy stem blight disease. Genetic inheritance and QTL analysis indicated that gummy stem blight resistance is controlled by an incompletely dominant effect of major QTLs.

*Corresponding Author: Tel. 063-238-6671, E-mail: lus4434@korea.kr

Genome-wide identification of the dehydrin genes in the *Cucurbitaceae* species

Sang-Choon Lee¹, Won-Kyung Lee¹, Ho Jun Joh¹, Inseo Kim¹, Jaehyeon Jeon¹, Sae Hyun Lee¹, Tae-Jin Yang^{1*}, Kihwan Song^{2*}

¹Department of Plant Science, Seoul National University, Seoul 08826, Republic of Korea

²Department of Bioresources Engineering, Sejong University, Seoul 05006, Republic of Korea

Dehydrins (DHNs) are hydrophilic proteins belonging to group II of the late embryogenesis abundant (LEA) protein family. DHNs have highly conserved lysine-rich K-segment and are considered as molecular chaperons playing important roles in plant growth and abiotic stress tolerance. In this study, DHN genes were identified through genome-wide searches in five Cucurbitaceae species including cucumber, wild cucumber, melon, watermelon, and bitter melon. A total of 32 DHN genes were found in the five species, which were further divided into several types depending on the presence and order of the major conserved motifs such as K-, Y-, and S-segments. *In silico* expression profiling using RNA-Seq data revealed high expression of SK₃-type DHN gene and very low expression of other DHN genes in cucumber. *In silico* promoter analysis identified a number of *cis*-acting elements related to abiotic stress-response, such as DRE and ABRE, in 2-kb upstream sequences from start codon of four cucumber DHN genes. DHN genes identified in this study will be valuable for understanding stress response mechanism as well as enhancing molecular breeding in Cucurbitaceae crops.

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*Corresponding Author: Tel. 02-880-4547, 02-3408-2905, E-mail: tjyang@snu.ac.kr, khsong@sejong.ac.kr

SSR 마커를 이용한 세포융합 감귤의 이질 4배체 판별

김민주*, 윤수현, 박재호, 박석만, 진성범

제주특별자치도 서귀포시 남원읍 국립원예특작과학원 감귤연구소

감귤 품종 중 운향과 금감속인 금감은 추위에 강해 내한성 육종 프로그램에 많이 사용되며 과피와 과육을 함께 먹을 수 있는 장점이 있다. 반면 감귤속인 길전네이블오렌지는 과육의 당도가 높고 신맛이 적으며 종자가 없다는 특징이 있다. 따라서 속이 다른 두 품종간의 장단점을 보완하면서 씨가 없고 과피와 과육을 함께 먹을 수 있는 감귤 품종 육성을 위하여 본 연구를 수행하였다. 길전네이블오렌지의 캘러스와 장실금감의 잎 조직을 재료로 세포 융합을 실시하였으며 융합된 세포를 직접 배지에서 배양하여 식물체를 얻었다. 얻어진 식물체에 대한 배수성은 Flow cytometry을 이용하여 검정하였다. 핵 DNA를 판별 할 수 있는 SSR 마커를 이용하여 핵 DNA가 금감과 길전네이블오렌지의 DNA를 모두 포함하고 있는 이질 4배체라는 것을 판별하였다. 또한 미토콘드리아와 엽록체 DNA 판별 마커를 이용하여 미토콘드리아와 엽록체가 어느 쪽에서 유래되었는지 확인할 수 있었다. 두 가지 품종의 핵 DNA가 모두 포함된 것으로 보아 향후 과실은 금감과 오렌지의 중간 형태를 나타내는 과실 특성을 나타낼 것으로 예상되며 차후에 새로운 품종으로 활용할 수 있을 것이다.

*주저자: Tel. 064-730-4143, E-mail: 88minju@korea.kr

녹색 품종형 고생장형 스프레이국화 ‘그린트리’ 육성

정재아¹*, 신학기², 김미선¹, 박종택¹

국립원예특작과학원 화훼과, 농촌진흥청 수출지원농업과

스프레이국화 ‘그린트리(Green Tree)’는 2007년 국립원예특작과학원 화훼과 국화육종온실에서 녹색 품종형 겹꽃인 ‘Leonardo’를 모본으로 연녹색 품종형 겹꽃 ‘Green Bird’를 부본으로 교배하여 종자를 채종하였다. 2008년 종자를 파종, 육묘 후 실생묘를 정식하여 자연개화후 선발하여 ‘07B1-140’계통번호를 부여받았다. 이후 1차, 2차 특성검정을 실시하였으며, 3차 특성검정을 실시하였다. 개화특성검정을 실시하고 축성재배, 자연재배, 억제재배의 주년생산성 검정 및 절화수명 등 소비자 기호성에 대해 조사되었다.

국화 ‘그린트리’ 품종은 10월 하순에 자연 개화하는 절화용 스프레이 추국이다. 화색은 YGN144A로 밝은 녹색 품종형 겹꽃으로 꽃크기는 4.2 ± 0.2 cm이며 화당 설상화수는 282.7 ± 10.9 매로 볼륨감이 있는 중형화로 디스버드형으로 재배도 가능하다. 초장은 106.1 ± 1.5 cm로 균일하가 잘 자라고 동시에 개화되고 고온기 화색발현이 균일한 특성을 가지고 있다. 착화수는 약 16.8 ± 2.3 개 정도이며 절화수명은 약 21일로 길다. 단일처리 후 연평균 개화반응은 7.5주이다. ‘그린트리’ 품종의 재배시 주의할 점은 고온이 지속될 경우 잎이 처리는 현상이 나타날 수 있으므로 과습되지 않도록 관수에 주의해야 한다. 그리고 억제재배기 개화지연을 방지하기 위해서 화아분화시 온도를 18도이상 유지시켜주는 것이 좋다.

*교신저자: Tel. 063-238-6811, E-mail: jabisung@korea.kr

흰녹병저항성 스프레이국화를 이용한 백색스탠다드국화의 변이 확대

정재아*, 이은혜, 신학기, 김미선, 박종택

국립원예특작과학원 화훼과

국화에서 흰녹병은 상업용 재배에서 가장 심각한 피해를 주는 병으로 수출검역대상이기도 하다. 하지만 전체 절화국화 재배면적의 80%를 차지하는 스탠다드 즉 대국은 현재까지 재배되는 주요품종 중에 흰녹병저항성 품종이 없다. 본 실험은 국화유전자원 중에 스프레이국화 내병성을 도입하기 위해 교배조합을 작성하고 교잡후대의 저항성유전과 국화꽃의 주요 유전형질에 대해 조사하였다. 흰녹병저항성 유전자원으로는 Dancer와 Gibaeg 품종을 교배친으로 이용하였으며 스탠다드국화 교배친으로는 주요한 육성계통과 상용품종을 이용하였다. 후대개체를 대상으로 3차에 걸친 포자비산법을 이용한 저항성 검정을 실시하고 흰녹병에 대한 1차선발을 실시하였다. 흰녹병에 대해서 Jinba × Dancer조합에서는 2:1, 08-1145 × Dancer는 4:1 분리비를 보였으며, 08-1145 × Gibaeg조합에서는 2:1 분리비를 보였다. 후대실생개체 89개체중 흰녹병저항성인 52개체를 선발하고 개화특성에 따라 스탠다드국화의 기본특성에 적합한 개체를 2차 선발하였다. 선발된 후대개체는 백색스탠다드국화와 다시 여교배하였다. 여교배한 후대는 482립을 채종하고 258개체를 정식하였으며 그중 다시 흰녹병저항성과 개화특성검정을 실시하여 50개체를 선발하였다. 현재 스프레이내병성 유전자를 도입한 흰녹병저항성 유망계통을 3계통 선발하였다.

*교신저자: Tel. 063-238-6811, E-mail: jabisung@korea.kr

Genotyping and bioinformatics analysis of single nucleotide polymorphism related to powdery mildew resistance in *Capsicum baccatum* and *Capsicum annuum*

Abinaya Manivannan¹, Yul-Kyun Ahn^{1*}, Tae-Hwan Jun², Eun-Young Yang¹, Sena Choi¹, Jinhee Kim¹, Eun-Su Lee¹ and Do-Sun Kim¹

¹Vegetable Research Division, National Institute of Horticultural and Herbal Science, Rural Development Administration, Jeonju-55365, Republic of Korea

²Department of Plant Bioscience, Pusan National University, Busan-46241, Republic of Korea

Rapid advancements in genome sequencing platforms provide ample opportunity for the development of DNA-based molecular markers. The present study deals with the genome wide identification, genotyping, and bioinformatics analysis of single-nucleotide polymorphism (SNP) markers related to powdery mildew (PM) resistance in two pepper varieties. *Capsicum baccatum* (PRH1- a PM resistant line) and *Capsicum annuum* (Saengryeg- a PM susceptible line), were re-sequenced to develop the SNP markers. The sequencing resulted in a total of 6,213,009 and 6,840,889 SNPs for PRH1 and Saengryeg respectively. Among the SNPs, 4,887,031 polymorphic SNP loci were identified between the two lines and 306,871 high-resolution melting (HRM) marker primer sets were generated. In order to understand the SNPs associated with the vital genes involved in diseases resistance and stress associated processes, chromosome-wise gene ontology analysis was performed. The gene ontology results revealed the occurrence of SNPs related to diseases resistance genes were predominantly distributed in chromosome 4. Furthermore, the chromosomes 5-8 consisted of SNPs-associated with genes involved in the nucleotide and ion binding processes. From the generated results, HRM primers were selected from each chromosome and evaluated in 46 F4 population of *Capsicum*. Among the tested primers, 19 primers discriminated the population into resistant, moderate, and susceptible varieties which has been corresponded with the physiological disease evaluation data. Thus, the current endeavor describes a novel approach for the identification of SNP markers that can be utilized for molecular breeding of pepper with powdery mildew resistance.

*Corresponding Author: Tel. 063-238-6674, E-mail: aykyun@korea.kr

Sequencing and *de novo* assembly of diploid perilla genome

Seon-Hwa Bae¹, Kyeong-Seong Cheon¹, Myoung-Hee Lee², Ki-Won Oh², Jeong-Hee Lee³, Ung-Han Yoon¹, Jundae Lee⁴, Tae-Ho Kim^{1*}

¹Genomics Division, National Institute of Agricultural Science, RDA, Jeonju, 54874, Korea

²UplandCropBreedingResearchDivision,NationalInstituteofCropScience,RDA,Milyang, 50424, Korea

³SEEDERS, INC. Daeduk Industry-Academic Cooperation Building, Daejeon 11-3, 30415, Korea

⁴Department of Horticulture, Chonbuk National University, Jeonju, 54896, Korea

Perilla is a self-pollinating annual herbaceous plant of the Lamiaceae family and has mainly been cultivated as an oil crop in East Asia. Here we report progress on the *de novo* genome assembly of *P. citriodora* (2n=2X=20). We undertook a draft *de novo* genome assembly by combining data from multiple sequencing platforms (Illumina, PacBio RS II) using various libraries with different insertions. The genome was assembled into 1,622 scaffolds with 12,325,979 bp (N50) with a total length of 643.9 Gb. Ten whole BAC sequences involved in omega-3 biosynthesis pathway were highly covered in the scaffolds. CEGMA showed that the percentage of completeness for this assembly was 92.74% and 97.58% for completely and partially aligned core eukaryotic genes, respectively. BUSCO analysis revealed a completeness score of about 95.5%. Repeat analysis showed that 61.47% of the assembled genome was predicted to be repetitive. A total of 196,413 *ab initio* gene models were predicted along with *Perilla* scaffolds using MAKER. Of them, 41,751 gene models were matched at least once with GO, Protein families DB and CCD. A total of 39,025 gene models were predicted along with the *Perilla* transcripts using Blastx. With the above evidences, we found that 55,418 gene models were involved at least once. GenBank showed that a total of 56,604 gene models were predicted. The results above will provide important information on the genome structure to understand the functional genomics of *Perilla*.

*Corresponding Author: Tel. 063-238-4563, E-mail: thkim1961@korea.kr

Genome-wide identification of the SOD, APX, and CAT gene families in the *Cucurbitaceae* species

Won-Kyung Lee¹, Sang-Choon Lee¹, Ho Jun Joh¹, Inseo Kim¹, Jaehyeon Jeon¹, Sae Hyun Lee¹, Tae-Jin Yang^{1*}, Kihwan Song^{2*}

¹Department of Plant Science, Seoul National University, Seoul 08826, Republic of Korea

²Department of Bioresources Engineering, Sejong University, Seoul 05006, Republic of Korea

Superoxide dismutase (SOD), ascorbate peroxidase (APX), and catalase (CAT) are key enzymatic antioxidants which play important roles in plant abiotic stress response and tolerance. In this study, SOD, APX, CAT gene families were identified through genome-wide searches in five *Cucurbitaceae* species including cucumber, wild cucumber, melon, watermelon, and bitter melon. As a result, 67, 59, and 27 genes were identified to encode SOD, APX, and CAT, respectively, in the five species. Through domain search, phylogenetic analysis, and *in silico* subcellular location analysis, features of the genes were characterized. *In silico* expression profiling using RNA-Seq data revealed diverse expression patterns of SOD, APX, and CAT genes in normal cucumber tissues. Antioxidant enzyme genes identified in this study will be valuable resource for understanding stress response mechanism as well as facilitating molecular breeding of *Cucurbitaceae* crops.

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*Corresponding Author: Tel. 02-880-4547, 02-3408-2905, E-mail: tjyang@snu.ac.kr, khsong@sejong.ac.kr

Molecular identification of *Allium ochotense* and *A. microdictyon* using multiplex-PCR based on single nucleotide polymorphisms

Yong Bog Kim¹, Rahul Vasudeo Ramekar², Byong Gon Choi¹, Ju Kyong Lee², Ik Young Choi³, Sun Gang Choi³ and Kyong Cheul Park^{3*}

¹Gangwon-do Agricultural Research & Extension Services, Chuncheon 24226, South Korea

²Department of Applied Plant Sciences, College of Agriculture and Life Sciences, Kangwon National University, Chuncheon 24341, Korea

³Department of Agriculture and Life Industry, Kangwon National University, Chuncheon 24341, Korea

Allium ochotense and *A. microdictyon*, commonly known as 'Mountain garlic,' are popular and economically important species in many countries including Korea, China, and Mongolia. Their leaves are often used as side dishes as well as in traditional medicines. In Korea, these two species are at risk of extinction due to damage to their natural habitat, and thus they need to be conserved and the subject of breeding programs. However, their identification relies mostly on morphological data, which have limitations and, until recently, led to classifying these two species under *A. victorialis*. In the present study, a simple and reliable method of molecular identification was developed, targeting four barcoding regions: the internal transcribed spacer (ITS), the *maturase K* gene (*matK*), the chloroplast *psbA-trnH* intergenic region, and the large subunit of the *ribulose-bisphosphate carboxylase* gene (*rbcL*). Single nucleotide polymorphisms (SNPs) were found in ITS and *matK* regions, but species-specific primers were designed based solely on the SNP at position 680 of the ITS region that differentiated *A. ochotense* from *A. microdictyon*. Using these primers in amplification refractory mutation system (ARMS)-PCR, *A. ochotense*, and *A. microdictyon* were simultaneously and efficiently distinguished. This study is the first to report a simple, rapid, and efficient method for discriminating *A. ochotense* and *A. microdictyon*, evidencing the utility of species-specific markers to accelerate conservation and breeding programs.

*Corresponding Author: Tel. +82-33-250-7770, E-mail: kyongcheul.park@kangwon.ac.kr

Construction of high-resolution map and analysis of stem related to QTL using Milyang23/Gihobyeyo recombinant inbred lines

Ye-Ji Lee^{1,4}, Kyeong-Seong Cheon¹, Eun-Ju Byeon¹, Hyeonso Ji², Gang-Seob Lee³, Ung-Han Yoon¹, Nam-In Hyung⁴, Tae-Ho Kim^{1*}

¹Genomics Division, National Institute of Agricultural Sciences, RDA, Jeonju 54874, Republic of Korea

²Genetic Engineering Division, National Institute of Agricultural Sciences, RDA, Jeonju 54874, Republic of Korea

³Biosafety Division, National Institute of Agricultural Sciences, RDA, Jeonju 54874, Republic of Korea

⁴Department of Plant and Food Sciences, Sangmyung University, Cheonan 31066, Republic of Korea

Rice (*Oryza sativa* L.) is one of the major crops for most Asians and grain production has dramatically increased over the past decade. However, severe weather conditions, such as strong winds, often cause yield reduction by stem lodging. To identify the loci related to lodging resistance, we studied QTL analysis using the recombinant inbred lines derived from 'Milyang23' and 'Gihobyeyo' (MGRILs). We generated 3,221 SNP markers from 162 MGRILs through resequencing analysis by Illumina HiSeq 2000. Recombination breakpoints were visualized on bin-map with SNPs compared to parental chromosome and used for the construction of the high-resolution genetic map. Subsequently, in 2017, the 12 QTLs in each internode diameter and culm length were detected from within the QTL regions of chromosome 1, 6, and 7 with high accuracy (LOD>8). In comparison with QTL regions of 2016, 11 QTLs were overlapped and new one (LOD>20) was detected in 2017. It will be possible to narrow down these candidate QTL regions to identify genes related to lodging resistance by map-based cloning.

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Corresponding Author: Tel. 063-238-4563, E-mail: thkim@rda.go.kr

qVDT11, a major QTL related to drought tolerance as stable tiller formation in rice

Su-Min Jo^{1*}, Tae-Heon Kim¹, Dongjin Shin¹, Saes-Beul Lee¹, Ji-Yoon Lee¹, Sang-Ik Han¹, Jun-Hyeon Cho¹, Kyung-Min Kim², Jong-Hee Lee³, You-Chun Song¹, Dong-Soo Park¹, Myung-Kyu Oh¹

¹Department of Southern Area Crop Science, National Institute of Crop Science, RDA, Miryang 50424, Republic of Korea

²College of Agriculture and Life Science, Kyungpook National University, Daegu 41566, Republic of Korea

³Research Policy Bureau, Rural Development Administration, Jeonju 54875, Republic of Korea

Recently drought caused by global climate change is seriously giving a threat to world rice production and food security in rice field. 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. In here, we screened 218 rice genetic resources for drought tolerance at vegetative stage and selected 32 highly drought-tolerant varieties in greenhouse. Under rain-fed conditions, Nagdong grain yield decreased by 53.3% from 517 kg/10a to 241 kg/10a when compare to irrigation condition. By comparison, Samgang yield decreased by 23.6% from 550 kg/10a to 420 kg/10a. The variety Samgang exhibited strong drought tolerance and stable yield in rain-fed conditions and was selected for further study. 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. qVDT2, flanked by markers RM324 and S2016, explained 8.8% of the phenotypic variance with LOD score of 3.3 and an additive effect of -0.6 . qVDT6 was flanked by S6022 and S6023 and explained 12.7% of the phenotypic variance with LOD score of 5.0 and an additive effect of -0.7 . 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 . qRWC11 was the only QTL for RWC to be identified; it was in the same locus as qVDT11. qRWC11 explained 19.6% of the phenotypic variance, with a LOD score of 4.0 and an additive effect of 9.7. To determine QTL effects on drought tolerance in 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. DH lines with both of these drought tolerance associated QTLs exhibited the most stable tiller formation. These results suggest that qVDT11 is important for drought tolerance and stable tiller formation under drought stress condition in field.

*Corresponding Author: Tel. 055-350-1175, E-mail: tnals88319@korea.kr

기계수확이 가능한 내병 장류 두부용 콩 ‘새금’

김현태^{1*}, 강범규¹, 한원영¹, 이병원², 이영훈³, 최만수³, 서정현¹, 고종민³, 윤홍태², 오기원¹, 하태정³, 곽도연¹

¹경남 밀양시 점필재로20 국립식량과학원 남부작물부

²경기도 수원시 수인로126 국립식량과학원 중부작물부

³전북 완주군 이서면 혁신로181 국립식량과학원

콩 다수확 품종 ‘대풍’은 뛰어난 재배안정성과 수량성에도 불구하고 종자가 작고 배꼽색이 갈색인 이유로 재배가 확대되지 못하고 있다. ‘대풍’의 이러한 종자상의 단점을 개선하고, 더하여 기계수확 적응성을 향상시키고자 시도해 온 결과 ‘새금’을 개발하였기에 여기에 소개한다. ‘수원190호’와 ‘대원콩’을 교배하여 육성한 대립 내재해성인 계통을 부분으로 하여 2003년에 ‘대풍콩’과 교배하였다. 2005년 F₂ 집단에서 선발한 개체를 2006년 아시아채소연구개발센터에서 3세대 세대진전후 2007년 F₆세대부터 국립식량과학원 시험포장에서 계통전개하여 선발하였다. 2009-2010년 생산력검정시험에서 종실색택이 좋고 다수성이며 기계수확적성이 높은 계통을 선발하여 ‘밀양232호’의 계통명을 부여하고, 2011-2013년 3년간 전국 11개소에서 지역적응성을 검정하였다. ‘새금’은 유한신육형으로 모용과 형색이 갈색이고 종피와 배꼽색은 황색이며 꽃색은 백색이다. 성숙기가 10월 17일로 ‘대원콩’보다 3일 정도 늦으며, 종실은 구형이고 100립중이 25.4g으로 대원콩보다 1.2g 무거운 대립품종이다. 키가 대원콩보다 크지만 표준재배에서의 도복정도는 대원콩과 비슷한 정도로 강하다. 포장에서의 자연이병정도와 8r 균주를 이용한 분무접종에서 불마름병에 저항성을 보였으며, 콩모자이크바이러스의 경우 자연이병 포장에서는 증상이 나타나지 않았으나 G7H, G6H, G5 strain의 즙액접종에서는 모자이크 반응을 보였다. 내탈립성이 강하여 시험포장에서 탈립이 잘 되지 않으며, 성숙 꼬투리를 40℃ 건조기에 48시간 두어도 꼬투리가 터지지 않았다. 도복에 강하고, 가장 낮은 꼬투리의 높이가 18cm로서 컴바인 등을 이용한 기계수확이 용이한 품종으로 생각된다. 그러나, 밀식재배에서는 도복에 약하며, 검은뿌리썩음병 이병주율이 대원콩보다 높다. 두부수율과 메주 청국장수율 및 발효적성은 대원콩과 비슷하였으며, 남부 적응지역의 평균수량이 3.02ton/ha로 ‘대원콩’과 비슷한 수준이다.

*주저자: Tel. 053-663-1107, E-mail: sojatae@korea.kr

Atomato flowering gene *SELF PRUNING 5G* promotes day-neutrality and early yield

Soon Ju Park^{1,2}, Sebastian Soyk², Jong Hyang Bae³, José M Jiménez-Gómez⁴, Zachary B Lippman²

¹Department of Biological Science and Institute for Basic Science, Wonkwang university 460 Iksandae-ro, Iksan, Jeonbuk, Korea

²Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, USA.

³Department of horticulture industry, Wonk wang University, Iksan 54538, Korea

⁴Department of Plant Breeding and Genetics, Max Planck Institute for Plant Breeding Research, Cologne, Germany.

In many plants, the signals for flower induction depends on seasonal variation in day length. Photoperiod response depends on cross-talk between light perception and the circadian clock, which function together to control expression of the flowering hormone florigen. Here we show that loss of day-length-sensitive flowering in tomato was driven by the florigen paralog and flowering repressor *SELF-PRUNING 5G* (*SP5G*). *SP5G* expression is induced to high levels during long days in wild species, but not in cultivated tomato because of cis-regulatory variation. CRISPR/Cas9-engineered mutations in *SP5G* cause rapid flowering and enhance the compact determinate growth habit of field tomatoes, resulting in a quick burst of flower production that translates to an early yield. Our findings suggest that pre-existing variation in *SP5G* facilitated the expansion of cultivated tomato beyond its origin near the equator in South America, and they provide a compelling demonstration of the power of gene editing to rapidly improve yield traits in crop breeding.

Corresponding Author: S.J.P. (sjpark75@wku.ac.kr),
J.M.J.-G. (jose.jimenez-gomez@versailles.inra.fr)
Z.B.L. (lippman@cshl.edu).

JMJ30-mediated H3K9me3 demethylation drives tissue identity changes to promote cellular reprogramming in *Arabidopsis*

Kyounghee Lee*, Ok-Sun Park & Pil Joon Seo

Department of Biological Sciences, Sungkyunkwan University, Suwon 16419, Republic of Korea

Plant somatic cells can be dedifferentiated by *in vitro* tissue culture methods, and massive genome-wide chromatin remodeling occurs particularly during callus formation. Since callus resembles lateral root primordium, tissue identity conversion is essentially required when leaf explants are used. Consistent with that differentiation state is defined by chromatin structure that permits limited gene profiles, epigenetic reprogramming would underlie cellular reprogramming for tissue identity changes. Although histone methylation suppressing leaf identity during callus formation has been demonstrated, it is still elusive which epigenetic factor is involved in activation of root identity. Here, we report that JUMONJI C DOMAIN-CONTAINING PROTEIN 30 (JM30) stimulates callus formation by promoting expression of a subset of *LATERAL ORGAN BOUNDARIES-DOMAIN* (*LBD*) genes that establish lateral root primordia. The JM30 protein binds directly to the *LBD16* and *LBD29* promoters with the help of AUXIN RESPONSE FACTOR 19 (ARF19) and activates expression of *LBD16*, *LBD17*, *LBD18*, and *LBD29*. In support of this, the *JMJ30*-deficient mutants displayed reduced callus formation with low transcript levels of *LBDs*. The ARF-JMJ30 complex catalyzes removal of methyl groups from H3K9me3 especially at the *LBD* loci to activate their expression. These results indicate that the JM30-ARF-LBD axis promotes callus formation.

*Corresponding Author: E-mail: kh10905@skku.edu

The MIEL1 E3 ubiquitin ligase negatively regulates cuticular wax biosynthesis in *Arabidopsis* stems

Hong Gil Lee^{1*}, Juyoung Kim², Mi Chung Suh² and Pil Joon Seo¹

¹Department of Biological Sciences, Sungkyunkwan University, Suwon 16419, Republic of Korea

²Department of Bioenergy Science and Technology, Chonnam National University, Gwangju, 61186, Republic of Korea

Cuticular wax is an important hydrophobic layer that covers the plant aerial surface. Cuticular wax biosynthesis is shaped by multiple layers of regulation. In particular, a pair of R2R3-type MYB transcription factors, MYB96 and MYB30, are known to be the main participants in cuticular wax accumulation. Here, we report that the MYB30-INTERACTING E3 LIGASE 1 (MIEL1) E3 ubiquitin ligase controls the protein stability of the two MYB transcription factors and thereby wax biosynthesis in *Arabidopsis*. MIEL1-deficient *miel1* mutants exhibit increased wax accumulation in stems, with upregulation of wax biosynthetic genes targeted by MYB96 and MYB30. Genetic analysis reveals that wax accumulation of the *miel1* mutant is compromised by *myb96* or *myb30* mutation, but *MYB96* is mainly epistatic to *MIEL1*, playing a predominant role in cuticular wax deposition. These observations indicate that the MIEL1 – MYB96 module is important for balanced cuticular wax biosynthesis in developing inflorescence stems.

*Corresponding Author: Mi Chung Suh, E-mail: mcsuh@chonnam.ac.kr; Pil Joon Seo, E-mail: pjseo1@skku.edu

국내 귀리 탈부특성 및 근연관계 분석

김경민¹, 신동진¹, 김경훈¹, 박효진¹, 권유리¹, 현종내¹, 오명규¹

¹경남 밀양시 점필재로 20, 농촌진흥청 국립식량과학원 남부작물부 논이용작물과

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 높은식이섬유인 베타글루칸이 3~6% 들어있어 식용으로도 그 가치를 인정받고 있다. 귀리는 두가지 종류로 종실에 껍질이 있는 겉귀리와 껍질이 없는 쌀귀리로 구분되는데 이런 이유로 겉귀리는 수확 후 껍질을 탈피하기 위한 노력이 필요하지만 쌀귀리는 탈곡과 함께 껍질이 제거되어 식용으로 이용하기에 유리해 국내에서 대부분 쌀귀리를 식용으로 이용하고 있다. 이에 겉귀리와 쌀귀리의 탈부특성과 근연관계가 연관성이 있는지 알아보고자 국내에서 재배되고 있는 겉귀리 7품종과 쌀귀리 5품종 총 12품종을 수집하여 공시하였다. 겉귀리와 쌀귀리의 탈부 여부는 수확 후 탈곡기를 이용해 탈곡되어 나오는 종실의 껍질의 유무로 탈부성을 확인하였고, 품종간의 근연관계는 분자마커를 활용하여 분석하였다. 분자마커는 University of Saskatchewan의 CMG-Lab에서 제공하는 61개의 SSR마커를 이용하여 분석하였고 그 중 22개의 마커가 다형성을 나타내었다. 이후 22개의 마커에서 확인되는 밴드패턴을 NTSYSpc 2.1 프로그램을 사용하여 Tree plot으로 나타내어 근연관계를 확인하였다. 그 결과, 탈곡 후 껍질이 벗겨지는 탈부특성은 겉귀리 7품종의 경우 탈부되지 않았고, 쌀귀리 5품종은 탈부되는 특성을 나타내었다. 근연관계는 Coefficient 1.20에서 겉귀리6품종과 쌀귀리1품종, 그리고 겉귀리 1품종과 쌀귀리4품종 2개의 그룹으로 나뉘어졌으며 대체로 겉귀리와 쌀귀리끼리 가깝게 그룹화 되는 경향을 나타냈다. 이 결과를 토대로 향후 더 많은 다형성 마커를 이용하여 귀리의 품종판별에 대한 기초자료로 활용하겠다.

*주저자: Tel. 055-350-1174, E-mail: raiders87@korea.kr

Resequencing of Gayabyeo, a Tongil-type brown planthopper (BPH) resistant rice variety, and development of single nucleotide polymorphism (SNP) markers

Hyun-Ju Kang¹, Eokkeun Ahn², Song Lim Kim¹, Inchan Choi¹, Jeongho Baek¹, Kyung-Hwan Kim¹, Hyeonso Ji^{1*}

¹Gene Engineering Division, National Institute of Agricultural Sciences, Jeonju 560-500, Republic of Korea

²Department of Central Area, National Institute of Crop Science, Suwon 441-707, Republic of Korea

Gayabyeo has been known to be resistant to various BPH biotypes collected in Korea. With a purpose of mapping genes of Gayabyeo conferring BPH resistance, we developed a F2 population derived from a cross between Gayabyeo and Taebaegbyeol which is a Tongil type BPH susceptible rice variety. Also, we performed whole-genome resequencing of these two varieties. The sequencing yielded 18.5×10^9 bp for Gayabyeo, and 17.9×10^9 bp for Taebaegbyeol. After quality trimming and read mapping onto Nipponbare reference sequence, the final average mapping depth was $27.6 \times$ for Gayabyeo and $25.5 \times$ for Taebaegbyeol. Totally, 284,501 putative SNPs between Gayabyeo and Taebaegbyeol were detected. Up to now, 96 CAPS (Cleaved Amplified Polymorphic Sequences) markers were developed based on the detected SNPs which were within restriction enzyme recognition sites, and they have been being used for genotyping 180 F2 plants derived from a cross between Gayabyeo and Taebaegbyeol. By comparison of resequencing data of Gayabyeo and the sequences of already reported BPH resistance genes (*Bph3*, *Bph14*, *BPH18*, *BPH26*), it was revealed that Gayabyeo has *Bph3* and *BPH26* resistance genes. We will confirm the BPH resistance genes of Gayabyeo by mapping experiment, and are developing selection markers for these genes.

*Corresponding Author: Tel. 063-238-4657, E-mail: jhs77@korea.kr

Genetic analysis of four dense green leaf mutant lines of rice and their genome resequencing

Jun Oh¹, Hyun-Ju Kang¹, Song Lim Kim¹, Jeongho Baek¹, Inchan Choi¹, Kyung-Hwan Kim¹, Hyeonso Ji^{1*}

¹Gene Engineering Division, National Institute of Agricultural Sciences, Jeonju 560-500, Republic of Korea

Dense green leaf mutants can be utilized in discovery of genes regulation leaf growth and development. We found four dense green leaf mutant rice lines which are Ds061942, Ds073406, Ds074081, 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 phenotype indicating that the dense green leaf trait was caused by a recessive gene in each mutant line. F2 segregation ratios were also fit to 3:1 (wild type : mutant type), which demonstrated that single recessive gene controls dense green leaf trait in each mutant line. Resequencing of the four 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 $26.55 \times$ - $28.75 \times$. By comparison with Dongjin resequencing data, 42,386-58,393 single nucleotide polymorphisms (SNPs) were found between each mutant line and Dongjin. Based on these results map-based cloning of the genes regulating the dense green leaf trait of the mutant lines will be carried out with F2 population derived from crosses between each mutant line and Dongjin.

*Corresponding Author: Tel. 063-238-4657, E-mail: jhs77@korea.kr

밝은 오렌지색 품종형 스프레이국화 ‘오렌지팝’ 육성

배민지¹, 진영돈¹, 안동춘¹, 정용모¹, 최시림¹, 홍광표², 황주천^{3*}

¹경남 창원시 경상남도농업기술원 화훼연구소

²경남 진주시 경상남도농업기술원 연구개발국

³경남 밀양시 경상남도농업자원관리원

경남농업기술원 화훼연구소에서는 2012년 10월에 화형과 화색이 우수한 분홍색 품종형의 ‘Lollipop’을 모본, 흰녹병 저항성이며 착화성이 우수한 황색 품종형 ‘Yellow Cap’을 부분으로 인공교배하여 교배조합으로부터 386개의 종자를 획득하였다. 그 후 교잡 1세대를 육묘하여 특성검정 후 화색이 선명하고 성장세와 착화성이 우수한 5개체(LY13-27, 63, 85, 126, 274)를 1차로 선발하였다. 이들 중 특성이 우수한 개체 LY-85(경남교CS-54호)를 삼목에 의해 개체증식 후 화훼연구소 비닐온실 내에 정식하였으며, 2014년부터 2016년까지 3년간에 걸쳐 1~2차 생육특성검정을 통해 안정성, 균일성과 흰녹병 저항성 등을 조사하였고, 2016년에는 계통번호 ‘경남교CS-54호’를 부여하여 3차 특성검정을 수행해 안정성과 균일성에 대한 연차별 재현성 그리고 주년생산성(자연, 축성, 억제재배) 및 품평회와 시장출하 등을 통해 생산자와 소비자의 기호성 평가를 받았다. 그 결과 기호성이 좋고, 화색 및 화형 등 품질이 우수하다고 판단되어 2016년 농작물 직무육성신품종심의회 심의를 거쳐 ‘오렌지팝(Orange Pop)’으로 명명하고 국립종자원에 품종보호출원 하였다. ‘오렌지팝’은 밝은 오렌지색(GON163C)의 품종형의 겹꽃 화형인 스프레이 국화로 착화성이 좋고 줄기가 강건한 특징이 있다. 자연개화기는 10월 28일로 대조품종(11월 4일)보다 7일정도 빨리 개화하는 특징이 있으며, 초장은 96.9cm로 대조품종(92.1cm)보다 길다. 꽃 직경은 5.2cm, 꽃자루 길이는 11.1cm이며, 설상화수는 12.2개 정도이다. 절화수명은 약 20일 정도이며, 비닐하우스 내에서 연중재배가 가능하다. 재배 시 초기 생육증진을 위한 영양분 관리가 중요하며, 하계 고온기 재배 시 화색발현을 위해 한 낮에 차광을 30% 정도의 한랭사로 차광을 해 주고 환기를 충분히 해 주는 것이 좋다.

*주저자: Tel. 055-254-1624, E-mail: baeminji@korea.kr

Detection of QTLs in interspecific *Perilla citriodora* x *P. hirtella* mapping population

Myoung Hee Lee¹, Ki Won Oh^{1*}, Myung Sik Kim¹, Jung In Kim¹, Eun Young Oh¹, Suk Bok Pae¹, Un Sang Yeo¹, Tae-Ho Kim², Jeong Hee Lee³, Do Yeon Kwak¹, Yong Chul Kim¹

¹Department of Southern Area Crop Science, NICS, RDA, Miryang, Korea

²National Institute of Agricultural Science, Wanju, Korea

³Seeders Inc., Daejeon, Korea

A interspecific cross between *P. citriodora* and *P. hirtella* constitutes ideal material for a linkage map construction in genome project of *Perilla*. The chromosomes of the species are same with $n=10$ and progenies of the cross are normal in growth and seed set. The phenotype of F2 population of the cross are normally distributed and this is a proof of the high affinity of the chromosomes during their sexual reproduction. Total number of 2,518 markers were mapped in 10 linkage groups with total length of 1,309 cM. Among the markers, 21 QTLs were associated with agronomic traits under LOD 3.0 condition. Purple leaf color related QTL, *qtl_lc-1*, was mapped in LG3 and two anthocyanin biosynthesis transcription factor like sequences, WD40 repeat-like superfamily protein and myb domain protein 43, were detected near from *qtl_lc-1*.

*Corresponding Author: Tel. 055-350-1131, E-mail: ohkw1004@korea.kr

High oleic acid 콩 육성을 위한 돌연변이 계통 PE451, PE2742, PE3058의 특성 검정

박은영¹, 이정동^{1*}

¹대구광역시 북구 산격동 경북대학교 농업생명과학대학

세계적으로 생산되는 식물성 기름의 주요 원료 중 하나인 콩은 기름 구성성분의 23%를 단일불포화지방산인 oleic acid가 차지하고 있다. Oleic acid는 높은 온도에서 기름의 안정성을 높여주고 혈압을 조절하는 기능이 있는 것으로 조사된 바 있다. Oleic acid 함량이 높은 계통을 선발하기 위해 EMS를 처리한 돌연변이 집단을 육성하였고, M4세대에서 고 oleic acid 함량을 보인 PE451(44.4%), PE2742(47.7%), PE3058(33.4%)을 선발하였다. 이들 돌연변이 계통과 wild type인 풍산나물콩과 다수성이며 대립품종인 우람을 인공 교배 하여 얻은 F₂₃집단의 지방산을 분석한 결과 oleic acid의 변이가 관찰되었다. Oleic acid에서 linoleic acid로 생합성 되는 과정에 Fad2-1A 유전자와 Fad2-1B 유전자가 관여하는 것으로 알려 졌고, 이들 유전자가 기능을 잃으면 oleic acid 함량이 높아지는 것으로 선행연구에서 보고되었다. 선발된 고 oleic acid 계통들의 Fad2-1A, Fad2-1B 유전자 염기서열을 풍산나물콩과 비교한 결과 엑손에서는 변이가 없는 것으로 확인이 되었다. 따라서 oleic acid 함량이 높은 돌연변이 계통에 대한 mapping 연구가 필요하면 이를 통해 oleic acid 함량을 높이는 새로운 genome 영역이나 유전자를 밝힌다면 콩의 oleic acid 함량을 높이는데 기여할 수 있을 것으로 기대된다.

*주저자: Tel. 053-950-5709, E-mail: jdlee@knu.ac.kr

분자표지를 이용한 탄저병 저항성 고추 ‘AR탄저박사’ 품종개발

도재왕^{1*}, 윤재복¹, 박석진¹

¹경기도 화성시 여울로 4길27 (주)고추와육종

고추 탄저병은 *Colletotrichum* spp.에 의해 발생하며 고추재배에 있어서 많은 피해를 주는 병중에 하나로 국내외에서 발생하여 농가소득의 감소를 초래하고 있다. 이러한 탄저병 피해를 줄이고자 약제를 이용한 화학적 방제보다는 식품으로서도 안전한 탄저병 저항성 품종의 육성을 시도하였고 ‘AR탄저박사’를 개발하게 되었다. 탄저병 저항성품종의 모계로 사용한 ‘8047’계통은 2009년도에 37개 상용품종의 F₂분리집단을 정식하고 GMS와 CMS 분자표지를 이용하여 웅성불임이 GMSK-MSms, CMS-Rf/f이며 원예적 특성이 우수한 개체를 선발하고 고정하기를 반복하였다. 최종적으로 ‘대들보’ F₈세대에서 노지포장에서 바이러스에 강하고 원예적 특성 및 조합능력이 우수한 개체를 선발하여 ‘8047’로 명명하였다. 탄저병 저항성인 부계 계통의 육성은 1998년부터 현재까지 국내에서 우점 병원균인 *Colletotrichum. acutatum* 균주를 사용하였고 대만의 AVRDC에서 도입한 PBC81(*Capsicum baccatum*) 계통을 microinjection방법으로 과실에 직접 접종하고 선발한 개체의 탄저병 저항성을 국내 주요 재배종인 *C. annuum*(SP26)계통으로 도입하였다. 그러나 종간교잡 불화합성으로 후대진전이 어려워 배배양을 통해 F₁개체를 생산하고 *C. annuum*(SP26)계통과 여교잡하여 BC₁F₁집단을 전개하였다. 이후 *C. acutatum* 균주로 기내 접종하여 저항성인 개체를 선발하고 BC₁F₂에서 원예적 특성이 우수한 *C. annuum*(H41)계통에 여교잡하여 BC₂F₂집단을 만들고 기내접종과 포장저항성으로 선발하였다. 또한 SP26과 PBC81을 이용한 BC₁F₁, BC₁F₂분리집단에서 QTL 분석을 통해 *C. acutatum*과 *C. capsici* 저항성과 연관된 QTLs를 동정함에 따라 개발된 분자표지로 탄저병 저항성을 보유한 개체를 선발하여 정식하고 기내접종을 병행하여서 탄저병에 강한 개체를 선발하였다. 분자표지와 탄저병 기내접종 및 포장저항성으로 선발하고 세대진전을 반복한 결과 BC₂F₈ 세대에서 탄저병 저항성이 강하고 수량성이 좋은 탄저병 저항성 부계 ‘42-13-3’계통을 선발하였다. 이렇게 만들어진 두 계통으로 예비조합을 작성하여 조합성능 검정과 농가 시교재배 시험을 거쳐 원예적 특성이 우수하고 탄저병에 강한 ‘AR탄저박사’를 육성하였다.

*주저자: Tel. 031-8003-0586, E-mail: wahng0@honmail.net

Mutation of *SPOTTED LEAF4 (SPL4)* encoding a microtubule severing protein produces reactive oxygen species (ROS) and delays leaf senescence in rice

Giha Song^{1*}, Da-Yea Park¹, Nam-Chon Paek¹

¹Department of Plant Science, Plant Genomics and Breeding Institute, and Research Institute of Agriculture and Life Science, Seoul National University, Seoul 08826, Republic of Korea

The mutants show autonomous lesion formation, spontaneous cell death without any pathogen attack and resistance to a pathogen are classified to lesion mimic mutants (LMMs). Through these phenotypes, LMMs were used to study the mechanisms of programmed cell death pathway and response to a pathogen. In this study, the *spotted leaf4 (spl4)* mutant which is derived from γ -ray irradiation were used to study the spontaneous cell death mechanism. It has been reported that many LMMs its encoding genes were identified but its molecular mechanism of lesion formation and pathogen resistance is still unclear. The reactive oxygen species (ROS) is the product of senescence and ROS can be found near the spots in LMMs during autonomous lesion formation in LMMs even though it is a developmental stage. Stay-green is the phenomena of delayed senescence and this is the one character that breeders want to achieve. Also, Scientists study this delayed senescence phenotype to elucidate the leaf senescence mechanism. In this study, we analyzed the rice *spl4* mutant, which shows autonomous lesion formation on leaf blades, ROS accumulation and shows the stay-green phenotype. The *spl4* locus was identified by map-based cloning. This locus encodes a putative microtubule severing protein, spastin. Our data may suggest that the malfunctioning of microtubule severing protein results in pleiotropic phenotypes of autonomous lesion formation, ROS accumulation and delayed senescence in *spl4* mutant.

*Corresponding Author: E-mail: rcnavic@snu.ac.kr

Mastering of terpenoid metabolic pathway via rice MYB transcription factor, OsMYBR22

Hyung-Keun Ku¹, Ye Sol Jeong^{1,3}, Min-Kyoung You^{1,2}, Dongho Lee³, Sun-Hyung Lim^{4*}, Sun-Hwa Ha^{1,2*}

¹Crop Biotech Institute, Kyung Hee University, Yongin, Korea

²Graduate School of Biotechnology, Kyung Hee University, Yongin, Korea

³Department of Biosystems and Biotechnology, Korea University, Seoul, Korea

⁴National Academy of Agricultural Science, RDA, Jeonju, Korea

Terpenoid, the largest group of naturally occurring organic chemical compounds, has been taken the steady concern as a target for genetic modulation because of the nutritional and economic significance of these compounds. To identify the regulatory genes of two secondary metabolisms in rice, blue light was selected because it simultaneously affected the highest content of total carotenoids and phenolic compounds when examined in different light treatments of white, blue, red, dark, and green. The seventeen transcription factor (TF) genes were discovered to show the up-regulated pattern in blue light (B) compared to white light (W) through microarray analysis. In particular, a TF13 gene, a member of the MYB transcription factor gene family, showed 2.7 fold higher expression levels in B/W and was selected one of the best candidates via further trans-activation assay of five promoters of anthocyanin and carotenoid biosynthetic genes. In this study, the function of TF13 on terpenoid biosynthesis was only analyzed. Firstly, meta-profiling analysis with TF13 and eight terpenoid biosynthetic genes based on microarray data sets showed dramatic circadian pattern of TF13 in rice leaves and roots at different stages, as well as, the expression patterns induced by ABA, drought, and cold stress conditions. To investigate the functional roles of TF13 in rice plants, we analyzed transgenic plants overexpressing TF13 and the T-DNA activation tagging mutant lines using qRT-PCR. The overexpression of TF13 resulted in the enhanced expression of terpenoid biosynthetic genes. Recently, we are producing the CRISPR/Cas9-induced TF13 KO lines in rice. We hope it might be very helpful to understand the regulation mechanism of plant secondary metabolism.

*Corresponding Author: E-mail: limsh2@korea.kr, E-mail: sunhwa@khu.ac.kr

Genome-wide DNA polymorphisms analysis of rice mutants by gamma-ray irradiation based on Whole genome re-sequencing

Lee Jae Woo*, Cheol Seong Jang

Plant Genomics Lab. Department of Applied Plant Sciences, Kangwon National University, Chuncheon 200-713, Korea

Recently, many mutation breeding studies have been used ionizing radiation such X-rays, gamma rays and neutrons in many major crops. Gamma-ray induced mutant rice has been also reported for breeding and genetic studies. However this genome-wide effect is still largely unknown. In this study, we carried out genome-wide effect identification by gamma-ray induced mutant rice. We obtained 3,000 mutant rice lines induced by gamma-rays of 200Gy and 300Gy applied to Donganbyeo (wild-type, WT) After that, we developed up to 8th generation, Among them we selected a total of 244 core individuals about abiotic stress tolerance and excellent quantitative traits. Among these selected mutants line, we performed whole genome re-sequencing at abiotic stress tolerance 20 line and excellent quantitative traits 40 line from an Illumina HiSeq4000 platform. Average 65,421,382 quality-filtered read were generated, with average sequencing depth of ~30X for each line. Filtered reads aligned on to the rice reference genome 'Nipponbare', its average mapped reads and mapping percentage are 62,739,789 and 95.88% respectively. Single nucleotide polymorphisms (SNPs) and insertions/deletions (InDels) were detected using Genome Analysis Toolkit (GATK). Average 164,152 SNPs and 41,752 INDELs were identified. We selected only homozygous variants from a total variants, where significant mutation were average SNPs 85, InDels 131 respectively. The effects of SNPs/InDels were classified four levels "HIGH effect" "MODERATE effect", "LOW effect" and "MODIFIER" according to SnpEff. A total 'HIGH effect' SNPs variation were 46 and InDels were 496 respectively. Additionally we will study gene functions for stress tolerance and quantitative traits.

*Corresponding Author: Tel. 032-250-6416, E-mail: csjang@kangwon.ac.kr

The expression of putative genes related to plant growth in dwarf soybean derived from crossing of *G. max* and *G. soja*.

Yong-Wook Ban^{1,2}, Taewook Kim³, Doori Park^{1,4}, Chanseok Shin³, Ik-young Choi^{1*}

¹Department of Agriculture and Life Industry, Kangwon National University, Chuncheon 24341, South Korea

²Department of Forestry Resources, Kangwon National University, Chuncheon 24341, South Korea

³Department of Applied Biology and Chemistry, Seoul National University, Seoul 08826, South Korea

⁴Department of Molecular Bioscience, Kangwon National University, Chuncheon 24341, South Korea

A plant growth type is one of the major important key to use for economical effect including high yield product in agriculture and industry. We tried to find differently expressed genes to classify and understand the regulation of genes related to plant growth in a mutant, dwarf soybean which are happened in F5 derived from crossing of *G. max* var. Peking and *G. soja* var. IT182936. The transcriptome sequencing are generated by Illumina high throughput sequencing platform in each 3 samples normal and dwarf lines, respectively. We found highly significantly up-/down-regulated genes in the comparing of gene expression in normal and dwarf soybeans. There are classified that the genes related to disease and stress responsive showed with the up-regulation in dwarf soybean. Such over-expression of disease resistance and other immune responsive genes could be targeted to understand the gene regulation how the immune genes regulate the response of plant growth. Otherwise, photosynthesis related genes are very low expression in dwarf lines. In plants, sucrose interacts with hormone signals, not only regulates many plant processes, but also affects gene expression of photosynthetic components. Lower concentrations of sucrose reduce the overall metabolism and adversely affect plant growth. In addition, expression of genes related to transport such as SAUR, which is responsible for auxin transport, sucrose-proton symporter, cation transporter were also low. The transcriptome expression and genes classified related plant growth could be useful resource to researchers studying plant growth.

*Corresponding Author: Tel. 033-250-7768, E-mail: choii@kangwon.ac.kr

곰취(*Ligularia fischeri*) 유전분석을 위한 microsatellite 마커 개발 및 평가

안혜림^{1,2}, 김영미¹, 조아르나^{1,2}, 권용락¹, 서용원², 정지희^{1*}

¹충북 충주시 수안보면 수회리로 72 국립산림품종관리센터

²서울특별시 성북구 안암로 145 고려대학교 생명공학부

곰취(*Ligularia fischeri*)는 국화과의 다년초로 최근 들어 산채 작물로 각광받으면서 재배 면적이 확대되어 주요 산촌 소득 종으로 자리 잡고 있다. 본 연구에서는 곰취에 대한 유전 육종 연구에 활용 할 수 있는 microsatellite 표지를 개발하고 적용 가능성을 평가 하였다. 강릉과 태백 두 지역에서 채집한 곰취 2개 샘플로부터 DNA를 추출하고 일루미나 HiSeq2500 플랫폼을 이용하여 250-bp PE sequencing 수행하였다. Genome-wide *in silico* 분석을 통해 두 샘플 간 8bp 이상 차이를 보이는 unique polymorphic microsatellite loci를 탐색하여 총 72개의 프라이머쌍을 디자인하였다. 강원도 강릉 4개, 태백 3개 집단에서 수집한 곰취 66개 샘플을 이용하여 증폭여부 및 변이 특성을 검증하여 최종적으로 다형성을 보이고 유전자형 식별이 뚜렷한 7개 primer를 선발하였다. Primer 별로 관찰된 대립유전자 수는 3-27개, 총 154개가 확인되었고, 이형접합도 관찰치 및 기대치 평균은 각각 0.624(0.480-0.768), 0.680(0.455-0.772)였다. Bayesian cluster 분석 결과 곰취 집단 간에 비교적 뚜렷한 차이가 확인되어 개발된 마커는 앞으로 곰취의 집단 유전학적 연구 및 분류학적 연구에도 유용하게 활용될 수 있을 것으로 기대된다.

*교신저자: Tel. 043-850-3383, E-mail: florajh@korea.kr

Assessment of parental genome in Asiatic x *L. longiflorum* Hybrids through genomic *in situ* hybridization analysis

Fahad Ramzan¹, Hyoung Tae Kim¹, Adnan Younis^{1,2}, Young Kwan Jo¹, Choi Yu Hyeon¹, Ki-Byung Lim^{1*}

¹Dept. of Horticulture, Kyungpook National University, Daegu 41566, Korea

²Institute of Horticultural Sciences, University of Agriculture, Faisalabad, 38040, Pakistan

In *Lilium*, development of interspecific hybrids imparts the significant traits (colors, resistance to diseases etc.) of the two sections in consequential hybrids. Verification of interspecific hybrids based on the presence of hybrid characteristics or not. In this regard, cytogenetic techniques, genomic *in situ* hybridization (GISH) has proved to be most precise and applicable approach for genome evaluations of resulting progenies. Chromosome analysis and genomic constitution identification are main objectives in GISH analysis. GISH technique discriminate the maternal as well as paternal genome in interspecific hybrids. In this study, F1 interspecific crosses were made by using Asiatic hybrids as maternal while *L. longiflorum* cultivars as paternal parent. According to GISH results, interspecific crosses (AL), one progeny of ID number 122665 showed equal genomic distribution of both parents i.e. 12 chromosomes of *L. longiflorum* & 12 chromosomes of Asiatic genome with two A/L genomic recombinations. Progeny (12268) showed 10 Asiatic chromosomes and 14 *L. longiflorum* chromosomes. Paternal parent genome influence were increased in the resulting progeny, verified the successful interspecific hybridization between two genomic sections. Consequently, GISH analysis confirmed the genomic presence of parents and discriminated the parental genomes in AL hybrids.

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*Corresponding Author: E-mail: kblim@knu.ac.kr

OsPhyB-mediating novel regulatory pathway for drought tolerance in rice root identified by a global RNA-Seq transcriptome analysis of rice genes in response to water deficiencies

Yo-Han Yoo¹, Anil Kumar N.C¹, Jong-Chan Park¹, Yun-Shil Gho¹, Sang-Won Lee¹, Gynheung An¹ and Ki-Hong Jung^{1*}

¹Graduate School of Biotechnology & Crop Biotech Institute, Kyung Hee University, Yongin 446-701, Republic of Korea

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 RING box E3 ligases in the ubiquitin-proteasome pathways are significantly stimulated by induced drought. We also analyzed the functions of 66 candidate genes that have been functionally investigated previously, suggesting the primary roles of our candidate genes in resistance or tolerance relating traits including drought tolerance through literature searches besides diverse regulatory roles of our candidate genes for morphological traits or physiological traits. Of these, we used a T-DNA insertional mutant of rice *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.

*Corresponding Author: Tel. 031-201-3474, E-mail: khjung2010@khu.ac.kr

Callus induction and plant regeneration from immature zygotic embryos of various maize genotypes (*Zea mays* L.)

Joon Ki Hong¹, Ki Jin Park², Gang-Seob Lee¹, Dool Yi Kim³, Ju-Kon Kim⁴, Seung Bum Lee¹, Eun Jung Suh¹, Kyung-Hwan Kim¹, Yeon-Hee Lee^{1*}

¹Agricultural Biotechnology Department, National Institute of Agricultural Sciences, Rural Development Administration, 370 Nongsaengmyeong-ro, Jeonju-si, Jeollabuk-do, 54874, Korea

²Maize Experiment Station, Gangwondo Agricultural Research and Extension Services, Hongcheon, 25160, Korea

³Crop Foundation Research division, National Institute of Crop Science, Rural Development Administration, 181 Hyeoksin-ro, Iseo-myeon, Wanju-Gun, Jeollabuk-do, Korea

⁴Graduate School of International Agricultural Technology and Crop Biotechnology Institute/GreenBio Science & Technology, Seoul National University, Pyeongchang 25354, Korea

Callus induction and plant regeneration ability of 16 maize genotypes including Korean inbred lines were investigated using 9 to 15 day-old immature zygotic embryos from maize grown in the pots and field culture. Immature zygotic embryos placed on MS medium supplemented with L-proline 0.7 g/L, MES 0.5 g/L, Dicamba 1.5 mg/L, 2,4-D 0.5 mg/L, AgNO₃ 4 mg/L, and Sucrose 20 g/L showed the highest frequency of callus induction. The highest number of shoots was regenerated upon transferring the embryogenic callus to MS medium supplemented with 5 mg/L zeatin. The root formation was observed when shoots were grown on MS medium supplemented with 0.2 mg/L indole-3-Butyric acid (IBA). Additionally, immature zygotic embryos from maize grown in the field produced high frequency of plant regeneration, under the same culture conditions above. Fifteen genotypes except one line showed callus induction and shoot regeneration. Among sixteen genotypes tested, H99, B98, HW3, and B73 gave the best plant regeneration. H99 showed the highest number of shoot formation from the primary embryogenic callus. The results suggest that genotypes and growth conditions of maize plants play a very important role for enhancing the embryogenesis competence of immature zygotic embryos. The successful regeneration from immature zygotic embryos of maize inbred lines provides a basis for molecular breeding of new cultivars by genetic transformation.

*Corresponding Author: Tel. 063-238-4690, E-mail: yhl2222@korea.kr

Identifying cold stress related genes of rice (*Oryza sativa* L.) at early young microspore stage using Genome-wide association study

Mijeong Kim¹, Taegyu Kim¹, Yoonjung Lee¹, Jisu Choi¹, Giwon Cho¹, Joohyun Lee^{1*}

¹Department of crop science, Konkuk University, Seoul 05029. KOREA

As rice is the model crop, many studies of abiotic stress is using rice. Cold stress, especially at fertility stage, is the affected to rice yield. In order to identify cold stress-related genes at early young microspore stage, genome-wide association study (GWAS) was conducted. Cultivated 110 rice germplasm were moved in the growth chamber under the condition of 12°C/RH70%(12h day/12h night when the rice plant was grown in 10 DBH(days before heading). Also, rice plant as control was moved in the green house under condition of 28°C/RH70%(12h day/12h night). After 4 days the plants were moved in a greenhouse. The fertility of rice plant were monitored after the grain were fully grown. The most tolerant rice germplasm to cold stress were Cheongdo-Hwayang-12 and IR38 as 63.1 and 61.8 of fertility and the most recessive rice germplasm were Cheongsongangmi as 0.45. As a result of GWAS with re-sequencing data and fertility after cold treatment germplasm using genome association and prediction integrated tool (GAPIT), the 18 candidate gene is on chromosome 6, 11 and 12.

*Corresponding Author: Tel. 02-450-0480, E-mail: joohyun00@gmail.com

Transcriptome profiling of fruit maturity genes in sweet persimmon (*Diospyros kaki* Thunb.)

Eun-Gyeong Kim^{1,3}, Ji-Young Son³, Yeo-Ok, Park³, Young-Han Lee³, Doo-Sang Park³, Youngmi Choi¹, Joonyup Kim², Younghoon Park^{1,2*}

¹Department of Horticultural Bioscience, Pusan National University, Miryang 627-706, Korea

²Life and Industry Convergence Research Institute, Pusan National University, Miryang 627-706, Korea

³Sweet Persimmon Research Institute, Gyeongsangnam-do Agricultural Research and Extension Services, Gimhae 50871, Korea

Flavonoids play crucial roles in biotic and abiotic stress responses that are tightly associated with quality of fruit crops. Proanthocyanidins (PAs), a class of plant flavonoids, are colorless phenolic oligomers or polymers synthesized from the anthocyanin branch of the flavonoid pathway. Persimmon (*Diospyros kaki* Thunb.; 2n=6x=90) fruits accumulate large amounts of PAs during fruit development, which often comprise more than 1% fresh weight at maturity that causes strong astringent sensation in the mouth. Although many approaches have been useful to remove the astringency, molecular understanding that underlie the process remains unclear. Here, we examined the transcriptomes of two commercially grown late (Fuyu) and early (Soshu) maturity cultivars to understand the differences that occur during the maturation of persimmon fruit. *De novo* transcriptome assembly and subsequent analysis were performed for four major stages (i.e., 9 WAB (week after blooming), 12 WAB, 15 WAB and 18 WAB) selected based on physiological changes examined in each cultivar. Average rates of read mapping for eight representative stages of all fruit maturity were 84.59%.

Overall, the results of transcriptome data well reflected the phenological and physiological changes such as free sugar content, physical characteristics of fruits, tannin contents unique to each cultivar. Clustering the differentially up- or down-regulated genes more than two-fold over maturation time in each cultivar (e.g., 9 WAB of Fuyu vs 12 WAB of Fuyu) or at maturation time between the cultivars (e.g., 9 WAB of Fuyu vs 9 WAB of Soshu) further revealed distinct expression profiles responsible for the fruit maturity.

*Corresponding Author: Tel. 055-350-5525, E-mail: ypark@pusan.ac.kr

Proteome analysis of leaves and roots of sorghum under copper stress

Swapan Kumar Roy¹, Seong-Woo Cho², Soo Jeong Kwon¹, Kabita Sarker¹, Zhanguo Xin³ and Sun-Hee Woo^{1*}

¹Department of Crop Science, Chungbuk National University, Cheong-ju, Korea

²Department of Crop Science and Biotechnology, Chonbuk National University, Jeon-ju, Korea

³Plant Stress and Germplasm Development Unit, USDA-ARS, 3810 4th Street, Lubbock, TX, USA

Copper (Cu) is an important micronutrient for plants growth and development. But it is extremely toxic to plants at high concentration and can inactivate and disturb protein structures. To investigate the molecular alterations that occur in response to copper stress, the present study was performed in ten-day-old Cu-exposed leaves and roots of sorghum seedlings. The growth characteristics were markedly inhibited, and ionic alterations were prominently observed both in the leaves and roots when the seedlings were exposed to different concentrations (0, 100, and 150 μ M) of CuSO₄. Using two-dimensional gels with silver staining, a total of 24 prote in spots (≥ 1.5 -fold) from Cu-exposed sorghum leaves were successfully analyzed by MALDI-TOF-TOF mass spectrometry. Of the 24 differentially expressed proteins from Cu-exposed sorghum leaves, 13 proteins were up-regulated, and 11 proteins were down-regulated. In the Cu root proteome, twenty-one (21) protein spots were found to be expressed differentially upon Cu stress, with more than 1.5-fold differences in abundances between the control and Cu-treated samples. Compared with the control seedlings, a total of 10 proteins were increased significantly while 11 proteins were decreased abundances. These findings suggest that the differentially expressed proteins involved in resistance to stress helped Sorghum bicolor to tolerate high levels of Cu. However, reductions in the abundance the translation and synthesis, photosynthesis and energy metabolism related proteins were observed in response to Cu stress. The results of the present study suggest that photosynthesis and energy metabolism was inhibited under oxidative stress caused by elevated Cu stress. The betaine-aldehyde dehydrogenase identified in this investigation displayed dynamic changes in abundance upon Cu stress, and these proteins are associated with carbohydrate metabolism. The enhancement of the antioxidant defense by this BADH enzyme seems to be one of the strategies to reduce the effect of oxidative damage caused by Cu stress. The resulting differences in protein expression patterns together with related morpho-physiological processes suggested that these results could help to elucidate plant adaptation to Cu stress and provide insights into the molecular mechanisms of Cu responses in C₄plants.

*Corresponding Author: Tel. +82-43-261-2515, E-mail: shwoo@chungbuk.ac.kr

Overexpression of *ICE1*, a regulator of cold acclimation, enhances cold tolerance in transgenic *Arabidopsis thaliana*

Zhi-Fang Zuo¹, Hana Jeong¹, Hyeon-Jin Sun², Mi-Young Park², Dae-Hwa Yang², Chang-Ho Eun², Hong-Gyu Kang^{2*}, Hyo-Yeon Lee^{1,2}

¹Department of Biotechnology, Jeju National University, Jeju 690-756, Korea, 2. Subtropical Horticulture Research Institute, Jeju National University, Jeju 690-756, Korea

Plenty of genes are known in regulating the cold response in plants. *Arabidopsis thaliana* *ICE1* (Inducer of *CBF* Expression1), a bHLH (basic-helix-basic) type transcription factor which binding to the MYC recognition cis-elements in the promoter of *CBF3/DREB* to regulate the transcription of *CBF*(Inducer of *CBF* Expression CRT/DRE Binding Factor) genes during cold stress. Although we know overexpression of *ICE1* increased the cold tolerance in *Arabidopsis thaliana*, the cold resistance mechanism has not been reported in detail. Here, the 1485 bp *ICE1* was cloned from *A. thaliana* and constructed into the binary vector pCAMBIA3301-*Pubi::ICE1*. After plant transformed by the floral dip transformation method, the transcription level in T₁ generation and segregation of T₂ transgenic plants analysis of 7 PPT resistance lines suggested that *ICE1* had been successfully integrated into T₂-3 and T₂-5transgenic *Arabidopsis* genome with single copy. The overexpression of *ICE1* in T₃-3 and T₃-5 showed big leaves, higher proline content, less MDA content, higher activities of superoxide dismutase (SOD), peroxidase (POD) at low temperatures. This is the detailed reason of overexpression of *ICE1* can increase the cold tolerance of transgenic *Arabidopsis* during chilling and freezing.

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*Corresponding Author: E-mail: honggyu@jejunu.ac.kr

Differential proteomic analysis of cadmium-responsive proteins in leaves and roots

Swapan Kumar Roy¹, Seong-Woo Cho², Soo Jeong Kwon¹, Kabita Sarker¹, Zhanguo Xin³ and Sun-Hee Woo^{1*}

¹Department of Crop Science, Chungbuk National University, Cheong-ju, Korea

²Department of Crop Science and Biotechnology, Chonbuk National University, Jeon-ju, Korea

³Plant Stress and Germplasm Development Unit, USDA-ARS, 3810 4th Street, Lubbock, TX, USA

Cadmium (Cd) stress may cause serious morphological and physiological abnormalities in addition to altering the proteome in plants. The present study was performed to explore Cd-induced morpho-physiological alterations and their potentiality associated mechanisms in Sorghum bicolor leaves and roots at the protein level. The most significant growth inhibition was observed in plants treated with a combination of the highest concentrations of Cd²⁺ ions (150 μ M). The accumulated level of Cd was significantly increased in plants exposed to the high concentration of Cd (150 μ M) compared to the untreated plants. The concentrations of Zn²⁺ and Ca²⁺ ions were decreased, whereas the Fe²⁺ ion concentration was increased when seedling leaves were exposed to Cd²⁺. Under Cd stress, quantitative image analysis revealed a total of 33 protein spots that exhibited more than a 1.5-fold changes in intensity and the 33 differentially expressed proteins were successfully analyzed using MALDI-TOF/TOF MS analysis. Among these proteins, a total of 15 proteins showed increased expression, and 18 proteins showed decreased expression in the treated samples compared to their levels in untreated seedlings. On the other hand, a total of 86 differentially changed proteins were identified at 15-day-old sorghum roots between Cd stress and control conditions ($p < 0.05$) whereas 39 increased and 45 decreased based on 3 biological replicated MaxQuant computational platform. The protein abundance involved in glycolysis and tricarboxylic acid cycle, including glyceraldehyde 3-phosphate dehydrogenase was changed in sorghum roots after Cd treatment. Cd toxicity may significantly alter the glycolytic pathway and the Cd-induced disorganization of the photosynthetic apparatus, and these effects may have a major impact on the plant's ability to withstand this type of stress. The up-regulation of GADPH protein may play an active role in supplying energy to Cd-treated plants via the glycolytic pathway. Cd has a strongly negative impact on proteins related to carbohydrate metabolism and that could limit ATP production, limit primary carbon metabolism, hamper photosynthetic machineries and inhibit plant growth and development. The observed down-regulation of this protein indicates that carbon fixation is inhibited in Cd-exposed plants, and these results suggest that photosynthesis machineries are also susceptible to Cd stress. On the other hand, the increased abundance of stress-related proteins (GSTs and CYPs) was strongly induced by Cd exposure that observed in the present study that involved in antioxidant defense and detoxification systems.

*Corresponding Author: Tel. +82-43-261-2515, E-mail: shwoo@chungbuk.ac.kr

제초제저항성 교배종 잔디(JG21-MJ) 계통의 후대 안정성 평가를 위한 분자생물학적 특성 검정

정하나², 좌지방², 선현진¹, 양대화¹, 강홍규^{1*}, 이효연^{1,2}

¹제주특별자치도 제주시 아라2동 제주대학교 아열대원예산업연구소

²제주특별자치도 제주시 아라2동 제주대학교 생명공학부

유전자변형 작물의 상업화를 위해서는 유전자변형 작물의 안전성과 환경에 미치는 영향에 관한 평가가 이루어져야한다. 본 연구는 제초제저항성 유전자변형 들잔디 JG21와 금잔디(*Z. meliloti*) 1)의 중간 인공수분을 통해 육성된 제초제저항성 교배종 잔디 계통(JG21-MJ)의 분자생물학적인 분석을 통해 유전자변형 작물의 환경 위해성 평가를 수행하였다. 제초제저항성 교배종 잔디들에 대한 후대 안정성을 분석하기 위하여 도입유전자에 대한 복수세대의 genomic Southern blot분석과 T-DNA의 게놈 내의 인접서열을 분석하였고, 도입유전자의 복수세대 별 발현을 확인하였다. T-DNA의 게놈내 삽입 인접서열을 바탕으로 제초제저항성 들잔디 이벤트(JG21)와 교배종 잔디(JG21-MJ)를 동정할 수 있는 프라이머를 제작하였고, 이를 이용한 검정방법을 수립하였다. 본 연구 결과로 환경위해성 평가를 위한 제초제저항성 교배종 잔디의 분자생물학적인 자료를 획득하였으며, 계통 특이 프라이머를 제초제저항성 유전자변형 들잔디 이벤트 JG21과 교배종 잔디 계통의 검출을 위하여 유용하게 사용할 수 있음을 확인하였다. 제초제 저항성 교배 잔디의 복수세대에 대한 후대안정성을 Southern blot과 T-DNA의 게놈 내의 인접서열을 분석한 결과, 제초제 저항성 교배종 잔디의 F1~F2세대에서는 도입된 모든 유전자들이 안정적으로 도입되어 있으며, backbone DNA는 제초제 저항성 들잔디 이벤트 JG21과 교배종 잔디 계통(JG21-MJ)에 삽입되지 않았음을 확인하였고, qRT-PCR을 통해 복수세대에서 제초제 저항성 교배종 잔디에서 목적 유전자들이 안정적으로 발현되고 있음을 확인하였다.

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*교신저자: Tel. 064-754-3985, E-mail: honggyu@jejunu.ac.kr

비린내 없는 소립 검정콩 “강원 152호” 육성

하건수^{1*}, 송윤호¹, 조윤상¹, 이지우¹

¹강원도 춘천시 충열로 강원도농업기술원 작물연구과

소립검정콩은 정선 등 여러 지역에서 쥐눈이콩으로 불리며 대립콩에 비하여 특수하게 이용되고 있다. 따라서 최근 소비자들이 선호하는 소립검정콩에서 비린내를 제거하고자 하였으며, 육성 모본으로는 비린내 유발 효소가 제거된 진품콩 2호와 소립검정콩인 다원콩을 이용하였다. 비린내유발 효소의 결핍 여부를 검정하기 위하여 효소검정방법과 전기영동법을 이용하였고, 또한 지방종 소립검정콩인 쥐눈이콩의 도복, 바이러스병해 등 내재해성을 보완하기 위하여 내도복성, 내병충성, 성숙기 및 수량성을 육성 지표로 하였다. 특히 전통적인 이용목적인 약용콩으로서 생리활성성분 함유 정도를 육성 지표로 하였다. 1999년 인공교배하여 2000년 F₁을 양성하였으며, 2001-2004년도에 F₂ - F₄ 세대를 경과하였다. F₅ 세대를 경과하며 GSL99104-2B-25-10-9-3 계통을 선발하였으며, 2005-2006년도에 실시한 생산력검정시험에서 생육특성이 우수하고 소립 다수성이며 내재해성 계통으로 비린내 유발 효소가 결핍된 ‘강원152호’를 육성하였다. ‘강원152호’는 안토시아닌 함량이 16,975μg/종피g 이고 이소플라본 함량이 2,437μg/g 으로 생리활성성분 함량이 많은 기능성 소립검정콩 계통이다.

*주저자: Tel. 033-248-6051, E-mail: redclover@korea.kr

Comparison of transcriptomic changes in *Miscanthus sinensis* under salt stress

Minjung Yook, Soo-Hyun Lim, Hyejin Yu, Do-Soon Kim*

Department of Plant Science, Seoul National University, Seoul 08826, Republic of Korea

Abiotic stress tolerance is the essential trait for second-generation bioenergy crops which compete with food/feed crops for farmlands. *Miscanthus* is generally known for its high abiotic stress tolerance, but has not been much studied. To cultivate *Miscanthus* in a marginal land including salt-stressed area, we need to understand the response mechanism to salt stress and how salt tolerance can be improved. Therefore, in this study, we performed transcriptome analysis between two *M. sinensis* accessions with contrasting salt tolerance, M119 (sensitive) and M131 (tolerant). The highest and second highest ligule leaves of M119 and M131 were harvested at 0, 24, and 48 hours after salt treatment for RNA sequencing. During the time-course, a total of 363 DEGs were obtained from the pair-wise comparison of the six cDNA libraries. For salt-sensitive accession, 143 genes were up-regulated during the first 24 hours after salt treatment, and keep the state of regulation in the subsequent 24 hours. For salt-tolerant accession, 178 genes were sharply up-regulated during the first 24 hours and turned to the normal state in the subsequent 24 hours. Particularly, 67 DEGs (48 annotated) were exclusively up-regulated in salt-tolerant accession and most of them were associated with signal transduction pathway to abiotic stresses in plants including transcription factors and receptor-like kinases. Thus, our results suggest that gene expression regulations of the upstream genes in the salt-tolerance cascades brought about diverse adaptability for salt stress in *M. sinensis*. The result of this study could be utilized for studying and improving salt stress tolerance in *Miscanthus*.

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*Corresponding Author: Tel. 02-880-4552, E-mail: dosoonkim@snu.ac.kr

Genetic diversity and relationship analysis of *Angelica gigas* using genetic SSR markers

Yurry Um¹, Dae Hui Chung¹, Gwang Hun Park¹, Jinsu Gil², Yi Lee², Chungryul Jung¹, Kwon Seok Jeon¹, ManJo Kim¹, Yunmi Park^{1*}

¹Forest Medicinal Resources Research Center, National Institute of Forest Science, Yeongju 36040, Republic of Korea

²Department of Industrial Plant Science & Technology, Chungbuk National University, Chungju 28644, Republic of Korea

Angelica gigas Nakai has been an important herbal medicine for women in Eastern Asia for a long time. However, the plant lack efficient information for genetics. In this study, we developed genomic simple sequence repeat (SSR) markers from the Illumina sequence reads of five *A. gigas* accessions using next generation sequencing (NGS) technology for molecular breeding base construction of *A. gigas*. We discovered 138,113 SSRs, motif types of di- to deca-nucleotides, from the 356,018,143 bp repeat regions of the genome of *A. gigas*. A total of 16,496 primer sets were successfully designed from the 138,113 SSR regions. From these candidates, we selected 848 SSR markers that show *in silico* polymorphism and we tested 23 tri-nucleotide motif type SSR primer sets for polymorphism using 30 *A. gigas* accessions. Twenty-one SSR markers showed high PIC value (PIC > 0.6) and we analyzed the genetic relationship of the 30 *A. gigas* accessions based on the 23 polymorphic SSR markers and constructed phylogenetic trees. These newly developed *A. gigas* SSR markers would be useful tools for molecular genetics, genotype identification, genetic mapping, molecular breeding, and species relationships study within the *Angelica* genus.

*Corresponding Author: Tel. 054-630-5645, E-mail: pym5250@korea.kr

The bicistronic expression of two non-mammalian Viral 2A sequences in plants using golden rice phenotype

Ye Sol Jeong^{1,2}, Young Joo Jung¹, Hyung-Keun Ku^{1,3}, Jae Kwang Kim⁴, Kyoung Bok Lee⁴, Mi Ran Ko^{1,3}, Min Kyoung You^{1,3}, Sun-Hyung Lim⁵, Ju-Kon Kim⁶, Dong ho Lee², Sun-Hwa Ha^{1,3*}

¹Crop Biotech Institute, Kyung Hee University, Yongin 17104, Korea

²Department of Biosystems and Biotechnology, Korea University, Seoul 02841, Korea

³Department of Genetic Engineering and Graduate School of Biotechnology, College of Life Sciences, Kyung Hee University, Yongin 17104, Korea

⁴Division of Life Sciences and Bio-Resource and Environmental Center, Incheon National University, Incheon 22012, Korea

⁵National Academy of Agricultural Science, Rural Development Administration, Jeonju 54874, Korea

⁶Graduate School of International Agricultural Technology and Crop Biotechnology Institute/GreenBio Science and Technology, Seoul National University, Pyeongchang 25354, Korea

The β -carotene biofortified rice showing golden color phenotype has been developed via bicistronic expression using a 2A sequence from foot and mouth disease virus (FMDV) that was known for a mammalian pathogenic virus. As a substitute for this FMDV-2A (F2A, 20 aa), 2A peptides of non-mammalian virus-origins, T2A (20 aa) from *Thosea asigna* virus and I2A2 (30 aa) from *Infectious myonecrosis* virus, were chosen considering of the reported cleavage efficiency. Their synthetic DNA sequences using rice codon usage were *in-frame* embedded between two synthetic genes for β -carotene production to generate two recombinant genes, *stPTAC* (*stPsy-T2A-stCrtI*) and *stPIAC* (*stPsy-I2A2-stCrtI*), respectively. Both transgenic rice plants displayed golden color in seed endosperms. Three independent lines being verified the single copy-insertion of T-DNA were selected for transgene analysis, respectively. Total amounts of carotenoids in *stPTAC* were an average of 1.66 μ g/g, which were 2.1-fold higher value than *stPIAC* seeds (0.81 μ g/g). Gene expression patterns of *stPsy* and *stCrtI* were similarly showed the highest level among *stPTAC* and the lowest level among *stPIAC* lines. Immunoblot analysis showed higher expression of proteins in *stPTAC* than *stPIAC* lines. None of large recombinant proteins was detected as a linked form of *stPSY* and *stCRTI* by T2A or I2A2 unlike F2A, demonstrating both T2A and I2A2 peptides are good system to simultaneously express two genes with better efficiency than a F2A peptide in plant system. In addition, highly elevated zeaxanthin level in *stPTAC* line 1 were identified by the integration of T-DNA into 1st intron region of zeaxanthin epoxidase (*ZEP*). As a result, *Zep* expression and conversion of zeaxanthin into antheraxanthin were entirely shut down.

*Corresponding Author: Tel. 031-201-2654, E-mail: sunhwa@khu.ac.kr

Growth characteristics and amino acids composition of quality protein maize lines

Hwan-Hee Bae*, Beom-Young Son, Jung-Tae Kim, Jin-Seok Lee, Sang Gon Kim, Seong-Bum Back

Department of Central Area Crop Science, NICS, RDA, Suwon, 16429, Republic of Korea

To date, many researches have been done for Quality protein maize (QPM). But there is few maize QPM varieties in Korea. In this reason, to develop maize QPM cultivars, investigation of the growth characteristics and amino acid composition among QPM lines was carried out. The range of siliking days was range from 60 to 69 days. In plant height, CML492 was shortest (152 cm) and CML143 was the tallest (295 cm). The ear height of CML492 was 66 cm and that of CML143 was 175 cm. Protein contents of maize QPM grains were from 9.07% to 12.67%. CML556 was the highest and CML493 was the lowest among maize QPM grains. The contents of fat were from 3.38% to 5.25%. The lowest and highest were CML141 and CML147, respectively. The contents of ash ranged from 1.22% to 1.78%. CML555 was the lowest and CML142 was the highest. carbohydrate contents were from 71.7% to 75.5%. CML557 was lowest and CML493 was the highest. The calories of each line ranged from 346 to 365 Kcal, CML140 was the lowest and CML492 was the highest. The composition of major amino acid in maize QPM grain is glutamic acid (16.34%), and proline (9.80%). The mean of lysine composition was 3.64%, and CML140 showed the highest 4.34%. It is anticipated that domestic adaptive QPM varieties will be developed through back-crossing with domestic maize lines, because CML 140, 141 and 493 contain more than 4% lysine.

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*Corresponding Author: Tel. 031-695-4042, E-mail: miami9@korea.kr

현사시나무 *GASA* 유전자 분리와 발현 특성 구명

최현모, 배은경, 이효신, 최영임*

경기도 수원시 권선구 국립산림과학원 산림유전자원부 산림생명공학과

GASA (*Gibberelic Acid Stimulated transcript in Arabidopsis*)는 식물 호르몬인 지베렐린에 의해 조절되는 식물 유전자로서 식물의 발달 및 생장, 그리고 다양한 스트레스 반응에 관여하는 것으로 알려져 있다. 토마토를 비롯하여 애기장대와 포도, 포플러에 이르기까지 다양한 식물 종에 보존되어 있고 여러 식물에서 유전자의 특성 구명 연구가 이루어지고 있다. 그러나 아직까지 임목에서는 *GASA*에 관한 연구가 거의 이루어지지 않은 실정이다. 본 연구에서는 *GASA* 유전자를 현사시나무(*Populus alba* × *P. glandulosa*)에서 분리하여 이를 *PagGASA*라 명명하였고 유전자의 구조와 발현 특성을 조사하였다. *PagGASA* 단백질은 95개의 아미노산으로 구성되었으며 N-말단에 signal peptide 영역과 C-말단에 12개 시스테인 반복 서열이 보존되어 있다. 유전자 발현 분석 결과, *PagGASA*는 꽃과 뿌리에서 높게 발현하였고, 지베렐린 뿐 아니라 앱시스산, 자스몬산, 살리실산과 같은 스트레스 관련 식물 호르몬에 의하여 발현이 증가하는 것이 확인되었다. 또한 *PagGASA* 유전자 발현을 증가시키는 형질전환 현사시나무를 제작하여 단수 조건에서의 일별 광화합효율을 측정한 결과 형질전환 현사시나무가 건조 내성에 효과가 있음을 확인하였다. 따라서 *PagGASA*는 스트레스 반응성 호르몬들에 의한 신호전달계에 매개되어 내건성 기작에서 역할을 할 것으로 보이며, 기후변화 대응 임목 개발을 위한 분자육종의 주요 대상 유전자로서 가치를 보여줄 것으로 기대된다.

*주저자: Tel. 031-290-1173, E-mail: yichoi99@korea.kr

A simple, rapid and systematic method for the developed GM rice analysis

So-Young Kim, Min Kang, Hye-min Lim, Jung-Il Cho, Hyeon-so Ji, Kang-Hyun Lee, Soo-Chul Park, Gang-Seob Lee*

National Institute of Agricultural Science, Rural Development Administration, Wanju-gun, Jeollabuk-do 55365, Republic of Korea

We have generated 383 independent transgenic lines that contained the 149 *PsGPD* (*Glyceraldehyde-3-Phosphate Dehydrogenase*), 118 *ArCspA* (*Cold Shock Protein*), 44 *BrTSR15* (*Triple Stress Resistance 15*) and *BrTSR53* (*Triple Stress Resistance 53*) genes under the control of a constitutive (*CaMV 35S*) promoter to generate genetically modified (GM) rice. TaqMan copy number assay was determined inserted T-DNA copy number. Also FSTs analysis was isolated from 203 single copy T-DNA lines of transgenic plants and sequence mapped to the rice chromosomes. In analyzing single copy lines, we identified 95 FSTs, among which 37 (38.9%) were integrated into genic regions and 58 (61.1%) into intergenic regions. About 27 homozygous lines were obtained through multi-generations of planting, resistance screening and TaqMan copy number assay. To investigate the transgenes expression patterns, the mRNA transcripts of homozygous lines were examined by quantitative real-time PCR analysis from leaf tissue. The transcript levels were significantly increased in all of the transgenic plants compared with wild-type. In several lines of myc-tagged *BrTSR15* and *BrTSR53* transgenic plants, the BrTSR15 and BrTSR53 proteins were highly expressed in mature leaves. These results may be useful for the large-scale production of transgenic plants or T-DNA inserted rice mutants.

*Corresponding Author: Tel. 063-238-4791, E-mail: kangslee@korea.kr

Establishment of hairy root cultures by *Agrobacterium rhizogenes*-mediated transformation of ginseng (*Panax ginseng*) for ginsenoside production

Min Jung Kim¹, Van Binh Nguyen¹, Vo Ngoc Linh Giang¹, Yun Sun Lee¹, Tae-Jin Yang^{1*}

¹Department of Plant Science, Plant Genomics and Breeding Institute, and Research Institute of Agriculture and Life Sciences, College of Agriculture and Life Sciences, Seoul National University, Seoul, Korea

Ginseng (*Panax ginseng*) is one of the most promising medicinal plant due to its pharmacologically valuable ginsenosides for human health. Cultivation of ginseng takes about 4-7 years with extensive efforts to control quality from biotic and abiotic factors. To overcome this difficulty, an in vitro tissue culture system has been developed to produce biomass of adventitious root. However, this method normally goes with plant hormone application which is toxic or not good for human health. In order to overcome this limitation, we developed an efficient system for ginsenoside production through hairy root biomass mediated by *Agrobacterium rhizogenes* transformation. Callus tissues of five *P. ginseng* cultivars and an F₁ hybrid species (*P. quinquefolius* x *P. ginseng*) have been investigated for transformation efficiency. Genomic PCR analysis of hairy roots confirmed that *rolB* and *rolC* were introduced in six transformed hairy root lines but not in normal untransformed adventitious roots. Especially, these transformed lines grew well in SH basic salt medium without any plant hormones. Taken together, our study will contribute to mass production of ginseng roots with high ginsenosides in the future.

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*Corresponding Author: Tel. 02-880-4547, E-mail: tjyang@snu.ac.kr

A putatively stress-related gene *BrTSR53* isolated from Chinese cabbage (*Brassica rapa*) confers salt stress tolerance in Yeast

Min Kang, So-Young Kim, Hye-min Lim, Jung-Il Cho, Hyeon-so Ji, Kang-Hyun Lee, Soo-Chul Park, Gang-Seob Lee*

National Institute of Agricultural Science, Rural Development Administration, Wanju-gun, Jeollabuk-do 55365, Republic of Korea

Crops are exposed to various environmental stresses. These have been affecting the growth of crops, resulting in the severe loss of agronomic production in many countries. Therefore, development of new varieties of resistant crops is required to assure the desired productivity of crops in stress conditions. In this study, a putatively stress-related gene *BrTSR53* was isolated from *Brassica rapa*. The *BrTSR53* is 481 bp long and contains ORF region of 234 bp. This ORF showed strong sequence similarities to the uncharacterized genes from *Arabidopsis*. The expression of *BrTSR53* was determined by quantitative real-time PCR analysis. After 3 hr, the highest quantities of mRNA were revealed in cold and salt stress treatments. In drought stress treatments, there was the highest expression after 36 hr. Therefore, it was confirmed that the ORF in *BrTSR53* should be a gene that confer increased resistance to *B. rapa* growing in different stress conditions. The ORF region of *BrTSR53* gene was cloned into an expression vector, pYES-DEST52, and a new protein with molecular weight of 13 kDa was detected by western blot analysis. Also, stress tolerance tests showed that *BrTSR53*-ORF transgenic yeast exhibited increased resistance to the salt stresses compared with the control. In conclusion, the present data predicts that novel ORF in *BrTSR53* can serve as an important genetic resource for abiotic stress resistance.

*Corresponding Author: Tel. 063-238-4791, E-mail: kangslee@korea.kr

복륜, 향기나는 한국 춘란 신품종 ‘삼국향’

김동용¹, 박소연², 왕형², 권순욱²

¹전라북도 군산시 대야면 새만금생명공학센터

²경상남도 밀양시 부산대학교 식물생명과학과

춘란(*Cymbidium goeringii*)은 잎이 작고 내한성이 강하여 심비디움류 중 가장 북쪽까지 분포 되어있는 종이다. 한국, 일본, 중국의 춘란은 3~4월에 개화하며 반 음지성 식물이다.

중국 등 주요 난 소비자들은 크기가 큰 동양란을 기피하고 향기가 있는 중소형 춘란을 선호하고 있으나, 이에 부합하는 품종 연구가 미흡하고, 여전히 자연 돌연변이 개체들이 재배되고 있는 실정이다. 새만금 생명공학센터에서 개발된 ‘삼국향’ 품종은 잎에 진녹색 바탕에 설백 복륜이 강하게 발현되고, 원판 복륜화로 향기를 갖는 품종이다. 또한 잎의 길이는 18cm정도의 소형종이고, 잎 폭은 1cm 정도로 권엽성을 보인다. 신품종 ‘삼국향’은 향기와 무늬를 갖춘 특유성을 가진 품종으로서 수출용으로 경쟁력이 높을 것으로 기대된다.

주저자: Tel. 0502-504-5724, E-mail: kdy5724@naver.com

Development of chloroplast DNA markers for classification of the collected species and for ecological restoration in *Rhus chinensis* (Anacardiaceae)

Inseo Kim¹, Yun Sun Lee¹, Jee Young Park¹, Ho Jun Joh¹, Hyun Oh Lee², Sang-Choon Lee¹, Tae-Jin Yang^{1*}

¹Department of Plant Science, Plant Genomics and Breeding Institute, and Research Institute of Agriculture and Life Sciences, College of Agriculture and Life Sciences, Seoul National University, Seoul, 08826, Republic of Korea

²Phyzen Genomics Institute, Seongnam, Gyeonggi-do, 13558, Republic of Korea

Rhus chinensis is a woody plant that is distributed throughout the tropical and temperate regions. Its remedial components have enabled *R. chinensis* to be used as a medicinal herb and for ecological restorations. However, a wide distribution of *R. chinensis* produced several geographically isolated populations that led to intraspecific diversity. Although *R. chinensis* have several ecological values, few studies have been conducted at the intraspecific level to classify populations for adequate use of the plants. In this study, a chloroplast genome of Chinese *R. chinensis* was generated through *de novo* assembly method. The length of chloroplast genome was 149,094 bp, which encoded 77 protein coding genes, 30 tRNAs genes, and 4 ribosomal RNA genes. Sequence comparisons to the reported Korean *R. chinensis* revealed 104 InDels and 463 SNPs between the two chloroplast genomes. These variations were confirmed by phylogenetic analysis conducted using 8 species from the order Sapindales. Then, three molecular markers were developed that could discriminate between Chinese *R. chinensis* and Korean *R. chinensis* successfully. As a result, we presume that the markers could be a suitable tool to distinguish different collections of *R. chinensis*. Ultimately, this research could be a basic data not only for further research of *R. chinensis* related to remedial effect that could lead to proper use as medicinal herbs but also for ecological restorations of Korean *R. chinensis* species through selection and breeding of local populations in Yang-gu that is known to be well preserved nature in Korea.

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***Corresponding Author:** Tel. 02-880-4547, 02-3408-2905, E-mail: tjyang@snu.ac.kr

A nonsense mutation of *Capsanthin/capsorubin synthase* controlling orange pepper fruit

Jeong Eun Kim^{1*}, Hee Ju Yoo¹, Byung-Cheorl Kang² and Je Min Lee^{1*}

¹Department of Horticultural Science, Kyungpook National University, Daegu, Korea

²Department of Plant Science, College of Agriculture and Life Sciences, Seoul National University, Seoul, Korea

Carotenoids are plant pigments that play a major role in conferring fruit color. Carotenoids or color variations are often controlled by genetic variation of the biosynthetic genes. The color of mature pepper fruit is mainly classified as red, orange, and yellow. Orange and yellow fruit colors are determined by mutations of phytoene synthase (*Psy*) and capsanthin-capsorubin synthase (*Ccs*), respectively. Unlike the previous fruit color model, we hypothesized that genetic variation in *Ccs* controls the orange fruit color in pepper. Ripe fruit of *Capsicum annuum* 'K146465' is orange, and its carotenoid profile obtained by HPLC analysis showed a lack of the major pepper carotenoid capsanthin but an abundance of lutein, zeaxanthin, and β -carotene as compared to red pepper. cDNA cloning and sequencing analysis detected a new nonsense mutation due to T¹⁰²⁶ insertion in the cDNA of *Ccs* but no DNA variation in *Psy*. We developed a derived cleaved amplified polymorphic sequence (dCAPS) marker to distinguish the nonsense mutation on *Ccs*. Genetic analysis of the F₂ population derived from *C. annuum* 'Sweet Banana'(red fruit color) × *C. annuum* 'K146465' revealed that orange fruit color was determined by a single recessive gene. The nonsense mutation on *Ccs* distinguished by the dCAPS marker was co-segregated with orange fruit color in the F₂ population. The germplasm coupled with the dCAPS marker and carotenoid profiling will facilitate marker assisted breeding to select orange fruit color and improve lutein, zeaxanthin, and β -carotene levels in pepper.

***Corresponding Author:** Tel. 053-950-5723, E-mail: jemin@knu.ac.kr

Inferring the genetic determinants of fruit colors in tomato by carotenoid profiling

Hee Ju Yoo¹, Gyu-Myung Lee¹, Chang-Sik Oh², Inhwa Yeam³, Je Min Lee^{1*}

¹Department of Horticultural Science, Kyungpook National University, Daegu 41566, Korea

²Department of Horticultural Biotechnology, College of Life Science, Kyung Hee University, Yongin, Gyeonggi 17104, Korea

³Department of Horticulture and Breeding, Andong National University, Andong, Gyeongbuk, 36729, Korea

Carotenoids are essential for plant and animal nutrition, and are important factors in the variation of pigmentation in fruit, leaf, and flower. Tomato is a model crop for studying the biology and biotechnology of fleshy fruits, and especially for the understanding of carotenoid biosynthesis. In commercial cultivars and germplasms of tomato, visual phenotyping of the colors of ripe fruits could be done easily. However, subsequent analysis of metabolic profiling should be demanded for hypothesizing genetic factors prior to time-consuming genetic analysis. We used high performance liquid chromatography (HPLC), employing C₃₀ reverse-phase column, to efficiently resolve six carotenoids and isomers of several carotenoids in yellow, orange, and red colored ripe tomatoes. High content of lycopene was detected in red tomatoes. The orange tomatoes contained three dominant carotenoids, namely, δ -carotene, β -carotene, and prolycopene. The yellow tomatoes showed low levels of carotenoids compared to red or orange tomatoes. Based on the HPLC profiles, genes responsible for overproducing δ -carotene and prolycopene were described as *lycopene ϵ -cyclase* and *carotenoid isomerase*, respectively. Subsequent genetic analysis using DNA markers in segregating population and germplasms were conducted to confirm the hypothesis. This study establishes the usefulness of metabolic profiling for inferring the genetic determinants of fruit color.

*Corresponding Author: Tel. 053-950-5723, E-mail: jemin@knu.ac.kr

Integrative transcriptomic and functional analyses to unveil distinct genetic influences on fruit ripening between pepper and tomato

Gyu-Myung Lee^{1*}, Hee Ju Yoo¹, Inhwa Yeam³, Doil Choi², Je Min Lee^{1*}

¹Department of Horticultural Science, Kyungpook National University, Daegu 41566, Korea

²Department of Plant Sciences, Seoul National University, Seoul 08826, Korea

³Department of Horticulture and Breeding, Andong National University, Andong, Gyeongbuk, 36729, Korea

Pepper and tomato provide suitable models for comparisons of fruit ripening processes. We present distinct molecular patterns of ripening between pepper and tomato by transcriptomic analysis. Our analyses unveil potential mechanisms of non-climacteric ripening and pepper-specific pigmentation due to defect of regulators and ethylene synthesis. Functional analysis of ripening regulators by virus induced gene silencing in pepper fruits are in progress. The *Golden-like 2* transcription factor is shown to distinct expression pattern rationalizing differential ripening pattern. The gene silencing effect of the *Golden-like 2* in pepper fruit is analogous to the *uniform* mutation. The integrated analysis allows us to better understand differential genetic factors of fruit development and ripening in pepper and tomato.

*Corresponding Author: E-mail: codelkm@naver.com

내한성이 강한 호두나무 신품종 ‘레이크볼’ 및 ‘한아름’ 육성

김재희, 박영기*, 김세현

경기도 수원시 국립산림과학원 특용자원연구과

추위에 강하고 대립 다수확성 호두나무 신품종을 육성하기 위하여 본 연구를 수행하였다. 연구결과를 요약하면 1983년에 경기도 광주에서 선발한 ‘산성4호’(♀)와 미국에서 도입한 ‘레이크’(♂)를 인공교배하여 얻어진 종자를 파종하여 교잡종 차대묘를 양성하여 수확량이 많고 우량개체를 대상으로 재배안정성 검정을 실시 한 후 품질이 우수한 ‘SL4-7’클론을 ‘레이크볼’이라 명명하였다. 또한 1982년에 미국에서 도입한 ‘맥킨스터’(♀)와 내한성이 우수한 ‘상촌’(♂)을 인공교배하여 교잡종 차대묘를 양성하여 품질이 우수한 ‘MS2-15’클론을 ‘한아름’이라고 최종 명명하였다. 신품종 ‘레이크볼’과실의 종경과 횡경은 각각 45.3mm와 42.5mm, 입중과 인중비는 17.6g과 52.8%였으며, 과피두께는 1.1mm이다. ‘한아름’과실의 종경과 횡경은 각각 46.1mm와 38.8mm, 입중과 인중비는 14.6g과 59.6%, 과피두께는 1.0mm로 과실형질이 일반종 호두나무 보다 우수하였다. 이 품종들은 2016년 신품종 보호출원(레이크볼: 2016-33, 한아름 : 2016-34)을 하였다.

*교신저자: Tel. 031-290-1093, E-mail: woodpark@korea.kr

고품질 다수확 호두나무 신품종 ‘골든볼’ 육성

박영기*, 김재희, 김세현

경기도 수원시 국립산림과학원 특용자원연구과

호두나무는 호두나무과(Juglandaceae)에 속하는 낙엽교목으로 우리나라에서 연평균 12℃ 정도 범위인 지역에서 안정적인 생장을 한다. 본 연구는 고품질 다수확성 호두나무 품종을 육성하기 위해 호두나무 주산지를 대상으로 병충해가 없고 수세가 강하며, 과실 형질이 우수한 우량개체들을 선발하였다. 선발된 우량개체 후보목들은 국립산림과학원 재배시험포지에 클론보존원을 조성하였고, 개화, 결실된 클론을 대상으로 품매검정을 통한 호두나무 특성을 검정한 결과 형질이 우수한 ‘NM2’ 개체를 선발하였다. 우량개체로 선발된 ‘NM2’는 2011년부터 2013년까지 결실 및 과실특성에 대한 안정성 검정을 실시한 후 특성이 안정적으로 발현되어 ‘골든볼’로 최종 명명하였다. 신품종 ‘골든볼’과실의 종경과 횡경은 41.1mm와 40.1mm, 입중과 인중비는 각각 16.8g, 41.3%였으며, 과피두께는 1.8mm였다. 이 품종은 2014년 신품종 보호출원을 하였다.

*교신저자: Tel. 031-290-1093, E-mail: woodpark@korea.kr

Characterization of low-temperature germinability QTL, *qLTG1*

Sun Ha Kim, Kyu-Chan Shim, Hyun-Sook Lee, Anh Quynh Le, Sang-Nag Ahn*

Department of Agronomy, College of Agriculture & Life Sciences, Chungnam National University, Daejeon 34134, Korea

Seed germination is being delayed or inhibited under several kinds of stress such as temperature, salt, and osmotic pressure. In direct-seeded rice method, low-temperature germinability is considered as one of the factors for stable stand establishment at temperate regions and high altitude areas. The *qLTG1* is a major quantitative trait locus (QTL) that plays a vital role in controlling tolerance to low temperature at seed germination stage (also termed as “low-temperature germinability”). To assess the function of *qLTG1*, a population derived from the cross between *Oryza rufipogon* (Rufi) and the Korean japonica cultivar, ‘Hwaseongbyeol’ (HS) was evaluated. A BC₃F₇ line (TR5) showed better low-temperature germinability than its recurrent parent. The Rufi allele enhanced the low-temperature germination rate, which accounted for 55.4% of total phenotypic variation. The *qLTG1*, including the 12 genes, was detected and located in RM10310-CRM14 on chromosome 1 within 68.2 kb region. To identify the genes targeted by *qLTG1*, the expression profiles of the identified candidate genes and germination behavior of *qLTG1* under different stress conditions were further investigated and compared to HS, Rufi, and TR5. Increased germinability was observed in TR5 and Rufi than HS at 13 °C, 250 mM NaCl, and 500 mM mannitol conditions. These results confirmed that *qLTG1* showed tolerance for several abiotic stresses such as salt, drought and low temperature. Furthermore, transgenic rice plants will also be developed to conduct a detailed investigation on low-temperature germinability.

*Corresponding Author: E-mail: ahnsn@cnu.ac.kr

Genetic diversity, population structure, and core collection of black soybean accessions with green cotyledon using 6K SNP marker

Ji Yun Lee^{1*}, Hong Jib Choi¹, Chang Suk Huh¹, Jeong Suk Bae¹, Se Jong Kim¹ and Jeong Dong Lee²

¹Division of Crop Breeding, Gyeongsangbuk-do Provincial Agricultural Research & Extension Services, Daegu 41404, Republic of Korea

²School of Applied Biosciences, Kyungpook National University, Daegu 41566, Republic of Korea

For the efficient breeding of black soybean, a core collection is needed using genetic diversity study. In this study we evaluated 470 black soybean accessions with green cotyledon from RDA gene bank, and analyzed their genetic diversity, population structure, and core collection using the SoySNP6K Illumina Infinium BeadChip. Recently SNP markers are broadly used in plant by development of genome complexity reduction sequencing technologies. For data analysis of genetic diversity, gene diversity and polymorphism information content (PIC) were calculated using the genetic analysis package PowerMarker V3.25. Phylogenetic dendrogram was constructed with UPGMA based on genetic distance matrix using the same software. Polymorphic information content (PIC) values ranged from 0.00 to 0.38 with an average of 0.19. The gene diversity also ranged from 0.00 to 0.50 with an average of 0.22. A core collection was selected 89 accessions using PowerCore V1.0. For evaluation about coverage of selected core collection, we have analysis data including agronomic traits and functional components. A model based program STRUCTURE 2.3.4 was used to study genetic relationship among individual accessions.

*Corresponding Author: Tel. +82-53-320-0283, E-mail: dock0409@korea.kr

Development of high resolution genetic map for Onion (*Allium cepa* L.) using reference free Genotyping-by-sequencing (GBS) and SNP assays

Jinkwan Jo^{1*}, Preethi M Purushotham¹, Koeun Han¹, Heung-ryul Lee², Gyoungju Nah³, Byoung-Cheorl Kang¹

¹Department of Plant Science, Plant Genomics and Breeding Institute, and Vegetable Breeding Research Center, College of Agriculture and Life Sciences, Seoul National University, Seoul 151-921, Republic of Korea

²Biotechnology institute, Nongwoo bio co., Ltd., Yeoju-si, Gyeonggi-do, 113-141, Republic of Korea

³NICEM (National Instrumentation Center for Environmental Management, Seoul National University, Seoul 151-921, Republic of Korea

Single nucleotide polymorphisms (SNPs) play an important role as molecular markers in plant genomics and breeding studies. Although onion (*Allium cepa* L.) is an important crop globally, relatively few molecular marker resources have been reported due to its huge genome size with high heterozygosity. Genotyping-by-sequencing (GBS) offers a greater degree of complexity reduction followed by concurrent SNP discovery and genotyping for species with complex genome. In this study, GBS was employed for SNP mining in onion that currently lacks reference genome. The segregating F₂ population derived from across between 'NW-001' and 'NW-002' as well as the multiple parental lines (M1, M2 from 'NW-001' and P1, P2 from 'NW-002') were used for GBS analysis. A total of 56.15 Gbp raw sequence data were generated and 1,851,428 SNPs were identified from the *de novo* assembled contigs. Stringent filtering resulted in 10,091 high fidelity SNP markers. Robust SNPs satisfying the segregation ratio and evenly distributed in the mapping population were applied for onion genetic map construction. The final map resulted in eight linkage groups and spanned a genetic length of 1,383 centiMorgan (cM) with an average marker interval of 8.08 cM. Moreover, these robust SNPs were further analyzed using high-throughput Fluidigm technology for marker validation. This is the first study in onion that developed genome wide SNPs using GBS. The developed SNP markers and linkage map will be a valuable tool for genetic mapping of important agronomic traits and marker assisted selection in onion breeding programs.

*Corresponding Author: Tel. 02-880-4563, E-mail: bk54@snu.ac.kr

Functional analysis of rice OsXRI5 gene related to bacterial blight

Hye Seon Kim, Seok-Jun Moon, Kyong Sil Lee, Duk-Ju Hwang, Il-Pyung Ahn, Shin-Chul Bae, Myung Ok Byun, Sang Ryeol Park*

Molecular Breeding Div. National Institute of Agricultural Sciences, Rural Development Administration, Jeonju, 54875, SouthKorea

The NPR1 (nonexpresser of pathogenesis-related genes) is key regulator of salicylic acid (SA)-mediated resistance and functionally conserved in diverse plant species, including rice (*Oryza sativa* L.). The rice genome contains five NPR1-like genes. In this study, one of rice homologous gene, OsNH5 was found to be induced by rice bacterial blight pathogen *Xanthomonas oryzae* pv. *oryzae*, and the defense molecules benzothiadiazole (BTH) and salicylic acid (SA). Over-expression of OsXRI5 conferred disease resistance to bacterial blight. OsXRI-overexpressed transgenic lines were shown the higher level expression of several pathogenesis-related protein genes, OsPR4, OsPR10 and OsPAL, than wild type rice. The OsXRI5-green fluorescent protein (GFP) fusion protein was localized in the nucleus. This study provides a practical approach for the improvement of disease resistance in rice.

*Corresponding Author: srpark@korea.kr

Diversity in composition and molecular weight distribution of endosperm proteins among Ethiopian tetraploid wheat genotypes

Daniel Hailegiorgis^{1,3}, Chong Ae Lee², Song Joong Yun^{1,2*}

¹Department of Crop Science and Biotechnology, Chonbuk National University, Jeonju 561-756, Republic of Korea

²Institute of Agricultural and Life Sciences, Chonbuk National University, Jeonju 561-756, Republic of Korea

³Department of Plant Science, Wollo University, Dessie, Ethiopia

The endosperm proteins of Ethiopian durum wheat varieties have been isolated and characterized. Sequential extraction method was used to separate individual protein fractions according to their solubility. Prolamins (also known as large monomeric gluten proteins), were identified to be predominant protein fractions (51.47%). Albumins and globulins accounted for only 27% of the total protein. Under reduced condition, polyacrylamide-gel electrophoresis has revealed a wide range of molecular weight (MW) for albumin and globulin proteins. The molecular weight range of globulin was 10-100 KDa. The electrophoretic pattern of globulin revealed more polymorphisms than that of albumin. High polymorphism, both in terms of band intensity and occurrence, was observed between 15 and 35 KDa. The presence of polymorphism in this region suggests that globulins could also be used as suitable and useful genetic markers to discriminate genotypes. In sum, five globulin dominant genes were identified with sizes of 15, 22, 35, 55, and 70 KDAs. The gel electrophoresis result of albumin proteins did not show any significant variation among the genotypes. The number and position of bands were similar for all varieties. When compared to globulins, albumin proteins had wider molecular weight range (10 KDa to 130 KDa). Unlike globulins, there were only two prominent bands in albumins (73 KDa and 9 KDa). The ratio of monomeric to polymeric proteins was close to 4:1. This ratio is among the highest reported so far and it has some implication in quality of processed products. The cutoff point of 100 in the dendrogram that was constructed based on the dissimilarity matrix of the total protein content and individual protein fractions discriminated the 20 durum wheat varieties into 3 major classes. Our results could be useful for plant scientists, bread and pasta making industries in selecting good raw materials with high protein quality for end-users.

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*Corresponding Author: E-mail: sjyun@jbnu.ac.kr

Analysis of QTL associated with flag-leaf angle using a doubled haploid genetic map in rice (*Oryza sativa* L.)

Jeong-Gwan Ham, Sopheap Yun, Rahmatullah Jan, A-Ra Cho, Jun-Hoi Kim, Xiao-Xuan Du, Kyung-Min Kim*

Division of Plant Biosciences, School of Applied Biosciences, College of Agriculture & Life Science, Kyungpook National University, Daegu, 41566, Korea

In this study, QTL analysis and physical map construction was performed by using Cheongcheong, Nagdong doubled haploid population for detect yield related flag-leaf angle genes. Investigated flag-leaf angle, photosynthetic efficiency, chlorophyll contents about doubled haploid population, RSM (Response surface methodology) was performed by Minitab 17 to analyze relationship between 3 factors. Genetic map was constructed by using Mapmaker (ver 3.0) and Mapchart (ver 2.2). QTL analysis was performed by using WinQTL cart (ver 2.2). When RSM analysis was performed, yield was increased by decreasing of flag-leaf angle, increasing of photosynthetic efficiency, increasing of chlorophyll contents. QTLs about flag-leaf angle was detected at chromosome 4, 12, QTLs about photosynthetic efficiency was detected at chromosome 3, QTLs about chlorophyll contents was detected at chromosome 11. When constructed physical map based on detected QTLs, 9 genes at *qFA4*, 2 genes at *qFA11*, 7 genes at *qPE3*, 6 genes at *qCC11* were detected. As flag-leaf is known to be expressed by differentiation of cell elongation, genes related to cell elongation were detected in this study. This study will be useful for basic data of development and breeding of rice cultivars.

*Corresponding Author: Tel. 053-950-5711, E-mail: kkm@knu.ac.kr

Construction of genetic map using EST-SSR markers in sweetpotato (*Ipomoea batatas* (L.) Lam)

Jin-Hee Kim, Jun-Hoi Kim, Xiao-Xuan Du, Sopheap Yun, Kyung-Min Kim*

Division of Plant Biosciences, School of Applied Biosciences, College of Agriculture & Life Science, Kyungpook National University, Daegu, 41566, Korea

According to the Food and Agriculture Organization (FAO) statistics, the world population will increase to about 91 million (Asia 51 million, Africa 19 million). A rise in the world's population means increased need for food. Sweet potato (*Ipomoea batatas* L.) is one of the alternatives to solving the problem. Thus, in the world breeding practice for improving the quality of sweet potato is ongoing. Recently, development of molecular marker for sweet potato demonstrated good potential to be used in genetic selection. In this study, cDNA library were constructed from total RNA. A total of 789 of cDNA were cloned in *E. coli* by employing pGEMT-easy vector. As many as 579 EST-SSR markers were designed (73.38%) from the known cDNA nucleotide base sequences. Developed EST-SSR marker expected length is range from 100 to 380bp. The motif sequence types of the EST-SSR markers were varied, of which most of the motif sequence types were di- and penta-, respectively, while the most found motifs was CAGAAT(29.0%) and TCT(2.8%). 21 cultivars and Yeseumi X Annoben populations used for construction of genetic map. molecular analysis on sweet potato could be done more efficiently. Thus, we can develop high quality sweet potato while overcoming the challenge from climate change and unfavorable conditions.

*Corresponding Author: Tel. 053-950-5711, E-mail: kkm@knu.ac.kr

Genetic analysis of chlorophyll content and leaf senescence using progeny from an interspecific cross in rice (*Oryza sativa* L.)

Kyu-Chan Shim, Luong Ngoc Ha, Sun Ha Kim, Yun-A Jeon, Hyun-Sook Lee, Xin Lu, Sang-Nag Ahn*

Department of Agronomy, Chungnam National University, Daejeon 305-764, Korea

In plant, chlorophyll content and leaf senescence is associated with grain filling and yield. We analyzed a QTL controlling chlorophyll content using introgression line (CR7501). CR7501 derived from a cross between *Oryza sativa* Hwaseong as a recurrent parent and wild species *O. grandiglumis* as a donor parent showed higher chlorophyll content than Hwaseong. For QTL analysis, 58 F₃ and 38 F₄ lines were developed from across between CR7501 and Hwaseong. A QTL for chlorophyll content (*qCC2*) was detected in chromosome 2 and explained 24.63% of phenotypic variation. To examine the senescence effect of *qCC2*, dark-induced senescence (DIS) was conducted. Detached leaves from Hwaseong and CR7501 were incubated on 3mM MES buffer (pH 5.8) at 27°C under complete dark condition. CR7501 has higher chlorophyll content with delayed senescence than Hwaseong. To know whether the *qCC2* has leaf functionality during the DIS, ion leakage test and Fv/Fm measurement were performed. In the Fv/Fm value, significant difference was observed at 6 days after incubation. But, ion leakage rate was not significantly different. These results might suggest that the *qCC2* is possibly associated with chlorophyll content and stay-green phenotype.

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*Corresponding Author: Tel. +82 42 821 7038, E-mail: ahnsn@cnu.ac.kr

토마토 유전자원 풋마름병 저항성 검정용 SNP 분자표지 개발

안영은^{1,2}, 하온숙^{1*}, 노나영¹, 고호철¹, 전영아¹, 성경숙¹, 이주희¹, 백형진¹, 이준대²

¹전북 전주시 완산구 농생명로 국립농업유전자원센터

²전북 전주시 덕진구 백제대로 전북대학교 농업생명과학대학 원예학과

풋마름병(bacterial wilt)은 열대, 아열대, 온대지역에 걸쳐 전 세계에서 약 50과 400종 이상의 식물에서 병해를 일으키며 특히 가지과 작물에 큰 피해를 입히고 있다. 이에 대한 다양한 방제 방법이 제시되고 있지만 현재 풋마름병 저항성 품종을 사용하는 것이 가장 효과적인 방법으로 알려져 있다. 따라서 토마토 풋마름병 저항성 유전자원을 탐색하기 위하여 효율적이고 정확한 풋마름병 저항성 평가체계를 구축하는 것이 필요하다. 병 저항성을 평가 방법으로는 생물검정과 마커검정 방법이 있는데 풋마름병은 유전적 요인은 물론 온도, 습도와 같은 환경적 요인에도 영향을 받기 쉬우므로 생물검정과 마커검정을 병행하여야 정확한 데이터를 얻을 수 있다. 따라서 본 연구에서는 토마토 풋마름병 저항성을 정확하게 검정할 수 있는 분자표지를 개발하고자 하였다. 식물재료로는 토마토 유전자원 61개와 저항성 대조구 4개, 이병성 대조구 1개를 사용하였고, 병원균은 국립원예특작과학원에서 분양받은 *Ralstonia solanacearum* WR-1 isolate를 사용하였다. 먼저 다양한 토마토 유전자원에 대해 풋마름병 생물검정을 실시하여 극단적으로 저항성과 이병성을 나타내는 각 48 개체를 선택하고 GBS 분석을 통해 저항성과 이병성 간 변이를 보이는 SNP를 탐색하였다. 이후 GWAS 분석으로 QTL을 분석한 후 QTL에 연관된 SNP를 선발하여 HRM 분자표지로 개발하였다. 두 개의 QTLs이 염색체 6번(*Bwr-6*)과 12번(*Bwr-12*)에서 탐색되었는데 12번에 있는 것이 주동 QTL이었다. 이 주동 QTL에 아주 가깝게 연관된 10개의 SNP를 이용하여 9개의 HRM 분자표지를 개발하였고, 개발된 분자표지를 다양한 유전자원에 적용해 본 결과 생물검정 결과와 100% 일치하는 분자표지를 2개(BWR12-HRM1과 BWR12-HRM2) 선발할 수 있었다. 이 과정에서 기존에 개발되어 있던 SSR 분자표지(SML12-8과 SML12-9)를 같이 실험하였지만 100% 일치하는 것은 없었다. 본 연구에서 개발된 2개의 SNP 분자표지는 앞으로 토마토 유전자원 풋마름병 저항성 검정에 활용될 수 있을 것이라고 생각되며, 앞으로 추가적인 연구를 통해 풋마름병 저항성 주동 유전자를 클로닝하는 데에 기여할 수 있을 것이라고 생각된다.

*주저자: Tel. 063-238-4952, E-mail: oshur09@korea.kr

Genome-wide association study for detection of disease resistance genes in grape vine

Kyo-Sang Lee, Hyun A Jang, Sang-Keun Oh*

Department of Applied Biology, College of Agriculture & Life Sciences, Chungnam National University, Daejeon 34134, Republic of Korea

Grapes have cultivated worldwide, specially grown for brewing purposes and accounting for about one-third of the world's fruits production. However, grape anthracnose 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 to prove the pathogenicity of the fungal isolates *Colletotrichum acutatum* and *C. gloeosporioides* which were inoculated onto healthy grape leaves by detached method. Results of pathogenicity test from 844 grape cultivars(obtained from RDA Korea) showed 726(87%) susceptible and 118(13%) resistance, respectively. Secondly, we finally selected 350 cultivars (118 resistance and 232 susceptible cultivars) and constructed the Genotyping-by-Sequencing(GBS) library with 96 barcode sets to find 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(Genome-Wide Association Study) 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 resistant genes. Therefore, additional studies should be carried out to confirm resistance genes which are related to current candidate genes.

*Corresponding Author: Tel. 042-821-5762, E-mail: sangkeun@cnu.ac.kr

Genetic variations on florigen related genes in tomato.

Min-Sung Kang¹, Jong Hyang Bae², Soon Ju Park¹

¹Department of biological science and Institute for Basic Science, Wonkwang university 460 Iksandae-ro, Iksan, Jeonbuk, Korea

²Department of horticulture industry, Wonkwang University, Iksan 54538, Korea

Dosage of florigen activation is one of most important yield trait in tomato because it controls tomato shoot growth. Fine-tuning of the dosage effect to shoot growth give a new window for manipulating tomato yield in the field. Here we studies new genetic variants effect in florigen activation complex in tomato, which are capable of using as genetic resources for high yield tomato breeding. We were isolated three new mutant alleles in *Self Pruning* (*SP*) locus, known as a tomato anti-florigen, from 200 semi-determinate core collection lines. A single amino acid substitution mutant, *sp-337* produced more sympodial shoots per plant with the potential to increase yield through whole life under determinate growth than the one of *sp* classic. IL 3-2-2 of *Solanum pennellii* producing two leaves on each sympodial shoot was caused by significant increase of *SFT* expression. IL5-4 carrying *S.penSP5G* results in late flowering time in *S. lycopersicum*. Additionally, *CR-sp5g*, 60bp deletion mutant induced by CRISPR/cas9 system, showed early flowering producing 6 leaves on primary shoot meristem. Altogether, these genetic variations are new resources working on a single florigen pathway for tomato breeding and they could be used as multiple genetic tools to overcome background issue on breeding process.

Author E-mail: duke0357@naver.com

Development of freezing tolerance molecular markers from *Brassica oleracea*

Hayoung Song and Yoonkang Hur*

Department of Biological Sciences, College of Biological Science and Biotechnology, Chungnam National University, Daejeon, Republic of Korea

Molecular markers are useful techniques to shorten the maintenance and management costs of crops through early selection. Therefore, it is very important to develop markers that are practically applicable to breeding materials. Cold stress, including freezing, limits crop yield and cultivation area. Freezing tolerance is one of the major horticultural features of cabbage plants. We developed cold - tolerant molecular markers for early selection of freezing-tolerant lines in cabbage cultivation. To develop gene-based molecular markers for freezing-tolerant cabbage, we focused on Circadian Clock Associates 1 (*CCA1*) and Cold shock domain containing protein 5 (*CSDP5*). *CCA1* is a core circadian clock component that affects metabolic pathways and confers cold tolerance by upregulating CBF pathway genes. *CSDP5* is known to help cells survive at temperatures below optimal growth temperatures. We cloned and analyzed *CCA1* (*BoCCA1s*), and *CSDP5* genes (*BoCSDP5s*) from seven inbred lines and one cultivar of *Brassica oleracea* ssp. *capitata*. Two types of alleles were detected: BN106-type (freezing-tolerant; *BoCCA1-1*, *BoCSDP5-106*) and BN107-type (freezing-susceptible; *BoCCA1-2*, *BoCSDP5-107*). Numerous InDels (insertions/deletions), SSRs (simple sequence repeats), and SNPs (single nucleotide polymorphisms) were found in the exons and introns of *BoCCA1s* and *BoCSDP5s*. Using InDels and SNPs, we designed PCR primer pairs to distinguish freezing-tolerant lines, which we validated using 102 cabbage lines and cultivars. In the case of allelic variation in *CCA1*, Inbred lines possessed either the BN106-type or BN107-type allele, but most cultivars had both alleles. Freezing-tolerant cabbage had BN106-type InDels and/or BN106-type SNPs regardless of the presence of BN107-type InDels and SNPs. BN106-type SNPs appear to be more widely detected in freezing-tolerant cabbages than BN106-type InDels. Such markers can best be utilized for cabbage breeding using several markers derived from different genes and independently established inbred lines from different seed companies.

Author E-mail: hayoung282@hanmail.net

Development of genetic markers in Korean cultivated peanut (*Arachis hypogaea* L.) by resequencing

Daewoong Lee¹, Tae-Hwan Jun^{1*}

¹Department of Plant Bioscience, Pusan National University, Miryang, Republic of Korea

Peanut or groundnut (*Arachis hypogaea* L.) is a major economic legume crop widely cultivated in tropical and subtropical regions of the world and an important source of protein and vegetable oil especially unsaturated fatty acid (such as oleic acid) for human nutrition. Cultivated peanut is an allotetraploid (AABB; $2n=4x=40$) with a relatively large genome size of 2800 Mb/1C, which is presumed to have derived from a single recent hybridization event between two diploid ancestors of *A. duranensis* (the A genome) and *A. ipaensis* (the B genome). We resequenced two Korean peanut cultivars “K-OI” (*Arachis hypogaea* ssp. *fastigiata* L.) and “Pungan” (*Arachis hypogaea* ssp. *hypogaea* L.), which were developed at the Department of Southern Area Crop Science, National Institute of Crop Science (NICS) in Milyang. We identified various types of genetic markers including single nucleotide polymorphisms (SNPs), insertions/deletions (Indels), simple sequence repeats (SSRs), and Cleaved Amplified Polymorphic Sequences (CAPS). To verify the availability of markers found in the study, we screened some of polymorphic markers for 96 peanut varieties that are made up of 5 different origins. Our results are likely to provide a valuable resource for the peanut breeders and researchers.

*Corresponding Author: Tel. 055-350-5507, E-mail: thjun76@pusan.ac.kr

Identification of novel pungency regulatory genes in the fatty-acid biosynthesis pathway in *Capsicum annuum*

Juhun Lee^{1*}, Min-Young Kang¹, Koeun Han¹, Doyeon Hwang¹ and Byoung-Cheorl Kang¹

¹Department of Plant Science, Plant Genomics and Breeding Institute, and Vegetable Breeding Research Center, College of Agriculture and Life Sciences, Seoul National University, Seoul, 151-921, Republic of Korea

It is reported that capsaicinoids synthase (CS) is encoded by the *Pun1* gene and synthesizes pungent causative compound, capsaicinoids. Because of the capsaicinoids, mammals can feel the pungency when they consume the peppers (*Capsicum* spp.). Until now most of the non-pungent peppers had mutation in the *Pun1* gene. We isolated a non-pungent mutant from 1480 M₂ mutant lines, originated from pungent ‘Yuwol-Cho’ (*C. annuum*). To figure out the novel locus which is controlling pungency, F₂ population between ‘Yuwol-Cho’ (*C. annuum*) and its isolated mutant line was analyzed. The segregation ratio of pungency in F₂ converged on 15:1, which means that duplicate gene action explains this phenomenon. However, the expression levels of *BCAT*, *ACL*, *KAS*, *FAT*, *PAL*, *Pun1* genes decreased in isolated non-pungent mutant parent. The expression levels of four fatty acid biosynthesis genes in the capsaicinoids biosynthesis pathway showed systematical decreases. This discordance between F₂ segregation ratio and the expression levels analysis by real-time PCR means that certain genes affected the activation of fatty-acid biosynthesis pathway genes. From this research, the novel gene regulating pungency will be elucidated.

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

벼 종자의 미량원소 QTL 분석

이현숙¹, 심규찬¹, 김선하¹, 송원용², 안상낙^{1*}

¹대전광역시 유성구 대학로99 충남대학교 농업생명과학대학

²경상북도 포항시 남구 청암로 77 포항공과대학교 생명과학과

식물의 미량원소 아연 (Zn), 철 (Fe), 구리 (Cu), 망간 (Mn), 칼슘 (Ca) 등은 다량원소와 함께 식물 생육에 중요한 요소이며 철, 아연과 같은 미량원소는 동물의 생육, 발달에 있어서 필수적인 원소이다. 본 연구에서는 벼 종자의 미량원소를 조절하는 양적형질 유전자좌 (QTLs)를 탐색하였다. 기존의 연구에서 납저항성으로 알려진 잡초벼 KH2J와 재배벼 밀양23호를 교잡한 F2 집단을 이용하여 QTLs 분석을 실시하였다. 벼 종자는 수확 후 현미를 65% 질산에 녹인 후 ICP-MS (inductively coupled plasma mass spectrometry)로 미량원소 아연, 철, 구리, 망간, 칼슘, 추가적으로 납 (Pb), 카드뮴 (Cd), 비소 (As)의 함량을 조사하였다. 120 개의 F2 집단을 총 92개의 SSR marker로 유전분석한 결과 총 8개의 원소에 대하여 single point analysis 분석으로 총 27개, CIM (composite interval mapping) 분석으로 22개의 유전자좌를 탐지하였고 이들 중 염색체 5번에 아연과 철, 망간을 조절하는 QTL이 공통적으로 탐지되었다. 아연 함량 조절 QTLs은 모든 분석에서 공통적으로 염색체 5번 이외에 8번과 10번에서도 탐지되었다. F2 집단에서 이들 QTLs을 포함하는 계통을 선발하여 아연함량을 비교한 결과, 밀양 23호가 24.5ng/mg, 선발된 CR4046 (CR5113)가 밀양23호 보다 높은 34.7ng/mg을 보였다. 이 계통을 다음 세대로 진전시켜 밀양23호와 현미 아연함량을 비교한 결과 밀양23호가 18.2ng/mg일 때 CR4046 (CR5113)은 33.7ng/mg로 높은 함량을 유지하였다. 추가적으로 KH2J 계통이 보이는 까락과 까락색에 관여하는 QTLs이 염색체 4번에서 공통적으로 탐지되었고 부선색에 관여하는 QTLs 또한 염색체 4번, 6번에서 탐지되었다. 본 연구에서는 벼 종자의 미량원소 조절 QTLs을 탐지하였고, 특히 아연 함량 조절이 우수한 계통을 선발하였다. 현재 이들 아연, 철 함량과 까락관여 유전자좌의 고밀도 지도 작성을 진행 중에 있다.

*주저자: Tel. 042-821-7038, E-mail: ahnsn@cnu.ac.kr

Development of genetic maps of *Allium cepa* using genotyping-by-sequencing

Daewoong Lee¹, YongSuk Chung², Changsoo Kim², Tae-Hwan Jun^{1*}

¹Department of Plant Bioscience, Pusan National University, Miryang, Republic of Korea

²Department of Crop Science, Chungnam National University, Daejeon, Republic of Korea

A population of 186 F2 individuals derived from a cross of 'Umjinara' x 'Sinsunhwang' and the two parental lines were used for this study. In general, *Allium* species including onion has very large genome sizes ranging from approximately 10 to 20 Gbp, which have complicated genomic studies and precluded genome sequencing until recently. For the development of framework map, various types of markers including SSRs, RAPD, SNPs, and CAPS makers have been used for polymorphism test. Especially, a lot of SNP and CAPS markers were obtained from the onion transcriptome sequence by RNAseq of two parental lines. The GBS libraries have been constructed based on a modified protocol from Poland Lab using a two-enzyme system. We have been developing polymorphic markers for two parental lines, and genotyping for all F2 individuals were completed for a number of polymorphic markers. For the construction of GBS libraries, a set of 192 barcoded adapters were generated from complementary oligonucleotides with XhoI overhang sequence and unique barcodes of 4-8 bp length. The optimum conditions were determined for GBS analysis, and sequencing for all 186 F2 lines has been conducted using NGS platform.

*Corresponding Author: Tel. 055-350-5507, E-mail: thjun76@pusan.ac.kr

Identification of candidate genes associated with bacterial wilt resistance in pepper (*Capsicum annuum* L.)

Daewoong Lee¹, YangJae Kang², Yul-Kyun Ahn³, Taehwan Jun^{1*}

¹Department of Plant Bioscience, Pusan National University, Miryang, Republic of Korea

²Plant Systems Biology, School of Life Sciences Weihenstephan, Technical University of Munich, Germany

³Vegetable Research Division, National Institute of Horticultural & Herbal Science, Rural Development Administration, Wanju-gun, Republic of Korea

Bacterial wilt (BW) caused by *Ralstonia solanacearum* is one of the most common soil-borne vascular diseases of many solanaceous crops such as pepper and tomato. This study aimed to identify QTL for bacterial wilt resistance in a 169 F₈ recombinant inbred line (RIL) population obtained from across of 'YCM334' x 'Taeon' using genotyping by sequencing approach. First, we resequenced YCM344 and Taeon that are the parental lines of recombinant inbred lines (RIL). Compared to the known SNPs, we could identify the novel variations only existing in both parental lines and we annotated the informative SNPs by neighboring genes that are already known for disease resistance such as R genes and stress response genes. Moreover, via comparative analysis, we retrieved the SNPs located in the genomic regions that are in synteny with tomato genome. The final genotype matrix from GBS analysis resulted in 2684 SNPs for all 169 individuals, and total 14 linkage groups were constructed while 10 linkage groups represent chromosome 3 to 12, chromosome 1 and 2 were comprised with two linkage groups for each. The genetic map was ranged from 68.8 (chr.11) to 154.8 (chr.03) cM with the mean length of 89.3 cM, and covered approximately 1250.7 cM with 1820 unique loci (or bins). The average distance between mapped loci was about 0.7 cM with a range from 0.1 to 11.8 cM. We found significant association with five SNP markers and phenotype segregation as QTL with LOD threshold in different five chromosomes based on the high density genetic map.

*Corresponding Author: Tel. 055-350-5507, E-mail: thjun76@pusan.ac.kr

GWAS for rice seed germinability under low temperature condition.

Ah-Rim Lee¹, Heng Wang¹, Seong-Gyu Jang¹, Da-Eun Im¹, Soon-Wook Kwon^{1*}

¹Department of Plant Bioscience, Pusan National University, Miryang 50463, Korea

Rice (*Oryza sativa* L.) is one of major crops and a staple food in Asia, which is cultivated in temperate regions and at high altitudes of tropical regions. Direct-seeding has become increasingly important in rice growing areas because direct seeding in rice can reduce the labor requirement and the labor costs. Low-temperature germinability is an important trait in direct seedling culture, where rice is sown directly. Low temperature condition during sowing stage decrease yields and increase weed competition in rice. Despite of the importance of low-temperature germinability in rice cultivation, the genetic mechanism of this trait is well unknown.

In this study, we evaluated the low-temperature germinability of 137 rice accessions and conducted GWAS to identify candidate genes related to low-temperature germinability GWAS analysis performed using the GAPIT with PCA + Kinship model.

These results could provide basic information to enable the introduction of genes related to low-temperature germinability and be useful to developing direct-seeding cultivars.

*Corresponding Author: Tel. 055-350-5506, E-mail: swkwon@pusan.ac.kr

Compartmentation of rice prenyltransferases for terpene precursors (GPP, FPP, GGPP, and SPP) in greening leaf protoplasts

Min Kyoung You^{1,2} and Sun-Hwa Ha^{1,2*}

¹Graduate School of Biotechnology, Kyung Hee University, Yongin 446-701, Korea;

²Crop Biotech Institute, Kyung Hee University, Yongin 446-701, Korea

Terpene metabolites are composed of isoprene building blocks (C₅), isopentenyl diphosphate (IPP) and dimethyl allyl diphosphate (DMAPP) biosynthesized by a plastidial methylerythritol 4-phosphate (MEP) pathway and a cytosolic mevalonate (MVA) pathway. The isoprene building blocks (C₅) are sequentially condensed to generate the major terpenoid precursors, geranyl diphosphates (GPP) for monoterpenoids, farnesyl diphosphates (FPP) for sesquiterpenoids, geranyl geranyl diphosphates (GGPP) for diterpenoids, and solanesyl diphosphates (SPP). These terpenoid precursors, GPP, FPP, GGPP, and SPP, are biosynthesized by GPS (GPP synthase), FPS (FPP synthase), GGPS (GGPP synthase), and SPS (SPP synthase), and are modified to generate various monoterpenes, sesquiterpenes, diterpenes, and ubiquinones through cyclization, reduction, glycosylation, and so on. In this study, 10 predictive rice genes as major prenyltransferase responsible for GPS, FPS, GGPS and SPS are identified using sequence based analyses on in silico databases, and their biochemical activity modules are predicted. Their expression patterns on different tissues and developmental stages were investigated using quantitative RT-PCRs, and the subcellular localizations were determined using their GFP-fusion constructions. The analysis of subcellular localization shows that the terpenoid precursors are predictively compartmentalized into cytosol, chloroplasts, mitochondria, and golgi apparatus. The predictively compartmentalization analysis could be useful for developing efficient and unique rice terpenoid metabolic engineering, when their biochemical activities would be completely identified.

*Corresponding Author: sunhwa@khu.ac.kr

A new semi-dwarf and white grain wheat variety, “Baekkang” with good baking bread quality

Chon-Sik Kang^{1*}, Kyeong-Hoon Kim², Young-Keun Cheong¹, Jae-Han Son¹, Jong-Chul Park¹, Yang-Kil Kim¹, Kyong-Ho Kim¹, Tae-Il Park¹, Young-Mi Yoon¹, Ouk-Kyu Han³, Gi-Heung Hong⁴, Jin-Kyeong Choi⁵, Jae-Ki Song⁶, Jeong-Suk Bae⁷, Bo-Kyeong Kim¹, Chulsoo Park⁸

¹National Institute of Crop Science, RDA, Wanju 565-851, Korea

²Department of Southern Area, National Institute of Crop Science, RDA, Miryang 627-803, Korea

³Department of Central Area, National Institute of Crop Science, RDA, Suwon 441-100, Korea

⁴Chungnam Agricultural Research & Extension Service, Yesan 340-861, Korea

⁵Jeonnam Agricultural Research & Extension Service, Naju 520-715, Korea

⁶Gyeongnam Agricultural Research & Extension Service, Jinju 660-985, Korea

⁷Gyeongbuk Agricultural Research & Extension Service, Daegu 702-320, Korea

⁸Department of Crop Science and Biotechnology, Chonbuk National University, Jeonju 561-756, Korea

“Baekkang”, a winter wheat (*Triticum aestivum* L.) cultivar was developed by the National Institute of Crop Science, RDA. It was derived from the cross “Topdong/Klasic” during 2005. “Baekkang” was evaluated as “Iksan366” in advance yield trial test in 2012. It was tested in the regional yield trial test between 2013 and 2015. “Baekkang” is an awned, semi-dwarf and hard winter wheat, similar to “Keumkang” and “Jokyoung” (check cultivar). The heading and maturing date of “Baekkang” were similar to “Keumkang” and “Jokyoung”. “Baekkang” had higher test weight (806 g/L) and 1,000-grain weight (47.5g) than “Keumkang” (710 g/L and 46.4g, respectively) and “Jokyoung” (805 g/L and 46.1g, respectively). “Baekkang” showed resistance to Fusarium head blight than “Keumkang” and “Jokyoung”. “Baekkang” showed higher protein content (12.4%), SDS-sedimentation volume (60.0mL) and gluten content (10.1%) to “Keumkang” (12.1%, 61.3mL and 9.9%, respectively) and “Jokyoung” (11.1%, 49.5mL and 8.3%, respectively). It showed higher lightness (92.40) in flour color than “Jokyoung” (91.75, respectively). “Baekkang” showed higher volume (950mL) of baking bread than “Keumkang” (860mL) and “Jokyoung” (900mL). “Baekkang” exhibited lower firmness (1.96N) of crumb compared to “Keumkang” (2.54N) and “Jokyoung” (2.14N). Average yield of “Baekkang” in the regional adaptation yield trial test was 5.05 MT/ha in upland and 5.20 MT/ha in paddy field, which was 10% and 18% higher than those of “Keumkang” (4.69 MT/ha and 4.45 MT/ha, respectively).

*Corresponding Author: Tel. 063-238-5227, E-mail: kcs1209@koera.kr

A new semi-dwarf and red grain wheat variety, “Saekeumkang” with resistance to pre-harvest sprout, fusarium head blight and good making noodles quality

Chon-Sik Kang^{1*}, Kyeong-Hoon Kim², Young-Keun Cheong¹, Jae-Han Son¹, Jong-Chul Park¹, Yang-Kil Kim¹, Kyong-Ho Kim¹, Tae-Il Park¹, Young-Mi Yoon¹, Ouk-Kyu Han³, Gi-Heung Hong⁴, Jin-Kyeong Choi⁵, Jae-Ki Song⁶, Jeong-Suk Bae⁷, Bo-Kyeong Kim¹, Chulsoo Park⁸

¹National Institute of Crop Science, RDA, Wanju 565-851, Korea

²Department of Southern Area, National Institute of Crop Science, RDA, Miryang 627-803, Korea

³Department of Central Area, National Institute of Crop Science, RDA, Suwon 441-100, Korea

⁴Chungnam Agricultural Research & Extension Service, Yesan 340-861, Korea

⁵Jeonnam Agricultural Research & Extension Service, Naju 520-715, Korea

⁶Gyeongnam Agricultural Research & Extension Service, Jinju 660-985, Korea

⁷Gyeongbuk Agricultural Research & Extension Service, Daegu 702-320, Korea

⁸Department of Crop Science and Biotechnology, Chonbuk National University, Jeonju 561-756, Korea

“Saekeumkang”, a winter wheat (*Triticum aestivum* L.) cultivar was developed by the National Institute of Crop Science, RDA. It was derived from the cross “Keumkang/Olgeuru” during 2007. “Saekeumkang” was evaluated as “Iksan367” in advance yield trial test in 2012. It was tested in the regional yield trial test between 2013 and 2015. “Saekeumkang” is an awned, semi-dwarf and semi-hard winter wheat, similar to “Keumkang” (check cultivar). The heading and maturing date of “Saekeumkang” were similar to “Keumkang”. “Saekeumkang” had higher test weight (808 g/L) and 1,000-grain weight (47.0g) than “Keumkang” (710 g/L and 46.4g, respectively). “Saekeumkang” showed resistance to winter hardiness and pre-harvest sprouting, which lower pre-harvest sprouting rate (8.1%) than “Keumkang” (16.5%, respectively). “Saekeumkang” showed moderate resistance to Fusarium head blight. “Saekeumkang” showed high milling rate (72.0%), and lower protein content (11.6%), SDS-sedimentation volume (41.8mL) and gluten content (7.6%) to “Keumkang” (12.1%, 61.3mL and 9.9%, respectively). It showed higher lightness (93.54) in flour color than “Keumkang” (91.75, respectively). “Saekeumkang” showed higher amylose content (24.7%) and peak viscosity (118BU) of to “Keumkang” (23.7% and 114BU, respectively). “Saekeumkang” exhibited lower hardness (3.65N), higher springiness (0.92) and higher cohesiveness (0.67) of cooked noodles compared to “Keumkang” (4.13N, 0.91 and 0.62). Average yield of “Saekeumkang” in the regional adaptation yield trial test was 5.59 MT/ha in upland and 5.66 MT/ha in paddy field, which was 20% and 28% higher than those of “Keumkang” (4.69 MT/ha and 4.45 MT/ha, respectively).

*Corresponding Author: Tel. 063-238-5227, E-mail: kcs1209@koera.kr

Screening techniques for stress tolerance against drought and salinity in rice seedlings

Jae-Young Song¹, Seon-Kyeong Song¹, Dal-A Yu¹, Me-Sun Kim¹, Sothea Ouk¹, Kwon Kyoo Kang², Yong-Gu Cho¹

¹Department of Crop Science, Chungbuk National University, Cheongju 28644, Korea

²Department of Horticulture, Hankyong National University, Ansong 17579, Korea

Rice (*Oryza sativa*) cultivars show impairment of growth in response to abiotic stresses such as drought, salinity, heat and cold at the early seedling stage. It is important to precisely screen valuable genetic resources for improving stress tolerance and understanding tolerance mechanism to abiotic stresses. Because there are differences of experiment designs for screening of tolerant plant in several studies related to abiotic stress, this study has performed to provide the rapid and efficiency screening method for selection of tolerance rice to drought and salinity stresses. Two week-old rice seedlings that reached about three leaf stage were treated with drought and salinity stresses and examined tolerant levels with tolerant and susceptible control varieties, and transgenic plants. To determine the optimum concentration for the selection of drought and salinity condition, tolerant, susceptible and wild-type plants were grown under three soil moisture contents (5, 10 and 20% water contents) and three NaCl concentrations (100, 200 and 250 mM) for 10 days at seedling stage. 200 mM NaCl concentration and 5% moisture content soil were determined as the optimum conditions, respectively. The described methodologies in this study are simple and efficiency, and it might valuable for the selection of drought and salinity stress tolerance in plants at the 3,4-leaf-seedling stage.

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Corresponding Author: ygcho@cbnu.ac.kr

A new wheat variety, “Johan” with winter hardiness resistance, early maturity, high yield and good noodle quality

Chon-Sik Kang^{1*}, Kyeong-Hoon Kim², Young-Keun Cheong¹, Jae-Han Son¹, Jong-Chul Park¹, Yang-Kil Kim¹, Kyong-Ho Kim¹, Tae-Il Park¹, Young-Mi Yoon¹, Ouk-Kyu Han³, Gi-Heung Hong⁴, Jin-Kyeong Choi⁵, Jae-Ki Song⁶, Jeong-Suk Bae⁷, Bo-Kyeong Kim¹, Chulsoo Park⁸

¹National Institute of Crop Science, RDA, Wanju 565-851, Korea

²Department of Southern Area, National Institute of Crop Science, RDA, Miryang 627-803, Korea

³Department of Central Area, National Institute of Crop Science, RDA, Suwon 441-100, Korea

⁴Chungnam Agricultural Research & Extension Service, Yesan 340-861, Korea

⁵Jeonnam Agricultural Research & Extension Service, Naju 520-715, Korea

⁶Gyeongnam Agricultural Research & Extension Service, Jinju 660-985, Korea

⁷Gyeongbuk Agricultural Research & Extension Service, Daegu 702-320, Korea

⁸Department of Crop Science and Biotechnology, Chonbuk National University, Jeonju 561-756, Korea

“Johan”, a winter wheat (*Triticum aestivum* L.) cultivar was developed by the National Institute of Crop Science, RDA. It was derived from the cross “96PYT115/Suwon262//Joeun” during 2003. “Johan” was evaluated as “Iksan372” in advance yield trial test in 2013. It was tested in the regional yield trial test between 2014 and 2016. “Johan” is an awned, semi-dwarf and hard winter wheat, similar to “Keumkang” (check cultivar). The heading and maturing date of “Johan” were earlier to “Keumkang”. “Johan” had lower test weight (806 g/L) and 1,000-grain weigh (38.7g) than “Keumkang” (815 g/L and 46.5g, respectively). “Johan” showed resistance to winter hardiness and pre-harvest sprouting, which lower withering rate on the high ridge (4.8%) than “Keumkang” (32.6 %, respectively). “Johan” showed lower protein content (10.0%), SDS-sedimentation volume (41.7ml) and gluten content (7.3%) to “Keumkang” (11.9%, 59.5ml and 9.9%, respectively). It showed higher lightness (92.18) in flour color than “Keumkang” (91.86, respectively). “Johan” showed higher lightness (83.75) of noodle dough sheet than “Keumkang” (83.00). “Johan” exhibited similar hardness (4.25N) and higher springiness and cohesiveness of cooked noodles (0.90 and 0.63) compared to “Keumkang” (4.35N, 0.89, and 0.60, respectively). Average yield of “Johan” in the regional adaptation yield trial test was 5.56 MT/ha in upland and 5.17 MT/ha in paddy field, which was 24% and 22% higher than those of “Keumkang” (4.47 MT/ha and 4.22 MT/ha, respectively).

*Corresponding Author: Tel. 063-238-5227, E-mail: kcs1209@koera.kr

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

Joonki Kim^{1§}, Hye-Jung Lee^{1§}, Wricha Tyagi², Michael Kovach², Megan Sweeney², Susan McCouch^{2*}, Yong-Gu Cho^{1*}

¹Department of Crop Science, Chungbuk National University, Cheongju 28644, Korea

²Department of Plant Breeding and Genetics, Cornell University, Ithaca 14853, USA

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.

§ These authors contributed equally to this work.

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*Corresponding Author: ygcho@cbnu.ac.kr

A new long spike and numerous wheat variety, “Taejoong” with resistance to lodging and fusarium head blight and good noodle quality

Chon-Sik Kang^{1*}, Kyeong-Hoon Kim², Young-Keun Cheong¹, Jae-Han Son¹, Jong-Chul Park¹, Yang-Kil Kim¹, Kyong-Ho Kim¹, Tae-Il Park¹, Young-Mi Yoon¹, Ouk-Kyu Han³, Gi-Heung Hong⁴, Jin-Kyeong Choi⁵, Jae-Ki Song⁶, Jeong-Suk Bae⁷, Bo-Kyeong Kim¹, Chulsoo Park⁸

¹National Institute of Crop Science, RDA, Wanju 565-851, Korea

²Department of Southern Area, National Institute of Crop Science, RDA, Miryang 627-803, Korea

³Department of Central Area, National Institute of Crop Science, RDA, Suwon 441-100, Korea

⁴Chungnam Agricultural Research & Extension Service, Yesan 340-861, Korea

⁵Jeonnam Agricultural Research & Extension Service, Naju 520-715, Korea

⁶Gyeongnam Agricultural Research & Extension Service, Jinju 660-985, Korea

⁷Gyeongbuk Agricultural Research & Extension Service, Daegu 702-320, Korea

⁸Department of Crop Science and Biotechnology, Chonbuk National University, Jeonju 561-756, Korea

“Taejoong”, a winter wheat (*Triticum aestivum* L.) cultivar was developed by the National Institute of Crop Science, RDA. It was derived from the cross “Xian83(104).11/Keumkang” during 2005. “Taejoong” was evaluated as “Iksan370” in advance yield trial test in 2013. It was tested in the regional yield trial test between 2014 and 2016. “Taejoong” is an awned and hard winter wheat, similar to “Keumkang” (check cultivar). The heading and maturing date of “Taejoong” were later to “Keumkang”. “Taejoong” had lower test weight (757 g/L) and higher 1,000-grain weigh (48.3g) than “Keumkang” (812 g/L and 46.1g, respectively). “Taejoong” showed similar resistance to winter hardiness and pre-harvest sprouting and higher resistance to Fusarium head blight than “Keumkang”. “Taejoong” showed lower protein content (11.1%), SDS-sedimentation volume (34.2ml) and gluten content (8.8%) to “Keumkang” (11.9%, 59.5ml and 9.9%, respectively). It showed similar lightness (91.90) in flour color to “Keumkang” (91.86, respectively). “Taejoong” showed similar lightness (83.02) of noodle dough sheet than “Keumkang” (83.00). “Taejoong” exhibited similar hardness (4.24N), springiness and cohesiveness of cooked noodles (0.89 and 0.61) to “Keumkang” (4.35N, 0.89, and 0.60, respectively). Average yield of “Taejoong” in the regional adaptation yield trial test was 5.29 MT/ha in upland and 4.61 MT/ha in paddy field, which was 21% and 13% higher than those of “Keumkang” (4.36 MT/ha and 4.09 MT/ha, respectively).

*Corresponding Author: Tel. 063-238-5227, E-mail: kcs1209@koera.kr

Comparative expression analysis of rice and *Arabidopsis* peroxiredoxin genes suggests conserved or diversified roles between the two species and leads to the identification of tandemly duplicated rice peroxiredoxin genes differentially expressed in seeds

Yun-Shil Gho^{1*}, Sun-A Park^{1*}, Sung-Ruy Kim^{1,2*}, Anil Kumar Nalini Chandran¹, Gynheung An¹ and Ki-Hong Jung^{1*}

¹Graduate School of Biotechnology & Crop Biotech Institute, Kyung Hee University, Yongin 446-701, Republic of Korea

²Plant Breeding, Genetics, and Biotechnology Division, International Rice Research Institute, Metro Manila, Philippines

Peroxiredoxins (Prxs) have recently been identified as plant antioxidants. However, the biological functions in rice, a model crop plant, have not been well studied. In this study, we carried out a comparative transcriptome analysis of 10 rice and 10 *Arabidopsis* Prxs. As a result, Our phylogenetic analysis revealed that one subgroup contains three rice and three *Arabidopsis* Type-II PRXs that are expressed ubiquitously. This suggests that they are involved in housekeeping functions to process reactive oxygen species (ROS). A global expression analysis of the PRX family in rice identified tandem duplicates, Os1-CysPrxA and Os1-CysPrxB, in the 1-CysPrx subgroup that are differentially expressed in developing seeds and germinating seeds. Analysis of the cis-acting regulatory elements (CREs) revealed unique CREs responsible for embryo and root or endosperm-preferential expression. In addition, the presence of leaf/shoot-preferential Prxs in rice suggests that they are required in that crop because those plants must tolerate a higher light intensity in their normal growth environment when compared with *Arabidopsis* Prxs. Downregulation of two Prxs in the 1-deoxy-D-xylulose 5-phosphate reductoisomerase (dxr) mutant caused an albino phenotype, implying that those genes have roles in processing ROS produced during photosynthesis. Network analysis of four Prxs allowed us to model regulatory pathways that explain the underlying protein interaction network. Taken together, a systematic expression analysis of rice Prx family presented in this study will be a useful indicator for further functional studies of rice Prxs in morphological or physiological aspect.

*Correspondence: khjung2010@khu.ac.kr

Transcriptome profiling of flowering genes in Chinese cabbage and comparison with the radish flowering gene expression

Won Yong Jung^{1,†}, Areum Lee^{1,2,†}, Youn-Sung Kim^{3*}, Hye Sun Cho^{1,2*}

¹Plant Systems Engineering Research Center, KRIBB, Daejeon, 34141, Korea

²Biosystems and Bioengineering Program, University of Science and Technology (UST), Daejeon, 34113, Korea

³Department of Biotechnology, NongHyup Seed Anseong, 17558, Korea

Chinese cabbage (*Brassica rapa* ssp. *pekinensis*) is a typical species which requires vernalization to flowering. Flowering time is an economically important characteristic of Chinese cabbage crop with high leafy head yields and lateness of flowering is a favorable trait. However, there have been few reports on the flowering time-related genes and the flowering mechanism in Chinese cabbage. Here, we conducted genome-wide transcriptome analysis using an inbred line of Chinese cabbage, '4004', which showed the characteristics of early flowering in response to vernalization. In total, 1,677 differentially expressed genes (DEGs) were identified between with and without vernalization. From the transcriptome analysis result, 229 homologs of Arabidopsis flowering-time genes were identified in Chinese cabbage and 56 of these genes were responded to vernalization. qPCR analysis of major flowering genes showed that majority of flowering enhancers were up-regulated in response to vernalization, whereas most of flowering repressors were down-regulated in the condition. Among the major flowering genes, *BrFT*, *BrSOC1/2*, *BrFLC1/2/3*, and *BrMAF* gene expression were greatly affected by vernalization. Comparative analysis of flowering gene expression between Chinese cabbage and radish showed that expression of GA pathway-related genes was notably different: *BrGAI* and *BrGID1A* were expressed in reverse to that in radish. In addition, a number of major flowering genes of radish such as *RsFT*, *RsFRI*, *RsAPI*, and *RsLFY*, were not expressed, whereas, most of major flowering genes were expressed well in Chinese cabbage. These results suggest that different flowering mechanism may act between Chinese cabbage and radish under vernalization.

*Corresponding Author: Tel. 042-860-4469, E-mail: hscho@kribb.re.kr

Xanthomonas oryzae pv. *oryzae* triggers complex transcriptomic defense network in rice

Marjohn Nino¹, Franz M. Nogoy¹, Me-Sun Kim¹, Jae-Young Song¹, Kwon-Kyoo Kang², Yong-Gu Cho^{1*}

¹Department of Crop Science, Chungbuk National University, Cheongju 28644, Korea

²Department of Horticulture, Hankyong National University, Ansong 17579, Korea

High throughput transcriptome investigations of immunity in plants highlight the complexity of gene networks leading to incompatible interaction. To identify genes crucial to resistance against *Xanthomonas oryzae* pv. *oryzae*, functional genetic analysis of selected differentially expressed genes from our microarray data set was carried out. A total of 13 overexpression vector constructs were made using 35S CaMV promoter which drive constitutive expression in rice. Most of the genes are developmentally expressed especially during maximum tillering stage and are commonly highly expressed in the leaves. When screened against *Xoo* strain K2, the transgenic plants displayed shorter lesion length compared with wild type Dongjin which indicates partial resistance. The levels of ROS continuously magnified after inoculation which indicates robust cellular sensing necessary to initiate cell death. Elevated transcripts levels of several defense-related genes at the downstream of defense signal network also corroborate the phenotype reaction of the transgenic plants. Moreover, expression assays revealed regulation of these genes by cross-communicating signal-transductions pathways mediated by salicylic and jasmonic acid. These collective findings revealed the key immune signaling conduits critical to mount full defense against *Xoo*.

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*Corresponding Author: ygcho@cbnu.ac.kr

Genetic diversity analysis of pear (*Pyrus* spp.) germplasm based on genotyping-by-sequencing

Keumsun Kim^{1,2}, Sewon Oh^{1,2}, Hyeondae Han^{1,2}, Kidong Hwang^{1,2}, Min-Gi Lee^{1,2}, Suji Ahn^{1,2}, Jiyeon Kim^{1,2}, Yoon-Kyeong Kim³, Daeil Kim^{1,2*}

¹Department of Horticulture, Chungbuk National University, Cheongju 28644, Korea

²Brain Korea 21 Center for Bio-Resource Chungbuk National University, Cheongju 28644, Korea

³Pear Research Station, National Institute of Horticultural & Herbal Science, Rural Development Administration, Naju 58220, Korea

Estimation of genetic diversity among *Pyrus* spp. is often very difficult owing to the low morphological diversity, lack of differentiating characters among species, and widespread crossability. In present study, we conducted genotyping-by-sequencing technology to estimate the genetically diverse collection of 231 pear accessions and detected 10,186 SNPs. Phylogenetic tree was constructed using MEGA6 with neighbor-joining method and population structure was estimated by using STRUCTURE v.2.3.4. based on the set of 10,186 SNPs. Analysis of phylogenetic tree and genetic structure substantiate the identification of tree distinct subpopulations. The first subpopulation contains mainly *P. communis*, 4 primary pears (*P. glabra*, *P. amygdaliformis*, *P. nivallis*, and *P. elaeagnifolia*), and hybrids between *P. pyrifolia* and *P. communis*. The second subpopulation includes Japanese pears (*P. pyrifolia*) and the third subpopulation comprises Chinese pears (*P. bretschneideri*, *P. ussuriensis*, and *P. betulifolia*) and Korean native pears. Genetic analysis within each subpopulation revealed patterns of diversity associated with geographical origin. Finally, our findings could be useful for developing a core collection of pear genetic data.

*Corresponding Author: Tel. 043-261-2527, E-mail: dkpomo@cbnu.ac.kr

Comparative transcriptional profiles of compatible and incompatible interactions between *Xanthomonas oryzae* pv. *oryzae* and rice

Marjohn Nino¹, Joon ki Kim¹, Franz M. Nogoy¹, Dal-A Yu¹, Sothea Ouk¹, Jae-Young Song¹, Kwon-Kyoo Kang², Yong-Gu Cho^{1*}

¹Department of Crop Science, Chungbuk National University, Cheongju 28644, Korea

²Department of Horticulture, Hankyong National University, Ansong 17579, Korea

Bacterial blight, caused by *Xanthomonas oryzae* pv. *oryzae*, is an emerging disease of rice in Korea causing damage to rice quality and yield. To understand the transcriptional gene network that is crucial to resistance against *Xoo*, a whole-genome oligonucleotide microarray of Dongjin, a japonica rice which is susceptible to BB, and Jinbaek, which is resistant cultivar were used to infer transcripts of inducible genes between compatible and incompatible interactions at 48 hour post inoculation. Comparison of expression profiles between two cultivars revealed a complex and prominent gene network involved in resistance against bacterial blight. A total of 1,721 differentially expressed genes, designated as K2-induced differentially expressed genes (K2-DEGs), were identified. A large number of inducible genes are more evident in the resistant cultivar, which is threefold higher than in susceptible plant. Functional annotations revealed at least ten categories that are common in both interactions, of which signaling is most abundant, followed by transcription, metabolism, defense, and transport among others. Extensive upregulation of these genes presumably signifies that gene regulatory network leading to incompatible interaction is orchestrated by defense signals and robust cellular reprogramming. Most of the DEGs were assigned in cytoplasm and nucleus, corroborating the idea that critical resistant gene components may be targeted to the nucleus to trigger full immunity response to pathogen.

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*Corresponding Author: ygcho@cbnu.ac.kr

Comparative analysis of phylogenetic trees assessed by SSR and SNP markers in Asian pears (*Pyrus* spp.)

Keumsun Kim^{1,2}, Kidong Hwang^{1,2}, Sewon Oh^{1,2}, Hyeondae Han^{1,2}, Min-Gi Lee^{1,2}, Suji Ahn^{1,2}, Jiyeon Kim^{1,2}, Yoon-Kyeong Kim³, Daeil Kim^{1,2*}

¹Department of Horticulture, Chungbuk National University, Cheongju 28644, Korea

²Brain Korea 21 Center for Bio-Resource Chungbuk National University, Cheongju 28644, Korea

³Pear Research Station, National Institute of Horticultural & Herbal Science, Rural Development Administration, Naju 58220, Korea

Genotyping-by-sequencing (GBS) is a cost effective and straightforward technology for discovering single nucleotide polymorphisms (SNPs). However, the most important problem is the limit of fragment size to read and this phenomenon can influence on reliability of GBS. In this study, to evaluate the reliability of GBS, we analyzed genetic relationship among Asian pears (*Pyrus* spp.) using standard set of simple sequence repeats (SSRs) and SNPs derived from GBS, respectively. The genetic diversity was analyzed in 45 pear accessions (2 primary pears, 42 Asian pears, and 1 reference pear). Phylogenetic tree using SSRs was classified into a total of 5 groups. Group I consisted of 24 *P. pyrifolia* accessions except for 'Hori'. Group II, III, and IV consisted of accessions belonged to *P. bretschneideri* and *P. ussuriensis* except for 'Japanese Golden Russet (JGR) × Mikado Decline Resist. (MDR)', 'Yakumo', and 'Yandangseolri'. Group V contained *P. fauriei*, 'Bartlett', and other cultivars that consisted of 'Kiyomaro', 'Ooharabeni', and 'Taiheiyō'. These cultivars are accessions of interspecific cross between Asian pear and *P. communis*. This group was out-grouped and served as a reference to determine the relationship among Asian pear accessions. Even though phylogenetic tree using SNPs was divided into 3 groups, it was similar to using SSRs. The only difference is that group II, III, and IV drawn from SSRs were combined into group II in the phylogenetic tree using SNPs. Our study suggests that GBS is reliable and this results may be used for the management and development of pear germplasm collections

*Corresponding Author: Tel. 043-261-2527, E-mail: dkpomo@cbnu.ac.kr

Analysis of genetic diversity and population structure for *Actinidia arguta* using SNPs derived from genotyping-by-sequencing

Sewon Oh^{1,2}, Keumsun Kim^{1,2}, Hyeondae Han^{1,2}, Kidong Hwang^{1,2}, Min-Gi Lee^{1,2}, Suji Ahn^{1,2}, Jiyeon Kim^{1,2}, Mockhee Lee³ and Daeil Kim^{1,2*}

¹Department of Horticulture, Chungbuk National University, Cheongju 28644, Korea

²Brain Korea 21 Center for Bio-Resource Chungbuk National University, Cheongju 28644, Korea

³Namhae Branch, National Institute of Horticultural and Herbal Science, Rural Development Administration, Namhae 52430, Korea

The *Actinidia arguta* is wild genetic resource of hardy kiwifruit in Korea. In order to provide useful information to germplasm collection, the genetic relatedness and population structure were investigated within *A. arguta* and other *Actinidia* accessions (*A. polygama*, *A. macrosperma*, *A. rufa*, *A. chinensis*, and *A. deliciosa*). Those other *Actinidia* accessions were used as references. The phylogenetic relationship and population structure were obtained using single nucleotide polymorphisms derived from genotyping-by-sequencing. Relationship between *Actinidia* accessions was revealed by neighbor-joining method. In phylogenetic tree, the outgroup contains *A. polygama*, *A. macrosperma*, *A. rufa*, 'Hort16A' (*A. chinensis*), and 'Hayward' (*A. deliciosa*). The *A. arguta* accessions are classified into major two groups. In addition, three clusters were observed in population structure. The maximum delta *K* was detected at *K* = 3, which indicates the most likely number of genetic clusters. Cluster I and II are composed of *A. arguta* accessions and Cluster III is consisted of outgroup species in phylogenetic tree. Therefore, the result of phylogenetic analysis is consistent with population structure. These results could provide an information to develop a core germplasm set for *A. arguta*. Moreover, additional data such as agronomical traits may be need to classify the *A. arguta* accessions in detail.

*Corresponding Author: Tel. 043-261-2527, E-mail: dkpomo@cbnu.ac.kr

Identification of genetic structure for kiwifruits (*Actinidia* spp.) using genotyping-by-sequencing

Sewon Oh^{1,2}, Keumsun Kim^{1,2}, Hyeondae Han^{1,2}, Kidong Hwang^{1,2}, Min-Gi Lee^{1,2}, Suji Ahn^{1,2}, Jiyeon Kim^{1,2}, Mockhee Lee³ and Daeil Kim^{1,2*}

¹Department of Horticulture, Chungbuk National University, Cheongju 28644, Korea

²Brain Korea 21 Center for Bio-Resource Chungbuk National University, Cheongju 28644, Korea

³Namhae Branch, National Institute of Horticultural and Herbal Science, Rural Development Administration, Namhae 52430, Korea

In kiwifruits, the classification of *Actinidia chinensis* and *A. deliciosa* is difficult. Morphologically, the two species are very similar and have close phylogenetic relationship. To classify those two species, single nucleotide polymorphisms (SNPs) derived from genotyping-by-sequencing (GBS) were used for constructing phylogenetic tree and population structure in 50 kiwifruits. In the phylogenetic tree, the kiwifruit accessions are divided into 2 groups. The 22 *A. chinensis*, 18 *A. deliciosa*, and 3 hybrids are belonged in first group and classified into two subgroups. Subgroup I is consisted of *A. chinensis* accessions and 2 hybrids, 'Jacy Green' and 'Mega Gold' (*A. chinensis* × *A. deliciosa*). Subgroup II is composed of *A. deliciosa* accessions and 'Bangwoori' (*A. arguta* × *A. deliciosa*). The second group as an outgroup is consisted of *A. polygama* ('S8'), *A. arguta* var. *purpurea* ('S3'), *A. arguta* ('Chiak', 'K5-1-8', 'K5-2-3', 'K5-3-18'), and *A. arguta* × *A. deliciosa* ('Skinny Green'). In addition, population structure analysis showed that identified $K = 3$, which means the kiwifruit accessions are divided into three clusters. Our results suggest that the GBS derived SNPs could distinguish *A. chinensis* and *A. deliciosa*.

*Corresponding Author: Tel. 043-261-2527, E-mail: dkpomo@cbnu.ac.kr

Molecular characterization of *TaGAST1*, one of wheat *GAST* family of small polypeptides during spike development

Jae Yoon Kim^{1*}, Chang-Ho Kim¹, Yong Weon Seo²

¹Department of Plant Resources, College of Industrial Science, Kongju National University, Yesan 32439, Republic of Korea

²Department of Biotechnology, Korea University, Seoul 136-713, Republic of Korea

Gibberellic acids (GAs) are influential plant hormones that function during a plant's whole lifetime. GAs regulate major growth and developmental processes such as seed germination, stem elongation, flowering, and fruit development. Among numerous GA-responsive genes, the *GAST* family are known to be important growth inducers and regulators of development that act in response to GA. In this study, four GA-stimulated genes were isolated from wheat and designated *TaGAST1*, 2, 3, and 4 (*Triticum aestivum* gibberellic acid stimulated transcript 1, 2, 3 and 4). All *TaGAST* family members encode approximately 100 amino acid residues and include highly conserved cysteine-rich domains termed GASA domains in their C-terminal regions, along with divergent intermediate N-terminal regions. The expression of the *TaGASTs* was analyzed at the inflorescence development stage, in different tissues, and under the application of phytohormones. *TaGAST1* was prominently expressed at the inflorescence development stage in response to phytohormone treatment. However, *TaGAST1* was not expressed in the seedlings except under abscisic acid (ABA) treatment. *TaGAST2* and *TaGAST3* showed moderate expression in the spike but vigorous transcript accumulation in the seedling. *TaGAST4* was predominantly expressed only in the seedling. To identify putative interacting proteins of the *TaGAST* genes during spike development, a yeast two-hybrid assay was conducted and wheat cyclophilin A-1 (*TaCypA1*) was identified as a *TaGAST1* interacting protein. The expression pattern of *TaCypA1* in the developing spike was opposite to that of *TaGAST1*. A bimolecular fluorescence complementation assay revealed that the interaction of *TaGAST1* with *TaCypA1* is targeted to the plasma membrane.

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*Corresponding Author: Tel. 041-330-1203, E-mail: jaeyoonkim@kongju.ac.kr

Assessment of Genetic relationship using genome-wide single nucleotide polymorphisms developed by genotyping-by-sequencing in apples (*Malus* spp.)

Hyeondae Han^{1,2}, Keumsun Kim^{1,2}, Sewon Oh^{1,2}, Kidong Hwang^{1,2}, Min-Gi Lee^{1,2}, Suji Ahn^{1,2}, Jiyeon Kim^{1,2}, Sunheum Cho¹, Daeil Kim^{1,2*}

¹Department of Horticulture, Chungbuk National University, Cheongju 28644, Korea

²Brain Korea 21 Center for Bio-Resource Chungbuk National University, Cheongju 28644, Korea

This study was performed to evaluate genetic diversity between various apple (*Malus* spp.) accessions using single nucleotide polymorphisms which derived from genotyping-by-sequencing. The genetic relationship among 73 apple accessions was evaluated using a phylogenetic tree, which clustered all the accessions into four groups. Group I is contained three major subgroups with the following characteristics. Subgroup I consisted of wild species (*M. prunifolia*, *M. sieboldii*, and others) and both subgroup II and III are composed of crab apples and *M. × domestica* accessions. Group II is characterized by the apple cultivars bred in Korea and their parents accessions. Group III is composed *M. × domestica* accessions which are introduced cultivars and Korean bred cultivar of 'Seokwang'. Group IV consisted of wild species (*M. floribunda*, *M. asiatica*, and others), 'Mollie' s Delicious', and 'Honey Crispy'. These results indicate that the 73 apple accessions are mainly divided into wild species and cultivated species. Moreover, the estimated clusters revealed by the population structure showed an optimum value of 3 ($K=3$), that represented the 73 apple accessions could be categorized into three clusters. Our results are useful for consideration of parental selection in apple breeding.

*Corresponding Author: Tel. 043-261-2527, E-mail: dkpomo@cbnu.ac.kr

Use of SNP derived CAPS markers for identification of apple sports based on genotyping-by-sequencing

Hyeondae Han^{1,2}, Keumsun Kim^{1,2}, Sewon Oh^{1,2}, Min-Gi Lee^{1,2}, Kidong Hwang^{1,2}, Jiyeon Kim^{1,2}, Suji Ahn^{1,2}, Sunheum Cho¹, Daeil Kim^{1,2*}

¹Department of Horticulture, Chungbuk National University, Cheongju 28644, Korea

²Brain Korea 21 Center for Bio-Resource Chungbuk National University, Cheongju 28644, Korea

Cleaved amplified polymorphic sequence (CAPS) markers are techniques for identifying polymorphisms at a particular locus that is amplified by polymerase chain reaction (PCR), followed by digesting with restriction enzymes. The purpose of this research was to develop a new cost effective PCR based CAPS marker set using the high-throughput single nucleotide polymorphism (SNP) genotypes developed by the genotyping-by-sequencing (GBS) to distinguish the apple sports. SNP survey was comprised of using 18 apple sports genotypes ('Fuji', 13 sports of 'Fuji', 'Hongro', and 3 sports of 'Hongro') via GBS that resulted in 11,136 polymorphic SNP markers. After filtering out the polymorphic SNPs using recognition sequences of the 8 restriction endonucleases as a query, 79 SNPs were randomly selected. PCR primers were designed to amplify 450 to 550 bp sequences of each locus and their polymorphisms were visualized on 2% agarose gel. The genetic diversity in sports of 'Fuji' and 'Hongro' was very low, only 'Sobeak No.3' (sports of 'Fuji') and 'Sobeak No.2' (sports of 'Hongro') were distinguished by using CAPS markers. In this study, we succeeded in converting SNP sites into CAPS markers and distinguishing 2 sports of apple accessions. It is anticipated that these putative SNPs could be applied in apple genetic research and breeding.

*Corresponding Author: Tel. 043-261-2527, E-mail: dkpomo@cbnu.ac.kr

Tissue specific roles of 4-hydroxy-3-methylbut-2-enyl diphosphate reductases on rice terpenoids metabolism

Yeo Jin Lee^{1,2,†}, Min Kyoung You^{1,2,†} and Sun-Hwa Ha^{1,2*}

¹Graduate School of Biotechnology, Kyung Hee University, Yongin 446-701, Korea;

²CropBiotechInstitute, KyungHeeUniversity, Yongin446-701, Korea;

In plants, terpenoid precursors are produced through two independent pathways, the cytosolic mevalonate (MVA) pathway and the plastidial methylerythritol 4-phosphate (MEP) pathway. Isopentenyl diphosphate (IPP) and dimethylallyl diphosphate (DMAPP), which are precursor for the supply of terpenoid catalyzed by six enzymes of the MEP pathway. 4-hydroxy-3-methylbut-2-enyl diphosphate reductases (HDR or *IspH*) is essential enzyme in the last step of MEP pathway. Two *IspH* genes have been found in *Oryza sativa*. To profiling of expression patterns, transcript level of *OsIspH* genes were analyzed among developmental stages and tissues. *OsIspH1* is constitutively expressed higher in the leaves, whereas *OsIspH2* is expressed in the roots. *OsIspH1* complemented that functionally an *E. coli* *IspH* deficient mutant (DLYT1) in enzyme activity. *OsIspH1* fused sGFP protein was detected only into chloroplasts. Knock-out mutant of *OsIspH1* by T-DNA insertional mutagenesis in rice (*osisph1*) had albino phenotype, and signified that *OsIspH1* is critical functions for provide plastidial IPP/DMAPP in the leaves. Also, the *osisph1* were observed to be altered in roots of it, in which the number of roots, total weight, and length. In addition, transcript level of *OsIspH2* was detected to increase in roots of *osisph1* homozygous mutant than wild type plants, but not detected in shoots. These root phenotypes might be concern with transcript level of *OsIspH2* increased in roots of *osisph1* mutant. We conclude that *OsIspH1* and *OsIspH2* has tissue specific roles in terpenoids metabolism of shoots and roots, respectively.

†: equally first authors

*Corresponding Author: sunhwa@khu.ac.kr

BA와 NAA 호르몬 처리가 기내 알스트로메리아 절편체로부터 싹, 뿌리 및 근경 발생율에 미치는 영향

양환래, 박선경, 이상희, 김종보*

충북 충주시 충원대로 268 건국대학교 글로벌캠퍼스 의료생명대학 생명공학과

알스트로메리아 (*Alstroemeria*)는 세계 10대 절화에 속하는 중요한 절화 작물 중 하나이다. 알스트로메리아는 화색과 화형이 다양하고 절화 수명이 비교적 길며 특히, 저온적응성이 높아 고소득 화훼작물로서 생산자들에게 인기가 많아 국내 시장에서 시장규모가 증가하는 추세이다. 그러나 낮은 증식률과 장기간의 번식기간 그리고 바이러스 감염율이 높기 때문에 우량 품종의 대량증식이 어려운 현실이다. 따라서 기존의 근경(rhizome)을 이용한 증식 시스템을 개선하고 또한 다른 절편체인 엽병이나 배발생캘러스 그리고 체세포를 이용한 새로운 대량 증식 시스템을 확립하는 과정이 향후 필요하다. 본 연구진은 알스트로메리아의 근경을 이용하여 조직배양 시 cytokinin과 auxin을 조합하여 기내 식물체 성장에 효과적인 호르몬 농도조합을 선정하기 위해 본 연구를 수행하였다. 실험에 사용된 알스트로메리아는 국내 육성 계통 D187이고 이 계통의 근경을 절편체로 사용하였는데, 이 근경은 sucrose 30 g · L⁻¹, gelrite 0.25 %, BA(0.0, 0.5, 및 1.0) mg · L⁻¹와 NAA(0.0, 0.10 및 0.20) mg · L⁻¹ 가 혼용 첨가된 MS배지에 치상하여 23±1°C 그리고 16시간 명조 조건 하에서 4주 간격으로 계대배양 하였다. 2주마다 데이터 수집을 수행하여 총 10주간 측정 하였으며, 생체중, 싹길이, 뿌리길이, 뿌리 개수 그리고 rhizome 개수를 측정 하였다. 그 결과 호르몬 무처리구에서는 싹발생개수가 2개 미만이었지만 호르몬 처리구에서는 싹개수가 전부 2개 이상 발생하였다. 특히 BA 0.5 mg · L⁻¹ 와 NAA 0.20 mg · L⁻¹ 혼용처리를 하였을 때 뿌리개수가 2.23개로 가장 많이 발생하였고, 생체중 증가량 또한 3.37g으로 가장 높게 측정되었으며, 알스트로메리아 생장에 필요한 근경 발생개수가 2.64개로 5개의 호르몬 조합 중에 가장 많았다. 이러한 결과를 적용하면 향후 국내 우량 알스트로메리아 품종 대량생산 시스템 구축에 기여하여 우량품종의 고효율의 증식 및 농가 보급에 기여할 것으로 기대된다.

*주저자: Tel. 043-840-3549, E-mail: jbhee1011@kku.ac.kr

ERF group VII genes predicted as candidates of terpene synthesis regulator under blue light

Heebak Choi^{1*}, Sun-Hwa Ha¹

¹Crop Biotech Institute, Kyung Hee University, Yongin,

In plants, the terpene synthesis pathway generates more than 30,000 types of second metabolites including phytohormones (GA, ABA, cytokinin and strigolactone) and beneficial products. Interests for terpene synthesis pathway are increasing, but a sophisticated control of terpene synthesis seems difficult to achieve by direct modification of functional enzyme due to its severe defects. We purposed the blue light signal as appropriate condition for screening transcription factors and found ERF group VII family as negative regulator of terpene synthesis pathway. In here, prediction of relationship between ERF group VII family and terpene synthesis were presented. In addition, the characteristic of ERF group VII and comparison of its cis-elements with differential expression patterns were analysed.

***Corresponding Author:** Tel. 031-201-2653, E-mail: backy28@khu.ac.kr

Genetic variation architecture of mitochondrial genome reveals the differentiation in Korean landrace and weedy rice

Wei Tong¹, Qiang He¹, Yong-Jin Park^{1,2}

¹Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 32439, Republic of Korea.

Mitochondrial genome variations have been detected despite the overall conservation of this gene content, which has been valuable for plant population genetics and evolutionary studies. Here, we describe mitochondrial variation architecture and our performance of a phylogenetic dissection of Korean landrace and weedy rice. A total of 4,717 variations across the mitochondrial genome were identified adjunct with 10 wild rice. Genetic diversity assessment revealed that wild rice has higher nucleotide diversity than landrace and/or weedy, and landrace rice has higher diversity than weedy rice. Genetic distance was suggestive of a high level of breeding between landrace and weedy rice, and the landrace showing a closer association with wild rice than weedy rice. Population structure and principal component analyses showed no obvious difference in the genetic backgrounds of landrace and weedy rice in mitochondrial genome level. Phylogenetic, population split, and haplotype network evaluations were suggestive of independent origins of the indica and japonica varieties. The origin of weedy rice is supposed to be more likely from cultivated rice rather than from wild rice in mitochondrial genome level.

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Corresponding Author: Tel. 041-330-1201, E-mail: yjpark@kongju.ac.kr

Lectures of statistical models and population genetics for crop breeding

Kyu-Won Kim¹, Soon-Chun Jeong², Ji-Hye Hwang³, Hye-Won Chang⁴, Hee-Jong Koh⁴, Jung-Kyung Moon³, Yong-Jin Park^{1,5}

¹Center for crop genetic resource and breeding (CCGRB), Kongju National University, Yesan 32439, Korea

²Bio-Evaluation Center, Korea Research Institute of Bioscience and Biotechnology, Cheongwon, Chungbuk 34141, Korea

³National Institute of Crop Science, Rural Development Administration, Wanju 55365, Korea

⁴Department of Plant Science and Research Institute for Agriculture and Life Sciences, Seoul National University, Seoul 08826, Korea

⁵Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 32439, Korea

As genetic information for a large amount of crops can be collected rapidly via the next-generation sequencing (NGS) method or DNA chip, population genetics, which was previously described theoretically, has been applied to the field of crop breeding in recent years and its importance has been highlighted. In addition, crop gene mapping techniques based on statistical analysis methods such as genome-wide association study (GWAS) and genomic selection (GS) are emerging as important analytical methods. In order to keep the research level for the national crop breeding program global, a deeper understanding of statistical breeding is needed. We invited world-renowned academics in the field of statistical breeding and held lectures on statistical and bioinformatics tools to organically link genomic information with molecular breeding. More than 50 graduate students from all over the country participated in the study to gain a basic understanding of the various statistical models used in crop breeding and population genetics. Through this training, we hope that breeding research based on population genetics and statistical models will be promoted and thus contribute to cultivating new varieties.

Corresponding Author: Tel. 041-330-1201, E-mail: yjpark@kongju.ac.kr

Identification of candidate defense genes for rice blast supported by orthology identification, eQTL mapping and GWAS

Kyu-Won Kim¹, Won-Hee La², Il-Pyung Ahn³, Yong-Jin Park^{1,2}

¹Center for crop genetic resource and breeding (CCGRB), Kongju National University, Yesan 32439, Korea

²Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 32439, Korea

³National Institute of Agricultural Science, Rural Development Administration, Jeonju 54874, Korea

Rice blast is a serious disease that causes a decrease in rice yield. In Korea, it has implemented a considerable blast resistant cultivation system, but the epidemic of blast can occur at any time. In order to cope with rapidly evolving strains of blast disease, it is necessary to maintain sufficient resistance gene pool and to secure new resistance genetic resources continuously. We identified candidate genes for blast resistance in domestic rice populations. Using various evidences of the blast resistance genes such as sequence homology, transcriptional and genomic association, we summarized those evidences to narrow the defense candidate genes.

Corresponding Author: Tel. 041-330-1201, E-mail: yjpark@kongju.ac.kr

The development of algorithms, to enable comparative genomic analysis from many-to-many orthologs.

Kyu-Won Kim¹, Jung-Rye Nam¹, Yong-Jin Park^{1,2}

¹Center for crop genetic resource and breeding (CCGRB), Kongju National University, Yesan 32439, Korea

²Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 32439, Korea

Orthologs are divided into one-to-one orthologs, with one copy of orthologous gene per species, and many-to-many orthologs with multiple copies of orthologous genes per species. Many-to-many orthologs (n: n orthologs) account for a considerable proportion of all types of orthologs. Although, there is no model for comparative analysis from many-to-many orthologs, many studies have used only one-to-one orthologs. If we can make it that many-to-many orthologs are available, then we can compare the function of genes that have not previously been compared. We have developed an algorithm to enable comparative genomic analysis from many-to-many orthologs, by converting many-to-many orthologs to one-to-one orthologs. The algorithm we have developed is applied to monocotyledonous and dicotyledonous plants. A number of many-to-many orthologs were identified and converted to be compared with their functions. The results of this study are expected to contribute to the identification of new gene functions, by analyzing gene function of crops.

Corresponding Author: Tel. 041-330-1201, E-mail: yjpark@kongju.ac.kr

Construction of rice haplotype/INDEL information for rice functional study

Kyu-Won Kim^{1*}, Jung-Rye Nam^{1*}, Yong-Jin Park^{1,2}

¹Center for crop genetic resource and breeding (CCGRB), Kongju National University, Yesan 32439, Korea

²Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 32439, Korea

In order to effectively utilize the results of genome-wide association study (GWAS) to the researches for the fields of molecular biology, haplotype, well-made database which is suitable for genetic functional study is needed. Indel has a higher rate of mutation than SNP, and it has a significant effect on gene function changes through frame shift as well as SNP. Indel information is therefore of considerable importance in studies of gene function. However, it is difficult for researchers to easily and freely access Indel information. We constructed haplotype and indel information for rice as a model crop. We expect that the use of indel information will be activated through our study.

*These authors contributed equally to this work.

Corresponding Author: Tel. 041-330-1201, E-mail: yjpark@kongju.ac.kr

A comparison of pipelines for quantifying transcript expression from RNA-Seq data of Korean rice core collection

Jung-Rye Nam^{1*}, Kyu-Won Kim^{1*}, Yong-Jin Park^{1,2}

¹Center for crop genetic resource and breeding (CCGRB), Kongju National University, Yesan 32439, Korea

²Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 32439, Korea

RNA-Seq is a technique for analyzing the presence and amount of RNA molecules in a given sample based on NGS technology. To estimate transcription quantity from RNA-Seq data, the sequence readings are aligned to the reference genome or transcriptome, and then the amount of expression is estimated by their alignment. Practically, various techniques are used for implementation. Estimation method for transcription quantity of each technique is slightly different. We focused on different features on estimation by different pipelines and compared between pipelines, and in particular, traced genes that differ significantly by pipelines. We distinguished several cases of features where the differentiation is made. We hope that this study will provide a more accurate estimate of quantification of transcripts in the field of crop research.

*These authors contributed equally to this work.

Corresponding Author: Tel. 041-330-1201, E-mail: yjpark@kongju.ac.kr

Tolerance of anaerobic conditions caused by flooding during direct seeding and germinated seedling

Win Htet Oo¹, Yong-Jin Park^{1,2}

¹Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 32439, Korea.

²Center for crop genetic resource and breeding (CCGRB), Kongju National University, Yesan 32439, Korea

Rice is semi-aquatic, adapted to a wide range of hydrologies, from aerobic to anaerobic soils and flooded condition, to even deeply submerged soils in flood-prone areas. Flooding is a frequent hazard in lowland rice environments and is expected to intensify with climate change. Tolerance of anaerobic conditions exposed to complete submergence exploit two contrasting suites of traits, escape or quiescence, to survive this stress. In this study, comparison of anaerobic tolerance between two conditions, direct seeding and germinated seedling, to screen submergence tolerance variety from Korean Rice Heuristic Set. The “quiescent and elongation strategies” under control by the quantitative trait locus SUBMERGENCE 1 (SUB1) has been considered as a major mechanism controlling submergence tolerance in rice. Modern rice varieties are sensitive to flooding during germination and early growth but few landraces capable of germination under these conditions have recently been identified, enabling research into tolerance mechanisms. Further characterization of contrasting genotypes would help in elucidating the genetic and biochemical regulatory and signaling mechanisms associated with tolerance.

Corresponding Author: Tel. 041-330-1201, E-mail: yjpark@kongju.ac.kr

Transcriptome wide association studies reveal complex regulation network of rice eating and cooking quality

Qiang He¹, Kyu-Won Kim¹, Weiguo Zhao³, Yong-Jin Park^{1,2}

¹Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan, 32439, Republic of Korea.

²Center for crop genetic resource and breeding (CCGRB), Kongju National University, Yesan, 32439, Republic of Korea

³School of Biology and Technology, Jiangsu University of Science and Technology, Sibaidu, Zhenjiang, Jiangsu, 212018, PR China

Improvement of rice eating and cooking quality (ECQ) is among the most important aims in current breeding programs. Genome-wide association studies (GWAS) and other methods have identified many loci associated with rice ECQ traits, however, many genetic variants influence complex traits by modulating gene expression, the biological mechanisms remain largely unknown. Here, we performed a transcriptome-wide association study (TWAS) to identify significant expression-trait associations with 10 ECQ traits using 84 *Japonica* rice accessions and 42,205 transcripts. There were 285 significant transcript associations for ECQ traits (FDR < 0.05), among 58 for ACC, 175 for PRO, 19 for PV, 16 for CS, 6 for PeT and 52 for PTemp. These associated genes mainly involved in the metabolic, biosynthesis of secondary metabolites and peroxisome pathways. For the genes associated with ECQ traits, variation in expression could be explained by expression quantitative trait loci (eQTLs). Total 66,905 eQTLs for 285 e-traits ($p < 1e-16$), including 21,747 cis-eQTLs (32.5%) and 45,158 trans-eQTLs (67.5%), corresponding to 47,941 unique SNPs that affect the expression of 43 genes. The co-expression network for the genes associated with ECQ traits also constructed, 130 genes (45.6%) produced at least one network. Our results showcased the power of integrating genotype, gene expression and phenotype to gain insights into the genetic basis of ECQ traits, and will be providing an informative resource for studying rice ECQ traits molecular regulation mechanisms and be useful for rice molecular assistant selection breeding program aimed at developing new varieties with a high level of ECQ.

Corresponding Author: Tel. 041-330-1201, E-mail: yjpark@kongju.ac.kr

조생 황색 찰옥수수 신품종 “황찰옥”

최홍집¹, 오태영², 허창석¹, 이지윤¹, 배정숙¹, 김세종¹

¹대구광역시 북구 칠곡중앙대로 경상북도농업기술원 작물육종과

²경상북도 봉화군 봉성면 경상북도농업기술원 봉화약용작물연구소

우리나라 찰옥수수 생산규모는 재배면적 15,000~20,000ha, 생산량은 80,000톤 정도이며 전체 시장규모는 3,000억 원 정도로 추정되고 있다. 그러나 재배되고 있는 대부분의 옥수수가 국내에서 보급되고 있는 흰색 찰옥수수이다. 본 연구에서는 베타카로틴, 지아산틴 등 기능성 물질이 함유된 유색찰옥수수 품종을 개발 보급하기 위해 2002년부터 황색찰옥수수 유전자원을 수집하여 교배 및 인공수분을 통해 계통을 육성하여 2008년도에 GYW1과 GYW4 양친계통을 육성하였고, 2011년도에 GYW4를 종자친으로 하고 GYW1을 화분친으로 하여 유망교잡종으로 선발하였다. 2012년부터 2013년까지 2년간 특성평가와 성능검정을 수행하였으며 2014년부터 2016년까지 3년간 전국 5개 지역에서 지역적응성 시험을 수행하여 성능평가와 균일성, 안정성 시험을 거쳐 “황찰옥”으로 품종명칭을 정해 2016년 12월 품종보호출원 하였다. 황색 찰옥수수 신품종 “황찰옥”은 단교잡종으로 웅수색과 자수색이 담녹색이며 원통형이다. 이삭특성으로 이삭길이는 18cm, 직경 4.2cm, 착립장률 98%, 평균 이삭중 200g 정도였다. 10a당 이삭 수는 6,543개로 표준품종인 일미찰에 비해 3% 많았다. 한편 파종에서 출사까지의 소요일수는 62일로 표준품종인 일미찰에 비해 9정도 빨라 조기 수확이 가능한 품종으로 확인되었다. “황찰옥”의 채종시험 결과 모본과 부본을 2:1 비율로 파종하였을 때 10a당 132kg을 수확할 수 있었다.

***주저자:** Tel. 053-320-0226, E-mail: chj1217@korea.kr

CRISPR/Cas9 기반 천연독성 솔라닌 생합성 조절을 위한 기초연구

김미진^{1,2*}, 문기범¹, 사미나단수브라야², 장지영¹, 배상수³, 이금주², 김현순¹

¹대전광역시 유성구 과학로 125 한국생명공학연구원 식물시스템공학연구센터

²대전광역시 유성구 대학로 99 충남대학교 농업생명과학대학 원예과

³서울시 성동구 왕십리로 222 한양대학교 자연과학대학 화학과

감자 (*Solanum tuberosum* L.)는 세계 4대 작물 중의 하나로서 전세계인의 중요한 식량자원일 뿐 만 아니라 표준유전체가 밝혀져 연구모델로서도 그 가치가 우수한 작물이다. 감자에는 솔라닌이라는 천연독성 물질이 존재하는데, 이 솔라닌은 가지과에 일반적으로 있는 Glycoalkaloid 독성으로 아린맛, 구토, 식중독, 현기증 등 사람에게 부작용을 유발할 수 있다. 수확 후에도 합성이 진행되고 취급방법이나 저장조건에 따라 화합물이 증가하는 것으로 알려져 있다. 따라서 맛과 안전성을 고려한 감자의 활용도 증가를 위하여 연구가 필요하고 판단하였고, 유전자가위 CRISPR/Cas9(Clustered Regularly-Interspaced Short Palindromic Repeats/CRISPR associated protein 9)을 이용해 솔라닌 생합성에 관여하는 유전자를 교정하여 솔라닌 생합성 조절을 위한 기초연구를 수행하였다. 유전자의 교정여부를 확인하는 방법으로 Deep sequencing과 HRM (High resolution melting)을 수행하였고, Deep sequencing 결과 염기 삽입, 결실 등이 일어났으며 0.2~2.2%에 변이율을 확인하였다. HRM분석 결과에서는 또한 Wild type과 CRISPR/Cas9 처리한 유전자 간 뚜렷한 Melting curve 차이를 확인함으로써 유전적 변이가 일어났다고 판단할 수 있었다.

*주저자: Tel. 042-860-4494, E-mail: mijin364@kribb.re.kr

Transcriptome analysis of putative MYB-bHLH-WD40 transcription factors in purple and yellow seeds of wheat (*Triticum aestivum* L.) during seed development

Paulina Calderón Flores, Dae Yeon Kim, Yong Weon Seo*

Department of Biosystems and Biotechnology, Korea University, Seoul 136-713, Republic of Korea

Transcription factors (Tfs) naturally act as master regulators of cellular processes. They have broad functions such as regulation of floral organ development, photomorphogenesis, epidermal cell differentiation, hormonal responses, and flavonoid biosynthesis, also they act in concert with other regulations, the same transcription factor can be used repeatedly, with the outcome of the DNA binding event determined by which other regulators act in concert or opposition. The transcription complex composed of a WD40, a bHLH and a MYB protein regulates the expression of multiple distinct target genes in a range of plant species. It has been reported in rice, *A. thaliana*, *petunia hybrida* and *Zea mays*, that the bHLH interact with several MYB proteins.

In this study, we performed transcriptome analysis of two samples of wheat seeds, Deep Purple (P) and Yellow (Y) during three developmental stages (early, middle, and late stage), 10 Days After Flowering (DAF), 20 DAF, and 30 DAF. Furthermore, we performed a Differential Expression Analysis to investigate which Tfs (MYB, bHLH or WD) are up or down-regulated and in which stage, and to analyze if there was difference between Yellow and Deep Purple samples.

It seems that most of the Transcription Factors involved during the seed development between the Yellow and Purple samples are not the same and if the same Tf is shared, they are not expressing at the same time, we speculate that testa color is involved, further research need to be done to research if this Transcription Factors are working together to create some MYB-bHLH-WD complex to regulate gene expression.

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*Corresponding Author: Tel. +82-2-3290-3005, E-mail: seoag@korea.ac.kr

Differential gene expression of transcription factors related to the flavonoid pathway in the transcriptome of yellow and purple seeds of wheat (*Triticum aestivum* L.) during seed development

Paulina Calderón Flores, Dae Yeon Kim, Yong Weon Seo*

Department of Biosystems and Biotechnology, Korea University, Seoul 136-713, Republic of Korea

Transcription factors (Tfs) naturally act as master regulators of cellular processes. They have broad functions such as regulation of floral organ development, photomorphogenesis, epidermal cell differentiation, hormonal responses, and flavonoid biosynthesis.

The transcription complex composed of a WD, a bHLH and a MYB protein regulates the expression of multiple distinct target genes in a range of plant species. It has been reported in rice, *A. thaliana*, *petunia hybrida* and *Zea mays* that the bHLH interact with several MYB proteins, furthermore in other plant species it has been reported the requirement for a WD-bHLH-MYB transcription complex for the control of anthocyanin biosynthesis. We performed transcriptome analysis during early [10 Days after Flowering (DAF)], middle (20 DAF) and late (30 DAF) stages of seed development to identify putative MYB-bHLH and WD transcription factors related to the flavonoid, more specific to the proanthocyanidin, pathway. We cloned and sequenced some putative genes and found some amino acid differences between samples, even insertions or deletions of several amino acids. We need to further analyze using yeast two hybrid to prove if actually there is interaction between these Transcription factors and know if they are working together in the flavonoid production, moreover, to investigate if the deleted or inserted amino acids are related to the interaction between these MYB-bHLH-WD complex function.

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*Corresponding Author: Tel. +82-2-3290-3005, E-mail: seoag@korea.ac.kr

Transcript analysis during wheat grain filling period under the heat stress

Chan Seop Ko¹, Meong Kyu Ou², Jong Nae Hyun², Kyung Hun Kim², Jin Baek Kim³, Min Jeong Hong³, Yong Weon Seo^{1*}

¹Department of Biosystems and Biotechnology, Korea university, Anam-ro 145, Seong-Buk, Seoul, Korea.

²Department of Southern Area Crop Science, NICS, Miryang-si, Gyeongsangnam-do, Korea

³KAERI Advance Radiation Technology Institute, Jeongeup-si, Jeollabuk-do, Korea

Hexaploid wheat (*Triticum aestivum* L.) represents about 30% of the world's cereal numbers, with over 220 million ha cultivated worldwide. Heat stress is one of the major environmental factors that give detrimental effect on crop yields as well as quality. The increased temperature during reproductive phase of plant growth has emerged as a serious problem all over the world. Korean wheat cultivars that were developed for various characteristics such as winter hardness, earliness, and pest resistance have been released since 1960s. However, heat stress which was minor consideration up to 1990s, is now increasing problem. We used "Baegjoong" which is developed for noodle making and its growing area is increasing. Plants were grown at optimum environment until 8 days after flowering. Plants that are subjected to heat stress are moved to phytotron set 33°C/31°C (day/night). The heat treated plants were brought back to normal environment until harvest. Whole spikes were collected on stressed periods (DAF8, DAF10, DAF12) and soothing period (DAF15) for total RNA extraction. The transcript results showed that most of the transcripts share treated and control, and only 45 and 6 high and low expression, respectively, during heat stress were found. Differentially expressed genes will be validated for further elucidation of gene functions.

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*Corresponding Author: Tel. +82 2 3290 3005, E-mail: seoag@korea.ac.kr

Transcript and protein expression analysis of colored-grain wheat during grain development

Dae Yeon Kim¹, Min Jeoung Hong², Yong Weon Seo^{1*}

¹Department of Biotechnology, Korea University, Seoul 136-713, Republic of Korea

²Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, 29 Geomgu, Jeongseup 580-185, Republic of Korea

Hexaploid wheat is one of the most important cereal crops for human nutrition. Molecular understanding of the biology of the developing grain will assist the improvement of yield for different environments. In this study, we demonstrate transcript and protein expression analysis during seed development to understand the process of accumulation of phytochemicals in colored-wheat. The transcriptome from three different stages of developing spikelets in colored-wheat was determined using RNA sequencing. About 1200 and 3100 of significant transcripts (p-value < 0.05) from middle and late stages of grain development comparing with early stage of grain development were aligned to IWGSC1+popseq DB which is composed of over 110,000 transcripts including 100,934 coding genes. Gene ontology analysis were conducted and KEGG mapping was performed to show expression pattern of biosynthesis genes related in flavonoid, isoflavonoid, flavons and anthocyanin biopathway. Expression patterns of flavonoid biosynthesis pathway genes and candidate MYB – bHLH – WD40 (MBW) complex genes in RNAseq analysis during seed development were displayed by heatmap. Moreover, proteins shown high expression pattern at DAF 20 and DAF 30 compared to DAF 10 were selected by a k-means clustering method and identified by MLDI-TOF analysis for peptide mass fingerprinting.

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***Corresponding Author:** Tel. +82-2-3290-3005, E-mail: seoag@korea.ac.kr

Genetic analysis of dwarf wheat mutant generated by gamma ray irradiation

Eun Jeong Lee, Jin Seok Yoon, Yong Weon Seo^{*}

Department of Biosystems and Biotechnology, Korea University, Seoul 136-713, Republic of Korea

Wheat (*Triticum aestivum* L.), managing about 35% of the human population, is one of the most significant staple crops; moreover, consumption of crops has been increasing rapidly as the population grows over the decades, but the production rate can't keep up with the growing population. Therefore, advances in grain yields are the main ways to solve the challenge and meet the global demand. One approach for improving grain number and yield was the reduced plant height (dwarfing plants) that led to impressive increases in grain numbers and yields during the green revolution in wheat. It has been known that the genes associated with the dwarf stature in wheat are "Reduced Height Genes" (*Rhts*). Those dwarfing genes confer the reduction in stem elongation by a limited response to the phytohormone resulting in lodging resistance, improved harvest index, increase in partitioning of assimilates to the grain, more fertile spike, efficient utilization of the favorable environment, and yield benefits. In this study, genetic constitute of *Rhts* and their relationship with phenotype was investigated using F₂ segregation populations derived from crosses between "Keumkang" (tall) and "15DSPL014" (short line). Molecular markers that are relevant to dwarf genes are applied to individual plant for marker validation. The results could provide novel information about the effect of the dwarfing genes on plant height, and demonstrate potential availability for improving grain numbers and yields in wheat.

***Corresponding Author:** Tel. +82-2-3290-3005, E-mail: seoag@korea.ac.kr

Development and flowering in wheat relative to vernalization period

Cheol Won Lee, Yong Weon Seo*

Department of Biosystems and Biotechnology, Korea University, Seoul 136-701, Republic of Korea

Flowering is a critical change which transit from vegetative stage to reproductive stage. In wheat, various environmental and endogenous cues determine flowering time. These factors and flowering pathways interact with each other and work as regulatory networks. Of these, vernalization, the induction of a plant's flowering process by exposure to the prolonged cold, specially works on flowering through the regulation of various vernalization genes and transcription factors. To clarify an influences of vernalization on the wheat flowering, we set experimental groups with different exposure length under low temperature. With this, we also analyzed other phenotype results such as leaf and shoot length. We used two Korean cultivars, Keumgang and Yeongkwang, which have different maturity. They were exposed under the -4°C , treated different period per five days. The longer wheat were exposed under low temperature, the more gap of flowering time was increased between two cultivars. However, spike primordium were ranked same stages at same wheat development stages although the treatment of vernalization period was different. The obtained results will provide valuable information to understand the role of vernalization for flowing regulation in wheat aimed at establishing the mechanism of wheat flowering.

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*Corresponding Author: Tel. 02-3290-3005, E-mail: seoag@korea.ac.kr

RNA-seq analysis of wheat-rye translocations under cold stress

Woo Joo Jung, Yong Weon Seo*

Department of Biosystems and Biotechnology, Korea University, Seoul 136-701, Republic of Korea

Cold stress is one of the most fatal abiotic stresses affecting the wheat production. Plants adjust to temperature changes by up-regulating cold-tolerant genes at non-freezing low temperature, which is called acclimation. Though wheat-rye translocation lines are known for their high adaptiveness to harsh environments and tolerance to biotic stresses, molecular mechanism in the process of acclimation is not fully understood. In the present study, we performed an RNA-seq analysis of 1BL.1RS translocation and its near-isogenic line under normal and low temperatures (4°C). Total RNA extracted from the wheat seedlings were used to synthesize cDNAs and construct a sequencing library. The high-throughput sequencing was done using the Illumina HiSeq 2500 platform. After trimming low-quality reads from raw reads, HISAT2 was utilized to map the raw reads to the IWGSC RefSeq v1.0. Gene function was annotated using BLAST2GO program based on NCBI nr protein database, InterProScan, Gene Ontology (GO) and KEGG pathways. Differentially expressed genes (DEG) with an adjusted p-value ≤ 0.05 and fold changes ≥ 2 were selected using featureCounts and DEseq. A Venn diagram analysis revealed that a certain group of genes was up-regulated specifically in 1BL.1RS under the cold treatment. Finally, real-time PCR analysis was performed to verify the DEGs. The results of this study show the process of gene expressions under low temperature in both 1BL.1RS and normal wheat. Further studies will be needed to fully investigate the roles of the identified genes in cold tolerance.

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*Corresponding Author: Tel. 02-3290-3005, E-mail: seoag@korea.ac.kr

qCRS12, a major QTL related to cold tolerance at seedling stage in rice

Tae-Heon Kim¹, Su-Min Jo¹, Saes-Beul Lee¹, Ji-Yoon Lee¹, Sang-Ik Han¹, Jun-Hyeon Cho¹, Jong-Hee Lee², You-Chun Song¹, Dong-Soo Park¹, Myung-Kyu Oh¹, Dongjin Shin^{*1}

¹Department of Southern Area Crop Science, National Institute of Crop Science, RDA, Miryang 50424, Republic of Korea

²Research Policy Bureau, RDA, Jeonju, 54875, Republic of Korea

Rice is a staple food crop for more than half of the world population. Rice production is largely affected by various environmental conditions such as cold, heat and flooding annually. Especially rice is a highly sensitive to low temperature below 15-20 °C because of originating from tropical or subtropical climates. Seedling of rice is easily damaged to low temperature and result in yellowing, growth retardation, reduced tillering, which can cause severe yield losses. In addition, more frequent and intense cold damage of rice has been occurred in recent years by global climate change. A sharp decrease in rice production on account of cold damage constitute a threat to global food security. We used a recombinant inbreeding lines (RIL) population of 384 individuals derived from a cross between Hanareum 2, a highly cold sensitive variety and Unkwang, a cold tolerant variety for molecular mapping of QTLs related to cold tolerance. Seedling discoloration of each lines and parents caused by cold response were investigated in field condition after transplanting in 2016-2017. The seedling of each lines and parents was subjected to low temperate by 5~13 °C during 14 days. The cold recovery score (CRS) of RILs was recorded after 4 days recovery period according to standard evaluation system (SES, IRRI). Total of 10 QTLs were detected on chromosome 1, 6, 7, 8, 10, 11 and 12 using cold tolerance traits, seedling discoloration and cold recovery score in 384 RILs. The *qCRS12*, which detected on chromosome 12 between two flanking markers id12002113, id12002563 (1.1 Mbp) showed 25 LOD score with 26% of phenotypic variation of cold recovery score in RILs population. The positive allele contributing to cold tolerance came from the cold tolerant parent Unkwang. The result may provide useful information for a marker-assisted breeding program to improve cold tolerance in rice.

*Corresponding Author: Tel. 055-350-1185, E-mail: jacob1223@korea.kr

Improved method for reliable HMW-GS identification by RP-HPLC and SDS-PAGE in common wheat cultivars

Jong-Yeol Lee^{*1}, You-Ran Jang¹, Susan B Altenbach², Sun-Hyung Lim¹, Young-Mi Kim¹

¹National Academy of Agricultural Science, RDA, Jeonju, 560-500, Korea

²USDA-ARS, Western Regional Research Center, 800 Buchanan Street, Albany, CA 94710

The accurate identification of alleles for high-molecular weight glutenins (HMW-GS) is critical for wheat breeding programs targeting end-use quality. RP-HPLC methods were optimized for separation of HMW-GS, resulting in enhanced resolution of 1By and 1Dx subunits. Statistically significant differences in retention times (RTs) for subunits corresponding to HMW-GS alleles were determined using 16 standard wheat cultivars with known HMW-GS compositions. Subunits that were not identified unambiguously by RP-HPLC were distinguished by SDS-PAGE or inferred from association with linked subunits. The method was used to verify the allelic compositions of 32 Korean wheat cultivars previously determined using SDS-PAGE and to assess the compositions of six new Korean cultivars. Three cultivars contained subunits that were identified incorrectly in the earlier analysis. The improved RP-HPLC method combined with conventional SDS-PAGE provides for accurate, efficient and reliable identification of HMW-GS and will contribute to efforts to improve wheat end-use quality.

*Corresponding Author: E-mail: jy0820@korea.kr

Proteomic analysis of gliadin fractions in a common wheat

Jong-Yeol Lee^{*1}, You-Ran Jang¹, Sun-Hyung Lim¹, Kyoungwon Cho¹

¹National Academy of Agricultural Science, RDA, Jeonju, 560-500, Korea

Wheat gliadins confer the dough elasticity and extensibility through forming the gluten complex with glutenins and contain dominant epitopes to cause celiac disease (CD) and wheat-dependent exercise-induced anaphylaxis (WDEIA). The gliadins, including α -/ β -, γ - and ω -gliadins, in hexaploid wheat cultivars are encoded at *Gli-1*, *Gli-2* and *Gli-3* loci on homoeologous group 1 and 6 chromosomes. The large sizes of their gene families, the similar genetic structure and the large proportion of pseudogenes and the lack of genomic data make it difficult to study the composition of gliadin in hexaploid wheat variants. In this study, to challenge the difficulty using the improved proteomic tools, we extracted ethanol-soluble gliadin fractions from flour of a Korean wheat bread cultivar Keumkang (*Triticum aestivum* cv. Keumkang). Total 98 spots from the fraction were separated on 2-DGE gel, digested with chymotrypsin and then subjected to a nanoUPLC qTOF-MS/MS. Using Scaffold program linked to NCBI *Triticeae* and Butte 86-specific protein databases, α -/ β -gliadins, γ -gliadins, LMW-GSs, ω -gliadin and non-gluten proteins were identified to be present as the major protein in thirty-one (40.8%), twenty-eight (27.7%), eleven (10.6%), one (0.5%) and seven spots (5.3%) of 96 spots, respectively. The composition and repetitive number of CD- and WDEIA-relevant epitopes in the gliadin sequences indicate the potential riskiness of wheat cv. Keumkang flour in patients with CD and WDEIA and suggest the way forward for improving the food processing qualities and reducing the gliadin-derived adverse health effects.

***Corresponding Author:** E-mail: jy0820@korea.kr

RNA interference-mediated simultaneous suppression of seed storage proteins in rice grains

Jong-Yeol Lee^{*1}, You-Ran Jang¹, Sun-Hyung Lim¹, Kyoungwon Cho¹

¹National Academy of Agricultural Science, RDA, Jeonju, 560-500, Korea

Seed storage proteins (SSPs) such as glutelin, prolamin and globulin are abundant components in some of the most widely consumed food cereals in the world. Synthesized in the rough endoplasmic reticulum (ER), SSPs are translocated to the protein bodies. Prolamins are located at the spherical protein body I derived from the ER, whereas glutelins and globulin are accumulated in the irregularly shaped protein bodies derived from vacuoles. Our previous studies have shown that the individual suppression of glutelins, 13-kDa prolamins and globulin caused the compensative accumulation of other SSPs. Herein, to investigate the phenotypic and molecular features of SSP deficiency transgenic rice plants suppressing all glutelins, prolamins and globulin were generated using RNA interference (RNAi). The results revealed that glutelin A, cysteine-rich 13-kDa prolamin and globulin proteins were less accumulated but that glutelin B and ER chaperones, such as binding protein 1 (BiP1) and protein disulfide isomerase-like 1-1 (PDIL1-1), were highly accumulated at the transcript and protein levels in seeds of the transformants compared to those in the wild-type seeds. Further, the transcription of starch synthesis-related genes was reduced in immature seeds at two weeks after flowering, and the starch granules were loosely packaged with various sphere sizes in seed endosperms of the transformants, resulting in a floury phenotype. Interestingly, the rates of sprouting and reducing sugar accumulation during germination were found to be delayed in the transformants compared to the wild-type.

***Corresponding Author:** E-mail: jy0820@korea.kr

Enhancing of flower color with combinatorial expression of transcription factor genes, mPAP1 and B-Peru

Da-Hye Kim^{*1}, Jung Ae Park¹, Sung Ok Park¹, Sang-Kyu Park¹, Jong-Yeol Lee¹, Sun-Hyung Lim¹

¹National Academy of Agricultural Science, Rural Development Administration, Jeonju, 54874, Republic of Korea

Flower color is one of the main target traits in the flower breeding. To production of novel flower color in transgenic plants, it requires transgene that confer a useful trait and flower-specific promoters. To get the flower specific promoter, we focused on the late biosynthetic gene of anthocyanin, which is exclusively accumulated in flower of tobacco plant. Anthocyanidin synthase (ANS), a key enzyme in the late stages of the biosynthesis of anthocyanins, was cloned from flowers of the tobacco plant (*Nicotiana tabacum*). Analysis of the spatial regulation of expression of tobacco ANS gene has revealed that levels of its transcript are particularly abundant in flower tissues. To investigate activity of the promoter of the NtANS1 gene, transgenic tobacco plants with β -glucuronidase (GUS) under the control of the NtANS1 promoter (NtANS1-P) exhibited the authentic flower-specific expression. To enhance flower colors, the mPAP1 and B-Peru TF genes were both expressed in tobacco plant under NtANS1-P. Transgenic tobacco plants showed the normal growth and distinct reddish colors in flowers compared to nontransgenic tobacco plants. Structural genes and regulatory genes of anthocyanin biosynthetic pathway were significantly upregulated in transgenic tobacco flower. Consistent with gene expression profiles, anthocyanin content was significantly higher in transgenic tobacco flower. This result suggests that combination both of target trait gene, TFs and flower-specific promoter, NtANS1-P can show a reddish flower color in transgenic tobacco without any detrimental phenotype such as growth retardation. In conclusion, it might have valuable components for flower color modification through metabolic engineering.

***Corresponding Author:** E-mail: kimdh143@naver.com

Chromosomal assignment of gliadin fractions in Chinese spring and its aneuploid lines using RP-HPLC, SDS-PAGE, A-PAGE and 2-DGE

You-Ran Jang^{*1}, Sun-Hyung Lim¹, Jong-Yeol Lee¹

¹National Academy of Agricultural Science, RDA, Jeonju, 560-500, Korea

Gliadins, which account for 40-50% of total proteins, contribute to viscosity and elongation and play an important role in the formation of wheat dough. The genes encoding gliadins are mainly located on the short arms of chromosome 1 and 6. Gliadins are divided into four groups ω 5-, ω 1,2-, α - / β -, γ -gliadin. The ω 5-gliadin, encoded on wheat chromosomes 1, is the major antigen of wheat dependent exercise-induced food anaphylaxis (WDEIA). γ -gliadin encoded on chromosome 1 and α - / β -gliadin present on chromosome 6 are the major antigens of celiac disease. We conducted RP-HPLC, SDS-PAGE, A-PAGE and 2-DGE in gliadin fractions using Chinese Spring and its aneuploid lines of chromosome 1 and 6 to assign the individual gliadins to their chromosome encoded. In RP-HPLC, all peaks except one peak could be explained, but much 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. From the above results, we conclude cautiously that there might some gliadin proteins encoded on other chromosomes than chromosome 1 and 6. To prove this, additional experiments are required with the MS / MS identification of these 11 spots and analysis of CS aneuploid lines except for chromosome 1 and 6 as further study.

***Corresponding Author:** E-mail: jang6122@jbnu.ac.kr

Accurate and reliable analysis of LMW-GS alleles using Aroona NILs and standard cultivars

Su-Jin Cho^{*1}, Jin Sun Kim¹, You-Ran Jang¹, Sun-Hyung Lim¹, Jong-Yeol Lee¹

¹National Institute of Agricultural Science, RDA, Jeonju, 54874, Korea

Glutenin is a protein that is soluble in alkali even in gluten, which is a major component of wheat storage proteins. Glutenin is divided into high-molecular weight glutenin subunits (HMW-GS) and low-molecular weight glutenin subunits (LMW-GS) according to molecular weight size in SDS-PAGE. The effect of each alleles of glutenin on wheat quality properties is very important, each alleles is different from each other. Therefore, we need to know and identify each exact allele. In particular, LMW-GS plays an important role in the extensibility of wheat. On the other hand, HMW-GS alleles have been studied to some extent. However, LMW-GS allele studies are very insufficient and difficult to identify exact alleles of LMW-GS because there are many variations of allele and mobility is overlapped with gliadin fraction. In previous studies, the standard cultivar was checked by 2-DGE for the LMW-GS allele assay, but it was not clearly distinguishable. In this study, a comprehensive allele was analyzed by both 2-DGE and RP-HPLC experiments using the Aroona LMW-GS NILs (near isogenic lines) for more accurate and rapid LMW-GS allele validation. NIL refers to one line in which only one target LMW-GS allele is different and the remaining genetic composition is same. As a result of comparison of 2-DGE and RP-HPLC in the Aroona NILs, it was possible to establish more accurate alleles than existing alleles which was not distinguished by standard cultivars. These results are expected to contribute faster screening of improved wheat varieties development when breeders identify alleles.

***Presenting Author:** Tel. 063-238-4616, E-mail: bartbox@naver.com

Cloning and functional characterization of floral scent full length genes in *Cymbidium* Cultivar ‘Sunny Bell’ Flowers

Mummadi Reddy Ramya, Hye Ryun An, Pue Hee Park^{*}

Floriculture Research Division, National Institute of Horticultural & Herbal Science (NIHHS), Rural Development Administration (RDA), Wanju, 55365, Korea

Flower volatiles are valuable for many floricultural crops. Floral scents play key role to attract the pollinators and ensure the fertilization. The genus *Cymbidium* belongs to the Orchidaceae family and is economically important due to many species having beautiful and fragrant flowers. *Cymbidium* cultivar ‘Sunny Bell’ flowers are highly fragrant and small size pink flowers. Based on the richer volatiles in this plant we needed to isolate the floral scent pathway full length genes. In this paper, three genes encoding 1- deoxy-D-xylulose-5-phosphate synthase (DXS), 1-deoxy-D-xylulose-5-phosphate reductoisomerase (DXR), and linalool synthase (LIS) involved in the monoterpene biosynthesis pathways were cloned and sequenced by using topo cloning kit. In functional characterization LIS gene 81% matches Rose, and DXS and DXR sequences similar to *Ricinus communis* and *Hevea brasiliensis*. The variations in the constituent and content of volatile monoterpenes including linalool and geraniol For expression analysis among the three genes LIS were highly expressed in all flower stages. In addition DXS, and DXR also expressed in full flowering stages at low level and down regulated in early developmental stages. According to bioinformatics analysis the deduced amino acid sequences were 382, 342 and 359 respectively. However the full length floral scents genes which as LIS, DXR and DXS highly expressed in all floral organs and floral developmental stages. According to these results we confirmed that monoterpene pathway might be leading pathway. In further we will focus on regulation model through floral scent in *Cymbidium* cultivar ‘Sunny Bell’.

Identification of nitrogen-use-efficiency coding and noncoding transcripts in *Oryza sativa* L..

Seon-Ju Shin¹, Jae-Hee Lee¹, Hongryul Ahn², Inuk Jung³, Sun Kim^{2,3}, Hawk-Bin Kwon^{1*}

¹Department of Biomedical Sciences, Sunmoon University, Asan 336-708, Republic of Korea

²Department of Computer Science and Engineering, Seoul National University, Gwanak-Gu, Seoul, 151-744, Republic of Korea

³Interdisciplinary Program in Bioinformatics, Seoul National University, Gwanak-Gu, Seoul, 151-747, Republic of Korea

Nitrogen concentration in soil is one of the main factors directly affecting crop yield. However, the use of large amounts of nitrogen fertilizer to promote growth causes environmental problems. Therefore, we sought to identify genes involved in nitrogen metabolism that could improve the nitrogen metabolism efficiency in rice. In this study, we identified several novel nitrogen-use-efficiency (NUE) regulatory coding and noncoding transcripts in *Oryza sativa* L., using the next generation sequencing (NGS) technique and bioinformatics analyses. We investigated the functions of the activated/suppressed differentially expressed genes under nitrate treatment by Gene Ontology (GO) enrichment analysis. We identified the coding and noncoding transcripts (and clusters) that responded differently upon increasing or decreasing the nitrogen concentration. We then analyzed the transcription factors controlling the expression of these gene clusters through gene module analysis, and analyzed interactions between coding and noncoding genes through gene expression networking

***Corresponding Author:** Tel. 041-530-2288, E-mail: hbkwon@sunmoon.ac.kr

Reconstruction of composite comparative map including ten legume species

Chaeyoung Lee¹, Jin-Hyun Kim¹, Joo-Seok Park², Yoram Choi², Min-Gyun Jeong² and Hong-Kyu Choi^{3*}

¹Department of Medical Bioscience, Dong-A University, Busan, Republic of Korea

²Department of Applied Bioscience, Dong-A University, Busan, Republic of Korea

³Department of Molecular Genetics, Dong-A University, Busan, Republic of Korea

The Fabaceae (legume family) is the third largest and the second of agricultural importance among flowering plant groups. In this study, we report the reconstruction of a composite comparative map composed of ten legume genomes, including seven species from the galegoid clade (*Medicago truncatula*, *Medicago sativa*, *Lens culinaris*, *Pisum sativum*, *Lotus japonicus*, *Cicer arietinum*, *Vicia faba*) and three species from the phaseoloid clade (*Vigna radiata*, *Phaseolus vulgaris*, *Glycine max*). To accomplish this comparison, a total of 209 cross-species gene-derived markers were employed. The comparative analysis resulted in a single extensive genetic/genomic network composed of 93 chromosomes or linkage groups, from which 110 synteny blocks and other evolutionary events (e.g., 13 inversions) were identified. This comparative map also allowed us to deduce several large scale evolutionary events, such as chromosome fusion/fission, with which might explain differences in chromosome numbers among compared species or between the two clades. As a result, useful properties of cross-species genic markers were re-verified as an efficient tool for cross-species translation of genomic information, and similar approaches, combined with a high throughput bioinformatic marker design program, should be effective for applying the knowledge of trait-associated genes to other important crop species for breeding purposes. Here, we provide a basic comparative framework for the ten legume species, and expect to be usefully applied towards the crop improvement in legume breeding.

***Corresponding Author:** Tel. 051-200-7508, E-mail: hkchoi@dau.ac.kr

Efficient FISH analysis method using synthetic oligomers for conserved high copy repeat blocks

Nomar Espinosa Waminal^{1,2}, Remnyl Joyce Pellerin¹, Sung-Min Youn¹, Tae-Jin Yang^{2*} and Hyun Hee Kim^{1*}

¹Chromosome Research Institute, Department of Life Science, Sahmyook University, Seoul, 01795, Republic of Korea

²Department of Plant Science, Plant Genomics and Breeding Institute, and Research Institute of Agriculture and Life Sciences, College of Agriculture and Life Sciences, Seoul National University, Seoul, 08826, Korea

Fluorescence *in situ* hybridization (FISH) is a highly efficient molecular cytogenetic tool to visualize distribution of DNA elements in a genome. Conventional FISH procedure involves preparation of fluorescence-labeled probes that is time-consuming and requires technical experience. To improve this process, we designed oligodeoxynucleotide (ODN) probes for three commonly used targets, 5S, 45S rDNA, and telomere repeats. We designed twelve, four, and one ODN probes for 45S rDNA and 5S rDNA, and telomere tandem arrays, respectively. The rDNA probes has universal utility for plants including gymnosperms and angiosperms, animals, and fungi and telomere probe can be utilized for most of plants harboring *Arabidopsis*-type, (TTTAGGG)_n, telomere array. Use of different fluorochromes conjugated to the 5' end of each ODN probes permitted the simultaneous visualization of the genomic loci of the three target sequences which are commonly the most distinct feature of a chromosome complement. Utilization of pre-labelled ODN probes reduced efforts and time for FISH analysis. It greatly reduced the FISH hybridization time from ~16h at 37°C for conventional FISH to as short as 5 min at room temperature. The ODN probes can be ideal for routine FISH analysis even for species without preliminary chromosomal data. The method is efficient, reliable, and rapid in simultaneously detecting several target repeats, and is particularly useful in rapid chromosomal analysis of crop collections in breeding studies.

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***Corresponding Authors:** Tae-Jin Yang: Tel. 02-880-4547, 02-3408-2905, E-mail: tjyang@snu.ac.kr
Hyun Hee Kim: Tel. 02-3399-1715, E-mail: kimhh@syu.ac.kr

Function of fibrillin1a, 1b and 2 genes in highlight stress in *Arabidopsis*

Inyoung Kim, Hyun Uk Kim*

Department of Bioindustry and Bioresource Engineering, Plant Engineering Research Institute, Sejong University, Seoul, 05006, Republic of Korea

Fibrillin (FBN) 1a, 1b and 2 are lipid-associated proteins of plastids and accumulated under abiotic stress. In high light stress, FBN1a and 1b accumulation are regulated by abscisic acid (ABA) response regulators ABA-insensitive 1 (ABI1) and ABI2. It enhances resistance of photosystem II photoinhibition. The phenotype of triple *FBN1a, 1b, -2* suppressed transgenic plants generated by RNA interference (RNAi) using common sequences from three *FBN1a, 1b* and 2 show a lower shoot growth development and reduced anthocyanin accumulation under high light/cold stresses. These phenotype of transgenic plants are restored by jasmonate (JA) treatment. As a results, FBN1a, 1b, and -2 are expected to mediate by JA biosynthesis. In previous research, the functions of FBN2 is not well known. Our data suggest that the FBN2 interacted with PTM, a chloroplast envelope-bound transcription factor involved in retrograde signaling to mediate activation ABI4 transcription. To investigate detail molecular function of FBN1a, 1b and -2 under the high light/cold stress, we generated each of single and double mutants of *fbn1a* and *1b* using selection of T-DNA insertional mutants, and *FBN2* suppressed transgenic plant of using *FBN2-RNAi*. Also, we are generating triple mutants of *fbn1a, 1b, -2* combined with CRISPR/Cas9 gene editing system.

***Corresponding Author:** Tel. 02-3408-4318, E-mail: hukim64@sejong.ac.kr

Characterization of trichome morphology and aphids resistance of cultivated potato and its wild species

Kwang-Soo Cho*, Min-Kwon, Hong-Sik Won, Ji-Hong Cho, Ju-Seong Im, Jang-Gyu Choi and Young-Eun Park

Highland Agriculture Research Institute, National Institute of Crop Science, Rural Development Administration, Pyeongchang 232-955, Korea

Trichomes are specialized epidermal structures that protect plants from abiotic and biotic stresses. Cultivated potato (*Solanum tuberosum*) is known to have glandular and non-glandular trichomes. However, the classification of trichome types have not been studied in detail. In addition, little is known about what types of trichomes exist in its wild species. Here, one representative cultivated potato and 17 wild potato species were examined with FESEM (Field Emission Scanning Electron Microscopy) to compare trichome types, morphology, and density. Cultivated potato has two glandular and two non-glandular trichome types based on their morphology. All wild potato species tested here also have similar trichome types and have no unique trichome types. Among solanaceous species tomato trichome types (I-VII) were well characterized. So we designated potato trichome types with tomato trichome types. Previously known potato glandular type A and B (tomato trichome type VI and VII) were characterized by a very short stalk with irregularly shaped multi-celled heads (4 to 8) and by a short multi-cellular stalk with four-celled globular heads, respectively. Two potato non-glandular trichomes, previously not named, were characterized by a long multi-cellular stalk with multi-cellular bases (tomato trichome type II) and by a multi-cellular stalk with unicellular base (tomato trichome type III), respectively. Based on the trichome density, we could classified wild relative potato clones into four groups. First group (2 species) *S. berthaultii* and *S. hugaii* have high density of glandular type in abaxial and adaxial side. Second (1 species), *S. mochiense* have high density only non-glandular type trichomes only in abaxial side Third group (13 species), *S. raphanifolium*, *S. jamesii*, *S. cardiophyllum*, *S. hjertingii*, *S. stoloniferum*, *S. acaule*, *S. brevicale*, *S. chacoense*, *S. kurtzianum*, *S. verrucosum*, *S. pinnatisectum*, *S. iopetalum* have similar density of glandular and non-glandular type trichomes that of *S. tuberosum*. Fourth group (2 species), *S. microdontum* and *S. verni* have high density non-glandular type trichomes in abaxial and adaxial sides. To test infestation degree by aphids (*Macrosiphum euphorbiae*), four species include *S. tuberosum* were used. The lowest number (13.1) and highest (30.0) of honey dew spots secreted by aphids was shown in *S. hugaii* and *S. mochiense*, respectively. The degree of infestation by aphids was strongly negative correlated with total number of glandular trichome in potato abaxial and adaxial leaf sides.

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*Corresponding Author: Tel. 033-330-160, E-mail: kscholove@korea.kr

밀 육종 프로그램 이용을 위한 전분 특성 비교

조성우¹, 김학신², 최용현³, 최용석³, 박철수^{1*}

¹전북대학교 농업생명과학대학 작물생명과학과, ²국립식량과학원, ³사조동아원 (주) 중앙연구소

밀의 전분 특성은 국수와 빵의 부드러운 식미를 결정하는 주요 인자로 주로 아밀로스 함량에 영향을 받는다. 그러나, 비슷한 아밀로스 함량이라고 하더라도 전분의 팽윤(Swelling)과 호화(Pasting) 및 노화(Staling) 특성은 다양하게 나타나기 때문에 아밀로스 함량 측정만으로 식미가 우수한 자원 선별에는 한계가 있다. 그러므로 본 연구에서는 전분 특성을 평가하는 방법 간 비교를 통하여 육종에 효율적으로 이용이 가능한 분석 방법을 제시하고자 한다. 본 연구에는 2014년과 2015년에 수확한 15개 품종에 대해서 밀가루와 전분의 팽윤 및 호화 특성을 비교 분석하였다. 밀가루와 전분의 팽윤 및 호화 특성은 년차간 변이 보다는 품종간 변이에 영향을 많이 받는 것으로 나타나서 이들 특성을 육종 프로그램의 선발 지표로 이용이 가능할 것으로 보인다. 아밀로스 함량은 팽윤 특성과 높은 상관을 나타내었으며, 호화 특성에서도 setback값을 제외하고 높은 상관을 나타내었다. 밀가루와 전분의 팽윤 특성 간에는 높은 정의 상관을 나타내었고, 호화특성에서는 식미 특성과 높은 상관이 있는 peak viscosity와 breakdown이 밀가루와 전분 간에 높은 정의 상관을 나타내었다. 이를 통하여 단백질 및 전분 함량이 밀가루의 팽윤 및 호화 특성에 영향을 줄 수는 있지만 전분과 밀가루의 전분 특성 결과 간에 높은 상관이 나타나기 때문에 육종 프로그램에서는 밀가루를 이용한 전분 특성이 크게 문제가 되지 않을 것으로 생각되며, 분석에 시료가 적게 드는 팽윤 특성이 육종 프로그램에 이용이 보다 효율적일 것으로 보인다. 그러나 팽윤 부피와 무게 (Swelling volume and power) 분석간 차이는 발견하지 못했다. 그러나 밀가루를 이용한 팽윤 특성이 육종 프로그램에 이용된다고 하더라도 제분 과정이 필요하기 때문에 실제 육종에서 이용하기 위해서는 통밀(Wholemeal) 분쇄를 이용한 팽윤 특성 분석을 실시가 필요하다. 통밀을 이용할 경우 여러 가지 요인을 고려해야하기 때문에 이에 대한 연구는 추후 진행하고자 한다.

*주저자: Tel. 063-270-2533, E-mail: pc89@jbnu.ac.kr

국내 밀 육종 프로그램의 믹소랩 이용 품질 평가

조성우¹, 김학신², 최용현³, 최용석³, 박철수^{1*}

¹전북대학교 농업생명과학대학 작물생명과학과, ²국립식량과학원, ³사조동아원 (주) 중앙연구소

믹소랩은 반죽의 단백질 특성 뿐만 아니라 전분화 호화 및 노화특성을 평가할 수 있기 때문에 반죽 물성을 평가하는 믹소그래프나 파리노그래프와 전분호화특성을 평가하는 아밀로 그래프를 이용한 평가를 동시에 할 수 있는 장점이 있다. 믹소랩 분석 결과, 국내 밀 품종의 가수량과 반죽시간은 연질밀이나 박력분과 비슷하였으나, 반죽의 안정도 그리고 단백질 연화 정도는 경질밀이나 중강력분 수준을 보였다. 믹소랩으로 측정된 국내 밀 품종의 전분 특성은 경질밀의 전분특성과 유사함을 보였다. 믹소그래프와 믹소랩의 상관에서 반죽의 가수량은 정적 상관을 보인 반면에 반죽시간이나 안정도는 상관이 없는 것으로 확인되었다. 아밀로그래프의 최고점도와 브레이크 다운은 호화 및 조리의 안정도 그리고 노화정도와 상관을 보였다. 믹소랩의 반죽 및 단백질 특성은 빵 부피, 삶은 국수의 경도 및 과자 직경과 높은 상관을 보였고, 삶은 국수의 탄성 및 점성은 단백질 특성 및 전분의 호화정도와 노화 특성과 상관이 있는 것으로 나타났다.

*주저자: Tel. 063-270-2533, E-mail: pc89@jbnu.ac.kr

찰당질미 신품종 “스위트드림1세”

이원도¹, 강시용², 박용진³, 권순욱⁴, 이영상⁵, 조유현^{1*}

¹경기도 수원시 권선구 매실로 85 농업회사법인 (주)시드피아

²전라북도 정읍시 금구길 29 한국원자력연구원 첨단방사선연구소

³충청남도 예산군 예산읍 대학로 54 공주대학교 산업과학대학 식물자원학과

⁴경상남도 밀양시 삼랑진읍 삼랑진로 1268-50 부산대학교 식물생명과학과

⁵충청남도 아산시 신창면 순천향로 22 순천향대학교 의료생명공학과

‘스위트드림1세’는 밥쌀용 쌀 소비 감소와 쌀 재고량 증가로 인한 쌀 산업 위기를 극복하고자 소비자 요구에 다양성을 제공하고, 당질미를 활용한 다양한 가공적성 쌀 품종을 공급하기 위하여 농업회사법인 주식회사 시드피아에서 육성되었다. 2007년 해외 수집 조생찰의 sugary 변이체(KNUR42225M(1132)-79-12-3-1)를 부분으로하고 화영벼 모본으로 하여 교배하여 2008년부터 2014년까지 매년 포장에서 계통재배하면서 찰벼이며 당질미 특성을 갖는 계통을 선발, 유전적으로 온전히 고정하였다. 선발된 계통을 SP47로 계통명을 부여하고, 2015년 ~ 2016년에 난괴법 3반복으로 생산력검정을 수행하여 품종의 균일성과 안정성을 확인하여 ‘스위트드림1세’라고 명명하였다. ‘스위트드림1세’는 중부지역 보통기 재배에서 8월 20일경에 출수하는 중만생종으로 간장이 79.2cm이며 주당수수 14.5개 정도이다. 현미천립중은 19.0g, 장폭비 1.70로 단원형이다. 백미 수량은 418kg/10a로 추정벼 대비 80% 수준으로 기존 당질미에 비해 대단히 높은 편이다. 특히 ‘스위트드림1세’는 유리당 함량이 5.5%로 일반 품종에 비해 5배 가량 높으며, 식이섬유함량도 100g당 10.91g로 다량으로 함유하고 있어 가공식품 원재료로 활용이 기대된다.

*주저자: Tel. 070-4125-7959, E-mail: seedpia.001@gmail.com

거대배를 갖는 신품종 벼 “예농2호”

이원도¹, 강시용², 박용진³, 권순욱⁴, 조유현^{1*}

¹경기도 수원시 권선구 매실로 85 농업회사법인 (주)시드피아

²전라북도 정읍시 금구길 29 한국원자력연구원 첨단방사선연구소

³충청남도 예산군 예산읍 대학로 54 공주대학교 산업과학대학 식물자원학과

⁴경상남도 밀양시 삼랑진읍 삼랑진로 1268-50 부산대학교 식물생명과학과

‘예농2호’는 고기능성 거대배 신품종 육성을 목적으로 육성되었으며, 2007년 하계에 신동진 거대배 돌연변이체를 모본으로 하고, 변이모본인 다수확, 내도복 특성을 갖는 신동진벼를 부분으로 여교배하여 2007년부터 2009년까지 계통재배하면서 거대배 특성을 갖고, 임성, 초형이 양호한 KJ13-15-3-5-1 계통을 선발 고정하였다. 선발된 계통을 YN-007로 계통명을 부여하고, 2011년 ~ 2012년에 난괴법 3반복으로 생산력검정을 수행하여 품종의 균일성과 안정성을 확인하여 ‘예농2호’ 라고 명명하였다. ‘예농2호’는 중부지역 보통기 재배에서 8월 18일경에 출수하는 중만생종으로 간장이 87.1cm이며 주당수수 12.8개 정도이다. 현미의 장폭비는 1.81의 중원형이고, 현미 천립중은 원품종인 신동진벼 27.7g 보다 가벼운 23.6g 수준이다. 그러나 예농2호의 쌀눈 무게는 신동진벼 보다 2.8배 무거웠다. 예농 2호는 α -tocopherol이 대조품종 보다 2.5배 높은 함량을 보였고, 전 토코페롤 함량에서도 2배 정도로 차이가 났으며, δ -tocopherol은 6.5배 수준으로 나타났다.

*주저자: Tel. 070-4125-7959, E-mail: seedpia.001@gmail.com

향취성을 가지는 중만생 벼 신품종 “천지향1세”

이원도¹, 김태형², 박용진³, 권순욱⁴, 이영상⁵, 조유현^{1*}

¹경기도 수원시 권선구 매실로 85 농업회사법인 (주)시드피아

²서울특별시 중구 동호로 330 CJ제일제당

³충청남도 예산군 예산읍 대학로 54 공주대학교 식물자원학과

⁴경상남도 밀양시 삼랑진읍 삼랑진로 1268-50 부산대학교 식물생명과학과

⁵충청남도 아산시 신창면 순천향로 22 순천향대학교 의료생명공학과

‘천지향1세’는 글로벌 소비자 기호에 적합하고 농가 소득향상과 함께 미래 식문화 변화에 대응하고자 우수한 향 특성이 가미된 품종개발을 목적으로 농업회사법인 주식회사 시드피아에서 육성되었으며, 2004년 하계에 초형이 우수하고 약한 정도의 향을 갖는 HJ-11계통을 모본으로 하고, 현미 외관 품위가 양호하고 약한 정도의 향을 갖으며, 초형이 우수한 J-42 를 부분으로 교배하여 2004년부터 2012년까지 매년 포장에서 계통재배하면서 유전적으로 온전히 고정된 계통을 선발, 고정하였다. 선발된 계통에 대해 2013년 ~ 2015년에 난괴법 3반복으로 생산력검정을 수행하여 품종의 균일성과 안정성을 확인하여 ‘천지향1세’ 라고 명명하였다. ‘천지향1세’는 중부지역 보통기 재배에서 8월 19일경에 출수하는 중만생종으로 간장이 79.3cm이며 주당수수는 15.4개 정도이다. 현미 천립중은 18.6g, 장폭비 1.71로 단원형이다. 메벼로서 현미의 아밀로스함량과 단백질 함량은 각각 19.3%, 6.5% 정도이며, 백미 수량은 5.28MT/ha로 추청벼와 비슷한 수준이다. ‘천지향1세’는 쌀에서 은은한 팝콘향이 나는 향미 품종으로 재배 확대가 기대된다.

*주저자: Tel. 070-4125-7959, E-mail: seedpia.001@gmail.com

저장기간 및 조건에 따른 현미의 발아율과 생산연도 판별

홍지화^{1*}, 이영길¹, 강지선², 이민휘¹, 박영준¹, 김현태¹, 이재환¹, 김동민³

¹경상북도 김천시 울곡동 국립농산물품질관리원 시험연구소

²경상북도 상주시 성하동 국립농산물품질관리원 경북지원 상주사무소

³경상북도 김천시 울곡동 국립종자원 종자검정연구센터

양곡관리법의 양곡의 혼합금지 조항에 따라 생산연도(연산)가 다른 양곡(쌀, 현미)의 혼합이 금지되어 있으나 신곡과 구곡을 혼합하여 거짓으로 표시하는 사례가 증가하고 있어 이를 판별할 수 있는 방법 개발이 필요한 실정이다. 현미는 쌀에 비해 영양성분이 풍부하고 발아가 되기 때문에 이를 이용하여 현미의 생산연도 판별이 가능한지에 대한 연구를 수행하였다. ‘일품’ 품종의 연산별 시료(2012년산, 2013년산, 2014년산, 2015년산 각10점)를 대상으로 국제종자검정협회의 발아율 검정 방법을 이용하여 발아율을 조사한 결과 각 연산별 평균 발아율은 각각 0%, 7%, 56%, 97%로 나타나 생산연도별 시료의 발아율에 차이가 나타났고 통계분석 결과 신곡과 구곡 간에 유의한 차이를 나타내었다. 발아율과 생산연도 판별의 상관성을 알아보기 위하여 상주의 양곡보관창고를 지정하여 저장기간(6개월, 8개월, 10개월, 12개월)과 저장조건(상온, 저온)에 따른 현미의 발아율을 시험하였다. 동일한 시료라도 상온보관에 비해 저온보관 시 발아율이 더 높게 나타났고 저장기간이 길어질수록 발아율이 낮아지는 경향이였다. 상온조건에 보관된 시료의 저장기간에 따른 현미의 발아율을 검정한 결과 시료를 수확시점으로부터 8개월 정도 보관한 시료는 2015년산과 2014년산 간에 유의차가 없었으나, 10개월에서 1년간 보관 시에는 신곡과 구곡이 통계적인 유의차를 나타내었다. 반면 저온조건에 보관된 시료의 경우는 6개월 정도 보관 시에는 2015년산과 2014년산 간에 유의차가 없었으나 8개월에서 1년간 보관 시에는 신곡과 구곡 간에 유의차를 나타내었다. 시료를 단기간 보관 시에는 상온과 저온 조건이 신곡과 구곡의 발아율에 크게 영향을 주지 않았으나 시료를 장기간 보관 시에는 저장온도 조건에 따라 신곡과 구곡 시료의 발아율에 영향을 주는 것을 알 수 있었다. 본 연구에서 수집한 일품 벼의 연산별 발아율은 각 연산 간에 발아율 범위가 중복되지 않은 것으로 나타나 향후 현미의 단일 연산 또는 신·구곡을 판별하기 위한 기초자료로 활용이 가능할 것으로 사료된다.

*주저자: Tel. 054-429-7722, E-mail: hongjh19@korea.kr

쌀 신곡과 구곡의 판별을 위한 지표물질 선별과 휴대용 검정 키트 개발

홍지화^{1*}, 이솔화², 손민식², 박영준¹, 김현태¹, 이재환¹

¹경상북도 김천시 울곡동 국립농산물품질관리원 시험연구소

²대전광역시 유성구 전민동 (주)바이오어세이

쌀의 신곡과 구곡의 판별을 위한 지표물질로 기존에 활용중인 인지질 지표물질 외에 신규 지표물질을 탐색하기 위하여 안정동위원소 분석, 무기원소 분석, 유기성분 분석, 전자코 분석을 시도하였다. 하지만 신곡과 구곡 단일곡에 대한 판별 정확도가 95% 이하로 나타나 지표물질로 선별하지 못하였다. 이에 국립농산물품질관리원에서 고시한 쌀의 신선도 감정법을 신곡과 구곡의 판별법 개발 연구에 적용해 본 결과 신곡과 구곡인 단일곡의 경우 95% 이상의 정확도로 판별되는 것으로 나타났다. 신선도 감정법은 Guaiacol, Oxydol, *p*-phenylenediamin 3종의 시약 처리를 통하여 쌀에 포함된 효소의 산화효소 작용의 정도를 알아보는 방법으로 발색된 시약의 착색 정도를 육안으로 감정하는 방법으로 규정되어 있다. 따라서 효소활성도를 쌀의 신곡과 구곡 판별을 위한 지표물질로 추가 선정하였으나 본 감정법은 시약을 조제하는 사람에 따라 감정 결과가 상이하고, 시약 조제에 시간이 많이 소요되는 등 현장 업무에 직접 활용하기에는 제약이 존재하여 현재의 방법에 대한 신속화와 검정 표준화 시스템 구축이 필요한 실정이다. 이에 현장 휴대용으로 활용하기 위하여 기존의 시약 원액을 이용하여 수집된 시료에 대한 시약 조제별 안정성 시험을 수행하였고 Guaiacol 1%, *p*-phenylenediamin 0.2%를 기질로 Sodium Perborate 1%에 안정제를 첨가한 시약을 개발하였다. 개발된 키트를 이용한 검정 결과는 기존에 시약을 직접 조제하여 검정한 결과와 동일한 착색반응을 나타내었다. 본 연구를 통해 개발된 키트는 쌀의 신선도뿐만 아니라 신곡과 구곡 단일곡을 판별하는 도구로 활용이 될 것으로 기대된다.

*주저자: Tel. 054-429-7722, E-mail: hongjh19@korea.kr

풋고추 농산물의 표준규격 개발을 위한 매운맛 함량 실태조사

홍지화*, 최경후, 김은옥, 연영자, 박영준, 김현태, 이재환

경상북도 김천시 울곡동 국립농산물품질관리원 시험연구소

풋고추 농산물의 매운맛 성분에 대한 표준규격 개발을 위하여 시중유통 풋고추 111점을 수집한 후 매운맛 함량을 분석하여 매운맛 규격 설정이 가능한지 알아보았다. 풋고추 캡사이신 추출 방법을 확립하기 위하여 풋고추 꼭지와 씨를 제거한 후 건조시켜 분쇄 후 고춧가루 KS규격 설정 시 활용된 매운맛 분석법을 활용하여 분석조건을 확립하였다. LC 분석 결과 고추 매운맛 표준물질인 capsaicin 및 dihydrocapsaicin의 피크 머무름 시간(Retention time, RT)은 각각 4.2분, 6.8분으로 나타났고 표준물질 검량식의 상관관계수 값(R^2) 값은 0.999이상으로 나타났다. 풋고추 공시시료의 매운맛 함량은 4.4ppm~4379.3ppm의 범위를 나타냈고 평균 매운맛 함량 값은 967.4ppm으로 나타났다. 풋고추에 표시된 상품별 평균 매운맛 함량 값(ppm)은 풋고추(697.9), 모닝고추(43.9), 룡그린(48.2), 청양(2494.8), 오이맛·아삭이(95.2), 매운고추(3521.4), 과일(23.2), 애기초(398.6)로 분석되었고 분석횟수 간의 상대표준편차(% RSD) 값은 0.08~5.14로 나타나 재현성과 정밀도가 높게 나타났다. 풋고추 포장재 표시사항별 평균 매운맛 함량을 살펴보면 풋고추(품종 포함)로 표기된 시료의 매운맛 함량 분포는 청양고추, 매운고추, 오이맛·아삭이, 과일고추, 애기초고추, 모닝고추, 룡그린고추의 매운맛 분포범위를 모두 포함하여 매운맛 정도의 변이가 큰 것으로 파악되었다. 따라서 시중에 유통되는 풋고추의 매운맛 수치는 값의 변이가 존재하여 향후 등급안(매우매운맛, 보통매운맛, 순한맛 등) 마련이 가능할 것으로 판단된다. 또한 공시시료를 대상으로 CS(capsaicinoid synthetase) 유전자 포함 유무를 분석한 결과 111점 모두 연관 마커에서 증폭이 되는 것으로 나타났다. 본 연구를 기반으로 풋고추의 매운맛 성분에 대한 표준규격이 설정된다면 풋고추 농산물의 품질관리뿐만 아니라 매운맛 성분육종 등의 분야에도 유용하게 활용될 것으로 사료된다.

*주저자: Tel. 054-429-7722, E-mail: hongjh19@korea.kr

차나무 신품종 ‘장원 2호’의 기능성 성분 및 생리활성 특성

이민석¹, 고건희¹, 이정대¹, 유주¹, 이진호¹

¹아모레퍼시픽 그룹, (주)오설록농장 오설록연구소

제주도 소재 오설록연구소에서 고기능성 고품질 차나무 신품종 개발을 위하여 한국, 일본, 중국에서 수집된 차나무(*Camellia sinensis* L.) 유전자원에 대하여 작물학적 특성 과 잎의 기능성 성분 및 재차 품질특성에 대한 평가를 실시하였다. 그 결과 2007년 4월에 기능성 성분과 품질이 뛰어난 유전자원에 대하여 1차 선발을 실시하였고, 삼목방법을 통하여 계통육성을 실시하였다. 이렇게 정식을 한 21개의 계통을 성목이 될 때까지 3년간(2008~2010)육성하며 모수의 유전형질이 안정적으로 유지되는지에 대해서 2차 평가를 실시 하였다. 그중 내한성, 내병성 등 생육특성이 뛰어나고 차의 기호성에 관여하는 TFAA, Teanin 함량이 기존 도입품종인 야부기다 보다 1.5배 높은 계통을 최종적으로 선발하여 ‘장원 2호’라 명명하고 한국생명공학 연구소에 종자기탁과 특허등록을 완료 하였다(특허:10-1213200-000). 본 연구결과 국내 육성 차나무 품종인 ‘장원 2호’는 기존 도입품종들과 비교 하였을때 맛과 향의 기호성에서 우수한 특징을 나타 내었을 뿐만 아니라 피부 보습효과도 뛰어난 것으로 밝혀졌다. 이는 새로운 신품종을 활용한 기호성이 뛰어난 다류제품 뿐만 아니라 부가가치가 높은 화장품 원료로서도 그 가치가 뛰어난 것을 알 수 있다.

*주저자: Tel. 064-794-6491, E-mail: leems@osullocfarm.com

Analysis of powdery mildew susceptible genes in Korea melon lines to develop the powdery mildew molecular marker

Hyung Seong Lee, Haeun Jung, Seongbin Hwang, Hyun Uk Kim*

Department of Bioindustry and Bioresource Engineering, Plant Engineering Research Institute, Sejong University, Seoul, 05006 Republic of Korea

Melon (*Cucumis melo* L.) is an economically important fruit crop because of its productivity in worldwide. However, powdery mildew (PM) diseases, the main factor of reducing crop yields, affect melon farming these days. For this reason, we are developing the molecular makers to detect PM resistance in melon breeding lines. We got 8 PM resistance melon lines, and chose some genes as the candidate of molecular makers. We first chose the Mildew Locus O (MLO) genes that is known as susceptible genes. If they are lost their function by mutation, the melon lines get resistance to PM. We found 14 MLO genes in melon database, and categorized into six clades. Among of them, MLO genes in clade5 are susceptible factor to PM. CmMLO3, 5, and 12 are grouped in clade5. We get their cDNA from 8 resistance lines, and analysis the gene expression and sequence. Unfortunately, There is no differences between susceptible and resistance lines. So we found another susceptible genes, named PMR. On the basis of previous researches, PMR4, 5, and 6 are susceptible factor to PM, so we searched the PMR genes in melon, and get cDNA from 8 resistance lines. We will identify cDNA sequence of these lines, and compare to reference genes. Finding differences between susceptible and resistance lines will guide us to identify where the loss of function mutation is occurred. It can help to develop the PM molecular marker.

*Corresponding Author: Tel. 02-3408-4318, E-mail: hukim64@sejong.ac.kr

Development of molecular markers for screening salt tolerant and sensitive accessions in *Glycine max* and *Glycine soja*

Seokhyung Lee¹, Gyu Tae Park¹, Jagadeesh Sundaramoorthy¹, Jeong-Dong Lee¹, Hak Soo Seo², Jong Tae Song^{1*}

¹School of Applied Biosciences, Kyungpook National University, Daegu, Republic of Korea

²Department of Plant Bioscience, Seoul National University, Seoul, Republic of Korea

Soybean [*Glycine max* (L.) Merr.] is one of the major agricultural crops, which is widely known as a salt sensitive crop and may result in low yield in salt-affected areas. Therefore, it is necessary to develop salt tolerant soybean varieties for increasing yield in salt-affected areas. In a previous study, a dominant gene (*GmSALT3*) for salt tolerance was identified and nine haplotypes (H1 to H9) were detected among a total of 221 soybean accessions from China. The purpose of the present study is to develop molecular markers for screening salt tolerant and sensitive lines among *G. max* and *G. soja* accessions distributed in Korea, Japan and China depending on haplotypes in *GmSALT3* gene. Sequence analysis for *GmSALT3* gene from a total of 102 lines of *G. max* and 119 lines of *G. soja* showed various polymorphisms in coding regions. Depending upon the polymorphisms we identified 37 novel haplotypes and three formerly reported haplotypes (H1, H2, and H5). Among 40 haplotypes indentified, eight haplotypes showed tolerant and 32 haplotypes showed sensitive phenotypes. To confirm whether the polymorphisms detected in coding regions influence the *GmSALT3* expression, we performed reverse transcription-polymerase chain reaction. As a result, we detected expression of *GmSALT3* in all tolerant and in most of sensitive haplotypes. Therefore, currently we are looking for the other possibilities to explain the relationship between haplotypes and phenotypes.

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

안토시아닌 자원을 활용한 다양한 색 미백2호 품종 개발

박기진*, 박종열, 류시환, 서영호, 최재근, 남궁민, 용우식, 윤석원, 최준근

강원도 홍천군 두촌면 장남길 26 강원도농업기술원 옥수수연구소

국내 옥수수 재배는 풋옥수수 용도인 찰옥수수가 중심이 되면서 그동안 연농1호(일명 대학찰, 1999), 미흑찰(2004), 찰옥4호(2004), 미백2호(2005), 일미찰(2005) 등 품질이 우량한 품종들이 개발되어 현재까지 재배되고 있다. 하지만 이들 품종을 능가하는 품질이 우량한 품종이 지속 개발되지 못하고 있는 실정으로 삶거나 단순가공 등 부가가치가 낮은 소비 형태로 지속하여 왔는데, 이제는 부가가치를 창출할 신품종 개발이 시급하다. 옥수수연구소는 2000년부터 관상용옥수수에서 안토시아닌이 다량 함유된 계통을 선발하고 육종모집단을 구성하거나 여교잡을 실시하여 안토시아닌이 우량한 계통을 개발하여 왔다. 그동안 육종모집단으로 부터 색소1호(flint, 안토시아닌 포엽 이용), 청춘찰(waxy, 안토시아닌 풋옥수수), 색소2호(semi-flint, 안토시아닌 알곡 이용) 품종을 개발하는 성과를 거두었다. 최근에는 미백2호의 종자친과 화분친에 대하여 각각 3~4회 여교잡을 통하여 다양한 색을 가진 여교잡 계통을 확보하였으며 이를 상호 교잡하여 미백2호와 상당히 유사한 다양한 색의 교잡종을 구성하여 적응시험을 추진하고 있다. 특히 이들 다양한 색의 교잡종은 미백2호와 품질과 수확시기가 비슷하여 칼라 찰옥수수를 상품화하는데 많은 도움이 된다. 안토시아닌 함량의 차이에 따라 흰색, 분홍색, 갈색, 검정색 등으로 분리함으로써 식가공 재료로 직접 활용할 수 있는 제품이나 상품개발이 이루어지게 되면 옥수수의 부가가치를 높일 수 계기가 될 것이다.

*주저자: Tel. 033-248-6911, E-mail: kjp@korea.kr

국산밀 품종의 용도별 품질등급 기준설정

김정곤¹*, 박문웅¹, 성병열¹, 최재성¹, 박미자¹

¹경기도 수원시 권선구 서둔동 (주)바이오맥연구소

국산밀의 품질규격화를 위한 밀 품종별 용도에 따른 품질등급 기준을 마련하기 위하여 농가산 밀 원곡과 밀가루의 품질 분석을 통하여 본 연구를 수행하였다. 연구결과를 요약하면, 조경밀은 강력밀가루(제빵용)용으로 적합하였는데 1등급은 해당 품종이 95% 이상을 기준으로, 이종곡물 및 타품종 비율이 5% 이내 이어야 함(전품종 공통사항). 조경밀은 용도가 제빵용이므로 단백질의 양과 질이 높을수록 유리함. 따라서 조경밀 1등급의 단백질 함량은 13% 이상, 2등급은 12% 이상으로 설정하였음. 초자율은 원맥의 내부 형질이 유리질과 같이 단단하고 투명한 상태를 말하는 것으로 초자질이 높은 밀은 단백질 함량이 높음. 조경밀 1등급은 초자질 함량이 75% 이상, 2등급은 50% 이상으로 설정하였음. 원맥 Falling Number는 발아 정도를 판단할 수 있는 항목으로 FN값 300 sec 이상은 정상이라고 판단할 수 있음. 발아된 밀로 생산한 제빵용 밀가루는 반죽이 끈적이고, 급수량이 낮아져 완제품 품질이 떨어지게 됨. 참고로, 밀가루의 단백질과 침전가 항목은 원맥의 단백질 함량과 정의 상관관계를 갖는 항목이며, 조경밀 원맥 등급의 참고자료로 활용할 수 있음.

금강밀의 용도를 제빵과 제면용으로 정했을 때 준강력 수준의 단백질 함량이 바람직함. 금강밀 1등급의 단백질 함량은 12.5% 이상, 2등급은 11.5% 이상으로 설정하였음. 금강밀 1등급은 초자질 함량이 50% 이상, 2등급은 25% 이상으로 설정하였음. 원맥 Falling Number는 발아 정도를 판단할 수 있는 항목으로, FN값 300 sec 이상은 정상이라고 판단할 수 있음. 발아된 밀로 생산한 제빵용 제면용 밀가루는 완제품 품질을 떨어뜨리게 함. 해당 금강밀은 등급 기준을 설정하기에는 샘플수가 부족하여 과거에 분석된 자료를 감안하여 기준을 설정하였음.

수안밀의 용도는 중력밀가루(제면용)에 가까우므로 원맥 1등급의 단백질 함량을 10% 이상으로 설정하였음. 초자율 등급기준의 설정은 불필요함. 원맥 Falling Number는 발아율뿐만 아니라 전분의 호화점도 특성을 판단할 수 있고, FN가 높은 원맥은 밀가루의 호화점도가 높으며 면의 식감이 향상됨. 따라서 수안밀 1등급의 FN는 350 sec 이상으로 설정하였음.

백종밀과 연백밀의 용도는 박력밀가루 제과용으로 단백질 함량이 낮을수록 유리함. 원맥 1등급의 단백질 함량을 10% 이하, 2등급은 11% 이하로 설정하였음. 초자율 등급기준의 설정은 불필요함. 발아 피해를 입은 원맥은 케익과 과자 품질을 떨어뜨리므로 1등급은 FN 300 sec 이상으로 설정하였음.

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*주저자: Tel. 031-892-6644, E-mail: kimjgon22@naver.com

방사선을 이용한 소형 심비디움 속빛무늬 잎 돌연변이 품종 육성

강경원^{1*}, 김백준¹, 조영득², 강시용²

¹경기도 남양주시진건읍 진관리 286 바보난농원

²전라북도 정읍시 금구길 29 한국원자력연구원 첨단방사선연구소

동양계 심비디움은 산채에 의해 수집되거나 주로 중국 및 대만에서 수입되어 상품화되고 있는데, 서양계 심비디움에 비해 조직배양에 의한 묘의 생산 기간이 길고 재배가 까다로워 산업화에 어려움이 있다. 서양계 심비디움은 조직배양에 의한 증식 및 재배가 용이한 반면, 대부분 일본에서 육종되어 도입된 품종이 주를 이루고 있어 관상가치가 높은 국산 품종개발이 요망된다. 본 연구에서는 테이블위에 화분 재배에 적합한 식물체가 소형이면서, 잎에 무늬가 있어 관상가치가 높아 소비자가 선물용으로 수요가 높고, 생산능력은 작은 면적에서 대량생산이 가능한 동양계 심비디움의 수입을 대체할 수 있는 국산 품종을 육성하여 보급하고자 하였다. 원품종 황금곰은 잎에 황금색의 속빛무늬가 있는 품종이다. 생장점을 배양한 기내 protocom-like body (PLB)를 한국원자력연구원 첨단방사선연구소 감마선조사시설에서 30, 50, 70Gy의 선량으로 24시간 조사하였다. 조사한 배양체를 계대배양하면서 배양병내에서 잎의 변이 발생을 관찰한 결과, 이듬해에 50Gy 조사구에서 원품종보다 단엽성이면서 잎의 갓줄무늬 녹색이 뚜렷한 변이체를 기내 선발하였다. 이 변이체를 조직배양에 의한 증식 및 고정 과정을 거치고, 온실에서 순화 및 재배 과정을 거쳐 변이 특성이 고른 계통을 최종 선발하였다. 선발 계통의 초장은 6.5cm로 원품종 16cm에 비교하여 아주 작아진 왜성변이체이다. 선발계통의 잎 폭도 0.7cm로 원품종 0.9cm에 비교하여 작고, 잎 두께도 두꺼워졌다. 그리고, 잎의 가장자리에 남아있는 녹색의 줄 무늬도 원품종에 비교하여 두껍고 진하여 뚜렷하다. 따라서, 선발된 변이 계통은 초형이 작은 왜성으로 조직배양묘의 순화 및 순환재배가 용이하고 단위면적당 생산 효율도 높은 장점이 있다. 또한, 원품종 속빛무늬보다 단엽성이며 잎의 녹색 갓줄 무늬도 뚜렷하여 관상성 및 소비자 선호도가 높을 것으로 사료되어, 앞으로 품종보호권 등록 및 대량생산 상품화를 추진할 예정이다.

*주저자: Tel. 031-573-2643, E-mail: dawin7@hanmail.net

중산간 지역에서 벼 품종 “설레미” 재배시 적정 재식밀도 및 시비량

김정주^{1*}, 신운철², 정재혁³, 강위금¹

¹경상북도 상주시 화서면 중화로 2161 국립식량과학원 상주출장소

²전라북도 완주군 이서면 혁신로 181 국립식량과학원 기획조정과

³전라북도 완주군 이서면 혁신로 181 국립식량과학원 작물재배생리과

중산간 지역에서 관행적인 조기이앙, 질소질 비료 과용 등으로 쌀의 외관품질과 밥맛이 떨어지는 문제가 발생하고 있어 이앙시기 및 적정 질소질 비료 살포량을 설정하여 적기에 이앙하고 균형시비를 함으로써 조생종 쌀의 품질향상에 기여할 수 있다. 2011년에 육성된 중산간지 적응 조생종 벼 품종, “설레미”는 수량성이 높고 도정특성이 우수하여 중산간 지역에서 재배면적이 점차 증가하고 있는 추세이다. “설레미”는 2주간격(5월 6일, 5월 20일, 6월 5일, 6월 20일)으로 이앙하여 주요 농업적 특성 및 완전미 수량 등을 조사한 결과 이앙적기를 6월 5일로 설정한 바 있다. 질소질 비료 살포량 4수준(0, 5, 10, 15kg/10a)과 재식밀도 4수준(60, 70, 80, 90주/3.3m²)을 처리하여 2015년과 2016년, 2개년간 주요 농업적 특성 및 완전미 수량 등을 조사한 결과는 다음과 같다. 1. 2년 평균 출수기는 연차간 차이는 있으나 재식밀도 및 질소시비량에 관계없이 8월 7~8일로 비슷하였고, 질소시비량이 많을수록 간장과 수장이 커지는 경향이었음 2. 질소시비량 15kg/10a 시험구는 재식밀도와 상관없이 수당립수와 천립중의 증가로 대부분 도복되었음 3. 질소시비량이 증가할수록 재식밀도별 m²당 수수, 수당립수는 증가하는 경향을 보였고, 등숙비율은 감소하는 경향을 나타냈음 4. 백미수량은 질소시비량이 많을수록 증가하여 질소시비량 15kg/10a 수준에서 674~688kg/10a 범위로 높게 나타났음 5. 질소시비량이 많을수록 단백질 함량은 높아지는 경향을 보였고 완전미 비율은 낮아지는 경향이었으며 이에 따라 완전미 수량도 낮아지는 경향이었음. 따라서 중산간지 적응 조생종 벼 품종 “설레미”를 재배할 때 재식밀도는 완전미 수량을 고려하여 80~90주/3.3m² 수준이 적절할 것으로 보인다. 또한, 질소질 비료는 15kg/10a를 살포하였을 때 도복에 따른 수량 및 미질 저하의 우려가 있을 뿐만 아니라 등숙률의 저하로 완전미 수량이 감소하므로 적정 질소질 비료 살포량은 쌀의 외관품질 및 완전미 수량을 고려했을 때 본답의 양분상태에 따라 도복의 위험을 고려하여 10kg/10a 내외가 적절하다.

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*주저자: Tel. 054-533-0465, E-mail: jjkim74@korea.kr

벼흰잎마름병 저항성 유전자 집적 고품질 중만생 벼 ‘신진백’

박현수^{1*}, 김기영², 백만기¹, 조영찬¹, 김보경¹, 남정권¹, 고재권¹, 신운철¹, 김우재¹, 고종철¹, 김정주¹, 김현순¹, 이점호², 정종민¹, 강경호¹, 정지웅¹, 전재범¹, 이영복¹

¹전라북도 완주군 이서면 혁신로 181 농촌진흥청 국립식량과학원

²전라북도 전주시 완산구 농생명로 300 농촌진흥청

‘신진백’은 벼흰잎마름병 저항성 유전자를 집적한 고품질 중만생 벼 품종으로 기후변화에 의한 고병원성 신규 레이스의 분화로 인한 피해확산에 대비하고자 농촌진흥청 국립식량과학원에서 개발하였다. 2007/2008년 동계에 벼흰잎마름병 저항성 유전자 *Xa3*와 *xa5*를 가지고 있는 ‘익산493호’(이후 ‘진백’으로 명명)를 모본으로 하고, 최고품질 품종이면서 *Xa3*를 보유하고 있는 ‘호품’에 야생벼에서 유래한 *Xa21*을 도입한 자포니카형 근동질 계통 ‘HR24670-9-2-1’을 교배한 F₁을 부분으로 하여 삼원교배하였다. 집단육종법과 계통육종법을 이용하여 벼흰잎마름병균에 대한 생물검정과 함께 저항성 유전자와 연관된 분자표지를 이용한 MAS로 세 개의 저항성 유전자 *Xa3+xa5+Xa21*이 집적된 저항성 계통을 선발하였으며, 표현형이 우수한 계통에 대해서 생산력검정시험을 수행하였다. 출수기가 남평보다 늦은 중만생종으로 벼흰잎마름병균에 광범위 고도저항성을 나타내며 도열병과 줄무늬잎마름병에도 강한 복합내병성으로, 쌀의 외관품위와 밥맛이 양호한 단간 내도복 계통 HR27814-B-B-47-1-1을 선발하여 ‘익산575호’로 계통명을 부여하였다. 2014-2016년 3년간 실시된 지역적응성 검정시험 결과 ‘익산575호’는 벼흰잎마름병에 대한 저항성이 증진된 복합내병성 계통으로 밥맛이 양호하고 도정 특성이 우수한 점이 인정되어 직무육성 신품종 선정심의위원회에서 품종명 ‘신진백’으로 명명되었다. ‘신진백’은 우리나라 벼 품종 중에 최초로 *Xa21*을 도입하여 세 개의 벼흰잎마름병 저항성 유전자 *Xa3+xa5+Xa21*가 집적되어 기존의 저항성 품종들에 비해 벼흰잎마름병에 대한 저항성이 향상된 복합내병성 실용 품종이다. 또한 외관품위와 밥맛 등이 우수한 고품질 밥쌀용 품종으로 흰잎마름병 발병상습지 및 친환경 재배단지에 활용할 수 있어 안전하고 밥맛 좋은 쌀 생산에 기여할 것으로 기대된다.

*주저자: Tel. 063-238-5216, E-mail: mayoe@korea.kr

Morphological variation of accessions of *Perilla* Crop from north areas of China

Shi Jun Ma, Ju Kyong Lee*

Department of Applied Plant Sciences, College of Agriculture and Life Sciences, Kangwon National University, Chuncheon, 200-701, Korea

To better understand the morphological variation for *Perilla* crop in north areas of China, we studied the morphological variation of 87 *Perilla* accessions by examining 7 quantitative and 10 qualitative characters. As a result, morphological variation determined that between cultivated var. *frutescens* and cultivated var. *crispa*, showed significant morphological differences in 5 quantitative traits including effective number of branches (QN2), number of internodes (QN3), number of branches (QN4), length of the largest inflorescence (QN5), and days from seedling to flowering (QN7). However, two quantitative traits—plant height and number of floret of the largest inflorescence—did not show significant differences between cultivated var. *frutescens* and cultivated var. *crispa*. In principal components analysis (PCAs), five quantitative characters [plant height (QN1), effective number of branches (QN2), number of internodes (QN3), number of branches (QN4), and days from seedling to flowering (QN7)] and 6 qualitative characters [fragrance of plant (QL1), color of reverse side of leaf (QL3), degree of pubescence (QL5), color of flower (QL6), shape of leaf (QL7), and hardness of seed (QL10)] contributed to the positive direction on the first axis. The other quantitative and qualitative characters contributed to the negative direction on the first axis. Most accessions of cultivated var. *frutescens* and cultivated var. *crispa* were clearly separated by the first axis. In addition, most accessions of cultivated var. *frutescens* from high latitude and middle latitude areas were clearly separated by the first axis, except for several accessions. These findings in this study will provide useful information for understanding the morphological variation of *Perilla* crop according to the geographical distribution in high latitude and middle latitude areas of China.

*Corresponding Author: Tel. 033-250-6415, E-mail: jukyonglee@kangwon.ac.kr

시중 중화면 제조 기계를 이용한 국산 밀 품종의 중화면 면대 특성 및 식미 평가

윤영미¹, 김지은², 조성우², 강천식¹, 정영근¹, 박철수^{2*}

¹전라북도 완주군 이서면 국립식량과학원 작물육종과

²전라북도 전주시 덕진구 전북대학교 농업생명과학대학 작물생명과학과

국내 식품회사에서 중화면 제조에 이용되는 국내 기계와 연구기관에서 주로 사용하는 일본 기계를 이용하여 중화면을 제조하여 식미 특성을 비교 분석하였다. 국수 기계의 롤러의 크기와 무게의 차이로 국내 기계는 일본 기계에 비해서 가수량이 5% 높고, 반죽 휴지시간이 30분 짧았다. 국내 품종에서는 국수 면대 두께는 단백질 함량과 믹소그래프의 가수량에서 제조 기계와 상관없이 정 상관을 보였다. 단백질 함량이 다른 3 품종의 면대 두께는 두 기계 모두에서 단백질 함량, 침전가 및 믹소그래프 반죽 시간과 정 상관을 나타내었다. 부분 찰밀과 찰밀의 면대 밝기는 국내 기계에서만 아밀로스 함량에 정 상관을 보였다. 삶은 국수 특성을 살펴보면, 국내 기계가 일본 기계에 비해서 경도가 높고 탄성은 낮았으며 점성은 차이가 없었다. 단백질 함량이 다른 3 품종에서는 기계 종류와 상관 없이 단백질 함량이 증가할수록 삶은 국수의 경도는 증가하였지만, 탄성과 점성은 상관이 없었다. 부분 찰밀과 찰밀에서는 두 기계에서 모두 아밀로스 함량과 setback은 삶은 국수의 경도, 점도, 탄성과 정 상관을 보였고, 손상 전분과 breakdown은 부의 상관을 보였다.

*주저자: Tel. 063-270-2533, E-mail: pcs89@jbnu.ac.kr

중산간 지역에서 오대벼 재배시 벼 생육 및 식물체내 양분 변화의 연차간 변이에 대한 미세온도변화의 영향

김정주^{1*}, 신운철², 강위금¹, 조현숙³, 양창인⁴, 강신구⁵

¹경상북도 상주시 화서면 중화로 2161 국립식량과학원 상주출장소

²전라북도 완주군 이서면 혁신로 181 국립식량과학원 기획조정과

³전라북도 완주군 이서면 혁신로 181 국립식량과학원 작물재배생리과

⁴강원도 철원군 동송읍 태봉로 2346 국립식량과학원 철원출장소

⁵경기도 수원시 권선구 수인로 126 국립식량과학원 중부작물부 재배환경과

벼는 생육기간 중 온도 및 일사조건에 의해 벼 생육, 수량 및 품질에 크게 영향을 받는다. 기후변화에 따른 온도 상승으로 쌀 수량 감소 뿐만 아니라 쌀의 배백, 심복백 발생 및 동할미 증가 등 쌀 품질이 저하되고 온도 변화, 일조의 다소 및 강우일수 증감 등의 변화에 따라 벼 생육 특성의 연차간 차이를 나타낸다. 따라서 중산간 지역인 경북 상주시 화서면(해발 285m)에 소재하고 있는 국립식량과학원 상주출장소 시험연구포장에서 2014년~2016년, 3개년간 오대벼를 재배하여 벼 재배 군락 주위의 미세온도변화와 벼 생육 양상 및 양분 관련 특성의 연관성을 추정하기 위하여 벼 재배 군락 주위의 온도 변화, 작물학적 특성 및 벼 생육시기별 식물체내 양분변화를 조사하였다. 작물학적 특성 및 식물체내 양분(N, P, K)은 이앙기, 분얼초기, 분얼성기, 유수형성기, 출수기, 수확기로 나누어 생육단계별로 조사하였고 온도는 대기와 군락내 온도, 수온, 지온을 5월21일부터 9월20일까지 3개년간 조사하였다. 대기 및 지온의 적산온도는 2016년도에 높게 유지되었고 군락내 온도 및 수온의 누적온도는 2014년도에 낮게 유지되었다. 출수기 전까지 대기의 연차간 온도 변화는 2015년에 낮게 유지되었고 지온의 변화는 2016년도에 높게 유지되었으며 수온 및 군락내 온도 변화는 큰 차이를 보이지 않았다. 벼키의 변화는 2014년, 2015년, 2016년 순으로 증가 속도가 빨랐고, 건물생산량의 변화는 2014년도에 증가속도가 빨랐다. 대기의 온도와 지온이 높게 유지된 2016년도에 벼 생육이 진행됨에 따른 식물체내 양분 함량의 변화가 적었다. 따라서 식물체내 양분의 흡수, 이동에 따른 벼 생육 및 건물생산은 대기의 온도 및 지온의 영향이 클 것으로 보인다. 벼 재배지역의 미세 환경 변화에 의해 벼 생육 반응 및 양분의 흡수, 이동에 영향을 주므로 재배지역의 미세온도변화, 양분의 흡수 및 이동과 벼 생육 양상의 연관성을 추정하기 위해서는 각각의 데이터를 장기적으로 확보하여 분석할 필요가 있다.

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*주저자: Tel. 054-533-0465, E-mail: jjkim74@korea.kr

Difference of stachyose content between *RS2* dominant allele and *rs2* recessive allele in soybean seed

Jin-A Kim, Sung-Jin Han, Sang-Woo Choi, Dong-Hui Kang, Su-Jin Lee, Jong-Il Chung*

Division of Applied Life Science, Graduate School, Gyeongsang National University, Chinju 52828, Republic of Korea

Soybean [*Glycine max* (L.) Merr.] is an important source of protein and oil for humans and animals. Sucrose, raffinose, and stachyose are major soluble sugars present in mature soybean seeds. Stachyose is the most nutritionally undesirable in the soybean, because it causes flatulence and diarrhoea. Soybean cultivars with genetically low levels of stachyose enhance the utilization of soybean in food as well as feed uses. The objective of this research is to obtain the information on selection possibility of soybean lines with low stachyose content using DNA marker based on *RS2(rs2)* gene. Genetic population was developed from the crosses of 116-13 (low stachyose content) and PI417227 (normal stachyose content) parents. Twenty F₂ plants of *RS2*_ genotype and twenty F₂ plants of *rs2rs2* genotype from each populations were harvested. Content of stachyose was detected by HPLC. Stachyose contents (g/kg) of 116-13 and PI417227 were 3.7, 23.7, respectively. Stachyose content 20 F₂ plants with *RS2*_ genotype was 14.8 – 24.1 and stachyose content 20 F₂ plants with *rs2rs2* genotype was 2.1 – 4.7. Mean difference between *RS2*_ genotype and *rs2rs2* genotype was highly significant. From this results, selection of genetic lines with low stachyose content by DNA marker based on *RS2(rs2)* gene will be possible.

*Corresponding Author: Tel. 055-772-1872, E-mail: jongil@gnu.ac.kr

Agronomical traits of advanced soybean line with low indigestible carbohydrates

Su-Jin Lee, Sung-Jin Han, Sang-Woo Choi, Dong-Hui Kang, Jin-A Kim, Jong-Il Chung*

Division of Applied Life Science, Graduate School, Gyeongsang National University, Chinju 52828, Republic of Korea

Soybean [*Glycine max* (L.) Merr.] seed is one of the major food sources for protein, oil, carbohydrates, isoflavones, and many other nutrients to humans and animals. Raffinose and stachyose are main antinutritional factors in soybean seed. Both raffinose and stachyose are carbohydrates, belonging to the raffinose family of oligosaccharides (RFOs). RFOs are not readily digested in humans and cause flatulence or diarrhea. Genetic reduction of raffinose and stachyose content in mature soybean seed will improve the nutritional value of soybean. The objective of this research was to evaluate agronomic traits with 10 F₆ strains selected from breeding populations derived from the cross by seven parents. Content of raffinose and stachyose in mature seed was detected by HPLC. Agronomic traits such as flower color, flowering date, harvesting date, lodging, plant height, seed coat color, hilum color, 100 seed weight, and yield were evaluated. Total 10 intermediate parents with low raffinose and stachyose content were improved. 883-1 intermediate parent has small seed size. Six intermediate parents (15A1, 15D1, RS-5, RS-33, RS-64 and RS-70) have medium seed size and two intermediate parents (14G20 and RS-21) have large seed size. RS-21 intermediate parent has black seed coat and green cotyledon. Four intermediate parents (883-1, 14G20, RS-5 and RS-21) have elite agronomic traits. New intermediate parents developed through this study will be used to improve new soybean cultivars with low raffinose and stachyose content.

*Corresponding Author: Tel. 055-772-1872, E-mail: jongil@gnu.ac.kr

Identification of quantitative trait loci related to germinability under low oxygen condition

Jong-Min Jeong^{1*}, Woon-chul Shin¹, Man-Kee Baek¹, Hyun-Su Park¹, Chun-Song Kim¹, Jeong-Kwon Nam¹, Young-Chan Cho¹

¹Crop breeding division, National institute of crop science(NICS), Wan-ju 565-851, Republic of Korea

Stable germination and seedling establishment is an important factors for the success of direct seeding cultivation. In order to develop rice cultivars adaptable to wet direct seeding, it is necessary to investigate genetic resources, providing basic knowledge to allow the introduction of genes involved in Anoxia germination (AG) ability from accessions into elite cultivars. 139 recombinant inbred lines derived from Tongil-type rice cultivar 'Milyang 23' and Japonica rice cultivar 'Gihobyeo' were used a mapping population. Evaluation of AG was performed at phytotron in NICS (Jeon-ju, Korea) under temperature variation of 20±5°C per day. After sowing, 10cm depth of water was irrigated and the germination rate was measured at 15 days after sowing. In the QTL analysis using composite interval mapping, we identified two putative QTLs associated to AG tolerance at germination stages. These QTLs located on chromosome 2 and explained 9.43% and 14.75% of the phenotypic variance for AG, respectively. We would be to confirm the detected QTLs through fine mapping and detection of candidate gene. This result would be helpful to facilitate MAS system for improvement of AG resistance in rice variety breeding program for wet direct seeding.

***Corresponding Author:** Tel. 063-238-5217, E-mail: jjm0820@korea.kr

GWAS study for traits influencing chemical and pasting characteristics of eating quality in 96 Japonica rice germplasm

Jong-Min Jeong^{1*}, Woon-chul Shin¹, Man-Kee Baek¹, Hyun-Su Park¹, Chun-Song Kim¹, Jeong-Kwon Nam¹, Young-Chan Cho¹

¹Crop breeding division, National institute of crop science(NICS), Wan-ju 565-851, Republic of Korea

In order to secure competitiveness of our rice and increase consumption of rice, it is necessary to develop high quality new varieties that have our own unique taste to meet consumers' preferences. In this study, We carried out a genome wide association study (GWAS) for 10 traits related to the eating and cooking qualities using 96 Korean japonica rice germplasm. The 96 Korean japonica germplasm consist of 24 varieties, 26 landraces, 22 weedy rices, 19 breeding lines and five Japanese japonica varieties. The traits for eating and cooking quality, amylose content (AC), protein content (PC), alkali digestion value (ADV), glossiness of cooked rice (GCR) and 6 parameters for pasting properties from the rapid viscosity analyzer (RVA) were measured. In the GWAS analysis, a total of 3 marker-trait associations at $P < 0.0001$ for the break down (BD) were identified on chromosomes 1 and 6. Among them, 2 SNP makers associated BD, ab06000994 and ab06000453 on chromosome 6 located in the interval of wx loci, and explained 48.4% and 47.4% of the total variation in BD, respectively. These SNP marker closely linked to the wx gene could be applied to rice eating quality improvement with marker-assisted selection.

***Corresponding Author:** Tel. 063-238-5217, E-mail: jjm0820@korea. kr

Expand phenomics matrix with non-visible spectrum (hyperspectral) in *Brassica rapa* subsp. *chinensis* (bok choy)

Hyo-suk Kim^{1,3}, Sungyul Chang^{2*}, Youngchul Chung³, Hyeong Seok Kim² and Jae Hun Kim¹

¹Sensor System Research Center, Korea Institute of Science and Technology (KIST), Seoul, Republic of Korea

²Natural Products Research Center, Korea Institute of Science and Technology (KIST), Gangneung, Gangwon-do, Republic of Korea

³Department of Electronics and Communications Engineering, Kwangwoon University, Seoul, Republic of Korea

Selecting and implementing non-destructive methods to study complex biological system was active research topic in both plant and animal kingdom, since it could measure the complex system continuously in vivo. Recently, phenomic matrix that only contained visible morphological spectrum images (visible phenotypic marker) enhanced our understanding of complex biological traits greatly. However, visible spectrum data alone was not enough to study complex functional food trait. Hence, we implemented hyperspectral (multiple spectrum ranges) imaging technique to detect anthocyanin presence in multiple bok choy cultivars. The results showed that the method accurately detected anthocyanin concentration compared to traditional destructive chemical assays (HPLC). Furthermore, the method was sensitive enough to detect anthocyanin expression patterns influenced by environment factors in an identical bok choy cultivar. The fast and reliable method coupled with multi-omics data might obtain the complete picture of complex biological trait.

*Corresponding Author: Tel. 033-650-3683 E-mail: schang8@kist.re.kr

파종시기 및 질소 시비가 사료용 옥수수 및 수수×수단그라스 교잡종의 사료가치에 미치는 영향

김영진*, 정종성, 황태영, 김지혜, 김원호

국립축산과학원 축산자원개발부, 충남 천안시 서북구 성환읍 신방1길 114

본 연구는 충남 천안에서 수행하였으며, 옥수수 품종은 조사료용인 ‘광평옥’을 이용하였다. 파종은 2016년 4월 25일과 5월 12일에 75x16cm 재식거리로 ha당 40kg의 종자를 점파하였다. 질소 시비량은 200kg/ha와 220kg/ha를 처리하였으며, 기비는 50%, 추비는 생육 7~8엽기에 50%로 나누어 시용하였다. 수수×수단그라스 교잡종 품종은 출수형인 ‘SX-17’을 이용하였다. 파종은 2016년 4월 20일과 5월 9일에 주간거리 50cm로 ha당 40kg의 종자를 세조파 하였으며, 각 시험구 면적은 12m²(3×4m)로 하였다. 질소 시비량은 250kg/ha와 300kg/ha를 처리하였으며, 기비는 40%, 생육기에 30%, 1차 예취 후에 30%로 나누어 시용하였다. 옥수수의 사료가치(TDN)는 4월 25일 파종에서 71.75%로 가장 높았으며, 조단백질은 5월 12일 파종에서 9.26%로 가장 높았다. 반면 소화율은 5월 12일 파종에서 77.05%로 가장 높은 수치를 보였다. 질소 200kg/ha 처리가 220kg/ha 처리보다 사료가치(TDN)가 높고, 소화율도 좋았으나, 조단백질 함량은 약간 적은 경향이였다. 또한 질소 분시는 기비:추비 100:0% 처리가 50:50% 처리보다 사료가치(TDN)가 높고 소화율도 좋으며 조단백질 함량도 높은 경향이였다. 수수×수단그라스 교잡종의 사료가치(TDN)와 조단백질 함량은 1차 예취시에는 4월 20일 파종에서 가장 높았으며, 2차 예취시에는 5월 9일 파종에서 가장 높았다. 질소 300kg/ha 처리에서의 사료가치(TDN)는 250kg/ha 보다 1차 예취시 높았으며, 소화율도 양호했다. 질소 분시 사료가치(TDN)는 2차 예취시 40:30:30%가 50:50%에서 보다 양호했으며 조단백질 함량도 높았다.

*주저자: Tel. 041-580-6768, E-mail: yjikim@korea.kr

Effect of Stratification, GA₃ and kinetin treatment on germination in *Panax ginseng* C.A. Meyer

Jung-Woo Lee^{1*}, Jang-Uk Kim¹, Ick-Hyun Jo¹, Ji-Eun Hong¹, Kyong-Hwan Bang¹, Kee-Choon Park¹, Young-Chang Kim²

¹Department of Herbal Crop Research, National Institute of Horticultural and Herbal Science, Rural Development Administration, Eumseong 27715, Republic of Korea

²Department of Planning and Coordination, National Institute of Horticultural and Herbal Science, Rural Development Administration, Wanju 55365, Republic of Korea

Korean ginseng is propagated by seeds, which are required 3-4 years to produce mature seeds from their mother plants. It is very important to improve germination rate since ginseng seeds take a long time to be set and the price is high. Also it is required to establish the early breaking dormancy techniques in order to reduce the breeding cycle. In this study, we conducted to investigate the effect of kinetin and/or gibberellin on seed germination in *Panax ginseng* C.A. Meyer. Ginseng berries were harvested when they are mature completely from a research field of the Department of Ginseng research, National Institute of Horticultural and Herbal Science, RDA Eumseong, Korea in July 2016. Dehiscent seeds for germination test were immersed in a solution containing 50 mg/L or 100mg/L GA₃ for 24 hours, respectively at room temperature. Also, in order to confirm the combination effect of kinetin and GA₃, the seeds were immersed in a solution containing 50mg/L kinetin+100mg/L GA₃. GA₃ treatment has a little effect on breaking dormancy and germination, but could not be substituted for chilling requirement in *P. ginseng* due to characteristic of deep physiological dormancy. Kinetin has a significant effect on breaking dormancy and germination although a short period of cold treatment was required. Combination of GA₃ and kinetin treatments was more effective than each hormone treatments.

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***Presenter Corresponding Author:** Tel. +82-43-871-5612, E-mail: enzymer@korea.kr

Effect of Stratification, GA₃ and kinetin treatment on zygotic embryo development in *Panax ginseng* C.A. Meyer

Jung-Woo Lee^{1*}, Jang-Uk Kim¹, Ick-Hyun Jo¹, Kyong-Hwan Bang¹, Kee-Choon Park¹, Young-Chang Kim²

¹Department of Herbal Crop Research, National Institute of Horticultural and Herbal Science, Rural Development Administration, Eumseong 27715, Republic of Korea

²Department of Planning and Coordination, National Institute of Horticultural and Herbal Science, Rural Development Administration, Wanju 55365, Republic of Korea

The ginseng seeds separated from sarcocarps are surrounded by hard and impermeable seed coat acting a mechanical inhibitor. It probably takes about 21 months to achieve germination owing to delayed embryo development when the seeds detached naturally from their mother plants. In order to shorten the period, the seeds are placed in wet sand for over 90 days with periodic watering at 15-20°C known as warm stratification or dehiscence. In completely dehiscent seed, zygotic embryo is still immature and required for additive embryo development to overcome morphological dormancy. In this study, we conducted to investigate the effects of stratification periods, kinetin and/or gibberellin treatment on zygotic embryo development in *Panax ginseng* C.A. Meyer. Dehiscent seeds for measuring embryo development were immersed in a solution containing 50 mg/L or 100mg/L GA₃ for 24 hours, respectively at room temperature. Embryo and endosperm length were measured at intervals of 15 days for 90 days using light microscope after cutting ten seeds in half and then embryo to endosperm ratio was calculated. The embryo grew gradually as the cold stratification period increased, but it was rapidly increased between 30 and 60 days. The germination characteristics of seeds treated by kinetin were excellent when compared with GA₃ treatment and control during the same treatment period. The maximum embryo to endosperm ratio (0.99) observed at GA₃+kinetin treatments with 90 days cold stratification, but there is no difference with kinetin treatment.

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***Corresponding Author:** Tel. +82-43-871-5612, E-mail: enzymer@korea.kr

Resistance of strawberry cultivars to *Phytophthora cactorum*

Ye Rin Lee¹, Myeong Hyeon Nam², Won Suk Jang², Jin Hoon Lee¹, Jundae Lee^{1*}

¹Department of Horticulture, Chonbuk National University, Jeonju 54896, Republic of Korea

²Nonsan Strawberry Experiment Station, Chungcheongnam-do Agricultural Research & Extension Services, Nonsan 32914, Republic of Korea

Crown rot caused by *Phytophthora cactorum* is a serious disease damaging strawberry (*Fragaria x ananassa* Duch.) in worldwide. In this study, we aimed to identify resistant strawberry cultivars against *P. cactorum* through bioassay. A total of 104 strawberry cultivars including 'Sulhyang', 'Santa' and 'Akihime' were inoculated with an isolate, *P. cactorum* 'PC151111', obtained from the Nonsan Strawberry Experiment Station. The zoospore suspension was diluted in autoclaved sterilized water to approximately 10^4 - 10^6 spores \cdot mL⁻¹. The inoculated strawberry plants were incubated at 25 \pm 3°C and 16h/8h (light/dark), and the resistance was evaluated through observation of symptom development for 3 weeks. Disease index was scored on a scale from 0 to 4. In result, the disease index scores varied from 0 to 2.7 and the 14 cultivars, 'Sinyeobong', 'Yeohong', 'Sulhong', 'Sukyeong', 'Santa', 'Gwanha', 'Kamarosa', 'Festival', 'Flamengo', 'Okmea', 'J&Q's early', 'Goryeong', 'Gumsil', and 'Diamante', were highly resistant to *P. cactorum*. These resistant resources will be useful for the genetic analysis and breeding of strawberry resistant to crown rot.

*Corresponding Author: Tel. 063-270-2560, E-mail: ajfall@jbnu.ac.kr

감귤 신품종 '윈터프린스'

박석만^{1*}, 고상욱², 윤수현¹, 박재호¹, 김민주¹, 이동훈³, 최영훈¹

¹농촌진흥청 국립원예특작과학원 감귤연구소

²농촌진흥청 국립원예특작과학원 온난화대응농업연구소

³농촌진흥청 국립원예특작과학원 기획조정과

현재 제주지역에서 재배되고 있는 감귤류는 85%이상이 노지 온주밀감이며 나머지가 시설에서 재배되고 있는 만감류 품종이다. 1990년대 말 부지화(상품명: 한라봉)가 본격적으로 재배되기 시작하면서 제주지역의 만감류 재배 면적은 급격하게 늘어나게 되었다. 만감류는 일반적으로 온주밀감과 구분되어 해를 넘겨 수확되고 온주밀감보다 과피가 두꺼우며 교잡을 통해 육성된 품종들을 말한다. 그러나 근래에 들어 육종기술의 발달로 과거에는 교잡이 힘들었던 온주밀감과 다양한 품종들과의 교잡 품종이 육성되면서 만감류의 특성을 가지면서도 연내에 수확되는 품종들이 육성 되고 있다.

현재 제주에서 재배되고 있는 연내수확형 만감류는 일본에서 육성된 '하레히메'와 '에히메과시제28호'(상품명: 황금향)가 있으며 '에히메과시제28호'는 재배면적이 급증하고 있다. 그러나 '에히메과시제28호'는 과피 벗김이 어렵고 특유의 향을 보유하고 있어 소비자들의 평가에 있어 호불호가 분명한 품종이다.

이에 따라 본 연구는 '에히메과시제28호'의 단점을 극복하여 소비자들의 기호를 보다 충족시키는 품종을 육성하고 자 수행하였다. 윈터프린스는 2007년 '하레히메'를 모본으로 '태전병감'을 교배하여 육성된 교배 실생으로 2008년 실생을 탕자에 접목하여 2014년 1차 선발을 실시하여 2016년에 최종 선발하여 올해 5월 품종보호 출원을 실시하였다.

과실 특성은 10월 하순부터 착색이 시작되어 12월 상순에 완전 착색되며 과실은 옅은 오렌지색이다. 과실 크기는 평균 150g내외이며 성숙기 당도가 12°Brix 정도이고, 산함량은 0.8%로 당산비가 높고 과즙이 많고 과육이 부드럽다. 나무의 특징은 부분인 병감과 유사하여 수세가 강하고 가시가 발생하지 않는다. 또한 자가불화합성으로 종자가 발생하지 않는다. 윈터프린스의 경우 '에히메과시제28호'의 가장 큰 단점인 과피 벗김에 있어 과피가 두껍고 강도가 있어 온주밀감과 같이 매우 쉽게 벗겨낼 수 있다.

*교신저자: Tel. 064-730-4142, E-mail: babau2000@korea.kr

Evaluating three priming sources to surge kenaf seed germination in non-stress and stress conditions

In-Sok Lee*, Chan-Ho Kang, Ki-Kwon Lee

Division of Agro-food Development, Jeollabuk-do Agricultural Research & Extension Services, Iksan 54591, Republic of Korea

Kenaf (*Hibiscus cannabinus* L.) is a real jack of all trades in terms of using such as fiber, forage and fuel. However, kenaf seeds are reported to have poor physiological quality limiting biomass productivity. In this study, the effects of different concentration of three priming sources such as Hydro, KNO₃ and PEG on kenaf seed have been investigated to determine the optimal conditions for surging germination. A variety was Jangdae released from KAERI. The germination rates, MGD (mean germination days) and dry weight of the treated sample seed were compared with those of the untreated seed germinated under non-stress and salt stress conditions. First, there was significant difference in germination rate of kenaf compared non-stress and salt stress (0.1, 0.2, 0.3, 0.4 and 0.5% NaCl) in 24 hours. However, we could not find some difference of germination in 62 hours. It was possible for us to find significant difference in both shoot and root growth degree after 5 days. And, there was no difference in dry weight regardless of stress treatment. RD50 (salt concentration of causing 50% growth reduction) was 0.2~0.3% NaCl based on the shoot and root growth degree. The seeds were treated with Hydro, KNO₃ and PEG. It was found that germination of the treated kenaf seeds was sharply increased compared with that of the untreated seeds in 12 hours under non-stress (distilled water) and 0.3% salt stress conditions. As to MGD, a significant difference was shown in comparison with the treated and untreated kenaf seeds under two conditions. In dry weight (mg/10 plants), sample's dry weight treated with Hydro and KNO₃ was increased under non-stress condition compared with that of the untreated one. But, we found an opposite result under stress condition. The results showed significant effects of priming at 10% PEG concentration under non-stress. Up to 20% PEG, a dry weight of plants cultivated under 0.3% salt concentration was increased, since then, decreased. Three priming techniques proved to be efficient in reducing the germination period. The results suggest that priming with Hydro, KNO₃ and PEG optimized seed germination and vigor and is therefore recommended for kenaf seed invigoration before planting.

*Corresponding Author: Tel. 063-290-6038, E-mail: bioplant325@korea.kr

벼 흰잎마름병과 줄무늬잎마름병에 강한 조기출하용 조생종 '조일'

남정권¹, 박현수¹, 김기영², 김보경¹, 조영찬¹, 고재권¹, 김현순¹, 백만기¹, 김정주², 김우재¹, 신운철¹, 고종철¹, 이점호³, 정종민¹, 정지용¹, 강경호¹, 이영복¹

¹전라북도 완주군 이서면 혁신로 181 농촌진흥청 국립식량과학원

²경상북도 상주시 화서면 중화로 2161, 국립식량과학원 상주출장소

³전라북도 전주시 완산구 농생명로 300 농촌진흥청

우리나라 벼 재배면적 중 중만생 품종의 재배면적이 약 85%를 점유하고 있어 수확기 홍수출하에 따른 쌀값 하락 현상이 매년 반복되고 있는 실정이다. 밥맛이 좋고 병해에 저항성이면서 수량성이 높은 조생 품종을 개발하여 재배면적이 확대되면 중만생종 집중 출하에 따른 쌀값 하락 방지, 콤바인 등 농기계 작업시기 분산 등의 효과를 거둘 수 있다. 국립식량과학원은 2006년 하계에 조생종인 운봉37호를 모본으로 하고 진부와 운광이 교배된 F1을 부본으로 인공교배를 하였으며, F3 이후는 계통육종법에 따라 우량 계통을 선발하였다. 생산력 검정시험에서 조생, 다수성이면서 흰잎마름병과 줄무늬잎마름병에 강한

우량계통 HR27273-90-90-2-1-1에 '익산570호'로 계통명을 부여하였다. '익산570호'는 2013~2015년까지 3년간 지역적응시험 결과, 그 우수성이 인정되어 '조일'로 품종명을 부여하였다. 평야지 조기재배에서 '조일'의 출수기는 7월 16일로 '조평'과 비슷한 조생종이며, 간장은 72cm로 단간이며 내도복성이다. '조일'은 벼흰잎마름병(K1~K3)과 줄무늬잎마름병에 저항성이나 도열병에는 중 저항성이다. '조일'의 수발아율은 10.9%로 조평의 25.2%에 비해 낮은 편이다. '조일'의 쌀 수량은 2013~2015년 실시한 지역적응시험 보통기 보비재배에서 5.39MT/ha로 '조평'보다 3% 증수되며 쌀알은 맑고 심복백이 거의 없다. '조일'의 적응지역은 경기이남 평야지대와 소득작물 후작지이다. '조일'은 평야지 특히 남부평야지에서 추석전 조기 출하용으로 적합한 조생종이다.

주저자: Tel. 063-238-5202, E-mail: namjk725@korea.kr

벼 최고품질 품종의 저장온도 및 저장기간에 따른 도정특성 변화

남정권^{1*}, 신운철¹, 박현수¹, 정종민¹, 김춘송¹, 백만기¹, 조영찬¹, 고재권¹, 정희재¹, 김보경¹

¹전라북도 완주군 이서면 혁신로 181, 국립식량과학원 작물육종과

쌀 시범사업 연계 산업용 RPC 도정특성 및 가공적성 평가를 위하여 벼 최고품질 품종인 삼광, 하이하미, 수광 등 13품종을 저온(15℃)과 상온에서 6개월 및 9개월 저장 후 품종별 밥의 윤기치와 도정 특성을 분석하였다. 저장전 시료의 밥의 윤기치(Toyo 식미치)는 삼광 74.6, 윤광 75.5, 하이하미 81.2, 영호진미 77.9, 수광 76.0, 해품 73.8이었다. 저온(15℃)과 상온에서 6개월간 저장한 시료들의 밥의 윤기치는 68.6~76.4로 저장온도간에는 차이를 거의 보이지 않았다. 저장 후 9개월에서는 저장전의 식미치에 비하여 7.0~22.0 정도 낮았다. 특히, 조생종인 윤광과 해당쌀의 식미치 저하는 중만생종인 삼광, 수광, 칠보의 밥의 윤기치 저하 폭이 컸고, 상온 저장에서 저온 저장보다 감소폭이 더 컸다. 도정율은 저장기간이 길어질수록 동할미 발생 증가하여 도정율이 낮아지는 경향이었다. 특히 상온저장에서 저온저장의 도정율보다 1.0~3.0% 정도 낮은 경향을 보였다. 이상의 결과에서 조생종은 저장기간이 길고, 저장온도가 높아지면 중만생종보다 밥맛 저하가 크므로 기온이 상승하기 전에 소비를 하는 것이 유리하다. 또한 RPC 저장시설 부족으로 벼가 야적되는 경우가 많은데, 이는 밥맛과 도정율을 저하시키는 원인으로 품질 유지를 위한 품종별 최적의 저장조건을 산업용 RPC에 제시하여 쌀 소비촉진에 기여하고자 한다.

*주저자: Tel. 063-238-5202, E-mail: namjk725@korea.kr

건식 쌀가루 전용 뽕안에 ‘한가루’의 농업적 특성

원용재^{1*}, 안억근¹, 장재기⁶, 이상복², 이정희⁴, 정국현¹, 김명기¹, 양창인³, 하운구¹, 현웅조¹, 정웅기⁶, 조영찬⁴, 오세관¹, 윤미라¹, 김보경⁴, 김병주¹

¹경기도 수원시 권선구 수인로 125 국립식량과학원 중부작물부

²강원도 춘천시 충열로 251 국립식량과학원 춘천출장소

³강원도 철원군 동송읍 태봉로 2346, 국립식량과학원 철원출장소

⁴전북 완주군 이서면 혁신로 181 국립식량과학원 작물육종과

⁵전남 무안군 청계면 무안로 199 국립식량과학원 바이오에너지작물연구소

⁶충북 음성군 소이면 비산로 92 국립원예특작과학원 인삼특작부

쌀 소비를 높일 수 있는 방안으로 쌀가루산업 활성화에 적합한 건식제분 전용 신품종 ‘한가루’를 개발하였다. 건식 쌀가루 전용 벼 ‘한가루’는 2007년 하계에 중만생종이면서 현미천립중이 34.8g인 대립으로 쌀 튀김성과 현미 튀김 정립률이 좋은 ‘대립벼1호’를 모본으로, 밥맛이 우수한 ‘일품’의 돌연변이로 뽕안 멍쌀 특성을 가져 양조용으로 산업화에 성공한 ‘설갱’을 부분으로 교배하여 술을 담글 때 원료곡 생산성을 높일 수 있는 대립과 뽕안 멍쌀의 특성을 조합하여 국내 최초로 건식 쌀가루 전용으로 개발된 품종이다. ‘한가루’의 이삭 패는 시기는 8월23일로 중만생종이다. 벼키는 79cm로 ‘화성’보다 작고, 현미천립중은 32.9g으로 ‘화성’보다 1.5배 정도 무거우며, 쌀 수량은 542kg/10a 이다. 쓰러짐에 강하지만 병해충에 약하고, 수발아에 중정도의 반응을 보여 재배적응지역은 중부평야 및 호남평야 북부지역이다. ‘한가루’는 쌀알의 굳기가 연질이면서 배유내 전분구조가 밀과 같이 둥글어 건식 쌀가루의 입자는 평균 60~70μm로 작고, 손상전분이 6.4%로 낮아 쌀가루용 쌀로 적합하다. ‘한가루’로 맥주를 만들었을 때 ‘설갱’보다 환원당함량이 높고 쓴맛이 낮으며 목넘김이 부드러워 양조용에도 적합한 품종으로 확인되었다.

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*주저자: Tel. 031-695-4030, E-mail: yjwon@korea.kr

Effect of mulching on wintering and growth of autumn sown faba bean (*Vicia Faba* L.).

Min-kyu Lee¹, Jaihyunk Ryu¹, Dong-Gun Kim¹, Jung Min Kim¹, Jin-Baek Kim¹, Si-Yong Kang¹, Bo-Keun Ha², Soon-Jae Kwon^{1*}

¹Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, 29, Geumgu-gil, Jeongeup-si, Jeollabuk-do, 56212, Korea

²Division of Plant Biotechnology, College of Agriculture and Life Sciences, Chonnam National University, Gwangju, Korea

Faba bean (*Vicia faba* L.) is an important grain legume extensively grown as a spring crop to avoid freezing damage. However, the expected benefits in the harvest time and grain yields prefer autumn sowing to spring sowing faba bean. Recently, oversupply of rice was issue in South Korea, since high grain yield and developed farming system. The winter faba bean is going to fill as economic crop the time between harvest and transplant of rice field. Plastic mulching provide many positive advantages in crop cultivation such as earlier and higher overall yields, reduced evaporation, and fewer weed problems. The purpose of this study is to compare the difference in growth between PE film mulching field and non-mulching field in 256 individual lines of faba bean. Total 50 seeds were sown in PE film mulching field (22 seeds) and non-mulching field (28 seeds) at Korea Advanced Radiation Technology Institute in Jeongup, in middle Oct, 2015. Of the total 256 lines, zero percentage of survival rate was 63 lines in plastic mulching field and 78 lines in non-mulching field, respectively. Survival plants in PE mulching field had higher plant height than non-mulching field in middle of April, 2016, averagely 10 cm. Flowering started from 29 March, and mulching field was about 2 weeks faster than non-mulching field. In addition, this result was confirmed that the autumn sown faba bean was flowered one month earlier than the spring sown faba bean. These results will be very useful for the cultivation of pulse crop in South Korea, and faba bean will provide great opportunity for mutation breeding.

*Corresponding Author: Tel.: +82-63-570-3312, E-mail: soonjaekwon@kaeri.re.kr

Assessment of fatty acid composition in the different part of faba bean (*Vicia faba* L.) cultivars

Dong-Gun Kim¹, Jaihyunk Ryu¹, Min-kyu Lee¹, Jung Min Kim¹, Jin-Baek Kim¹, Chang-Hyu Bae², Si-Yong Kang¹ and Soon-Jae Kwon^{1*}

¹Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongup, 56212, Korea,

²Department of Life-resources, Graduate School, Sunchon National University, Sunchon, 59722, Korea

Faba bean (*Vicia faba* L.) is one of important versatile and cool-season pulse crop. As a protein-rich legume, faba bean is well adapting to most climatic areas of North Europe, Australia and Asia country for feed and food. This study was conducted to evaluate the fatty acid composition of 10 elite accessions. The fatty acid was extracted from leaves, green pods and matured seeds in each accessions. The most abundant fatty acids of leaves were α -Linoleic acid (C18:3)(n=3)(avg 61.9%), followed by Palmitic acid (C16:0)(avg 12.9%) and Linoleic acid (C18:2)(avg 12.7%). PI567883, PI284345 and PI369511 had highest α -Linoleic acid (63.7%), Palmitic acid (15.2%), Linoleic acid (13.5%) in leave, respectively. In green pods, Linoleic acid (C18:2)(avg 54%) were major fatty acid compound, Palmitic acid (C16:0)(avg 23.3%) and α -Linoleic acid (C18:3)(n=3)(avg 12.2%) were revealed less than 25%. Among 10 accessions, PI366039, PI614810 and PI430715 had highest Linoleic acid (58.9%), Palmitic acid (25.8%), α -Linoleic acid (20.4%) in green pod, respectively. The major fatty acids of matured seeds were Linoleic acid (C18:2)(avg 58.1%), Palmitic acid (C16:0)(avg 19%) and Oleic acid (C18:1)(avg 9.9%). PI252004, PI614810 and PI369511 had highest Linoleic acid (63.6%), Palmitic acid (20.8%), Oleic acid (12.7%) in seed, respectively. In this study, we assessed fatty acid of faba bean first adapted in Korea environment and will be useful for functional food using faba bean.

*Corresponding Author: Tel. 063-570-3312, E-mail: soonjaekwon@kaeri.re.kr

내병성 흰색 참깨 ‘누리(밀양55호)’

김성엽^{1*}, 이명희¹, 배석복¹, 오은영¹, 오기원¹, 정찬식², 여운상¹

¹경상남도 밀양시 점필재로 20 국립식량과학원 남부작물부

²전라북도 완주군 이서면 혁신로 181 국립식량과학원

참깨는 고온다습한 기후에서 재배 시 역병, 시들음병으로 인한 수량감소 피해가 크다. 따라서 국내에서 안정적으로 참깨 생산을 하기 위해서는 역병과 시들음병에 강한 품종육성이 필요하다. ‘누리’는 내병성 참깨 품종 육성을 목적으로 1999년 모본 ‘수원131호’와 부분 ‘양백(IT229436)’을 인공 교배하여 계통육종법으로 육성한 품종이다. 고유 특성은 초형은 소분지형이고 꼬투리는 3과성이며 꽃과 종피는 흰색이다. 또한 성숙기는 8월 23일로 표준품종인 ‘고품’보다 2일 느리며 경장은 138 cm로 크고 주당삭수가 82개로 대등한 수준이었다. 병해 및 도복저항성 포장검정결과 표준품종인 ‘고품’보다 역병, 시들음병, 흰가루병 및 도복에 강한 특성을 나타내었다. 특히 역병유묘검정 결과에서 저항성으로 나타났다. 종실수량은 ’14~’16년 3개년 간 전국 7개 지역 평균 118kg/10a으로 표준품종인 ‘고품’보다 17% 유의하게 높았다. 품질분석결과 조지방 함량은 49.0%, 단백질 함량은 26.1%으로 ‘고품’보다 3% 낮았으며, 세사민 함량은 293mg/100g으로 ‘고품’보다 19% 낮았다.

*주저자: Tel. 055-350-1227, E-mail: sesameup@korea.kr

쓰러짐에 강한 담적색 대립 신품종 팥 ‘해오름’

송석보^{1*}, 고지연¹, 우관식², 정태욱², 최명은¹, 김정인¹, 고종철³, 최유미⁴, 곽도연¹

¹경남 밀양시 점필재로20 국립식량과학원 남부작물부

²경기도 수원시 수인로126 국립식량과학원 중부작물부

³전북 완주군 이서면 혁신로181 국립식량과학원

⁴전북 전주시 완산구 농생명로370 국립농업과학원 농업유전자원센터

‘해오름’은 기계화 적성이 우수하고 가공적성이 뛰어난 팥 품종을 육성하고자 2008년 하계에 국립식량과학원에서 단간인 밀양7호(SA9709-2B-8-2-4-4-4)를 모본으로 하고 적색 대립인 K204656(Toyomidainagon)을 부분으로 인공교배하여 계통육종법으로 선발한 품종이다.

2013~2014년 생산력검정시험에서 쓰러짐에 강하고 수량성이 높아 “밀양27호”로 계통명을 부여하였다. 2014~2016년 지역적응시험을 실시한 결과, 가공적성이 우수하고 내재해성 품종으로 인정되어 2016년 농작물 직무육성 신품종 선정위원회에서 신규등록품종으로 결정되었다.

‘해오름’의 개화일수는 55일로 충주팥 보다 9일 정도 빠르고 생육일수가 92일로 2일 빠른 중만생종이다. 경장은 69cm이며 협당립수는 6.6개로 충주팥보다 많고 쓰러짐에 강하다. 100립중은 18.6g으로 맑은 적색의 종피색을 가진 대립 품종이다. 통팥 가공적성이 우수하고 앙금수율이 높아 팥 가공제품 제조시 품질면에서 유리하다. 수량성은 지역적응시험에서 평균수량이 2.04MT/ha로 다수성 품종이다. 적응지역은 강원도 산간고랭지를 제외한 전국 팥 재배 지역에서 재배가 가능하다. 기계수확이 가능한 ‘해오름’은 노동력과 생산비절감으로 생력화와 농가소득 증대에 기여할 것으로 기대된다.

*주저자: Tel. 055-350-1243, E-mail: songsb1254@korea.kr

L-dopa contents of three different parts of faba bean by UPLC

Jung Min Kim¹, Jaihyunk Ryu¹, Min-kyu Lee¹, Dong-Gun Kim¹, Jin-Baek Kim¹, Si-Yong Kang¹, Bo-Keun Ha², Soon-Jae Kwon^{1*}

¹Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongseup, 580-185, Korea

²Division of Plant Biotechnology, College of Agriculture and Life Sciences, Chonnam National University, Gwangju, Korea

Faba bean (*Vicia faba* L.) has rich L-dopa (3,4-dihydroxyphenyl-L-alanine), the precursor of dopamine, have long been used for the treatment of Parkinson's disease in ancient Eastern Indian ethnotherapeutics. The major objective of this study was to extract L-dopa in Faba bean from 10 accession by ultra performance liquid chromatography (UPLC), with data being gathered from matured seeds, green pod and leaves. The PI430715 contained highest L-dopa content as 15.69±0.10g, whereas PI252004 had lowest L-dopa contents in matured seeds. In green pod, PI430715 included highest L-dopa content (79.58±0.40g), PI655319 had lowest content (16.31±0.02g). In addition, PI284345 contained highest contents (39.82±0.28g) in leaves. The standard deviation of L-dopa in matured seeds, green pod and leaves showed 4.55, 23.16 and 3.65, respectively. However, green pod (34.73) had higher average of L-dopa contents than leaves (33.91). Ultimately, the new variety of faba bean had high content of L-dopa, should be needed for the functional foods. These results will provide valuable information to assist the potentially environmental friendly natural products of use to medicine and other purpose.

*Corresponding Author: Tel. 063-570-3312, E-mail: soonjaekwon@kaeri.re.kr

A new early-heading and high-yielding forage oat cultivar "Dakyeong"

Tae-Il Park^{1*}, Yang-Kil Kim¹, Hyoung-Ho Park¹, Ok-Kyu Han¹, Tae-Hwa Song¹, Jong-Chul Park¹, Jong-Ho Park¹, Chon-Sik Kang¹, Young-Jin Oh², Kyong-Ho Kim¹, Kyu-Hwan Choi³, Ki-Hong Hong⁴, Hyun-Seok Chae⁵, Young-Keun Cheong¹ and Bo-kyeong Kim¹

¹Department of Crop Breeding Division, National institute of crop science, Iseo-myeon, 55365, Korea

²Foundation of Agri. Tech. Commercialization & Transfer, Suwon-city, 16429, Korea

³Jeollabuk-do Agricultural Research & Extension, Iksan-city, 54591, Korea

⁴Chungcheongnam-do Agricultural Research & Extension, Sinam-myeon, 32418, Korea

⁵Subtropical Livestock Research Institute, National institute of animal science, Jeju-city, 63242, Korea

Oats have the characteristics of a high dry matter yield and good livestock palatability as well as feed value. So it's popular for livestock farming. In addition, being the recent climate warming and diversifying of crop rotation system in rice field of Korea, varieties of oats have been developed for forage use because the imported seeds can be also replaced. A new oat (*Avena sativa* L.) cultivar, 'Dakyeong' was released because of its earliness and high forage yield potential. Heading date was April 30 which was 6 days earlier than that of 'Samhan' as the standard one. Meanwhile, plant length is so high of 122cm, and rate of leaves showed higher of 14.7% than check variety of 10.9%. Over 3 years, forage yield based on fresh and dry matter yield were averaged 45ton ha⁻¹ and 15.7ton ha⁻¹ respectively. Dry matter yield was superior with an increase of 12% more than that of 'Samhan'. Also silage quality is good as the crude protein content was 6.1%, NDF and ADF were 60.0% and 33.9%, respectively, and TDN was 62.1%. TDN yield and silage grade were similar to check one. It was found out 'Dakyeong' would be suitable for areas with above -6°C of daily minimum temperature in January in Korean peninsula.

*Corresponding Author: Tel. 063-238-5222, E-mail: parktl@korea.kr

A new oat cultivar "Hi-Early" suitable in the paddy field of Korea

Tae-Il Park^{1*}, Yang-Kil Kim¹, Hyoung-Ho Park¹, Ok-Kyu Han¹, Tae-Hwa Song¹, Jong-Chul Park¹, Jong-Ho Park¹, Chon-Sik Kang¹, Young-Jin Oh², Kyong-Ho Kim¹, Kyu-Hwan Choi³, Ki-Hong Hong⁴, Hyun-Seok Chae⁵, Young-Keun Cheong¹ and Bo-kyeong Kim¹

¹Department of Crop Breeding Division, National institute of crop science, Iseo-myeon, 55365, Korea

²Foundation of Agri. Tech. Commercialization & Transfer, Suwon-city, 16429, Korea

³Jeollabuk-do Agricultural Research & Extension, Iksan-city, 54591, Korea

⁴Chungcheongnam-do Agricultural Research & Extension, Sinam-myeon, 32418, Korea

⁵Subtropical Livestock Research Institute, National institute of animal science, Jeju-city, 63242, Korea

Oats, which are known as one of the forage crops of Korea, have good livestock palatability and are popular with livestock farmers because of their high dry matter. However, the cultivation of double cropping in the rice field was reluctant due to the late maturing for farmers to plant rice continuously. A new oat (*Avena sativa* L.) cultivar, 'Hi-early', showed the heading date 10days earlier than that of check variety 'Samhan'. Average fresh and dry matter yield of 'Hi-early' in the regional adaptation yield trial test were similar of 40ton ha⁻¹ and 14ton ha⁻¹, respectively, but it was 20% of 38ton ha⁻¹ and 13ton ha⁻¹ higher than that of 'Samhan' in the paddy field with many tillers and 122cm of plant length, especially. Also, quality was good of silage grade II as the crude protein content was 6.2%, NDF and ADF were 61.9% and 35.3%, respectively, and TDN was 61.0% as the check one. 'Hi-early' would be adapted for areas with above -6°C of daily minimum temperature in January in Korean peninsula.

*Corresponding Author: Tel. 063-238-5222, E-mail: parktl@korea.kr

Biological responses and oxidative stress induced by acute and chronic gamma irradiation in *Oryza sativa* L.

Sung Min Han, Hong-Il Choi, Si-Yong Kang, Jin-Baek Kim*

Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongup, Jeonbuk 580-185, Korea.

Radiation breeding is a powerful tool for creating a new germplasm with various characteristics. Until now, KAERI has produced many rice varieties through radiation breeding techniques. In this study, we tried to compare physiological responses to acute and chronic irradiation, respectively. The rice plants (*Oryza sativa* L. cv Ilpum) were exposed to 100, 200, 300 Gy doses of acute for 8 hours or chronic for 10 days. The plant height, leaf length and leaf width were decreased with increase of a dose than the non-irradiated plants. The tiller number was increased by 100 Gy and 200 Gy chronic irradiation. DNA damage, chlorophyll fluorescence and free radical accumulation were increased. Induced gamma irradiation increases in the contents of H₂O₂ and malondialdehyde, decreases in the contents of glutathione and ascorbic acid, and increases in the superoxide dismutase and catalase activities. But the ascorbate peroxidase and peroxidase activities were different as gamma-irradiation patterns. Acute and chronic irradiation significantly increased the total phenols contents and phenylalanine ammonia-lyase activity induced under oxidative stress condition. Results suggest that the responses and defense providing reactive oxygen species scavenging systems prompted by irradiation exposure are dependent upon the gamma-ray pattern.

*Corresponding Author: Tel. 063-570-3313, E-mail: jbkim74@kaeri.re.kr

숙기가 빠르고 식미가 우수한 고당도 단옥수수 ‘고당옥1호’

이진석¹, 손범영¹, 김정태¹, 배환희¹, 백성범¹, 정태옥², 김상곤¹, 김성국¹, 정건호¹

¹경기도 수원시 권선구 수인로 126 국립식량과학원 중부작물부

²전라북도 전주시 완산구 농생명로 300 농촌진흥청

고당옥1호는 자식계통 KSE13을 종자친(모본)으로 하고 KSE37을 화분친(부본)으로 하는 단교잡종 단옥수수이다. 고당옥1호는 2006년과 2008년 생산력검정시험을 거쳐 2014년~2016년 3년간 전국 5개 지역에서 지역적응시험을 수행하였으며 그 우수성이 인정되어 2016년 농촌진흥청 직무육성 신품종으로 선정되었다.

고당옥1호는 sugary enhancer(*se*) 유전자를 보유한 단옥수수로 이삭의 색은 황백색을 나타내고 이삭 형태는 중간형을 나타낸다. 고당옥1호는 출사일수는 59일로 표준품종인 단옥3호와 차이가 없었고 이삭의 길이는 18.7cm로 단옥3호보다 길었으며 착립장률은 96%로 단옥3호보다 우수하였다. 고당옥1호의 깨씨무늬병, 그을음무늬병, 조명나방 등 병해충 저항성은 단옥3호와 유사하였으며 도복은 단옥3호보다 강하였다. 고당옥1호의 10a당 이삭수와 이삭중은 각각 6,530개/10a, 1,139kg/10a로 단옥3호와 유사하였다. 당도는 20.8°Bx로 단옥3호보다 높았고 백립중은 27.4g으로 단옥3호보다 작은 경향을 나타내었으며 관능평가 결과 전체기호도가 5.7로 식미가 우수하였다. 고당옥1호는 *se* 유전자를 보유하고 있어 일반옥수수, 초당옥수수(*sh*, *sh2*, *bt* 등), 일반단옥수수(*su*), 찰옥수수(*wx*) 등 다른 종류의 옥수수와 함께 재배 시 고유의 특성이 사라지므로 반드시 시간적 혹은 공간적으로 격리 재배하여야 하며 품질이 우수한 단옥수수 생산을 위하여 적기 수확이 반드시 필요하다.

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***주저자:** Tel. 031-695-4043, E-mail: z9813139@korea.kr

가공용 초다수성 복합내병성 벼 신품종 “한아름4호”

이지윤¹, 조준현¹, 이종희², 손영보¹, 박노봉³, 한상익¹, 오성환², 신동진¹, 송유천¹, 박동수¹, 박병명¹, 오인여¹, 남민희³, 오명규¹

¹경남 밀양시 점필재로 20 국립식량과학원 남부작물부

²전라북도 전주시 완산구 농생명로 300, 농촌진흥청

³경상북도 영덕군 병곡면 원황길 44 국립식량과학원 영덕출장소

“한아름4호”는 가공용 원료곡에 적합한 통일형 초다수성 품종을 만들기 위하여, 2007년 하계에 직립초형으로 수광태세가 우수한 금강과 수량성이 높은 한아름벼를 각각 모본과 부본으로 인공교배를 실시하였다. 2008년 하계에 F₁을 양성하였고, 2009년 F₂ 집단에서 80개체를 선발한 후 2009/2010년 국제미작연구소에서 F₃를 전개하여 계통 당 3계통씩 선발하였다. 이 후 2년 간 계통육종법으로 세대를 진전시켰으며, 2012년 예비선발시험과 2년 간의 생산력검정시험을 거쳐 밀양295호의 계통명을 부여하였다. 2014년부터 2016년까지 3년간의 지역적응시험 결과, 수량성이 높고, 줄무늬잎마름병 및 도열병 등에 저항성이고 수량성 등의 우수성이 인정되어 2016년 농작물 직무육성 신품종선정위원회에서 “한아름4호”로 명명되었다. “한아름4호”는 출수기가 8월 15일인 중만생종이며, 간장은 78cm로 “다산”보다 5cm 크고, 수장은 24cm로 “다산”보다 1cm 작다. “한아름4호”는 저온발아성과 등숙비율이 각각 70.0%와 82.6%이다. “한아름4호”는 쌀수량이 797kg/10a로 현재 개발된 벼 품종 중에서 수량성이 가장 높아 양조용 등 가공용 원료곡으로 적합한 품종이다.

***주저자:** Tel. 055-350-1164, E-mail: minitia@korea.kr

북한 수집 보리 유전자원의 중북부 지역에서의 월동율 및 출수기 변이

구자환*, 한옥규, 안중웅, 권순종

¹경기도 수원시 서둔동 국립식량과학원 중부작물과

북한에서 수집된 보리 유전자원에 대해서 북방 지역에서 재배가 가능한 유전자원을 탐색하고자 북한 원산의 보리 유전자원 209점과 국내에서 육성된 동보리1호, 올보리, 서둔찰보리, 유연보리를 비교품종으로 수원(2016년 10월 13일 파종), 연천(2016년 10월 7일 파종), 진부(2016년 10월 1일 파종)에 파종하여 월동율 및 출수기를 조사한 결과 수원지역에서 월동 중 동사한 유전자원 수는 4점(1.9%)이었고, 연천지역에서 월동 중 동사한 유전자원 수는 51점(24.4%)이었으며, 진부지역에서 월동 중 동사한 유전자원 수는 75점(32.8%)이었다. 국내에서 육성된 비교품종 동보리1호, 올보리, 서둔찰보리, 유연보리는 3개 지역에서 모두 월동이 가능하였다. 수원지역의 유전자원집단 평균 출수기는 4월 28일로 나타났으며, 연천지역의 유전자원집단 평균 출수기는 수원보다 10.6일이 늦은 5월 9일이었으며, 진부지역의 유전자원 집단 평균 출수기는 수원보다 11.1일이 늦은 5월 10일로 나타났다.

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***주저자:** Tel. 031-695-4053, E-mail: jhku@korea.kr

Polymorphic SSRs for genetic diversity and molecular breeding applications in sesame (*Sesamum indicum* L.)

Sovetgul Asekova*, Myung Hee Lee, Jung In Kim, Sung Up Kim, Suk Bok Bae, Un Sang Yeo, Eun Young Oh, Ki Won Oh, Do Yeon Kwak

Department of Southern Area Crop Science, NICS, RDA, Miryang, Korea

Sesame is one of the most ancient oil crop with high nutritional value beneficial to human health. It is widely grown in tropical, subtropical, and southern temperate regions of the world. Various types of molecular markers including RAPD, AFLP, EST-SSRs, ISSRs, SRAP were developed and used to detect genetic diversity for sesame germplasm. There is a limited study associated with genetic diversity of Korean sesame germplasm using SSR markers. SSR is one of very powerful genetic markers because they are hypervariable, relatively abundant, and provide extensive genome coverage. The primary goal of this project is to survey additional genomic SSR markers for polymorphism between 8 cultivars, and for assessing genetic diversity in sesame. The first draft genome sequence of sesame assembled *de novo* (274 Mb) of the elite Chinese sesame cultivar “Zhongzhi 13” was sequenced. Furthermore, 1500 SSR primer pairs were designed by whole genome survey. Among these, 218 polymorphic SSRs were developed and used to screen 31 sesame accessions. In the current study, we downloaded microsatellite DNAs with a known position on the chromosome in Excel file format (PMDBase database) referring to the first draft sesame genome. We randomly select 99 SSR primer pairs evenly distributed in 16 linkage groups (LGs) based on abundant repeat motifs of di- and tri-nucleotide repeats. Eight sesame cultivars (Milseong, Ansan, Galmi, Kangheuk, Daheuk, Kopoom, Chamhwang and Yangbaek) were evaluated by 99 SSR markers, of which 37 showed polymorphic bands. Among of them, 14 SSR polymorphic markers were reported earlier using 96 sesame accessions collected from 22 countries mainly from Asia and Africa. As a result, we found novel 23 SSR primer pairs amplified abundant, clear and repeatable fragments then they will employ to evaluate the genetic diversity. However, current result is primarily test for 8 Korean cultivars to confirm their suitability. The molecular studies on sesame carrying out for further assessing the level of genetic variation of Korean germplasm collection and worldwide sesame accessions.

***Corresponding Author:** Tel. 055-350-1239, E-mail: asekovasovetgul@korea.kr

Analysis of initial growth QTLs in rice using high-throughput plant phenotyping technology

Song Lim Kim, Hyenso Ji, Hongseock Lee, Eungyeong Lee, June Oh, Nyunhee Kim, Yoonkook Park, Jungmin Park, Inchan Choi, JeongHo Baek and Taek-Ryoun Kwon, Kyung-Hwan Kim*

Genetic engineering Division, National Institute of Agricultural Sciences, RDA, Jeonju, 54874, Korea

The initial growth rate is an important physiological trait to improve seedling establishment in direct seeding cultivation of rice. Plant phenomics provides nondestructive analyzing methods using image information of various plant phenotypes. In this study, 162 recombinant inbred lines from a cross between 'Milyang23' and 'Gihobyeo' (MGRIL) were used for analysis of initial growth using phenomics approaches. The main parameters from RGB images were number of pixels and plant height (PH) in image data. In addition, substantial measurements of shoot length (SL), fresh weight (FW), and dry weight (DW) were performed. Correlation coefficients (R) between image data and substantial measurement were revealed to be high among pixel, fresh weight, and dry weight (T-test<0.01). Several QTLs related with initial growth were found. In the 2 and 4 weeks old seedlings, *qPixel-1.1* (interval marker, *R1M47-STS01039*) and *qPixel-1.2* (interval marker, *STS01031-STS01039*) were nearly located at chromosome 1 with LOD (likelihood of odds) scores of 5.63 and 4.42, respectively. These two pixels related QTLs were similarly located not only with *qSL-1.1*, *qFW-1.1*, and *qDW-1.1* of 4 week old seedlings, but also with *qPH-1.1*, *qSL-1.2*, *qFW-1.3*, and *qDW-1.2* of 2 week old seedlings at chromosome 1. All of these QTLs were located at similar location with the semi-dwarf gene, *sd-1*. These results indicated that number of pixels might reflect plant biomass which is a result of initial growth rate. It is expected that phenomics approach will improve phenotyping accuracy, speeds, and efficiency for QTL analysis of agronomical traits.

*Corresponding Author: Tel. 063-238-4658, E-mail: biopiakim@korea.kr

국내산 밀 주요 재배지의 품종별 품질 분석

김경훈*, 김정민, 신동진, 권유리, 현종내, 오명규

경남 밀양시 점필재로 20, 농촌진흥청 국립식량과학원 남부작물부 논이용작물과

국내에서 생산되는 밀은 농가당 생산규모가 작고, 벼 중심의 밀재배에 따른 조기수확 등으로 품질균일도가 떨어져 수입밀보다 품질이 낮게 평가되고 있다. 이에 국내 지역별 밀 품종의 품질 변이를 알아보고자 이 실험을 수행하였다. 각 지역별로 대표품종에 대한 품질 분석한 결과, 전북 지역의 단백질 함량은 8.0%로 작년 대비 3.2% 낮아졌고, 전남 지역의 단백질 함량은 9.6%로 작년 대비 1.0% 낮아졌으며, 경남 지역은 9.3%로 2.9% 낮아졌다. 추가로 수집한 경북 지역, 충남 지역 원맥의 단백질 함량은 각각 9.2%, 11.7%를 나타냈다. 모든 지역의 단백질 함량이 작년과 평년에 비해서 낮았다. 전분 관련 요인인 아밀로스 함량의 큰 차이는 없었고, 단백질의 질적 특성을 나타내는 침전가 수치는 지역간 차이보다는 품종간 차이로, *Glu-D1* 유전자형(5+10)을 지닌 금강과 조경이 백중밀보다 높은 수치를 나타냈다. 지역간의 단백질 함량 차이는 전남북 지역은 백중의 재배면적 비율이 높고, 경남북 지역은 조경의 재배면적 비율이 높은 것에 기인한 것으로 생각된다. 특히적으로 충남 지역의 단백질 함량이나 질적 특성면에서도 우수한 것으로 나타났다. 같은 품종을 재배해도 지역별로 다른 품질의 원맥이 생산되는 점은 추후 연차별로 원맥 수집을 통해 재확인할 필요성이 있다. 향후 2017년 수확한 원맥의 품질을 추가로 조사·분석하여 지역별 생산되는 품종의 품질 차이를 보완·확인할 예정이다.

* 주저자: Tel. 055-350-1173, E-mail: k2h0331@korea.kr

Selection and characterization of soybean mutants with alteration in seed linolenic acid composition

Young Eun Jang, Min Jeong Hong, Soon-Jae Kwon, Joon-Woo Ahn, Sang Hoon Kim, Yeong Deuk Jo, Hong-Il Choi, Si-Yong Kang, Jin-Baek Kim*

Advance radiation technology institute, Korean atomic energy research institute, Jeongeup, Republic of Korea

Soybean (*Glycine max*) is one of the major oil crops. Soybean oil is consumed approximately 50 million metric tons per year that placing second highest in world vegetable oil consumption. Soybean seed containing 20 to 25 % lipid and most of the fatty acids are unsaturated fatty acid (18:1, 18:2 and 18:3). Linolenic acid (18:3n-3) is the dietary precursor for the long-chain omega-3 polyunsaturated fatty acids and it is not synthesized by human and other animals. In plant, linolenic acid is desaturated from oleic acid by sequential activity of fatty acid desaturases, FAD2 and FAD3 gene families. We measured seed fatty acid contents of 78 and 154 M₈ mutant progenies from 250 Gy gamma-ray radiated Danbaek (DB) and Daepung (DP) in 2016, respectively. Each 20 mutants of highest linolenic acid were selected from two mutant populations. We investigated agriculture characteristics, such as seed coat color, 100 seed weight, flowering and maturation. According to two year measurement of seed fatty acids, five lines from each mutant population were selected with high linolenic acid content. The average linolenic acid contents of selected lines from DB and DP mutant populations were 9.54% and 9.48%, respectively. For further research, we are searching for nucleotide polymorphism and gene expression changes of FAD2 and 3 gene families during seed development.

*Corresponding Author: Tel. 063-570-3313, E-mail: jbkim74@kaeri.re.kr

작물 표현체 분석 시스템 및 벼 생육 조건 최적화

최인찬, 김송림, 이홍석, 이은경, 김년희, 백정호, 지현소, 권택윤, 김경환*

전라북도 전주시 완산구 농생명로 370, 국립농업과학원 유전자공학과

최근 유럽, 호주와 미국 등 농업선진국에서는 식량 생산량의 증대를 위한 육종과 형질분석을 위해 식물 표현체(Plant Phenomics) 플랫폼을 구축하고 표현형 연구를 하고 있다. 이에 국립농업과학원은 스마트 온실에 식물운송 컨베이어, 이미지 센서와 챔버 그리고 워터링 시스템을 구축하였다. 이 시스템은 생장양상, 엽색, 엽면적, 물 공급량, 비료 시비, 스트레스, 형태학 등을 분석하여 식물의 특성을 파악할 수 있다. 먼저 카메라 Exposure, gain, gamma, 리프트 높이 및 회전 속도 조합을 설정하여 선명하고 흔들림 없는 이미지를 2분 30초안에 획득하여 대기시간을 단축시켰고 펌프의 1회 물 공급량과 속도, 화분에 대한 물의 총 공급량 설정, 컨베이어 스케줄링, 벼 재배에 적합한 토양을 선정하였다. 또한 이미지 계산값과 실측값인 픽셀, 엽면적, 크기, 초장, 건물중을 이용한 피어슨(Pearson) 상관관계 계수(R)는 0.96 이상으로 시스템의 실용성을 판단하였다. 이처럼 최적화된 식물표현체 시스템은 육안으로 판독하기 어려운 여러 가지 형질들을 고속 대량의 디지털 분석을 통해 벼 육종자원 개발 및 유전체분석기술과 연계될 수 있을 것이다.

*교신저자: Tel. 063-238-4658, E-mail: biopiakim@korea.kr

최근 10년간 벼 지역적응시험 계통의 내냉성 변화

이상복^{1*}, 현웅조², 정종민³, 이정희³, 서대하¹, 김병주², 성열규¹

¹강원도 춘천시 충열로 251 국립식량과학원 춘천출장소

²경기도 수원시 권선구 수인로 126 중부작물부 중부작물과

³전북 완주군 이서면 혁신로 181 국립식량과학원

우리나라는 1970년대 통일벼 품종의 보급됨과 더불어 벼 냉해에 대한 연구 필요성이 크게 대두 되었다. 1980년대의 냉해는 국내 벼 재배면적의 64.2%에 결정적인 피해를 주고 약 32%의 수확량 감소를 가져왔다. 그 후 1993년도 냉해는 1980년도와 유사한 극심한 냉해가 왔으나 그동안 냉해에 견디게 개량된 벼 품종의 보급으로 냉해의 피해를 크게 줄일 수 있었다.

1978년 농촌진흥청 작물시험장 춘천출장소가 설립된 이후 내냉성 검정 포장을 만들고 소양강댐의 냉수를 이용하여 내냉성 벼 품종육성 및 유전자원 탐색을 위한 검정사업을 지속적으로 수행하여 왔다. 특히 국내 벼 육종기관에서 육성한 우량계통들에 대한 포장 및 온실에서의 내냉성 검정을 통하여 벼 품종을 육성 해온 결과 내냉성이 크게 증진되었다.

지난 30년간 국립식량과학원 춘천출장소에서 벼 지역적응시험 공시된 우량계통에 대하여 냉수 처리로 포장 검정하고 조사한 계통들의 임실율을 보면 80년대에 29.8%, 90년대 43.7% 그리고 2000년대 50.3%로 점차 증가하여, 2000년대 평균은 80년대 대비 31%, 90년대 대비 약 7%가 증대되었다. 그러나 2010년 이후 2016년까지 연도별 우량계통들의 냉수처리 검정에 의한 평균 임실율은 42%로 감소하고 있으며 2014년 이후 최근 3년간은 36.7%의 임실율을 보이고 있다.

*주저자: Tel. 033-254-6328, E-mail: sabolee@korea.kr

이미지 센싱 기반 벼 생육 측정 모델 개발

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

전라북도 전주시 완산구 농생명로 370, 국립농업과학원 유전자공학과

최근 이미지 센서 기반으로 식물 표현체 연구가 활발히 진행되고 있다. 특히 생명자원 선발 효율성 증진 또는 유전자 기능 대량검정을 위한 식물표현체 분석 알고리즘은 다양한 작물 및 방법을 통해 개발되고 있다. 본 논문에서는 국내 벼 품종에 대한 생육 특성 분석 알고리즘을 연구하였다. 먼저 RGB 카메라를 이용하여 벼의 이미지를 획득하고 RGB 이미지를 Lab이미지로 변환하여 관심영역을 추출한다. 추출된 관심영역이미지를 연산하는 방법으로 다양한 알고리즘을 개발하였다. 4개 토양, 5개 품종에 대하여 비료투입 5일 전과 비료 투입 15일 후의 이미지를 획득하여 Lab, Lch 색영역에서 색상 변화를 판별하여 비료 투입여부에 대한 임계값을 설정하였다. 벼의 중요 생육특성인 생체중과 건물중의 예측을 위해서 면적, 높이, 폭을 영상에서 연산하여 비교 분석하였으며, 상관관계수(R^2)는 0.85 이상이 됨을 확인할 수 있었다. 또한 Convex hull, 식물 중심점 및 Compactness를 이용하여 새로운 생육특성을 제시하였다. 본 연구는 육안으로 확인하였던 생육특성을 개발된 알고리즘으로 대체 가능함을 보여주었고 다양한 알고리즘을 통해 생육특성에 대한 수치화, 정형화하여 새로운 해석방법을 제시하고자 한다.

*교신저자: Tel. 063-238-4658, E-mail: biopiakim@korea.kr

영상 분석 기술을 활용한 호접란의 표현형 분석

김년희¹, 김송림¹, 이은경¹, 이홍석¹, 백정호¹, 지현소¹, 최인찬¹, 박부희², 김정환^{1*}

¹전라북도 전주시 완산구 농생명로 370, 국립농업과학원 유전자공학과

²전라북도 완주군 이서면 농생명로 100, 국립원예특작과학원 화훼과

최근 호접란은 화훼 재배산업에서 가장 인기 있는 난초 중의 하나로 주로 열대 아시아 전역에 분포하고 있다. 부가가치가 높은 품종을 대량생산하기 위해 조직 배양 기술을 활용하고 있으며 조직배양 결과 특이한 표현형을 보이는 변이체가 발견되고 있다. 국립원예특작과학원에서 조직배양을 통해 육성한 17개 호접란의 꽃을 촬영하고 영상 처리 프로그램(Image J)으로 꽃의 크기, 색깔, 형태학적 특징 등을 이용해 표현형을 분석하였다. 먼저, 스케일 바를 이용하여 촬영된 이미지의 단위를 결정했고, 이미지의 노이즈를 제거하였다. 그 다음, 꽃의 이미지를 R, G, B 채널을 이용하여 영역추출을 하였고, 픽셀 값을 설정하여 배경과 꽃을 분리하였다. 분리된 이미지는 히스토그램, 면적, 폭, 높이, 측면의 길이, 둥근 정도, 퍼짐 정도, 균일성 등 형태학적 특징을 수치화하고 최소-최고 표준화를 통해 꽃의 형태, 꽃잎, 꽃받침에 대한 패턴을 분류 할 수 있었다. 본 연구는 호접란에 대한 특이 표현형 분석에 있어 중요한 지표로 향후 고부가 가치 난의 육종과 유전자 기능 분석에 이용될 수 있을 것이다.

*교신저자: Tel. 063-238-4658, E-mail: biopiakim@korea.kr

RGB 영상 분석을 통한 콩 종자 표현형 분석

이은경¹, 백정호¹, 한희정¹, 김송림¹, 김년희¹, 최인찬¹, 정남희², 최만수², 문중경³, 지현소¹, 김정환^{1*}

¹전라북도 전주시 완산구 농생명로 370, 국립농업과학원 유전자공학과

²전라북도 완주군 이서면 혁신로 181, 국립식량과학원 작물기초기반과

³전라북도 전주시 완산구 농생명로 370, 국립농업과학원 기획조정과

콩은 식물성 단백질 및 지방산의 주요한 공급원으로 세계적으로 중요한 식량자원이다. 국립식량과학원에서 콩 유전체 육종의 기반구축을 위해 모집단 4,382점에서 재배종 407점, 야생종 393점을 선발하여 핵심집단(Core SET-V2)을 작성하였다. 구축된 핵심집단은 종피색, 엽형, 백립중, 개화일수 등의 기본 형질을 조사하였다. 콩의 게놈전체연관분석(GWAS)을 위해 핵심집단에서 50계통의 종자를 RGB(Red Green Blue)영상을 활용하여 디지털 표현형분석(digital phenotyping)을 하였다. RGB영상은 위쪽과 측면 카메라를 이용하여 촬영하였으며 영상분석 프로그램(Image J)을 활용하여 콩 종자의 장폭, 단폭, 두께, 엽색, 제색, 원마도(Roundness) 등을 분석하였다. 특히 각 계통별 영상 데이터를 명암(Gray scale), 빨강(Red), 녹색(Green), 청(Blue)의 4가지 히스토그램과 로그 값으로 수치화 한 결과 정상적인 패턴이 대부분이었으나 4계통은 특이한 패턴을 나타내었다. 이 연구를 통해 실측에 의해서 분석이 어려운 콩 종자의 형태적 특성과 종피색, 제색 등의 색상 특성을 통해 게놈전체연관분석(GWAS) 가능성을 탐색하고자 하였다. 향후 더 많은 자원을 이용하여 영상 획득, 표현형 분석, 유전자기능 해석 등을 통해 유전체 육종에 활용하고자 한다.

*교신저자: Tel. 063-238-4658, E-mail: biopiakim@korea.kr

Relationship between Agronomic Traits and Canopy Structure in determining *Miscanthus* × *giganteus* Biomass Yield

Soo-Hyun Lim, Yeon-Ho Park, Do-Soon Kim*

Department of Plant Science, Seoul National University, Seoul 08826, Republic of Korea

Canopy structure of monocot crop is determined by vertical and horizontal plant growths mainly represented by stem height and stem distribution, respectively, and determine crop biomass yield. *Miscanthus* species have diverse growth habits and agronomic traits depending on species and thus show high diversity in biomass yield potential. This study was thus conducted to develop methods to assess canopy structure of *Miscanthus* and to investigate *Miscanthus* canopy structure in determining biomass yield of *Miscanthus*. The growth parameters of *M. × giganteus*, selected as a model *Miscanthus*, associated with canopy structure such as the spatial distribution of stems, stem height, and stem dry weight were assessed at harvest during the four years after planting and its canopy area and volume were estimated. In the first and the second year, canopy area and volume of *M. × giganteus* increased due to slow expansion of stem growth, but from the third year after planting increased dramatically, resulting in dramatic biomass yield. It is suggested that our method and results can be applied to other *Miscanthus* species for investigating relationship between agronomic traits and canopy structure in determining *Miscanthus* biomass yield and can be used to find target traits for *Miscanthus* breeding program.

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*Corresponding Author: Tel. 02-880-4552, E-mail: dosoonkim@snu.ac.kr

Identification and determination of phenolic compounds in seed of Kenaf (*Hibiscus cannabinus* L.) mutant Cultivars

Jaihyunk Ryu, Soon-Jae Kwon, Yeong Deuk Jo, Jung-Min Kim, Min-Kyu Lee, Dong-Gun Kim, Joon-Woo Ahn, Jin-Baek Kim, Si-Yong Kang*

Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongup, Jeonbuk, 56212, Korea.

Kenaf seeds have high antioxidant activity due to high amounts of phenolic compounds. This study was carried out to investigate phenolic compounds in three mutant kenaf cultivar (Jangdae, Baekma and Jeokbong) and two original cultivars (Jinju and C14). The phenolic compounds in seeds were determined by HPLC-MS. Three phenolic compounds (*N*-coumaroyl-3-hydroxytyrosine, ferulic acid and sinapic acid) were identified in early maturing cultivars (Baekma, Jeokbong and C14). Whereas, *N*-coumaroyl-3-hydroxytyrosine was not detected in mid-late maturing cultivars (Jangdae and Jinju). The ferulic acid content in all cultivars ranged from 1297.9 mg/kg to 2220.0 mg/kg; highest amount of ferulic acid was observed in Baekma. Ferulic acid content in Baekma is approximately 30% higher than it in mother cultivar C14. C14 cultivar showed highest amount of *N*-coumaroyl-3-hydroxytyrosine. Different amount of sinapic acid was observed between kenaf cultivars; Jinju and Jangdae displayed lowest (25.6 mg/kg) and highest level (924.1 mg/kg), respectively. Findings from the present study indicate that kenaf is a potential source of natural antioxidant and may be utilized for pharmaceutical production. In addition, early maturing cultivars contained *N*-coumaroyl-3-hydroxytyrosine which can be used as a marker compound to distinguish cultivars.

*Corresponding Author: Tel. 063-570-3310, E-mail: sykang@kaeri.re.kr

반매끈망으로 기호성이 우수한 청보리 신품종 ‘미한’

오영진¹, 박태일¹, 김양길¹, 박형호¹, 박종철¹, 강천식¹, 한옥규², 윤건식³, 홍기홍⁴, 배정숙⁵, 송재기⁶, 김정호¹, 정영근¹, 송태화¹, 박종호^{1*}

¹전북 완주군 이서면 혁신로 181 농촌진흥청 국립식량과학원

²경기도 수원시 서둔동 국립식량과학원 중부작물부 중부작물과

³충청북도 청주시 청원구 오창읍 가곡길 46 충청북도농업기술원

⁴충청남도 예산군 신암면 추사로 167 충청남도농업기술원

⁵대구광역시 북구 칠곡중앙대로136길 47 경상북도농업기술원

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 2001년에 도복 및 내한성이 강하며, 초형이 양호한 SB00T2064를 모본으로 하고, 양질 다수성으로 총체적성이 높은 수원385호(IT215831)를 부분으로 인공교배하여 까락이 반매끈망으로 부드럽고, 내한성 및 도복에 강하고, 사일리지 젖산함량이 높아 사일리지 품질이 우수한 ‘미한’을 개발하였다. ‘미한’은 직립초형으로 초장은 96cm로 ‘영양’보다 크며, 파성은 IV 정도로 가을파종에 적합하다. 답리작재배시 출수기는 4월 24일로 영양보다 3일 늦었으며, 황숙기는 5월24일로 ‘영양’보다 하루 늦었다. 줄기수는 m^2 당 665개로 다열성이며, 내한성은 ‘영양’보다 강하고, 호위축병은 나주(I형), 진주(IV)에서 저항성, 익산(III형)에서 중도저항으로 ‘영양’과 비슷한 내재해성 품종이다. 조사료 건물수량은 전작에서 13.8톤/ha로 ‘영양’에 비해 5%, 답리작에서 평균 10.6톤/ha로 ‘영양’에 비해 1% 감소하였다. 조사료 품질은 조단백질 함량이 10.3%, 총가소화영양분(TDN)은 68.2%로 영양에 비해 다소 낮았으나 젖산함량이 높고 초산 및 낙산함량이 낮아 사일리지 품질이 I 등급으로 매우 양호한 품종이다. ‘미한’의 적응지역은 1월 최저평균기온 $-8^{\circ}C$ 이상으로 북부 산간내륙지방을 제외한 전국에서 재배가 가능하다. ‘미한’은 추위 및 도복에도 강하고 반매끈망으로 가축기호성과 사일리지 품질이 좋아 금후 축산 농가들로 부터 큰 호응을 얻을 것으로 기대되며, 금후 신품종이용촉진사업을 통한 종자 생산단계를 거쳐 2019년부터 농가에 보급될 예정이다.

*교신저자: Tel. 063-238-5228, E-mail: ark0104@korea.kr

삼차망 다수성으로 기호성이 우수한 청보리 신품종 ‘유진’

오영진¹, 박태일¹, 김양길¹, 박형호¹, 박종철¹, 강천식¹, 한옥규², 윤건식³, 홍기홍⁴, 배정숙⁵, 송재기⁶, 김정호¹, 정영근¹, 송태화¹, 박종호^{1*}

¹전북 완주군 이서면 혁신로 181 농촌진흥청 국립식량과학원

²경기도 수원시 서둔동 국립식량과학원 중부작물부 중부작물과

³충청북도 청주시 청원구 오창읍 가곡길 46 충청북도농업기술원

⁴충청남도 예산군 신암면 추사로 167 충청남도농업기술원

⁵대구광역시 북구 칠곡중앙대로136길 47 경상북도농업기술원

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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 삼차망으로 내한성에 강하며, 초형이 양호한 수원406호/수원389호를 모본으로 하고, 장간으로 총체적성이 높은 SB961012/수원389호를 부분으로 인공교배하여 삼차망 다수성이면서 기호성이 우수한 우수한 ‘유진’을 개발하였다. ‘유진’은 직립초형으로 초장은 99cm로 ‘영양’보다 크며, 파성은 II 이다. 답리작 재배시 출수기는 4월 24일, 황숙기는 5월26일로 ‘영양’과 같다. 줄기수는 m^2 당 696개로 다열성이며, 내한성은 ‘영양’보다 강하고, 호위축병은 나주(I형), 진주(IV)에서 저항성, 익산(III형)에서 중도저항으로 ‘영양’과 비슷한 내재해성 품종이다. 조사료 건물수량은 전작에서 17.1톤/ha로 ‘유연’에 비해 19%, 답리작에서 평균 11.0톤/ha로 ‘유연’에 비해 2% 높다. 조사료 품질은 조단백질 함량이 10.6%, 총가소화영양분(TDN)은 69.1%로 유연에 비해 다소 높았으며, 젖산함량이 높고 초산 및 낙산함량이 낮아 사일리지 품질이 I 등급으로 매우 양호한 품종이다. ‘유진’의 적응지역은 1월 최저평균기온 $-8^{\circ}C$ 이상으로 북부 산간내륙지방을 제외한 전국에서 재배가 가능하다. ‘유진’은 삼차망이면서 추위 및 도복에도 강하고 총체수량이 높은 다수성으로 금후 축산 농가들로 부터 큰 호응을 얻을 것으로 기대되며, 금후 신품종이용촉진사업을 통한 종자 생산단계를 거쳐 2019년부터 농가에 보급될 예정이다.

*교신저자: Tel. 063-238-5228, E-mail: ark0104@korea.kr

Analysis of genetic variation in fruit color of *Capsicum* germplasm using SMRT sequencing

Min-Young Kang¹, Hyo-Bong Jeong¹, Ayoung Jung¹, Koeun Han¹, Moo-Chan Kang and Byoung-Cheorl Kang^{1*}

¹Department of Plant Science, Plant Genomics and Breeding Institute, and Vegetable Breeding Research Center, College of Agriculture and Life Sciences, Seoul National University, Seoul 151-921, Republic of Korea

In plants, carotenoid plays important roles in photosynthesis, photo-protection, and phytohormones synthesis such as ABA and strigolactone. In addition, carotenoid provides color to flowers and fruits for attracting insects or animals for pollination and seed dispersal. In *Capsicum*, ripe pepper fruits display various colors ranging from white to deep red. In the carotenoids synthesis pathway, capsanthin-capsorubin synthase (CCS), phytoene synthase (PSY1), β -Carotene hydroxylase (CrtZ-2) and lycopene β -cyclase (LcyB) genes are known for regulators of fruit color. In this study, total 132 accessions were used for sequence analysis of these genes using single molecule real time (SMRT) sequencing technology. We detected many variants in coding region of the each genes. The nucleotide sequences were aligned to those of red color fruit accessions. Sequencing analysis showed that 5 point mutations and 2 frame shift mutations in the coding region of the PSY1 gene. Among these mutations, one nonsense mutation and 2 frame shift mutations lead to premature stop codon. The CCS gene is consisted of one exon. In the coding region of CCS, 3 missense mutations, 5 nonsense mutations, and 5 frame shift mutations were identified. As for LcyB, we selected 23 accessions which had 4 missense mutations and 1 nonsense mutation. In coding region of the CrtZ-2 gene, 6 missense mutations and 1 frame shift mutation were detected. Specially, sequence analysis of the CrtZ-2 gene revealed a big structural mutation in the non-red color fruits that may result in no expression of this gene. Taken together, we revealed various genetic variations of PSY1, CCS, LcyB, and CrtZ-2 genes which are responsible for non-red color fruit in *Capsicum* spp.

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

조기재배 적합 다수성 중간질 고구마 ‘진율미’

이형운^{1*}, 이준설¹, 정미남², 남상식¹, 양정욱¹, 김재명³, 안승현⁴, 송연상¹, 한선경⁵, 황엄지¹

¹전남 무안군 무안로 199 국립식량과학원 바이오에너지작물연구소

²전북 전주시 완산구 농생명로 300 농촌진흥청 연구정책국 연구성과관리과

³전남 나주시 금천면 벽류길 121 국립원예특작과학원 배연구소

⁴전북 완주군 이서면 혁신로 181 국립식량과학원 작물재배생리과

⁵전북 전주시 완산구 농생명로 300 농촌진흥청 대변인실

최근 소비자는 단맛이 강하고 찢고구마 육질이 중간질 또는 점질로서 부드러우면서 간편하게 먹을 수 있는 적당한 크기의 고구마를 선호한다. 또한 고구마의 시장가격은 조기재배 고구마가 출하되기 시작하는 7월에 가장 높고 8월 가격은 보통기재배 고구마가 홍수 출하되는 10-11월보다 30~34% 정도 높기 때문에('14~'16년 3년 평균, 도매 상품 기준) 재배 농가는 품종 선택시 식미뿐만 아니라 조기재배 수량성도 중요하게 고려한다. 고구마 신품종 ‘진율미’는 농촌진흥청 국립식량과학원 바이오에너지작물연구소에서 식미가 우수하고 괴근 모양과 수량성이 양호한 ‘신천미(IT232328)’를 모본으로 하고 수량성이 양호하고 찢고구마 육질이 중간질인 ‘전미(IT258827)’를 부본으로 하여 2008년도에 교배하였다. 2009년에 실생개체선발시험에서 1,449개체 중 괴근의 모양과 비대가 양호한 98계통을 선발하였다. 2010년부터 2011년까지 계통선발시험, 2012년부터 2013년까지 생산력검정시험을 수행하여 괴근 육색이 담황색이고 모양, 수량성, 식미가 양호한 ‘MI2008-03-50’ 계통을 ‘목포90호’로 계통명을 부여하여 지역적응시험에 공시하였다. 2014년부터 2016년까지 3년간 지역적응시험을 수행한 결과, 수량성, 품질특성, 병해충저항성 등이 대비품종인 ‘율미’보다 우수하여 2016년 12월 농촌진흥청 농작물직무육성신품종선정심의회에서 신품종으로 선정되었으며 ‘진율미(Jinyulmi)’라 명명하였다. ‘진율미’는 잎모양이 심장형이며, 끝잎색은 자색, 엽색과 잎자루색, 줄기색은 녹색이다. 괴근의 껍질색은 홍색, 육색은 담황색이며 찢고구마 육질은 중간질로 부드러운 편이고 괴근 모양은 방추형이다. ‘진율미’는 덩굴조짐병과 고구마뿌리혹선충에 중도저항성이다. ‘진율미’는 식미점수가 3.6으로 대비품종보다 식미가 우수하며(대비품종 3.0) 생고구마 총유리당 함량은 8.8%(대비품종 4.9%), 감미도는 8.1(대비품종 4.8)로 대비품종보다 각각 80%, 69% 높다. 찢고구마의 감미도는 13.4(대비품종 11.9)로 대비품종보다 13% 높아 단맛이 더 강하다. ‘진율미’는 보통기재배시 상품괴근수량이 28.6 MT/ha이며, 조기재배시 상품괴근수량이 24.2 MT/ha으로 대비품종보다 각각 19%, 26% 많다. 상품괴근의 평균 무게는 137g으로 대비품종(178g)보다 작고 주당 상품괴근수는 3.6개로 많은 편이다. 식미가 우수하고 조기재배에도 적합한 ‘진율미’는 농가와 소비자 모두 선호할 것으로 기대된다(품종출원 번호: 출원-2017-148).

*주저자: Tel. 061-450-0141, E-mail: leehu79@korea.kr

간척지 단벌기 목재에너지림에 적합한 포플러 클론 선발

김현철*, 이현석, 이솔지, 강준원, 임혜민, 이위영, 장경환

경기도 수원시 오목천동 국립산림과학원 임목육종과

2009년 인천 서구 수도권매립지내에 위치한 간척지에 이태리포플러 3클론(Eco28, Dorskamp, Venziano), 미류나무 교잡종 3클론(Ay48, 97-18, 97-19), 현사시나무 3클론(72-30, Bonghwal, Clivus)을 1년 수확구, 2년 수확구 및 3년 수확구에 클론별로 각각 1반복 9본으로 3반복 총 27본씩 식재밀도 10,000본/ha으로 식재한 후 단벌기 목재에너지림 조성을 위해 지상 10 cm 부위에서 대절을 실시하였다. 수확구별 대절에 의한 맹아지 발생 수는 1년 수확구에서 11.1개로 가장 높았고, 2년 및 3년 수확구에서 7.0, 6.4개로 나타났다. 수확구별 연평균 바이오매스 생산량을 비교한 결과, 1년 수확구에서 평균 2.9 ton/ha/year로 나타났으며, 2년 및 3년 수확구에서 각각 평균 3.6, 4.3 ton/ha/year로 3년 수확구의 연평균 바이오매스 생산량이 가장 우수하였다. 클론별 연평균 바이오매스 생산량은 미류나무 교잡종들이 모든 수확구에서 다른 클론들 보다 우수하였으며, 특히 97-18 및 97-19 클론의 경우 3년 수확구에서의 연평균 바이오매스 생산량이 각각 9.5, 10.8 ton/ha/year으로 나타나 가장 우수하였다. 간척지 환경에서의 식엽충(leaf damage), 천공충(stem borer damage) 및 조기낙엽(early defoliation) 등의 피해도를 조사한 결과, 식엽충과 조기낙엽 피해는 모든 클론이 적었으며, 천공충 피해가 많이 나타났다. 바이오매스, 식엽충, 천공충 및 조기낙엽 피해 등을 지표로 사용하여 중요도에 따라 차등을 두어 가중치를 부여한 후 적응지수를 산출하였으며, 그 결과 미류나무 교잡종 97-18 및 97-19클론이 간척지 단벌기 목재에너지림에 가장 적합한 포플러 클론으로 나타났다.

*주저자: Tel. 031-290-1109, E-mail: hckim97@korea.kr

테다소나무 가계별 구과분석을 통한 종자생산 진단

이현석*, 김현철¹, 이솔지¹, 강준원¹, 임혜민¹, 이위영¹

¹경기도 수원시 오목천동 국립산림과학원 산림유전자원부

테다소나무(*Pinus taeda* L.)는 미국 남부지방에서 광범위하게 분포하는 것으로 알려져 있으며 우수한 성장력과 수간 통직성으로 인하여 현지에서는 주요 경제수종으로 이용되고 있다. 우리나라에는 해방 전 도입된 것으로 알려져 있으나 자료의 소실로 인하여 결과를 알 수가 없으며, 1964년부터 산지시험을 통하여 리기다소나무와 비교하여 3~4배 높은 것으로 알려져 있다. 하지만 내한성이 약하여 우리나라에서 생육 가능한 지역은 충청 이남으로 알려져 있다. 최근 기후변화로 인하여 테다소나무의 생육 가능지 확대 가능성에 대비한 우량 종자 확보 및 보급의 필요성이 대두되고 있다. 이를 위하여 가계별로 채취된 구과 및 종자특성을 구명함으로써, 유용 용재수 조립을 위한 종자 생산성 향상 방안을 모색하고자 본 연구를 수행하였다. 1981년 전남 보성에 조성된 테다소나무 시험림에서 총 14가계를 선발하였으며, 미국 농무성 구과분석 지침을 참고하여 종자생산능력, 종자생산효율 및 고사배주를 조사하였다. 구과 당 총 인편수는 평균 115.7개로 나타났으며, 임성인편수와 불임성인편수의 평균은 각각 63.2개와 52.6개로 조사되었다. 종자생산능력은 평균 111.3으로 조사되었으며 73.4~144.6 범위에서 나타나 가계 간 최대 2배 가량 차이를 나타내었다. 종자생산능력은 구과당 생산 가능한 종자 수의 생물학적 한계를 의미하며 구과 착과량이 증가함에 따라 종자 생산성이 저하될 수 있다. 고사배주수의 범위는 가계별로 1차에서 6~52개, 2차에서는 2.8~43.2개로 가계간 차이가 크게 나타났다. 성숙종자 수 중 비립종자와 충실종자는 각각 구과당 평균 각각 1.4~79.2개로 조사되었다. 임성인편수는 종자생산능력과 높은 정의 상관관계가 나타나($r=0.80$, $p<0.01$), 임성인편수가 증가할수록 종자생산능력이 높아지는 것을 확인할 수 있었다.

*주저자: Tel. 031-290-1107, E-mail: elvangoood@korea.kr

무인헬기를 이용한 이탈리아 라이그라스 파종시 생육특성 및 수량성 비교

박승민^{1*}, 김기용², 김지혜¹, 김영진¹, 김원호¹

¹충남 천안시 서북구 성환읍 신방1길 114 국립축산과학원 초지사료과

²전북 완주군 이서면 콩쥐팍쥐로 1500 국립축산과학원 축산환경과

본 연구는 최근 확산되고 있는 이탈리아 라이그라스의 무인헬기 파종과 기존의 산파 및 조파 파종방법의 생육특성을 비교하기 위해 수행하였다. 시험은 국립축산과학원 축산자원개발부 논 시험포장(천안 소재)에서 2017년 3월 9일부터 5월 30일까지 수행하였으며, 공시재료는 이탈리아 라이그라스(IRG) 코윈어리 품종을 이용하였다. 파종 방법은 무인헬기, 조파 및 산파를 하였으며, 파종량은 무인헬기 및 미스트기 산파시 60kg/ha, 조파시 40kg/ha로 하였다. 시비는 전량 기비로 하였으며, 시비량은 N-P₂O₅-K₂O=140-120-120 kg/ha를 살포 하였으며, 파종 후 답압하였다.

IRG 수량성을 비교한 결과, 무인헬기 시험구가 조파 및 산파에 비해 수량성이 낮았으며, 조파 시험구에서 수량성이 가장 높게 나타났다. 초장은 무인헬기 파종이 90cm로 가장 컸으며 산파에서 가장 작았다. 생초수량은 조파가 27,000kg/ha, 산파가 25,700kg/ha 및 무인헬기 파종에서 22,700kg/ha로 나타났다. 건물수량에서는 조파가 5,967kg/ha로 가장 많았으며 미스트기 산파가 5,680kg/ha, 무인헬기가 5,017kg/ha였으며, 건물물은 시험구 모두 22.1%로 나타났다. 이탈리아 라이그라스 파종방법에서 조파가 가장 우수한 것으로 나타났으며, 무인헬기 파종시는 산파에 비해 88%의 수량성을 보였다.

*주저자: Tel. 041-580-6765, E-mail: seung7min@gmail.com

수간석해를 통한 리기다소나무와 테다소나무 그리고 이들 수종의 중간 잡종인 리기테다소나무 생장 특성에 대한 연구

이솔지^{1,2*}, 김현철¹, 이현석¹, 임혜민¹, 강준원¹, 이위영¹, 김판기^{1,2}

¹국립산림과학원 산림유전자원부

²경북대학교 생태환경시스템학부

본 연구는 우리나라의 기후풍토에 적합한 용재수를 육성하기 위해서 중간 교잡육종된 리기테다소나무의 생장특성과 재적생장에 대한 육종효과를 검증·고찰하였다. 공시재료는 서울대학교 광양연습림에 조림된 47년생 리기테다소나무와 이것의 육종모수종(育種母樹種)인 테다소나무(49년생)와 리기다소나무(43년생) 5개체씩이다. 생장량분석은 공시재료를 지상 0.2m에서 벌도하여 1-2m간격으로 원판을 채취한 다음, 수간석해를 huber식 구분구적법에 따라서 실시하였다. 그 결과, 1영급 생장기간(1~10년) 중의 연평균수고생장량은 테다소나무가 0.56m로 리기다소나무(0.37m), 리기테다소나무(0.44m) 보다 높은 값을 나타냈다. 연평균흉고단면적생장량은 테다소나무가 3.83cm²로 리기다소나무(2.33cm²), 리기테다소나무(2.74cm²)보다 높은 값을 나타냈다. 그리고 연평균재적생장량은 테다소나무가 0.0025m³로 리기다소나무(0.0009m³), 리기테다소나무(0.0018m³)보다 높은 값을 나타내, 테다소나무가 가장 좋은 생장을 나타내고 있음을 알 수 있다. 2영급 생장기간(11~20년) 중에는 1영급과 마찬가지로 영급 생장기간(11~20년) 중의 평균수고생장량은 테다소나무가 0.80m로 리기다소나무(0.46m), 리기테다소나무(0.59m)보다 높은 값을 나타냈다. 평균흉고단면적생장량은 테다소나무가 10.5cm²로 리기다소나무(6.90cm²), 리기테다소나무(8.34cm²)보다 높은 값을 나타냈다. 그리고 평균재적생장량은 테다소나무가 0.0087m³로 리기다소나무(0.0037m³), 리기테다소나무(0.0059m³)보다 높은 값을 나타내 테다소나무가 좋은 생장을 나타내었다. 3영급 생장기간(21~30년)도 마찬가지로 평균수고생장량은 테다소나무가 0.70m로 리기다소나무(0.47m), 리기테다소나무(0.58m)보다 높은 값을 나타냈다. 평균흉고단면적생장량은 테다소나무가 10.88cm²로 리기다소나무(8.35cm²), 리기테다소나무(9.44cm²)보다 높은 값을 나타냈다. 평균재적생장량은 테다소나무가 0.0116m³로 리기다소나무(0.0062m³), 리기테다소나무(0.0092m³)보다 높은 값을 나타내 테다소나무가 좋은 생장을 나타내었다. 4영급 생장기간(31~40년)에 들어서면서 평균수고생장량은 테다소나무가 0.61m로 리기다소나무(0.41m), 리기테다소나무(0.53m)보다 높은 값을 나타냈다. 평균흉고단면적생장량은 테다소나무가 10.88cm²로 리기다소나무(9.13cm²), 리기테다소나무(10.44cm²)보다 높은 값을 나타냈다. 그리고 평균재적생장량은 테다소나무가 0.0155m³로 리기다소나무(0.0099m³), 리기테다소나무(0.0121m³)보다 높은 값을 나타내 테다소나무가 좋은 생장을 나타낸다. 그리고 전생장기간동안의 평균재적생장에서 테다소나무가 0.0086m³로 리기다소나무(0.0045m³)와 리기테다소나무(0.0068m³)에 비하여 좋은 재적생장을 나타낸다. 이러한 결과로 본 연구의 시험지역에서는 재적생장에 대한 리기테다소나무의 육종효과는 기대할 수 없으나, 테다소나무가 리기다소나무나 리기테다소나무보다 용재수 조림에 적합한 수종임을 알 수 있다.

*주저자: Tel. 031-290-1108, E-mail: solji730@korea.kr

Early maturity and white seed *Perilla* for edible seed ‘Deulhyang’

MyoungHee Lee*, JiMyoung Choi, EunYoung Oh, SungUp Kim, JungIn Kim, SukBok Pae, KiWon Oh, UnSang Yeo, DoYeon Kwak

Department of Southern Area Crop Science, NICS, RDA, Miryang, Korea

Perilla is one of oilseed crops in Korea and its seed is composed of lipid 35 ~ 45%, protein 20 ~ 25%. The proportion of omega-3 among fatty acids (α -linolenic acid) in *Perilla* oil is over 60%, which is the highest percentage among vegetable oils. A *perilla* variety ‘Deulhyang’ (*Perilla frutescens* (L.) Britton) for edible seed was developed at the Department of Southern Area Crop Science, NICS, in Miryang in 2016. It was originated from the cross between a pedigree of K015940 with white seed and a few branch, and YCPL647 with early maturity in 2005. ‘Deulhyang’ has white and soft seed, so its characters showed a great advantage to make a *perilla* powder in terms of color favor and yield as compared with brown seed. ‘Deulhyang’ has 100cm of main stem length and 12 branch numbers per plant, which is 4 numbers fewer than that of check variety ‘Saeyeopsil’. Maturing date of ‘Deulhyang’ was September 30, which is 5 days faster than that of ‘Saeyeopsil’. This variety has high oil content (45%) and linolenic acid(63%) in the fatty acid composition. The yield potential of ‘Deulhyang’ was about 1.24 ton/1ha in the regional yield trial.

*Corresponding Author: Tel. 055-350-1212, E-mail: emhee@korea.kr

Antioxidant activities and flavonoid contents of Korean black soybean landraces

Da-Young Baek^{1*}, Kyung Jun Lee¹, Myoung-Jae Shin¹, Gi-An Lee¹, Yang-Hee Cho¹, Kyung-Ho Ma¹, Yoon-Sup So², Jung-Ro Lee¹

¹National Agrobiodiversity Center, National Institute of Agricultural Sciences, RDA, Jeonju, 54874, Republic of Korea

²Dept. of crop science. Chungbuk National University, Cheongju, 28644, Republic of Korea

Black soybean (*Glycine max* L. Merr.) has been used as an excellent dietary source for the disease prevention and health promotion in Korea for hundreds over years. This study was carried out to evaluate the antioxidant activity and to determine the flavonoid contents in the 231 Korean black soybean landraces(KBSL), which conserved at RDA Gene bank. Antioxidant activities in the 231 KBSL were measured by using DPPH, TPC, TFC, ABTS and FRAP assay. The antioxidant activity assay of 231 KBSL showed the averages as follows; DPPH, 61.4 ± 33.4 (IC₅₀); TPC, 7.0 ± 2.8 mg gallic acid equivalent/g; TFC, 0.53 ± 0.15 mg quercetin equivalent/g; ABTS 4.9 ± 1.6 mg ascorbic acid equivalent(ASC)/g; and FRAP 1.10 ± 0.62 mg ASC/g. Based on the results of antioxidant activities, 31 representative KBSL were selected by using POWER CORE program. To compare the flavonoid content related to antioxidant activity, we measured the contents of myricetin, quercetin, kaempferol, and naringenin among the 31 representative collections. Myricetin contents of 231 KBSL were ranged from 0.06 to 0.23 mg/100g and IT178060 showed the highest myricetin content among them. Quercetin contents were ranged from 0.05 to 1.19 mg/100g and IT177342 showed the highest. Kaempferol and Naringenin were ranged from 0.15 to 1.66 mg/100g and 0.06 to 0.63 mg/100g, respectively and IT178054 showed the highest kaempferol and naringenin content. This study will be able to provide useful data for selecting seeds with high antioxidant activity and flavonoid content.

*Presenting Author: E-mail: dayung96@naver.com

Antioxidant activity in leaf extracts of Korean adzuki bean landraces

Kyung Jun Lee^{1*}, Myoung-Jae Shin¹, Jung-Ro Lee¹, Yang-Hee Cho¹, Kyung-Ho Ma¹, Gi-An Lee¹

¹National Agrobiodiversity Center, National Institute of Agricultural Sciences, RDA, Jeonju, 54874, Republic of Korea

Adzuki bean (*Vigna angularis* L.) is cultivated around the world, mainly in Asiatic countries, as diverse food sources. In Korea, the leaves of adzuki bean has been used as medicine and side dishes. *Sikryochanyo*, the Korean traditional medical book, described the leaves of adzuki beans that are helpful in treating and preventing diabetes. In this study, we investigated the antioxidant activity in the leaf extracts of 222 Korean adzuki bean landraces (KABL). Antioxidant activities of adzuki bean leaves extracts were analyzed by using DPPH, ABTS, ferric reducing antioxidant power (FRAP), reducing power (RP) total phenolic content (TPC), and SOD assays. Among the six antioxidant activities assay, DPPH showed wide variations, ranging from 12.6 to 178.5 (IC₅₀, CV 81.3%). ABTS, FRAP, RP, TPC and SOD in KABL ranged from 1.48 to 2.50 mg ASC/g, 0.39 to 6.03 mg ASC/g, 2.9 to 147 mg GAE/g, 0.37 to 14.7 mg ASC/g, and 7.8 to 38.2 (IC₅₀), respectively. According to the relative antioxidant capacity index (RACI), IT142500 (1.6) had the highest antioxidant activity, while IT142560 (-2.3) was the lowest. In clustering analysis, 222 KABL were classified into five groups. These results will expand the database for antioxidant activity and provide information on KABL which are valuable for development of functional foods and feed-additives resources.

***Presenting Author:** Tel. 063-238-4861, E-mail: lkj5214@korea.kr

Comparison of antioxidant activities in Korean common bean landraces

Xiao-Han Wang^{1*}, Kyung Jun Lee¹, Myoung-Jae Shin¹, Kyung-Ho Ma¹, Gi-An Lee¹, Yang-Hee Cho¹, Jung-Ro Lee¹

¹National Agrobiodiversity Center, National Institute of Agricultural Sciences, RDA, Jeonju, 54874, Republic of Korea

Beans are important dietary components with versatile health benefits. We analysed the extracts of 211 Korean common bean (*Phaseolus vulgaris*) landraces in order to determine their antioxidant activity. The antioxidant activities were measured by using total polyphenolic content (TPC), ABTS and FRAP assay. The results revealed that IT189598 had the highest TPC (3.46 mg gallic acid equivalent (GAE)/g) and FRAP (2.76 mg ascorbic acid equivalent (ASC)/g). In ABTS assay, IT110958 showed the highest antioxidant activity (1.49 mg ASC/g). TPC of 211 Korean common bean landraces showed a range of 0.60 to 3.46 mg GAE/g. FRAP and ABTS showed a range of 0.32 to 2.76 and 0.28 to 1.49 mg ASC/g, respectively. According to relative antioxidant capacity index (RACI), IT189598 (2.05) had the highest antioxidant activity, while IT102849 (-2.2) was the lowest. In clustering analysis, 222 common landraces were classified into four groups. This study will be able to provide useful data for selecting common bean landraces with high antioxidant activity.

***Presenting Author:** Tel. 063-238-4880, E-mail: wang@knu.ac.kr

Comparison of tocopherol composition in Korean black soybean landraces

Ga-Hee Kim^{1*}, Kyung Jun Lee¹, Myoung-Jae Shin¹, Gi-An Lee¹, Yang-Hee Cho¹, Kyung-Ho Ma¹, Yoon-Sup So², Jung-Ro Lee¹

¹National Agrobiodiversity Center, National Institute of Agricultural Sciences, RDA, Jeonju, 54874, Republic of Korea

²Dept. of crop science. Chungbuk National University, Cheongju, 28644, Republic of Korea

The aim of this study was to compare the tocopherols composition from the germplasms of Korean black soybean (*Glycine max* L.) landraces. Tocopherols are well known for their beneficial effects on human health such as antioxidant and anti-inflammatory activities. In this study, tocopherol contents in the seeds of 231 Korean black soybean landraces were analyzed using HPLC. Total tocopherol contents of 231 Korean black soybean landraces ranged from 5.4 to 255.5 ug/g with average of 80.7 ± 44.4 ug/g. The contents of α -tocopherol, $\beta + \gamma$ -tocopherol δ -tocopherol ranged from 2.3 to 327.3, 7.0 to 336.0, and 6.1 to 266.7 ug/g, respectively. Among 231 Korean black soybean landraces, IT177471 showed the highest total tocopherol contents. The highest contents of α -tocopherol, $\beta + \gamma$ -tocopherol δ -tocopherol were found in IT177459, IT177584, and IT177471 respectively. Among them, IT177220 had the lowest contents of all of tocopherols. These results describe the variations of tocopherol composition in the Korean black soybean landraces. The data obtained would be useful to both consumers and producers for manufacturing of traditional black soybean, which are commonly used in many countries.

*Presenting Author: Tel. 063-238-4880, E-mail: dayung96@naver.com

Morphological diversity in *Capsicum* spp. germplasm

Sea-Hee Han^{*}, Jung-Ro Lee, Gi-An Lee, Kyung-Ho Ma

National Agrobiodiversity Center, National Institute of Agricultural Sciences, RDA, Jeonju, 54874, Republic of Korea

The National Agrobiodiversity Center (NAS, RDA, Republic of Korea) has been committed to collect new valuable genetic resources continually. In this study, we regenerated conserved *Capsicum* spp. germplasm which could not be available due to seed quantity and quality, and we also investigated their morphological characters for sustainable utilization. A total of 192 *Capsicum* spp. accessions were regenerated and 15 morphological traits were surveyed according to the characterization guideline of RDA Genebank. Among the surveyed traits, flowering time ranged from June 7 to July 22 and 85% of tested accessions were mainly flowering in June. The maturity time ranged from June 3 to October 18 and main flowering time was October (45.6%) and September (37.8%). Main flower colors (FC) were white (46.6%) and pale green (43.0%). The fruit shape (FS) was various; flat round (7.8%), round (7.3%), heart shape (6.2%), quadrangle (10.9%), rectangle (6.7%), trapezoid (5.7%), triangular (13.0%), elongated (36.3%), Horn (5.7%). Principal component analysis (PCA) showed four principle components included PC-I (32.6%), PC-II (12.2%), PC-III (8.3%), and PC-IV (7.4%). Cumulatively four components explained 60.5% of the total variation in the data. PC-1 showed positive effect for some specific traits such as FC, maturity, fruit weight. PC-2 was more related to FC and FS, and PC-3 and PC-4 exhibited positive effect for plant type and density of stem hair. Our results provides insight into the characteristics of *Capsicum* spp., and the utilization basis of *Capsicum* spp. might be elevated for bio-industry.

*Presenting Author: Tel. 063-238-4870, E-mail: 2006024024@naver.com

Genome-wide identification of rice collar preferred genes using meta-expression analysis (RNA-seq) and construction of the regulatory network

Hyo-Yong Kim¹, Yun-Shil Gho¹, Ki-Hong Jung^{*}

¹Department of Plant Molecular Systems Biotechnology & Crop Biotech Institute, Kyung Hee University, Yongin 446-701, Korea

Little and tiny organ, ligule is able to have an effect on whole plant. The ligule is a thin and tongue-like white membrane in some plants including Rice. In rice, the ligule works many things as a column, umbrella and humidifier. However, we actually don't know the ligule specific gene and sequence. To effectively address this limitation, selection of useful candidate genes and identification of major regulatory factors through global approaches are necessary. So This paper used meta-expression analysis data and network analysis data from NCBI Gene Expression Omnibus about collar preferred gene to find out ligule specific gene. And identified 654 rice genes commonly differentially expressed under collar specific conditions. Gene ontology enrichment analysis show the quality and correlation about selected genes for ligule specific genes. Additionally, Regulation, Metabolism, Transcription and biotic stress overview were predicted with MapMan analysis. Using these methods, we will analyze the suitability of candidate genes. uncovering veiled information of the ligule specific genes should contribute to increase major crops production and aid additional experiment.

***Corresponding Author:** Tel. 031-201-3474, E-mail: khjung2010@khu.ac.kr

Lodging Tolerance and High Yield Barnyard Millet Variety 'Borajik'

Jeeyeon Ko^{1*}, Seokbo Song¹, Myeongen Choe¹, Kwansik Woo², Taewook Jeong², Doyeon Kwak¹, Kiyoun Kim³, Jongcheol Ko⁴, Inseok Oh²

¹Department of Southern Area Crop Science, NICS, RDA, Miryang, Korea

²Department of Central Area Crop Science, NICS, RDA, Suwon, Korea.

³Rural Development Administration, Jeonju, Korea.

⁴National Institute of Crop Science, RDA, Wanju, Korea.

Barnyard millet [*Echinochloa esculenta* (A. Braun)] is one of the small grain crops of millets, having balanced nutrients and abundant minerals. Recently there has been a growing interest in barnyard millet because it has characteristics that can be grow both in dry upland and waterlogged paddy field. 'Borajik', newly developed barnyard millet variety, was developed at the Department of Southern Area Crop Science, NICS, in Miryang in 2015. It was originated from K141287 in 2009 by pure line selection. The cultivation period of 'Borajik' were 95days at seeded in normal season(15th May) and 85days at seeded in double cropping season(15th June) which were 7~9 days later than that of check variety 'Sodamjik'. The column length were 120cm at seeded in normal season and 137cm at seeded in double cropping season and showed resistance to lodging. The yield potential of 'Borajik' were about 3.16 ton/ha at seeded in normal season(15th May) and 3.80 ton/ha at seeded in double cropping season(15th June) in replicated yield trials(RYT), which were 33~74% increased than that of check variety 'Sodamjik'. The endosperm characteristic of it showed non-waxy having 27% of amylose contents.

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

Evaluation of quality of perilla (*Perilla frutescens* var. *frutescens*) germplasms by using near infrared spectroscopy

Eun-Young Oh*, Myung-Hee Lee, Jung-In Kim, Sung-Up Kim, Suk-Bok Bae, Un-Sang Yeo, Sovetgul Asekova, Ki-Won Oh, Do-Yeon Kwak

Department of Southern Area Crop Science, NICS, RDA, Miryang, Korea

This study was carried out to investigate the quality of perilla (*Perilla frutescens* var. *frutescens*) seeds using non-destructive and time-saving Near-Infrared Spectroscopy method. Samples were tested on Unity Scientific Spectro2500-XL, which has the wavelength ranging from 680 to 2500nm by an interval of one. Crude fat, protein, rosmarinic acid content and fatty acid composition were analyzed by soxhlet extraction, Dumas combustion, liquid chromatography and gas chromatography, respectively. For calibration equation. 215 perilla lines including varieties and germplasms were tested for both NIR and component analysis. Among the perilla seeds, crude fat contents ranged from 27.4 to 51.2% at the average of 37.3% ($R^2=0.985$), protein contents varied from 14.5 to 30.8%, which has average of 19.5% ($R^2=0.936$). Rosmarinic acid content has 823 to 2815 $\mu\text{g/g}$ of variation and the average value of 1490 $\mu\text{g/g}$ ($R^2=0.844$). Coefficient of correlation of palmitic acid ($\text{C}_{16:0}$), stearic acid ($\text{C}_{18:0}$), oleic acid ($\text{C}_{18:1}$), and linoleic acid ($\text{C}_{18:2}$) composition were 0.896, 0.784, 0.914, 0.869, respectively. Linolenic acid ($\text{C}_{18:3}$) varied from 51.1 to 68.6%, which has average composition of 56.4% ($R^2=0.937$). Each tested component showed the strong positive linear correlation between NIR value and wet analysis. This NIR equation could be a useful tool for selecting line and gathering quality information in perilla breeding.

*Corresponding Author: Tel. 055-350-1232, E-mail: lavondy10@korea.kr

A new large grain and high yielding peanut variety "Tamsil"

Suk-Bok Pae^{1*}, Myung-Hee Lee¹, Sung-Up Kim¹, Eun-Young Oh¹, Un-Sang Yeo¹, Ki-Won Oh¹, Deok-Young Song², In-Seok Oh¹, Yong-Chul Kim¹

¹Department of Southern Area Crop Science, NICS, RDA, Miryang, Korea

²National Institute of Crop Science, RDA, Wanju, Korea

Korean usually like to consume large grain of peanut for the roasted or boiled. One of peanut breeding programs is also focused on developing large grain cultivar. A new peanut variety "Tamsil" (*Arachis hypogaea* ssp. *hypogaea* L.) with large grain and short stem was developed in the Department of Southern Area Crop Science, NICS, in Milyang 2016. This variety was developed from the crossing line between variety "Charmpyeong(Milyang26)" with short stem Virginia plant type and line "Milyang20" with semi-erect Virginia plant type. "Tamsil" which is short stem and semi-erect Virginia plant type has 31cm of main stem length, 42cm of branch length and 22 branch number per plant. Each pod has two grains with ellipse shape of brown testa and its yield components are composed of 44 mature pods of per plant, 111g of 100-seed weight, 78% of pod shelling ratio in the regional yield trials(RYT). Its seed quality show 28.8% of crude protein and 48.5% of crude oil and 53.2% of oleate in fatty acid composition. This also show resistant to early leaf spot, and more resistant to web blotch, stem rot, and lodging, compared with check variety "Daekwang". Owing to these superior growth characteristics of lodging resistance and source ability in late maturing stage, the average grain yield of "Tamsil" was more productive than reference variety by 19% with 4.97 MT/ha for grain production in 3 year regional yield trials.

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

Development of mutation populations by irradiation for breeding and functional genomics study in pepper

Yeong Deuk Jo¹, Han Sol Kang¹, Sang Hoon Kim¹, Jaihyunk Ryu¹, Jin-Baek Kim¹, Si-Yong Kang^{1*}

¹Radiation Breeding Team, Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongseup, Korea

Mutation breeding based on irradiation has been widely used for development of useful genetic resources for plant breeding. We have been developing mutation populations using diverse radiation sources, irradiation methods, and plant materials in pepper. First of all, M₂~M₃ populations that consist a total of 4,490 individuals were developed in 'Yuwolcho', a Korean landrace (*C. annuum* L.) that has early-flowering characteristics, by irradiation of gamma-rays and carbon ion beam, respectively, as standard populations for forward and reverse genetics studies. In the second place, we are developing M₁ population that consist of 1,666 individuals of 'Habanero', a *C. chinense* cultivar which is famous for its extreme pungency, to provide useful materials for practical breeding of cultivars for export and production of functional materials. Finally, populations were developed from crosses using irradiated pollens or pistils aiming the broader mutation spectrum or higher efficiency. In combination with optimized TILLING system based on capillary electrophoresis, these population will be used for breeding and functional genomics studies in pepper.

*Corresponding Author: Tel. 063-570-3310, E-mail: sykang@kaeri.re.kr

밥맛이 우수한 조생 최고품질 벼 ‘진광’

현웅조^{1*}, 이정희⁵, 원용재¹, 정국현¹, 안억근¹, 이상복², 김명기¹, 하운구¹, 양창인³, 성낙식¹, 조영찬⁴, 강경호⁴, 서대하², 김병주¹

¹경기도 수원시 수인로 125 국립식량과학원 중부작물부 중부작물과

²강원도 춘천시 충열로 251 국립식량과학원 춘천출장소

³강원도 철원군 동송읍 태봉로 2346, 국립식량과학원 철원출장소

⁴전북 완주군 이서면 혁신로 181 국립식량과학원 작물육종과

⁵전북 완주군 이서면 혁신로 181 국립식량과학원 기획조정과

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. 중부지역에 적응하는 밥맛이 우수한 조생품종 개발을 목적으로 진광은 단교배된 운광/고시히까리 F1과 호품을 각각 모부본으로 하여 2007년에 교배되었다. 세대단축을 위해 F1 세대의 약을 배양하여 AC3세대에서 초형과 쌀품질이 우수하고 도열병 및 흰잎마름병 저항성을 보인 SR31151-HB3104-29-1을 선발하여 수원575호의 계통명을 부여하였다. 2년간의 생산력검정시험과 3년간의 지역적응시험 결과 그 우수성이 인정되어 2016년 직무육성 신품종 심의회에서 최고품질벼로 선정되었다. ‘진광’은 조생종으로서 밥맛과 재배안정성이 우수하여 생산자부터 소비자까지 만족할 수 있고 다양한 작부체계에 적응할 수 있는 품종으로 역할이 기대된다.

사사: 본 연구는 농촌진흥청 연구사업(세부과제명 : 조 · 중생 고품질 벼 품종개발, 세부과제번호 : PJ009325012017)의 지원에 의해 이루어진 것임.

*Corresponding Author: Tel. 031-695-4028, E-mail: greathyunwj@gmail.com

중간모본용 완전단감 ‘단연 09-12-5’ 육성

손지영, 박여옥, 김은경, 이영한, 최성태, 김성철, 안광환, 박두상

경상남도농업기술원 단감연구소

단감의 주요 재배품종인 ‘부유’는 11월에 수확이 가능한 만생종으로 수확기 서리피해, 노동력 집중 등 많은 문제점을 가지고 있다. 따라서 수확이 빠르고 고품질의 특성을 지니며 떫은맛의 우려가 없는 완전단감 품종의 육성이 요구된다.

완전단감은 열성 형질로 완전단감과 교배조합에 의해 출현될 확률이 월등히 높다.

고품질의 완전단감을 육성하기 위해서는 요구 형질을 지닌 고품질의 완전단감 품종의 수가 많아야 하지만 완전단감 품종의 수는 극히 제한적이기 때문에 육성에 어려움이 많다.

따라서 단감연구소에서는 완전단감이면서 수확기가 빠르고 고품질의 특성을 지니는 품종을 육성하고자 시험을 수행하였다.

‘단연09-12-5’는 2009년 완전단감 ‘양풍’을 모본으로, ‘태추’를 부본으로 교배하여 얻은 완전단감 계통이다. 숙기가 10월 17일로 ‘부유’에 비해 빠르고 당도는 15 °Brix로 ‘부유’와 비슷하다. 과중이 370g으로 대과종에 속한다. 과실모양은 장형이다.

육질이 다소 치밀하고 감꼭지 부위의 과육 심부위가 넓은 특성을 보이지만, 단감말랭이로 가공하였을 때 우수한 식감과 품질을 나타냈다.

따라서, 수확기가 빠른 고품질 완전단감 육종의 중간모본용으로 사용 가치가 높고, 단감 가공용으로도 효용 가능성도 있어 이 계통을 선발하였으며, 추후 세부특성조사 수행 후 품종보호출원 예정이다.

Author E-mail: jjmm12@korea.kr

유색밀의 특성 및 추출용매별 색소 성분 분석

김경훈*, 윤성란, 신동진, 권유리, 김경민, 한상익, 현종내, 오명규

경남 밀양시 점필재로 20, 농촌진흥청 국립식량과학원 남부작물부 논이용작물과

유색밀은 종피에 자색 또는 흑색이 착색되어 색을 띠는 밀이다. 이러한 유색밀 자원의 색소 함량 분석을 위해서 추출 분석 방법을 설정하고자 한다. 식품원료에서 색소가 함유되어 있는 페놀산 추출 분석시 유기용매로 추출하는 방법이 주로 이용되고 있으나 추출하고 남은 잔사에도 결합형 형태의 페놀산 등의 유용한 물질이 존재하고 있다. 그러므로 이 실험에서는 유색밀의 색소 성분 추출시 기존의 추출방법인 에탄올, 메탄올 등의 용매별 분석하는 방법과 가수분해를 통한 결합형의 페놀산까지 분석하는 방법을 비교해보았다. 실험재료로 유색밀인 밀양42호, 일반밀(금강) 등을 통밀가루로 분쇄하여 50% 아세톤, 80% 메탄올, 80% 에탄올 용매로 추출하는 방법과 알칼리 가수분해 방법을 이용하여 결합형 탄닌, 총페놀성화합물, 항산화능 등을 분석하였다. 총페놀성화합물은 가수분해, 50% 아세톤, 80% 메탄올, 80% 에탄올 용매순으로 함량이 많았다. 유색밀의 결합형 탄닌, 총페놀성화합물의 함량은 각각 $423.33 \pm 83.27 (\mu\text{g catechin Eq./g})$, $1587.88 \pm 18.37 (\mu\text{g GAE/g})$ 로 일반밀인 금강밀에 비해서 모두 높았다. 항산화능 분석으로 Trolox equivalent antioxidant capacity (TEAC)은 $1456.25 \pm 28.64 (\mu\text{g trolox Eq./g})$ 로서 금강의 150.42 ± 4.77 보다 높았다. 그러므로 가수분해 방법은 결합형 페놀성 함량까지 알 수 있지만 항산화능을 측정할 수 없으므로, 추출용매 중에서는 50% 아세톤을 이용한 추출방법이 가장 적합한 것으로 생각된다.

*주저자: Tel. 055-350-1173, E-mail: k2h0331@korea.kr

The *PURPLE PERICARP* trait of black rice is defined as a complementary gene interaction between *Pb* and *Pp* genes by the extended Mendelian 9:7 ratio

Kyung Eun Lee¹, Jegeun Cho¹, Jong Bae Kim², Sang Gu Kang^{1*}

¹Molecular Genetics Laboratory, Department of Biotechnology, Yeungnam University, Gyeongsan 712-749, Korea; ²Institute of Health & Environment in Daegu, 215 Muhakro, Suseong-Gu, Daegu, 706-732 Republic of Korea

Rice *Purple Pericarp* (*Prp*) trait is required primarily to make black rice. *Prp* trait was known as a recessive epistasis following the Mendelian 9:3:4 ratios of purple, brown and white, respectively. However, self-pollination of the F₁ hybrid *Pbpb Pppp* genotype generated 4 different patterns of progenies with 3 dark purple : 6 medium purple : 3 brown : 4 white, resulted in differ to the typical recessive epistasis. The biochemical analysis of the progenies divided evidently into two groups; one contained cyanidin 3-*O*-glucoside (C3G) in the dark and medium purple seeds, but the other showing absence of C3G in brown and white seeds, resulting in the ratio of 9 C3G: 7 absences C3G, which fitted to the extended Mendelian 9:7 ratios of complementary gene interaction. Although black rice has been defined in either recessive epistasis or complementation depending on researchers, here we confirmed the *Prp* trait is defined as a complementary gene interaction of the *Pb* and *Pp* genes. Moreover, by assist with *Pb* allele genotyping, breeding convenience was achieved to select the black rice lines fixed with the two dominant alleles of *Pb* and *Pp* genes among complex allelic constitutions of the two genes in the hybrid progenies.

*Corresponding: E-mail: kangsg@yu.ac.kr

Testa color might not be a factor to determine seed dormancy in wheat (*Triticum aestivum* L.)

Paulina Calderón Flores, Yong Weon Seo*

Department of Biosystems and Biotechnology, Korea University, Seoul 136-713, Republic of Korea

The grain color of wheat has been related to the brightness of flour and to tolerance to preharvest sprouting. Grain color is controlled by dominant *R-1* genes located on the long arm of hexaploid wheat chromosomes 3A, 3B, and 3D (*R-A1*, *R-B1*, and *R-D1*, respectively). The *R-1* genes affect the sensitivity of embryos to abscisic acid (ABA) and the development of grain dormancy. *Tamyb10-A1*, *Tamyb10-B1*, and *Tamyb10-D1* genes, located on chromosomes 3A, 3B, and 3D, respectively. The red pigment of the grain coat is composed of catequin and proanthocyanidin (PA). These genes encode *R2R3*-type MYB domain proteins, similar to TT2 of *Arabidopsis*, which controls PA synthesis in testa. A single dominant allele is sufficient to result with red color, but grain redness increases in a gene-dosage-dependent manner. We choose publicly available markers which are known to related to the seed coat and the dormancy level based on the *R* gene of Yellow-Red wheat seeds to see if it is also related to the seed dormancy and testa color in our materials. We concluded that the testa color might not be a factor to determine dormancy in wheat or at least is not related to the deep purple testa color from our samples.

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*Corresponding Author: Tel. +82-2-3290-3005, E-mail: seoag@korea.ac.kr

보리호위축병 저항성 내도복 다수성 쌀보리 ‘호강’

김양길¹, 이미자¹, 박종철¹, 김경호¹, 강천식¹, 박종호¹, 한옥규¹, 최진경², 배정숙³, 송재기⁴, 박태일¹, 정영근¹, 김보경¹

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 다양한 건강식품이 개발되어 소비자들의 관심이 높아짐에 따라 채소는 물론 곡류에 있어서도 혼반용 곡류의 소비가 증가하고 있다. 따라서 이에 적합한 품종을 육성하기 위해 2004년에 쓰러짐에 강하고 다수성 등 특성을 가진 “수영보리”를 모본으로, 출수가 빠른 “극조숙55” 계통을 부분으로 인공교배하여, 도복에 강하면서 다수성인 혼반 및 보릿가루용 메성 쌀보리 ‘호강’을 개발하였다. ‘호강’은 6조이며 파성이 II 인 병성 쌀보리로 이삭의 형태는 중소수형이고, 까락이 길며 탈부성이 좋다. 출수기는 새쌀보리에 비해 익산(전주), 나주, 진주, 대구에서 4월 18일로 1일 빨랐다. 간장은 69cm로 새쌀보리보다 5cm 정도 짧은 중간형으로 내도복성이며, 수장(6.2cm)은 길고 1수립수(65개)가 많다. 천립중(34.6g)은 새쌀보리보다 4.1g 무거웠다. 병해저항성 중 보리호위축병은 저항성이며, 내한성은 새쌀보리와 비슷하였다. ‘호강’은 단백질(10.1%), 아밀로스(21.7%) 함량이 비슷하나 베타글루칸(5.5%), 백도(37.6) 높고, 흡수율, 퍼짐성이 좋았다. 조곡 수량성은 4.56톤/ha으로 7% 증수하였다. ‘호강’은 1월 평균기온이 -6℃ 이상인 지역에 보급 될 것으로 기대 된다.

*주저자: Tel. 063-238-5225, E-mail: kim5yk@korea.kr

내도복 다수성 보리차용 겉보리 ‘호향’

김양길¹, 박종철¹, 김경호¹, 강천식¹, 박종호¹, 한옥규¹, 윤건식², 배정숙³, 조수현⁴, 박태일¹, 정영근¹, 김보경¹

¹전북 완주군 이서면 혁신로 181 농촌진흥청 국립식량과학원

²충청북도 청주시 청원구 오창읍 가곡길 46 충청북도농업기술원

³대구광역시 북구 칠곡중앙대로 136길 47 경상북도농업기술원,

⁴강원도 춘천시 충열로 83 강원도농업기술원

최근 곡물을 이용한 차음료 시장 확대에 따른 다양한 기능성 음료가 개발되어 소비자들의 관심이 높아지고 있다. 따라서 이에 적합한 보리차 음료용 품종을 육성하기 위해 2005년에 보리호위축병에 강하면서 재해에 저항성인 특성을 가진 “새강보리”를 모본으로, 고품질의 “두루보리” 품종을 부분으로 인공교배하여, 쓰러짐에 강하고 다수성인 보리차용 겉보리 ‘호향’을 개발하였다. ‘호향’은 6조이며 파성이 II 인 병성 겉보리로 이삭의 형태는 밀수형이고, 까락이 길며 탈망성이 좋다. 출수기는 올보리에 비해 전작(수원, 춘천, 청원)에서 4월 23일로 1일, 답리작(대구, 익산, 전주)에서 4월 18일로 1일 빨랐다. 간장은 78cm로 올보리와 비슷한 장간형으로 내도복성이며, 수장(4.7cm)은 길고 1수립수(55개)가 많으며, 천립중(31.9g)은 올보리보다 3.6g 가벼웠다. 병해저항성 중 보리호위축병은 올보리보다 저항성이며, 추위 저항성 정도는 올보리와 비슷하였다.

‘호향’은 단백질(10.9%)과 베타글루칸(5.0%) 함량은 올보리와 비슷하나 폴리페놀 함량(0.19%)이 높다. 보리차 특성으로서 볶음 처리에 의한 동일한 조건에서의 보리차 색도(L)가 진하고, 적색(a) 및 황색(b) 높았다. 조곡 수량성은 전작에서 6.68톤/ha으로 6% 증수, 답리작 6.03톤/ha으로 9% 증수하였다. ‘호향’은 1월 평균기온이 -8℃ 이상인 지역에 보급 될 것으로 기대 된다.

*주저자: Tel. 063-238-5225, E-mail: kim5yk@korea.kr

Compositional variability in diverse maize hybrids (Literature review)

Mia Park¹, Gregory B. Tilton², Erin Bell³

¹Monsanto Korea, ²Monsanto Company, Missouri, USA, ³Monsanto Company, Missouri, USA

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.

Title of paper: Compositional Assessments of Key Maize Populations: B73 Hybrids of the Nested Association Mapping Founder Lines and Diverse Landrace Inbred Lines. Tyamagondlu V. Venkatesh, George G. Harrigan, Tim Perez, and Sherry Flint-Garcia (J. Agric. Food Chem. 2015, 63, 5282–5295)

Corresponding presenter: Tel. +82-2-3393-3763, E-mail: mia.park@monsanto.com

Growth characteristics and forage productivity of new tall fescue

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

National Agrobiodiversity Center, National Institute of Animal Science, RDA.

Tall fescue (*Festuca arundinacea* Schreb.) is a Gramineae perennial grass species and commonly used as a forage crop and developed to be used for soil retention or as lawn. A new tall fescue variety named “Greenmaster2ho” and “Greenmaster3ho” was developed by the National Institute of Animal Science, Rural Development Administration, in Cheonan, Korea from 2010 to 2014. For the synthetic seed production of this new variety, 5 superior clones were selected and polycrossed. The agronomic growth characteristics and forage production capability of the seeds were studied at Cheonan from 2010 onward, and regional trials were conducted in Cheonan, Hoengseong, Jeju, and Jinju from 2012 to 2014. New tall fescue variety showed resistance to disease, persistence, and regrowth ability that were all enhanced when compared with Fawn. This study developed a new tall fescue variety with excellent environmental adaptability, aiming to make a contribution to the vitalization of the Korean grassland industry

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***Corresponding Author:** Tel. 041-580-6757, E-mail: kiwon@korea.kr

질소시비량 및 등숙기간에 따른 기능성 성분 함량변화

함태호^{1*}, 권순욱², 류수노¹

¹서울 중로구 대학로 86 한국방송통신대학교 농학과

²경남 밀양 삼량진읍 부산대학교 생명자원과학대학 식물생명과학과

본 연구는 기능성 쌀인 슈퍼홍미에 함유된 성분인 Taxifolin과 질소시비량, 등숙시기에 따른 함량을 변화를 조사하여 환경 변화에 따른 기능성 성분의 변화 요인을 밝히고자 수행되었다. 만생종인 슈퍼홍미벼를 공시하고, 질소 시비를 (5, 9, 13kg/10a) 하여 2016년에 시험포장에서 수행한 실험 결과를 요약하면, 당노역제 성분인 타키폴린은 슈퍼홍미의 종실 내의 종피와 과피부위에 함유되었으며 등숙시기별 함량은 출수 후 빠를수록 높았으며 출수후 기간이 지남에 따라 점점 낮아졌다. 이는 등숙이 진행됨에 따라 taxifolin이 포함되지 않은 배와 배유 부분이 비대해짐으로 상대적으로 종피 부분이 낮아졌기 때문으로 판단된다.

슈퍼홍미는 흑진주벼와 수원 425호 교잡 후대 계통에서 선발된 C3GHi 계통과 종실이 큰 대립벼1호를 인공교배한 후대에서 계통육종으로 육성한 품종이다. 출수기는 9월 5일로 슈퍼자미보다 10일 늦은 만생종이며, 간장은 94.7 cm 로 슈퍼자미보다 13 cm 큰 장간이다. 포기당 이삭수는 5.4개로 적지만 이삭당 벼알수는 154.0 개로 슈퍼자미 보다 28% 많다. 현미의 천립중은 26.8g 으로 슈퍼자미와 비슷하다. 슈퍼홍미의 정조 길이는 9.05 cm이고 폭은 3.79 cm로 슈퍼자미보다 큰 대립이며 정현비율은 81.7% 이다.

기존의 갈색 유색미 품종인 건강홍미, 적진주, 홍진주와 교배 모본인 흑진주, 수원425호, C3GHi 품종, 그리고 같은 교배모본으로 육성된 슈퍼자미, 슈퍼자미2호 품종에 유색미 발현 관련 유전자 마커와 SSR 마커를 이용하여 유전자 특성을 조사하였다. 유전자 마커 분석결과 슈퍼홍미는 기존에 알려진 갈색 유색미 관련 유전자인 *Rc*, *Rd* 유전자가 아닌 다른 유전자에 의해 적갈색이 발현되고 있으며, 흑자색 유색미 관련 유전자인 *Pb* 유전자를 가지고 있는 것으로 조사되었다.

*주저자: Tel. 02-3668-4630, E-mail: lion78@daum.net

‘백일미’의 도열병 저항성 유전자위 표지를 위한 연관분석

정지웅*, 정종민, 강경호, 고재권, 김보경

전라북도 완주군 이서면 혁신로 181 국립식량과학원 작물육종과

다양한 돌려짓기 체계 개발을 촉진하여 농지활용도와 농가소득을 향상시키기 위한 목적으로 ‘고시히카리’에 대한 돌연변이 육종을 통해 극조숙 품종인 ‘백일미’가 육성되었다. ‘백일미’는 극조숙성과 더불어 도열병에 민감한 ‘고시히카리’ 보다 매우 안정적인 저항성도 함께 겸비하고 있음이 확인되었다. 포장에서 확보된 33개의 고병원성 균주들에 대한 저항성 평가(0:저항~5:민감)에서도 ‘고시히카리’는 4~5(33개 균주 평균 4.61)의 높은 이병성을 보인 반면, ‘백일미’는 3개 균주(88-031: 3, NC07-097: 3, NC14-096: 4)를 제외한 모든 균주에 대해 강한 저항성(0, 1)을 보였다(33개 균주 평균 0.64). ‘백일미’의 극조숙에 관여하는 유전자를 규명하기 위해 ‘고시히카리’와의 교잡후대로부터 145계통의 RIL집단을 육성하여 2개의 도열병 균주(NC14-020, NC14-054)에 대한 반응기작을 평가하였다. RIL 집단의 저항성 평균은 각각 4.0(NC14-020)과 3.0(NC14-054)을 보이며 좌편향 된 분포양상을 보였다. RIL집단에 대한 유전분석을 수행하기 위해 Genotyping-by-Sequencing(GBS)기법을 활용, 총 311개의 유의한 SNP를 확보하여 연관지도도를 작성하였다. Single Locus ANOVA 분석을 통하여 RIL계통들의 GBS 유전자형과 표현형(도열병 균주에 대한 저항성)간의 관련성 분석을 실시한 결과, 염색체 1번 말단 33.201Mbp 영역에서 두 균주 모두에 대해 안정적인 저항성을 발현하는 유전자위를 확인할 수 있었다. 해당 유전자좌는 RIL 집단 내 표현형 분산량의 32.5%(NC14-020)와 51.2%(NC14-054)를 설명하는 주동유전자였으며, ‘백일미’ 대립인자에 의한 저항성 증가정도는 ‘고시히카리’ 대비 각각 1.3(NC14-020)과 2.1(NC14-054)이었다. 본 연구를 통해 확인된 ‘백일미’의 변이 유전자는 향후 벼 품종의 도열병 저항성을 향상 시키기 위한 분자육종 재료로 활용될 수 있을 것으로 판단된다.

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*교신저자: Tel. 063-238-5236, E-mail: jrnj@korea.kr

고시히카리 돌연변이 후대 ‘백일미’의 극조숙 관련 유전자위 표지

정지웅*, 정종민, 김우재, 김현순, 김보경

전라북도 완주군 이서면 혁신로 181 국립식량과학원 작물육종과

농지활용도와 농가소득 향상을 위한 다양한 돌려짓기 체계의 개발에 활용코자 ‘고시히카리’(출수기 8월3일; 전주)에 대한 돌연변이 육종을 통하여 극조숙 벼 품종인 ‘백일미’(출수기 7월15일; 전주)가 육성된 바 있다. ‘백일미’의 극조숙에 관여하는 유전자를 규명하기 위해 ‘고시히카리’와의 교잡후대로부터 145계통의 RIL집단을 육성하고 출수기 분리양상을 조사하였다. RIL 집단 내에서 출수기는 7월12일(파종 후 64일)~8월22일(파종 후 105일)의 범위에서 파종 후 출수기까지의 평균 소요일수는 79.5일로 우편향 된(Skewness=0.82) 분포양상을 보였다. RIL집단에 대한 유전분석을 수행하기 위해 Genotyping-by-Sequencing(GBS)기법을 활용, 총 311개의 유의한 SNP를 확보하여 연관지도를 작성하였다. Single Locus ANOVA 분석을 통하여 RIL계통들의 GBS 유전자형과 표현형(파종 후 출수기까지 소요일수)간의 관련성 분석을 실시한 결과, 염색체 6번 8.643Mbp 영역과 염색체 7번 14.449Mbp 영역에서 유의한 유전자위들이 확인되었다. 각 유전자좌들은 RIL집단 내 표현형 분산량의 27%(염색체 6번)와 28%(염색체 7번)를 각각 설명할 수 있었으며, ‘백일미’ 대립인자에 의한 출수기 단축효과는 ‘고시히카리’ 대비 9.6일(염색체 6번) 및 10.3일(염색체 7번)로 각각 추정되었다. 본 연구를 통해 확인된 ‘백일미’의 두 대립인자들은 향후 극조숙 벼 품종육성을 위한 분자육종 재료로 활용될 수 있을 것으로 판단된다.

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***교신저자:** Tel. 063-238-5236, E-mail: jrnj@korea.kr

A study on enhancement of hydroxy fatty acid in transgenic *Arabidopsis* using CRISPR-Cas9-mediated gene editing

Mid-Eum Park¹, Kyeong-Ryeol Lee², Hyun Uk Kim^{1*}

¹Department of Bioindustry and Bioresource Engineering, Plant Engineering Research Institute, Sejong University, Seoul, 05006 Republic of Korea

²Department of Agricultural Biotechnology, National Institute of Agricultural Science, Rural Development Administration, Jeonju 54874, Republic of Korea

Plants produce triacylglycerol (TAG) that is an ester between glycerol and three fatty acids in seeds. Most of the plants produce five common fatty acids that are composed of palmitic acid (16:0), stearic acid (18:0), oleic acid (18:1), linoleic acid (18:2), linolenic acid (18:3). However, some plants produce uncommon fatty acids that are useful for industrial application. Castor bean plant have a 80~90% of hydroxy fatty acid (ricinoleic acid, 18:1-OH) in seeds, but they also have a toxin ricin and allergenic 2S albumin in seeds. To produce hydroxy fatty acids (HFAs) in transgenic plants, many researchers have tried to increase HFA accumulation in *Arabidopsis* as a model oil plant using transformation of genes that are related to HFA synthesis from castor bean plant. Expression of *RcFAH12* gene encoding a oleate Δ 12-hydroxylase in *Arabidopsis* can accumulate HFAs up to 17% in seed oil. Coexpression of *RcFAH12* and *RcPDAT1-2* encoding a phospholipid:diacylglycerol acyltransferase can accumulate HFAs up to 22~23% in seed oil. Additional expression of *RcDGAT2* encoding a diacylglycerol acyltransferase to *RcFAH12+RcPDAT1-2* transgenic *Arabidopsis* increased HFA up to 27% in seed oil. Currently, we designed a pair of single guide RNA (sgRNA) for gene editing and we cloned a CRISPR-Cas9 vector to knock-out genes encoding *Arabidopsis* PDAT and DGAT genes. We will eliminate the function of competitive endogenous genes that are related to TAG biosynthesis, thereby transgenic *Arabidopsis* will increase HFA more than current maximum 27% level. These result will contribute to produce better and more HFA in oil crops. In addition, this will help to understand lipid metabolism pathway.

***Corresponding Author:** Tel. 02-3408-4318, E-mail: hukim64@sejong.ac.kr

A new hybrid carnation 'Cream Magic' with light yellow flower color of spray type

Mi-Seon Kim, Bong-Sik Yu*, Jae-A Jung, Jong-Taek Park and Hak-Ki Shin

Floriculture Resesasrch Division, National Institute of Horticultural & Herbal Science, 100, Nongsaengmyeong-ro, Iseo-myeon, Wanju-gun, Jellabuk-do 565-852, Korea

카네이션은 우리나라 화훼산업에서 절화생산액이 131억원(2015, 화훼재배현황)로 비중이 높지만, 종묘의 자급률이 매우 낮다. 카네이션 수입품종의 묘값은 품종에 따라 다르나, 평균 주당 400원대로 비싸 농가의 경영부담이 매우 크다. 이러한 어려움을 해결하기 위해 국립원예특작과학원에서 절화용 카네이션 31품종이 개발하였다. 일부 품종은 농가에서 재배하여 시장출하를 하고 있으나 수입품종의 화색, 화형의 다양성에는 아직 매우 미흡하여 다양한 국산 품종개발, 보급이 요구되고 있다. 따라서, 2011년에 화사한 노랑색계의 'GumByul' 품종을 모본, 노랑색 바탕색에 빨강색 가는 테두리가 있는 황색계 'Picaro' 품종을 부분으로 하여 교배하였다. 실생계통 양성 및 특성검정은 2012~2016년에 걸쳐 3차의 개화 및 생육을 조사하여 균일성 등을 확인하여 최종적으로 원교 B2-70호 계통을 선발한 후 품평회를 거쳐 재배자, 유통업체 등의 기호도를 평가하여 2016년 직무육성심의회를 거쳐 'Cream Magic'이라 명명하여 품종화하였다. 카네이션 'Cream Magic'은 절화용 스프레이형으로 베이지색 바탕색에 분홍색의 줄무늬 테두리가 있는 투톤의 밝은 화색이며 개화가 빠르고 여름 고온기 적응성이 우수하고 생육이 강건하며 화형이 둥글고 꽃수가 꽃대 1개당 9.5개로 많아 볼륨감이 우수하다. 본 품종의 향기의 정도를 조사하기 위해 전자코(Fox α 2000)로 분석한 결과, 향기가 강한 '매리다' 품종과 비교시에도 향기의 정도가 약간 더 강하게 조사되어 품종의 우수성이 더 부각되었다. 더위에 매우 약한 카네이션의 특성상, 고온기 하우스내 온도가 30℃ 이상 7일 이상 재배시 품질이 떨어질 우려가 있으니 주의가 필요하다.

*교신저자: Tel. 063-238-6810, E-mail: kimms290@korea.go.kr

Copy number validation by using read coverage of NGS whole genome re-sequencing

Yang Qin, Hee-Jong Woo, Kong-Sik Shin, Myung-Ho Lim, Hyun-Suk Cho, Seong-Kon Lee*

National Institute of Agricultural Science, Rural Development Administration, Jeonju, 54874, Korea

With the development of a growing number of genetically modified (GM) crops, it is necessary to explore a detail, accurate and active molecular characterization method to select candidate events from a large pool of transformation events. Relative to traditional molecular analysis methods such as flanking sequencing and southern blot hybridization, the next generation sequencing (NGS) technology for whole genome sequencing of complex crop genomes had been proved to be useful for in-depth molecular characterization. In this study, five transformation events containing 1 Bt-resistant rice, 2 resveratrol-producing rices and 2 beta-carotene enhanced soybeans with one copy, two copies and three copies of foreign gene insertions respectively were conducted for southern blot hybridizations and NGS analysis, aim to reveal the relationship between copy number and read coverage. This finding might provide a useful way to confirm copy numbers of transformation events, consequently to cover the shortages of southern blot hybridization and flanking sequencing.

*Corresponding Author: E-mail: goryeong@korea.kr

환경이 강건하고 화색이 선명한 핑크색 대륜 질화용 거베라 ‘펠센스’ 육성

정용모^{1*}, 진영돈¹, 배민지, 최시림¹, 홍광표², 권오창³

¹경남 창원시 경남농업기술원 화훼연구소

²경남 진주시 경남농업기술원 연구개발국

³부산시 사하구 하단동 동아대학교 생명자원과학대학

경상남도농업기술원 화훼연구소에서, 기후변화에 대응하여 국내 재배환경에 적합하고 거베라 재배농가들의 핑크색 품종선택 기회를 더욱 많이 제공하며 외국품종의 로열티부담 경감을 위하여 2016년 화색이 선명한 핑크색 질화용 거베라 ‘펠센스’를 육성하였다. 2012년 3월 핑크색 대륜계의 ‘핑크센세이션’을 모본, 황색 대륜계의 ‘0845-07’을 부분으로 인공교배를 실시하여 4월 하순, 교배조합으로부터 364개의 종자를 획득하였다. 교배 후 결실이 된 종자는 4월 하순 경, 채종 즉시 파종하였으며, 그 중 321개의 종자가 발아(발아율 88.2%)하였다. 파종 1개월 후, 발아된 유묘는 본엽이 4~5매 전개되었을 때 화훼연구소 유리온실내의 선발 포장에 정식하였다. 정식 후 교잡 1세대를 육묘하여 2012년 11월 하순 경, 화색이 선명하고 수량이 많은 우수 개체(1224-17)를 1차로 선발하였다. 그 후 특성이 우수한 1224-17(경남교G-58호)개체를 2012년 12월, 성장점배양에 의해 개체증식 후 조직배양묘의 순화를 거쳐서, 2013년 10월 중순, 화훼연구소 유리온실내의 특성검정 포장에 정식하여 2016년 7월까지 3회에 걸쳐 생육 및 수량특성 검정을 실시하였다. 특성검정을 실시한 결과 화색, 화형, 수확량 등 품질과 수량이 우수하다고 판단되어 2016년 농작물 직무육성 신품종심의회 심의를 거쳐 ‘펠센스’(Pearl Sense)로 명명하였다. ‘펠센스’ 품종의 생육 및 개화특성 조사를 위하여 대조품종으로 ‘파티타임’ (234259)를 사용하였다. ‘펠센스’ 품종은 화색이 선명한 핑크색(62D) 반겹꽃으로, 화폭이 12.5cm 정도인 질화용 대륜화이다. 또한 포기당 연간 평균절화수량은 48.2송이 정도이며, 절화수명은 약 12.4일 정도이다. 개화소요일수는 91.5일로 대비품종 ‘파티타임’의 97.3일에 비하여 약 6일 정도 빠르며 이때 개화엽수는 약 9.7매 정도이다. ‘펠센스’ 품종의 설상화의 길이와 폭은 각각 5.8cm와 0.8cm 로 대조품종 ‘파티타임’의 4.8cm, 0.9cm와 비교하여 길이는 1.0cm 정도 길었지만 폭은 다소 작았다. 화경 직경은 상부와 하부 각각 0.6cm, 0.7cm 정도로 대조품종 ‘파티타임’의 상부 0.6cm, 하부 0.8cm와 비슷한 편이다. 재배상의 유의사항은 지온의 관리 및 양·수분의 흡수가 쉽도록 가능한 이랑을 높게 만들고, 여름철 고온기의 생리장해 및 고온에 의한 꽃봉오리의 유실 방지를 위하여 차광재배하여 온도상승을 막아주고 환기에 주의하는 것이 좋다.

*주저자: Tel. 055-254-1612, E-mail: ymchung@korea.kr

QTL analysis of the qBK^{WD} , a major QTL for bakanae disease resistance in rice

Sais-Beul Lee¹, Tae-Heon Kim¹, Su-Min Jo¹, Jun-Hyun Cho¹, Ji-Yoon Lee¹, Jong-Hee Lee², Sang-Ik Han¹, You-Chun Song¹, Myung-Kyu Oh¹, Dong-Soo Park^{1*}

¹National Institute of Crop Science, Miryang 50424, Republic of Korea

²Research Policy Bureau, RDA, Jeonju, 54875, Republic of Korea

Bakanae disease is one of the most serious problems in rice production in Korea, and has become serious in the hybrid rice growing area, worldwide, where involves increased use of seed beds for the raising platelets. In this research, we used F₄ population to locate a QTL for resistance against bakanae disease. The 200 RILs (F₄) were derived from a cross between Wonseadaesoo and Junam. The previous reported SSR markers (for indica and japonica rice) could not represent the polymorphisms between the two japonica rice parents used in this study. To make the linkage map, then we developed 338 InDel markers based on the NGS (next generation sequencing) data of Wonseadaesoo and Junam. QTL analysis using 200 F₄ population detected a QTL, qBK^{WD} , between InDel markers chr01_13542347 and chr01_15135218, 1.59Mb interval, on chromosome 1 with a LOD score of 8.29 and the QTL explained 20.2 % of the total phenotype variation. we also identified Gene pyramiding effect of two QTLs, previously developed $qBK1$ and qBK^{WD} , were also discussed. Results of this study are expected to provide useful information toward developing resistant rice lines harboring single or multiple major QTLs by pyramiding genes against bakanae disease.

*Corresponding Author: Tel. +82-55-350-1184, E-mail: parkds9709@korea.kr

A double freesia ‘Sunny Gold’ with dark yellow petals

Youn Jung Choi^{*}, Young Ran Lee, Su Young Lee, Yun Im Kang, Hae Ryong Cho

Floriculture Division, National Institute of Horticultural and Herbal Science, RDA, Wanju, 55365, Korea

Freesia (*Freesia hybrida* Hort.) is one of the popular ornamental crops over the world. Freesia ‘Sunny Gold’ was developed for the cut flower in the National Institute of Horticultural Herbal Science in 2016. This hybrid was crossed and selected from a seedling of ‘036010’ and ‘Golden Flame’ in 2010. Morphological characteristics of the selected freesia hybrid were investigated for 5 years from 2011 to 2016, and then it was named ‘Sunny Gold’ in 2015. ‘Sweet Lemon’ has single flower and lemon petals (RHS, YO17B). The average flower width is 5.4 cm and the average yield is 6.3. The growth of the plant shows vigorous and the average height is 98.3cm, and it is higher than about 24 cm that of control cultivar ‘Yvonne’. The average number of floret per stalk was 10.3, and stalk was 6.9 cm length that of control cultivar ‘Yvonne’, 8.7 and 9.5cm length, respectively. The average days to first flowering of ‘Sunny Gold’, 137.3 days, was approximately 8.7 days earlier than the control cultivar. It’s average vase life and yield is 9.0 days and 5.3 cornets per plant, respectively. The consumption of the yellow freesia such as ‘Gold Rich’, ‘Yvonne’, and ‘Shiny Gold’ is approximately 80% in Korean domestic cut flower market. Freesia ‘Sunny Gold’, as a mid-flowering freesia cultivar is expected to be popular to consumer.

*주저자: Tel. 063-238-6823, E-mail: lillium@korea.kr

A pink double freesia (*Freesia hybrida* Hort.) ‘Love Fiction’

Youn Jung Choi^{*}, Young Ran Lee, Su Young Lee, Yun Im Kang, Hae Ryong Cho

Floriculture Division, National Institute of Horticultural and Herbal Science, RDA, Wanju, 55365, Korea

Freesia (*Freesia hybrida* Hort.) ‘Love Fiction’ was developed for the cut flower in the National Institute of Horticultural Herbal Science in 2015. This hybrid was crossed and selected from a seedling of ‘Golden Crown’ and ‘White wing’, with ‘Teresa’ in 2008. Morphological characteristics of the selected freesia hybrid were investigated for 5 years from 2009 to 2014, and then it was named ‘Love Fiction’ in 2015. ‘Love Fiction’ has pink double petals (RHS, RPN74B). The average flower width is 6.6 cm and the average yield is 5.7. The growth of the plant shows vigorous and the average height is 101.7cm, and it is higher than about 34.6 cm that of control cultivar ‘Opala’. The average number of floret per stalk was 10, and stalk was 9.3 cm length that of control cultivar ‘Opala’, 11.7 and 10.5 cm length, respectively. The average days to first flowering of ‘Love Fiction’, 136.3 days and the average vase life and yield is 9.3 days and 5.0 cornets per plant, respectively. Despite the various colors of freesia flower, the consumption of the domestic cut-flower market is predominantly in the yellow freesia. This pink double freesia cultivar is expected to be useful for wedding bouquets not only in domestic market but also in overseas market.

*주저자: Tel. 063-238-6823, E-mail: lillium@korea.kr

신예감에 방사선 조사를 통한 무핵 계통 선발

박석만*, 박재호, 윤수현, 김민주

농촌진흥청 국립원예특작과학원 감귤연구소

국내의 감귤 소비시장은 90%가 생과로 소비되며 10% 정도가 가공용으로 이용되고 있다. 이러한 감귤 생과 시장에 있어 무핵여부는 소비자의 기호에 많은 영향을 미친다. 국내에 유통되는 감귤은 일부 금감을 제외하고는 대부분이 무핵 품종이다.

그러나 감귤 품종육성 기술이 발달하고 외국의 감귤 유전자원이 도입됨에 따라 다양한 교잡 계통 및 품종이 개발되고 이들 중에는 우수한 품질을 가지고 있으나 종자가 발생하는 단점을 가진 계통이 육성되기 시작하였다. 이러한 문제는 국내뿐만 아니라 감귤육종 프로그램을 운영하는 대부분의 국가에서 발생되고 있으며 이를 극복하기 위한 다양한 방법들이 연구되고 있다. 그중에 한 방법이 방사선 조사 방법이며 이러한 방법을 이용하여 이스라엘, 호주, 스페인 등에서는 무핵의 품종을 육성한 사례가 있으며, 중국감귤연구소에서도 이러한 연구를 수행하고 있다.

본 연구는 2012년에 육성된 유핵의 신예감을 이용하여 방사선 조사를 통해 무핵의 계통을 육성하고자 수행 되었다. 2013년 3월 신예감으로부터 접수를 채취하여 제주대학교 방사선연구원에서 60Gy와 100Gy의 감마선을 조사하였다. 이 접수를 그해 4월 탕자에 접목을 실시하였으며 1년간 생장을 시켰다. 2014년 생장한 접목묘로부터 다시 접수를 채취하여 8년생 탕자에 접목을 실시하였다. 이들 접목묘로부터 2016년 1월 12일에 60Gy 조사계통 48계통, 100Gy 22계통의 착과 과실을 수확하여 과실특성 및 종자 유무를 확인하였다. 그 결과 각각 7계통씩 총 14계통이 무핵임을 확인하였다. 무핵으로 확인된 계통을 대상으로 착화된 12계통에 대하여 2017년 5월에 화기 형태 및 꽃가루를 관찰하여 무핵의 원인을 규명하고자 하였다. 화기 형태 관찰결과 114-1 계통의 경우 수술이 매우 작았으며 현미경을 통한 화분수 관찰에서 정상 보다 매우 적은 화분의 수를 확인할 수 있었다. 이를 통해 이계통의 경우 웅성 불임에 의한 무핵이 유도 되었을 것으로 생각 된다.

*교신저자: Tel. 064-730-4142, E-mail: babau2000@korea.kr

Chalcone synthase I gene targeting using the *Agrobacterium tumefaciens*-mediated CRISPR-Cas9 system in carrot (*Daucus carota* L.)

Eun Ju Lee, Jun Young Choi, Sun-geum Jeong, Youn-Sung Kim*

Department of Biotechnology, NH Seed, Anseong 17558, Korea

The CRISPR-Cas9 system, a novel molecular tool for site-specific genome modification, was recently introduced into plants by transient or stable transformation. In carrot, *Agrobacterium tumefaciens*-mediated transformation system is well established, but a gene targeting using CRISPR-Cas9 system is not. Chalcone synthase is a rate-limiting enzyme in the biosynthesis of anthocyanin that accumulates in plant organs such as flowers, fruits and roots. The purpose of this study is to produce the transgenic plants with inhibition of anthocyanin biosynthesis using *A. tumefaciens*-mediated CRISPR-Cas9 system in carrot. *A. tumefaciens* GV3101 harboring *pHATC* containing genes encoding *Cas9*, *DcCHS1* sgRNA, and hygromycin phosphotransferase was used to infect hypocotyl explants. After 4 weeks of culture on selection medium, the explants produced embryogenic callus mainly at the cut edge. Plantlets were generated via embryo formation from the embryogenic callus after 8-12 weeks in culture. Under the selection with hygromycin, transgenic plants were selected and the insertion of transgenes into the transgenic plants was identified using PCR analysis. Targeted deep sequencing of transgenic plants revealed the deletion mutation at the target site. RT-PCR analysis showed the two bands, which may be obtained by the altered splicing. To confirm the root color of the transgenic plant, phenotype analysis was carried out, showing that the root color was changed from purple to yellow green. HPLC analysis showed that cyanidin was not detected in the transgenic line. These results showed that gene editing with CRISPR-Cas9 system in carrot could be useful for the development of the new valuable varieties.

*Corresponding Author: Tel. 031-652-5526, E-mail: yskim0907@naver.com

박 대목에서 CBF3 형질전환 식물체의 저온 스트레스 저항성 분석

조신환, 안윤균*, 김진희, 이은수, 김정호, 김도선

농촌진흥청 국립원예특작과학원 채소과

박이나 오이, 멜론, 수박과 같은 박과채소 작물을 재배할 경우 물이나 온도 등의 영향을 받아 생산량이 감소하게 되어, 이에 대한 저항성을 가진 작물 육종이 필요하다. 우리나라나 일본 등 몇몇 나라에서는 이런 불리한 환경을 극복하기 위해 박을 대목으로 하여 접목재배를 하고 있으며, 최근 EU에서는 형질전환체를 대목으로 하여 접목하는 기술을 NBT (New Breeding Technology) 중 하나로 정의하였다. 이 연구에서는 저온적응과 관련된 transcription factor 중 하나인 CBF3가 도입된 박(*Lageraria siceraria* Standl.)을 대목으로 하여, 시판중인 수박을 접목한 후 저온저항성이 있는지 확인하였다. 접목 한 식물을 저온 처리한 결과 3일차에서부터 점점 식물이 스트레스를 받는 것을 육안으로 확인할 수 있었으며, 4일차에서 비-형질전환체를 대목으로 한 식물체에서 고사 직전까지의 모습을 보이기도 하였다. 특히 저온 처리시 수박의 무게에서 급격한 감소가 나타났다. 비-형질전환체를 대목으로 식물체의 수박은 3일차에서 1001 g, 4일차에서 388 g으로 눈에 띄게 감소하였지만, 형질전환체를 대목으로 한 식물체에서는 3일차에서 1266 g, 4일차에서 1237 g으로 관찰되어 큰 차이를 보이지 않았다. 따라서 CBF3 형질전환체를 대목으로 사용할 경우 작물의 생장이나 생산량 증대에 많은 효과를 줄 수 있을 것으로 기대된다.

*교신저자: Tel. 063-238-6674, E-mail: aykyun@korea.kr

AVP1과 CBF3를 교배한 식물체에서 저온 스트레스 저항성 확인

조신환, 안윤균*, 김진희, 이은수, 김정호, 김도선

농촌진흥청 국립원예특작과학원 채소과

식물은 생장함에 있어서 생물학적, 비생물학적 스트레스의 영향을 받는다. 이러한 스트레스에 대한 저항성을 증진시키기 위한 많은 노력 중 하나로 저항성을 가진 두 종류 이상의 유전자를 집적시키는 방법이 있다. 한 개의 도입유전자를 가진 형질전환체를 서로 교배를 통해 두 가지 외부 유전자를 가진 식물체를 얻어 복합저항성 식물체를 개발할 수 있다. 이 연구에서는 H⁺-pyrophosphatase를 코딩하는 애기장대 AVP1 유전자를 도입시킨 형질전환체와 CBF3 형질전환체를 교배하여 AVP1과 CBF3 유전자 집적체통을 획득하였으며 저온저항성을 확인하였다. 저온처리 결과 비-형질전환체와 AVP1 형질전환체는 거의 고사하는 모습을 보였지만, CBF3 형질전환체와 교잡식물체는 살아있는 것을 육안으로 확인할 수 있었으며, 생육조사 결과 식물체의 키와 잎의 넓이 및 길이, 개수에서 차이를 보였다. 이는 CBF3 형질전환체와 교배를 통해 AVP1 형질전환체가 저온저항성을 나타내게 된 것이다. 따라서 교배를 통해 두 가지 이상의 유전자가 집적하게 된다면 복합저항성을 가진 식물체를 개발할 수 있으며, 작물의 생장이나 생산량 증대효과를 가져와 농가 소득 향상에 기여할 수 있을 것이다.

*교신저자: Tel. 063-238-6674, E-mail: aykyun@korea.kr

조기개화성 핑크색 홑꽃 분화용 국화 ‘가야베이비’ 육성

진영돈¹, 안동춘¹, 배민지¹, 정용모¹, 황주천¹, 최시림¹, 홍광표²

¹경남 창원시 경남농업기술원 화훼연구소

²경남 진주시 경남농업기술원 연구개발국

경상남도농업기술원 화훼연구소에서는 분화용 국화 로열티부담 경감과 생산비 절감을 위하여 2016년 핑크색 홑꽃 조기개화성 품종인 ‘가야베이비’를 육성하였다. 2014년 1월에 성장세가 균일하고 개화가 빠른 핑크색 ‘하모니핑크’를 모본, 흰녹병에 강하며 개화가 빠른 핑크색 ‘핑크아이’(CFC0087)를 부분으로 인공교배하여 교배조합으로부터 180개의 종자를 획득하였다. 채종 즉시 파종하고 발아시켜 1개월 정도 육묘한 후 10cm 화분에 정식하고 3주 재배 후 적심하고 단일처리하여 개화가 빠르고 화색이 우수한 ‘HPPI-10, 23, 57, 110’ 등 4계통을 우수개체로 선발하였다. 선발된 4계통을 2014년부터 2015년까지 2년간에 걸쳐 1~2차 생육특성 검정을 통해 기호성, 안정성, 균일성과 흰녹병 저항성 등을 조사하여 최종적으로 ‘HPPI-23’을 선발하였다. 2016년에 계통번호 ‘경남교CP-50호’를 부여하여 3차 특성검정을 수행해 생육과 개화특성, 안정성과 균일성, 품평회와 시장출하 등을 통해 생산자와 소비자의 기호성 평가를 받았다. 그 결과 시장성과 기호성이 좋고, 화색 및 화형 등 품질이 우수하다고 판단되어 2016년 농작물직무육성신품종심의회 심의를 거쳐 ‘가야베이비’으로 명명하고 국립종자원에 품종보호출원 하였다. ‘가야베이비’는 연핑크색(P75B) 홑꽃 화형으로 자연일장에서는 10월 25일경에 개화하는 추국이며, 축성 및 억제재배에서 단일처리 후 개화소요일이 5.5주 이하로 조기개화하는 품종이다. 꽃 크기는 4.0cm로 중형이며 암적색의 화실을 가지고 있으며 평균개화소요일이 36일로 짧다. 착화수와 분지수가 26.4개와 5.2개로 많아 상품성이 좋으며 흰녹병에 강하고 재배기간이 짧아 상품성이 좋은 품종이다. 화훼연구소에서 개발된 ‘가야시리즈’와 동시출하시 상품성이 높을 것으로 보이며 10cm 내외의 화분에 적심후에 일반적인 분화국화 재배법으로 재배하면 휴면성이 약해 연중생산이 가능하다. 재배상의 유의사항은 여름철 고온기의 화색퇴화 및 개화지연 방지를 위하여 차광을 해주고 서늘하게 관리하는 것이 좋다.

*주저자: Tel. 055-254-1623, E-mail: ydchin@korea.kr

고추의 shed-소포자 배양 시 전처리 온도, 배지의 조성, 탄소원의 종류 및 농도가 소포자배 발생에 미치는 영향

박은준*, 양은영, 채수영, 문지혜, 박태성, 김옥례, 김대영, 이선이, 김상규

농촌진흥청 국립원예특작과학원 원예작물부 채소과

다수성, 고품질과 더불어 생물학적 또는 비생물학적 스트레스에도 저항성이 있는 새로운 품종을 개발하기 위한 다양한 육종 기술이 요구되고 있다. 반수체와 배가반수체는 새로운 육종방법의 하나인 반수체 육종의 좋은 재료가 될 수 있다. 고추에서 반수체/배가반수체를 생산하는 방법으로 약배양, shed-소포자 배양, 나출 소포자 배양 등이 보고되고 있다. 현재까지 실제 육종에 이용되고 있는 방법은 약배양으로 각 회사 및 연구소에서 자체적으로 기술을 보유하고 있다. 그러나 최근 소포자 배양이 가능해지면서 약배양보다 높은 효율로 배를 생산할 수 있는 배양방법들이 보고되고 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 전처리 온도, 배양배지의 조성, 탄소원의 종류 및 농도가 소포자배 발생에 미치는 영향을 조사하였다. 전처리가 소포자배 발생에 미치는 영향을 조사한 결과 9℃에서 7일 동안 저온처리 후 Maltose가 8% 포함된 배지에서 배양 시 5.4개의 배가 발생하였다. 배양배지 조성, 탄소원에 따른 배발생 효율을 조사하기 위해 maltose와 sucrose가 포함된 1/2NLN, NLN, NN, MS2 배지를 사용한 결과 NLN 배지에서 가장 많은 소포자배가 발생하였으며, 탄소원의 종류에 따른 차이는 크지 않았다. 탄소원 농도의 영향을 조사하기 위해 액체배지 내 sucrose를 2, 4, 6, 8, 10% 농도로 첨가 후 28℃에서 배양한 결과 소포자배 발생에 영향을 미치는 최적의 sucrose 농도에 따른 차이는 크지 않았으나 밀양재래는 6%, long fruit 품종은 6, 10%에서 배발생이 높았다. 본 연구결과들은 shed-소포자 배양을 통해 반수체/배가반수체를 생산하기 위한 연구의 기초자료로 이용될 수 있을 것이다.

*주저자: Tel. 063-238-6613, E-mail: ejpark97@korea.kr

CRISP/Cas9 을 이용한 Glucoraphanin 고함량 브로콜리 계통 육성

이상협^{1*}, 황병호²

¹서울특별시 광진구 군자동 세종대학교 생명과학대학 생명시스템학부 바이오산업자원공학전공

²경기도 이천시 장호원읍 이항리 아시아종묘 생명공학육종연구소

브로콜리는 항암 작용을 비롯하여, 고혈압 및 심혈관 질환에 대한 예방 효과와 해독 효소의 유도효과가 크다고 알려져 있다. 따라서 2000년 이후 국내 소비량이 매년 상당히 증가되고 있는 실정이다. 브로콜리의 대표적인 유효 성분은 sulforaphane(S-methylsulfinylbutyl isothiocyanate)로 알려져 있고, 세포 조직이 마쇄될 때 전구물질인 glucoraphanin이 myrosinase에 의해 분해되면서 sulforaphane nitrile과 함께 생성된다고 알려져 있다. 따라서 glucoraphanin 고함량 브로콜리 육성은 브로콜리 육성 기술을 한 단계 높이는 계기가 될 것이다. 2011년 미국 몬산토사에서 Glucoraphanin 함량이 기존 재배종의 2~3 배 되는 Beneforte라는 품종을 전통 육종을 통해 출시하였다. vilosa라는 야생자원(Glucoraphanin 함량이 재배종의 2~3 배)을 십 수 년동안 back-crossing한 결과이다. 본 연구에서는 CRISP/Cas9이라는 분자생물학 기법을 적용하여 Glucoraphanin 함량을 높이고자 하는 시도를 추구한다.

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*주저자: Tel. 02-3408-4375, E-mail: sanglee@sejong.ac.kr

열대형 반수체 유기계통 및 반수체 옥수수의 특성평가

이진석^{1*}, 손범영¹, 김정태¹, 배환희¹, 김상곤¹, 백성범¹

¹경기도 수원시 권선구 수인로 126 국립식량과학원 중부작물부

국내 옥수수 반수체 유기계통을 개발하기 위하여 열대형 반수체 유기계통(TAIL, Tropically Adapted Inducer Line)의 특성 및 유기된 반수체 옥수수의 특성평가를 수행하였다. TAIL P1과 TAIL P1/P2는 생물학적 마커로 이용하기 위하여 제1엽의 엽초에 안토시아닌 색소를 발현하였고 출사일수는 모두 71일이었으며 화분비산 후 출사까지의 기간이 1~2일이었다.

TAIL의 반수체 유기율을 평가하기 위하여 광평옥, SK165, KS124, KS164, KY48 등을 검정친으로 하여 TAIL P1과 교배를 수행하였으며 R1-nj 유전자의 발현에 따라 반수체 유기율을 평가한 결과 R1-nj 유전자 발현에 의한 반수체 유기율은 10.5%였다. 이들을 50공 육묘 포트에 모두 파종한 후 제1엽 엽초의 안토시아닌 색소발현을 확인하였다. R1-nj 유전자 발현에 의해 이배체로 선발된 종자 중 2%는 반수체 종자였고 반수체로 선발된 종자 중 47.9%는 이배체 종자였으며 실제 반수체 유기율은 7.8%로 R1-nj 유전자 발현에 의한 유기율과는 차이가 있었다. 이배체와 반수체 식물체를 포장에 이식하여 반수체 옥수수와 생육특성을 비교한 결과, 반수체 옥수수는 간장, 엽폭, 간경 등이 이배체 옥수수보다 작았으며 출웅과 출사는 정상적으로 이루어졌으나 화분은 형성되지 않았다.

사사: 본 연구는 농촌진흥청 차세대바이오그린21 연구사업(세부과제명 : 옥수수 반수체 유기 유전자 도입 및 국내 적응 자원 개발, 세부과제번호: PJ011769032017)의 지원에 의해 이루어진 것이다.

*주저자: Tel. 031-695-4043, E-mail: z9813139@korea.kr

양배추 소포자배양에 효과적인 시기와 배양조건 구명

박민영^{1,2*}, 장하영^{1†}, 임용표², 이정수¹, 박수형^{1*}

¹농촌진흥청 국립원예특작과학원 채소과

²충남대학교 원예학과

십자화와 채소에서 소포자배양은 doubled-haploid (DH) 계통을 개발하는데 널리 사용된다. 육종가들은 유전적으로 동일한 상동 염색체를 갖는 DH 계통을 양친으로 사용하기를 선호하며 소포자배양기술을 이용한 육종은 단기간에 선택된 식물 재료로부터 DH 계통을 개발할 수 있다는 점에서 유용하다. 국립원예특작과학원에서는 유전적으로 다양한 양배추 자원들의 소포자배양을 통하여 효과적인 시기와 조건을 구명하기 위해 본 연구를 실시하였다. 그 결과, 배지조건의 경우 '2×NLN, AgNO₃ 1mg/L, 13 % Sucrose'의 조성이 배 생산에 효과적임을 확인할 수 있었다. 그리고 배양 재료로 사용된 다양한 세대의 양배추 자원 중 소포자로부터 유도된 배 발생 효율은 일대잡종 세대 보다 자가 수정 후대인 F₂ 또는 F₃ 세대에서 높았다. 이러한 결과를 통하여 양배추의 소포자배양 시, 목적하는 양배추 자원으로부터 유도된 배의 개수가 일대잡종 품종에서 계획한 양 만큼 도달하지 못했을 경우, 그의 자손 세대를 사용하여 소포자배양을 지속하는 것을 추천한다. 그리고 본 연구를 통하여 획득된 배 발생 개수와 토양 순화 개체 수는 소포자배양 전제기간 중, 개화 초기의 결과가 중기 및 말기보다 높았다. 토양 순화의 경우, 개화 초기에 수집한 꽃봉오리를 이용하여 소포자배양한 결과에서 식물체로 토양 순화된 비율이 전체 중 71.2% 로 중기와 말기의 각각 27.0%, 1.8% 결과 보다 월등히 높았다. 이러한 결과를 통하여 양배추의 소포자배양을 하고자 할 때, 저온처리 후 꽃봉오리가 발생하는 전체 기간 동안 배양을 진행하는 것보다, 짧게는 개화 초기(첫 개화 후 14일 까지)에만, 늦어도 개화 중기의 초기까지 배양을 진행하는 것이 배양 성공 면이나, 노동력 절감 면에서 더 효율적이라고 판단된다.

*교신저자: E-mail: psh@korea.kr

배가 반수체 기술을 이용한 국내최초 옥수수 계통 DHF1, DHW1 육성

류시환*, 최재근, 박종열, 남궁민, 용우식, 윤석원, 박기진, 최준근

강원도 홍천군 두촌면 장남길 26 강원도농업기술원 옥수수연구소

우량 계통육종은 옥수수 교잡종 육성을 위한 필수요소이다. 국내의 옥수수 계통육종은 순도 고정을 위해 7회 이상의 인공교배(selfing)를 수행하는 전통적인 방법에 의존하고 있다. 시간과 노력 소모가 많은 전통육종의 단점을 극복하고자 강원도농업기술원 옥수수연구소에서는 국제옥수수·밀연구소(CIMMYT)와 협력하여 배가반수체 기술의 국내 도입에 노력한 결과, 국내 최초로 신기술을 이용한 옥수수 계통육성에 성공하였다. 배가반수체 기술에 의한 옥수수 계통육성체계는 반수체 유기, 염색체 배가 및 계통생산, 그리고 계통의 특성평가 등의 3단계로 이루어진다. 2014년 반수체 유기체(Inducer)와의 교배를 통한 반수체 유기에서 종실용 옥수수 32P75 F2 집단과 찰옥수수 미백2호 F1 집단의 반수체 유기율은 각각 4.0%와 2.9%였다. 2015년 colchicine를 이용한 염색체 배가 및 계통생산에서 32P75와 미백2호 집단으로부터 각각 9계통과 38계통을 생산하였다. 2016년 각 집단에서 육성된 계통의 표현형적 특성평가를 실시하여 적응성, 도복, 내병성 등이 우수한 DHF1 및 DHW1을 선발하였다. DHF1은 출사일수 74일, 간장 175cm, 100립중 32g의 직립형 종실용 계통이다. DHW1은 출사일수 69일, 착수고율 40%, 이삭장 11.5cm의 조숙성 찰옥수수 계통이다. 육성된 계통은 기존의 엘리트 계통과의 교배를 통해 조합능력 및 생산력검정을 수행할 예정이며, 우량 교잡종 품종육성에 활용성이 높을 것으로 기대된다.

사사: 본 연구는 농촌진흥청 차세대바이오그린21사업(PJ011769012017)의 지원에 의해 이루어진 것임

*교신저자: Tel. 033-248-6913, E-mail: shr8921@korea.kr

Assessment of genetic diversity of rice germplasm with black purple and red pericarp color using simple sequence repeats (SSR) markers

Jae-Ryoung Park, Won-Tae Yang, Doh-Hoon Kim, Yong-Sham Kwon*

Department of Molecular Genetic Engineering, Dong-A University, Busan 49315, Korea

The assessment of genetic diversity investigated with SSR markers would benefit to make use of these germplasms as well as applying them in association mapping. The present study was conducted to evaluate the genetic diversity of rice germplasms with 376 black purple and 172 red pericarp color conserved by Dong-A university. The 600 pairs of simple sequence repeat (SSR) primers screened against 11 rice varieties. Sixteen informative primer pairs with high polymorphism information contents (PIC) value were used to assess genetic diversity in the collection. A total of 409 polymorphic amplified fragments were obtained by using 16 SSR markers. The number of alleles per locus ranged from 11 to 47 with an average of 25.6 alleles per locus. The average PIC was 0.913 ranging from 0.855 to 0.964. Four hundred nine three SSR loci were used to calculate Jaccard's distance coefficients for unweighted pair group method with arithmetic mean cluster analysis. These accessions were separated into several distinctive groups corresponding to morphological types. At present, we are analyzing population structure and the relationship between molecular markers and major agronomic traits such as seed and major morphological trait in 548 rice accessions. These results would provide valuable information for colored rice breeding program and the protection of important germplasm resources using molecular marker.

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*Corresponding Author: Tel. 051-200-7521, E-mail: yskwon3@dau.ac.kr

The Storage stability of perilla oil affected by storage conditions and fatty acid composition

MyoungHee Lee*, JiMyoung Choi, EunYoung Oh, SungUp Kim, JungIn Kim, SukBok Pae, KiWon Oh, UnSang Yeo, DoYeon Kwak

Department of Southern Area Crop Science, NICS, RDA, Miryang, Korea

The perilla oil is a Korean traditional oil, it has over 60% proportion of omega-3 among fatty acids, which is the highest percentage among vegetable oils. The perilla oil were studied on the changing properties according to storage condition and fatty acid composition after oil extraction. Perilla seed was roasted at 170°C, extracted with oil press and stored at 4, 10, 250°C. Their lipid peroxidation was monitored by the acid and peroxide value test method every month. We analyzed the composition of fatty acid in perilla varieties and germplasm for examine oxidative stability according to α -linolenic acid composition. The acid value and peroxide value of perilla oil at 25°C showed the increasing tendency in all the samples during the storage period. Though just a small changes was observed in the compositions of fatty acid but it was not affected seriously according to storage temperature and period.

*Corresponding Author: Tel. 055-350-1212, E-mail: emhee@korea.kr

Modification of seed colors via CRISPR/Cas9-targeted knockout of LDOX gene in rice

Shahina Akter¹, Hyo-Ju Lee¹, Ye Rim Lee¹, Yeo Jin Jung¹, Jong Hee Kim¹, Yong-Gu Cho³, Kwon-Kyoo Kang^{1,2}, Yu-Jin Jung^{1,2*}

¹Department of Horticulture, Hankyong National University, Ansong 17579, Korea

²Institute of Genetic Engineering, Hankyong National University, Ansong 17579, Korea

³Department of Crop Science, Chungbuk National University, Cheongju 28644, Korea

Genome modification technologies such as ZFN (Zinc Finger Nuclease), TALEN (Transcription Activator-Like Effector Nuclease) and CRISPR/Cas9 technology have been successfully applied to improve various crop traits. 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 seed colors in higher plants using rice. 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 used for production of transgenic rice plants via *Agrobacterium*-mediated transformation. Targeted mutations were analyzed in bar-resistant shoots by sequencing of the LDOX amplicons (PCR products) using NGS analysis. Transgenic rice plants clearly contained DNA mutations such as nucleotide substitutions, insertions and deletions at the target site, which varied depending on the transgenic lines. In the future, we will investigate seed color in transgenic lines. And these data will be discussing relationship between seed-color phenotypes and mutations in transgenic plants.

*Corresponding Author: E-mail: yuyu1216@hknu.ac.kr, kykang@hknu.ac.kr

High-frequency genome editing with the CRISPR/Cas9 system in rice

Hyo-Ju Lee¹, Sangsu Bae³, Geung-Joo Lee⁴, Pil Joon Seo⁵, Dong Hyun Kim¹, Jae Uk Lee¹, Yong-Gu Cho⁶, Kwon Kyoo Kang^{1,2*}, Yu Jin Jung^{1,2*}

¹Department of Horticultural Life Science, Hankyong National University, Ansong 17579, Korea

²Institute of Genetic Engineering, Hankyong National University, Ansong 17579, Korea

³Department of Chemistry, Hanyang University, Seoul 04763, Korea

⁴Department of Horticulture, Chungnam National University, Daejeon 34134, Korea

⁵Department of Biological Sciences, Sungkyunkwan University, Suwon 16419, Korea

⁶Department of Crop Science, Chungbuk National University, Cheongju 28644, Korea

The CRISPR/Cas9 is a core technology that can result in a paradigm for breeding new varieties. This study describes in detail the sgRNA design, vector construction, and the development of a transgenic plant and its molecular analysis, and demonstrates how gene editing technology through the CRISPR/Cas9 system can be applied easily and accurately. CRISPR/Cas9 facilitates targeted gene editing through RNA-guided DNA cleavage, followed by cellular DNA repair mechanisms that introduce sequence changes at the site of cleavage. It also allows the generation of heritable- targeted gene mutations and corrections. Here, we present detailed procedures involved in the CRISPR/Cas9 system to acquire faster, easier and more cost-efficient gene edited transgenic rice. The protocol described here establishes the strategies and steps for the selection of targets, design of sgRNA, vector construction, and analysis of the transgenic lines. The same principles can be used to customize the versatile CRISPR/Cas9 system, for application to other plant species.

*Corresponding Author: E-mail: yuyu1216@hknu.ac.kr, kykang@hknu.ac.kr

유전변이 기반 콩 분자마커 생산 모듈 개발

김남훈¹, 김혜식¹, 신명주¹, 이현오¹, 최범순¹, 유의수^{1*}

¹경기도 성남시 분당구 성남대로 331번길, 백궁프라자1 빌딩 605호, 파이젠 유전체 연구소

작물의 유전체 정보 생산은 차세대 유전체분석 방법의 발달로 급속히 증가하고 있으며, 대량의 유전변이 데이터를 확보하고 이들 정보의 효율적인 활용으로 작물에서 유전체 육종을 구현하기 위한 단계로 전환하고 있다. 따라서 많은 유전체 정보 중 분자유종에 적극적으로 이용할 수 있는 데이터베이스의 구축과 효율적이고 통합된 정보를 추출, 활용 이 가능하게 하는 인터페이스의 구축은 분자유종의 효율 향상에 많은 기여를 할 것으로 판단 된다. 본 연구는 “육종현장에서 사용이 가능한 유전체 육종 지원 시스템의 개발”의 일환으로 콩 표준유전체를 기반으로 유전체 재분석 기술을 이용한 NGS 데이터의 분석을 통해서 국내 보유 콩 유전자원 내에 존재하는 SNPs, indels, MIPs (MITE insertion polymorphism; MITEs=Miniature Inverted-repeat Transposable Elements) 등 유전변이를 확보하고 질적, 양적 형질의 동정 및 개체 선발에 적용하기 위한 다량의 분자마커를 개발을 위한 분자마커 생산모듈의 개발에 있다. MITE 기반의 마커 개발 과정, 콩 핵심집단 대상 대량의 SNP 및 indel 마커 개발 방법 등의 결과, 가시화 전략 등이 본 발표에 소개되며, 과제의 연구 결과는 관련 작물 유전체 정보의 집중화에 기여하고, 정보관리, 분석방법에 표준화를 제시하여 관련 유전체정보의 이용과 해석에 신뢰성을 더 하고, 분자 육종 시 필요한 polymorphic 한 다량의 마커 제작에 도움을 주어 분자 육종의 효율을 높일 것으로 기대한다.

***교신저자:** Tel. 031-716-0041, E-mail: yeisooyu@phyzen.com

Development of wheat transformation by biolastic approach in a Korean wheat cultivar “Keumkang”

Jin Sun Kim^{*1}, Su-Jin Choi¹, You-Ran Jang¹, Sun-Hyung Lim¹, Jong-Yeol Lee¹

¹National Institute of Agricultural Science, RDA, Jeonju, 54874, Korea

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 biolastic 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.

***Presenting Author:** Tel. 063-238-4616, E-mail: jskim220@korea.kr

AVMP (Assembly Verification using Mate Pair) 프로그램을 이용한 결명자 유전체 검증

박미소¹, 김남훈¹, 이승욱¹, 유의수¹, 강상호², 최범순^{1*}

¹경기도 성남시 분당구 성남대로 331번길, 백궁프라자1 빌딩 605호, 파이젠 유전체 연구소

²전라북도 완주군 이서면 농생명로 166, 농촌진흥청 국립농업과학원 농업생명자원부 유전체과

결명자 (*Senna tora* L.)는 콩과에 속하는 일년생 초본이다. 눈을 맑게 하는 씨앗이란 이름대로 예로부터 한의학에서 시신경보호, 혈압강하, 항균, 이뇨 등의 치료에 사용되어왔다. 결명자는 anthraquinone, flavonoid 등의 이차대사산물을 많이 함유하고 있고, 최근에는 emodin 성분이 항암 등에 효능이 있다고 알려져 산업적으로도 가치가 큰 식물이다. 결명자의 유전체크기는 600Mb 정도로 알려져 있으나, 아직까지 결명자의 유전체분석이나 의학적 효용이 있는 유전자들의 기능 및 pathway 연구는 거의 진행되지 않은 상태이다. NGS 기술의 발전은 수많은 신규 유전체분석을 가능하게 하고 있다. 주식회사 파이젠은 Illumina사의 HiSeq 플랫폼 기반의 짧은 염기서열을 *de novo* assembly에 이용한 뒤 생성되는 부정확한 scaffold의 오류를 줄이고자 하였다. 그 방안으로 완성된 유전체 서열에 mate pair 데이터를 다시 붙여봄으로써 span size를 확인하는 Assembly Verification using Mate Pair (AVMP) 프로그램을 파이젠 유전체 연구소에서 개발하였다.

AVMP (Assembly Verification using Mate Pair) 프로그램은 perl 5.10.1과 GD library 2.46을 이용하여 개발되었으며, 이는 결명자 유전체 검증뿐만 아니라 다양한 종에서 유전체정보를 검증함에 있어 많은 기여를 할 것이라 생각된다.

*주저자: Tel. 031-716-0041, E-mail: iamparkmiso@phyzen.com

Early maturing rice Variety, 'Gawaji 1', adaptable to climatic change and double cropping system in Gyeonggi-Do, northern area of South Korea

Ji-Hye Lee, Jung-Hee Jang, Byoung-Rourl Choi and Tae-Jin Won*

Gyeonggi-Do Agricultural Research & Extension Services(GARES), Hwaseong 283-33, Korea

'Gawaji 1', an early maturing and low amylose content rice variety adaptable to double cropping system with barley as later winter crop, was developed by the crop breeding team of Crop Research Division, GARES, Hwaseong, Korea in 2016. 'Gawaji 1' was derived from a cross between 'Baegjinju' and 'Sangmibyeo' in 2004. This variety had heading date of August 4 in Gyeonggi Province. It had a semi-elect plant type and resistance to lodging with strong culm. Its culm length was 67 cm. This variety had 15 tillers per hill and 104 spikelets per panicle. It was medium grain variety showing 1,000 grain weight of brown rice of 19.3g. Its protein contents of milled rice was 8.2% which was lower than 'Baegjinju'. Its milling ratio was 75.5% which was higher than 'Baegjinju'. The yield of milled rice was 5.0 MT/ha under the ordinary culture of the local adaptability test in 3 areas of Gyeonggi Province for three years. 'Gawaji1' is highly adaptable to Gyeonggi Province, especially to northern region of Han River.

*Corresponding Author: Tel. +82-31-229-5775, E-mail: wonboy@gg.go.kr

Overexpression of the *Oryza sativa* glutathione synthetase improved stress tolerance and productivity in transgenic rice plants under field conditions

Seong-Im Park¹, Young-Saeng Kim¹, Jin-Ju Kim¹, Il-Sup Kim², Ho-Sung Yoon^{1*}

¹Department of Biology, College of Natural Sciences, Kyungpook National University, Daegu 702-701, South Korea

²School of Life Sciences, BK21 Plus KNU Creative BioResearch Group, Kyungpook National University, Daegu 41566, Republic of Korea

Reactive oxygen species, which increase under various environmental stresses, have deleterious effects on plants. An important antioxidant, glutathione, is used to detoxify reactive oxygen species in plant cells and is mainly produced by two enzymes: gamma-glutamylcysteine synthetase (γ -ECS) and glutathione synthetase (GS). To evaluate the functional roles of the glutathione synthetase gene (*OsGS*) in rice, we generated four independent transgenic rice plants (TG1 – TG4) that overexpressed *OsGS* under the control of the constitutively expressed *OsCcl* promoter. When grown under natural paddy field conditions, the TG rice plants exhibited greater growth development, higher chlorophyll content, and higher GSH/GSSH ratios than control wild-type (WT) rice plants. Subsequently, the TG rice plants enhanced redox homeostasis by preventing hydroperoxide-mediated membrane damage, which improved their adaptation to environmental stresses. As a result, TG rice plants improved rice grain yield and total biomass following increases in panicle number and number of spikelets per panicle, despite differences in climate during the cultivation periods of 2014 and 2015. Overall, our results indicate that *OsGS* overexpression improved redox homeostasis by enhancing the glutathione pool, which resulted in greater tolerance to environmental stresses in the paddy fields.

*Corresponding Author: Tel. +82-53-950-5348, E-mail: hys@knu.ac.kr

Overexpression of a novel RING-type E3 ubiquitin ligase gene induces the coiled branch (*cbr*) mutant in Arabidopsis

Gyu Tae Park¹, Jagadeesh Sundaramoorthy¹, Seokhyung Lee¹, Jeong-Dong Lee¹, Hak Soo Seo², Jong Tae Song^{1*}

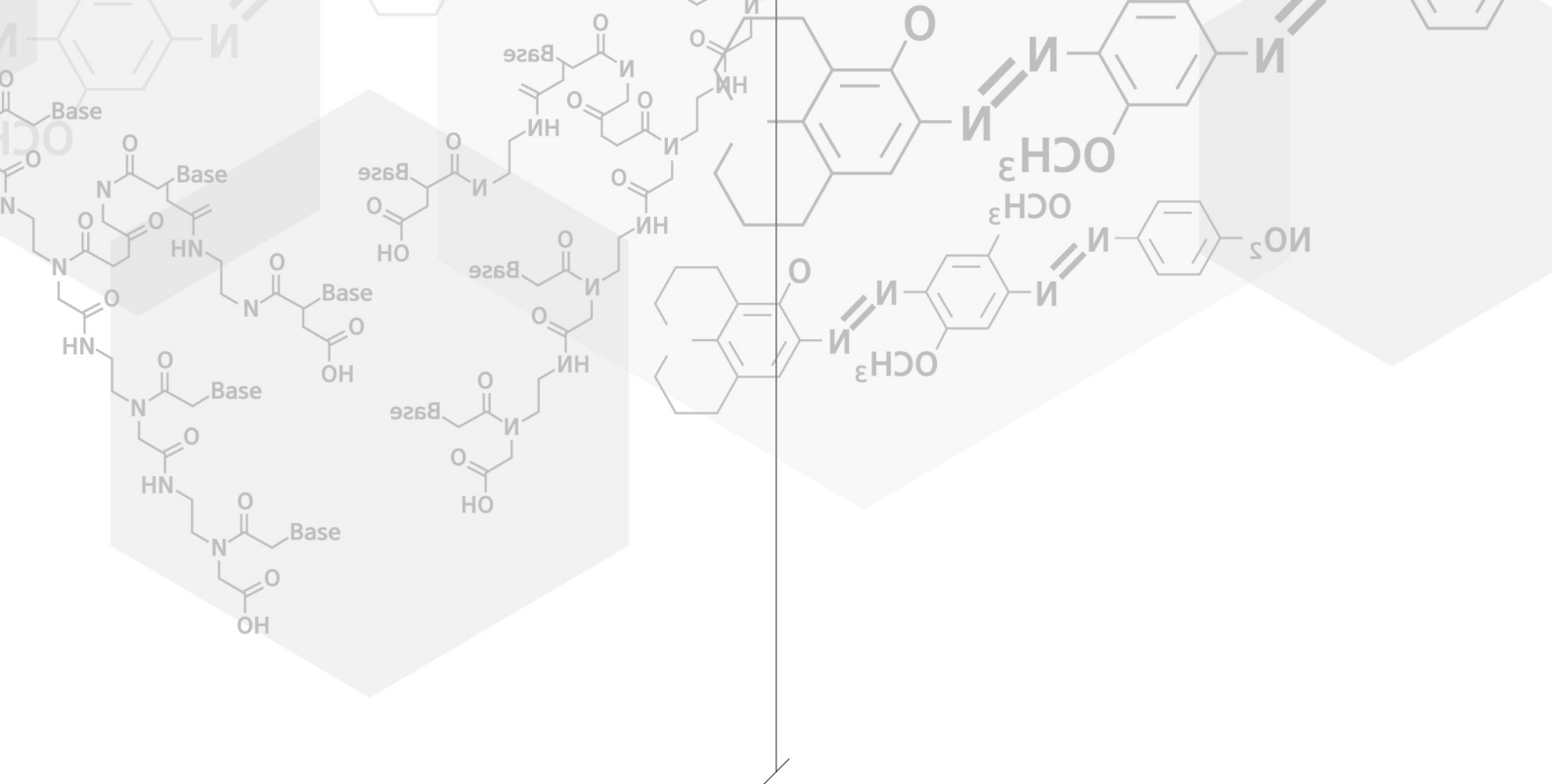
¹School of Applied Biosciences, Kyungpook National University, Daegu, Republic of Korea

²Department of Plant Bioscience, Seoul National University, Seoul, Republic of Korea

In nature, the wild relatives of soybean [*Glycine soja* Sieb. and Zucc.] have curly/wavy branches whereas cultivated varieties are upright. To investigate the molecular mechanism of coiling nature, screening was carried out from Arabidopsis activation tagging lines obtained by activation T-DNA treatment that have curly/wavy morphology. The mutant with a wavy and curly morphology with coiling branches was named *cbr*. Plasmid rescue and genomic southern blot analysis revealed the site of T-DNA insertion in the genome. RT-PCR was performed to evaluate the 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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*Corresponding Author: Tel. +82-53-950-7753, E-mail: jtsong68@knu.ac.kr



식물분자육종사업단 & GM작물개발사업단

일시 2017년 7월 7일(금), 09:00 ~ 10:40

장소 대구 엑스코

주관 식물분자육종사업단 & GM작물개발사업단



SP-LL-37, human antimicrobial peptide, enhances disease resistance in transgenic rice

In Hye Lee¹, Yu-Jin Jung^{1,2}, Yong Gu Cho³, Ill Sup Nou⁴, Md. Amdadul Huq^{1,2}, Franz Marielle Nogoy³, Kwon-Kyoo Kang^{1,2*}

¹Department of Horticultural Life Science, Hankyong National University, Ansong, Korea,

²Institute of Genetic Engineering, Hankyong National University, Ansong, Korea,

³Department of Crop Science, Chungbuk National University, Cheongju, Korea,

⁴Department of Horticulture, Suncheon National University, Suncheon, Korea

As rice is the main food source for more than half of the world's population, fluctuation in production can indirectly make a significant impact on the world economy. Bacterial leaf blight and blast are the most important diseases affecting rice production. They are difficult to control because the speed of diffusion is very fast. The usual way to control such type of pathogens is to spray pesticides. However, continuous and extensive use of such pesticides causes longterm exposure of the environment to contamination. In addition, many microorganisms can acquire resistance to chemical pesticides [Daoubi et. al., 2005]. The most effective and environment friendly way to control bacterial leaf blight and blast diseases is deployment of resistant cultivars. Classical plant breeding for resistant varieties requires complex system development like identification of source for donor genes, time and cost of breeding, stability of resistance and multiple location tests. Biotechnology can be used to complement the shortcomings of traditional breeding, and a number of success stories have already been reported. Antimicrobial peptides (AMPs) are components of the defense system of animals and plants against pathogens and are generally shorter than 50 amino acid residues per peptide. AMPs are controlled by a single gene, and can destroy microorganisms, including bacteria, fungi, mycoplasma, and viruses, with minimum energy consumption during the initial infection. Because of this huge advantage, scientists used AMPs as one of the important sources for breeding resistant varieties [Rahnamaeian M, 2011]. Human LL-37 is a multifunctional antimicrobial peptide of cathelicidin family. It has been shown in recent studies that it can serve as a host's defense against influenza A virus. We now demonstrate in this study how signal peptide LL-37 (SP-LL-37) can be used in rice resistance against bacterial leaf blight and blast. We synthesized LL-37 peptide and subcloned in a recombinant pPZP vector with pGD1 as promoter. SP-LL-37 was introduced into rice plants by *Agrobacterium* mediated transformation. Stable expression of SP-LL-37 in transgenic rice plants was confirmed by RT-PCR and ELISA analyses. Subcellular localization of SP-LL-37-GFP fusion protein showed evidently in intercellular space. Our data on testing for resistance to bacterial leaf blight and blast revealed that the transgenic lines are highly resistant compared to its wildtype. Our results suggest that LL-37 can be further explored to improve wide-spectrum resistance to biotic stress in rice.

*Corresponding Author: Tel. 031-670-5104, E-mail: kykang@hknu.ac.kr

Optimization of crop productivity in tomato by manipulating genetic variations in florigen related genes

Soon Ju Park^{1*}, Sebastian Soyk², Min-Sung Kang¹, Zachary B Lippman²

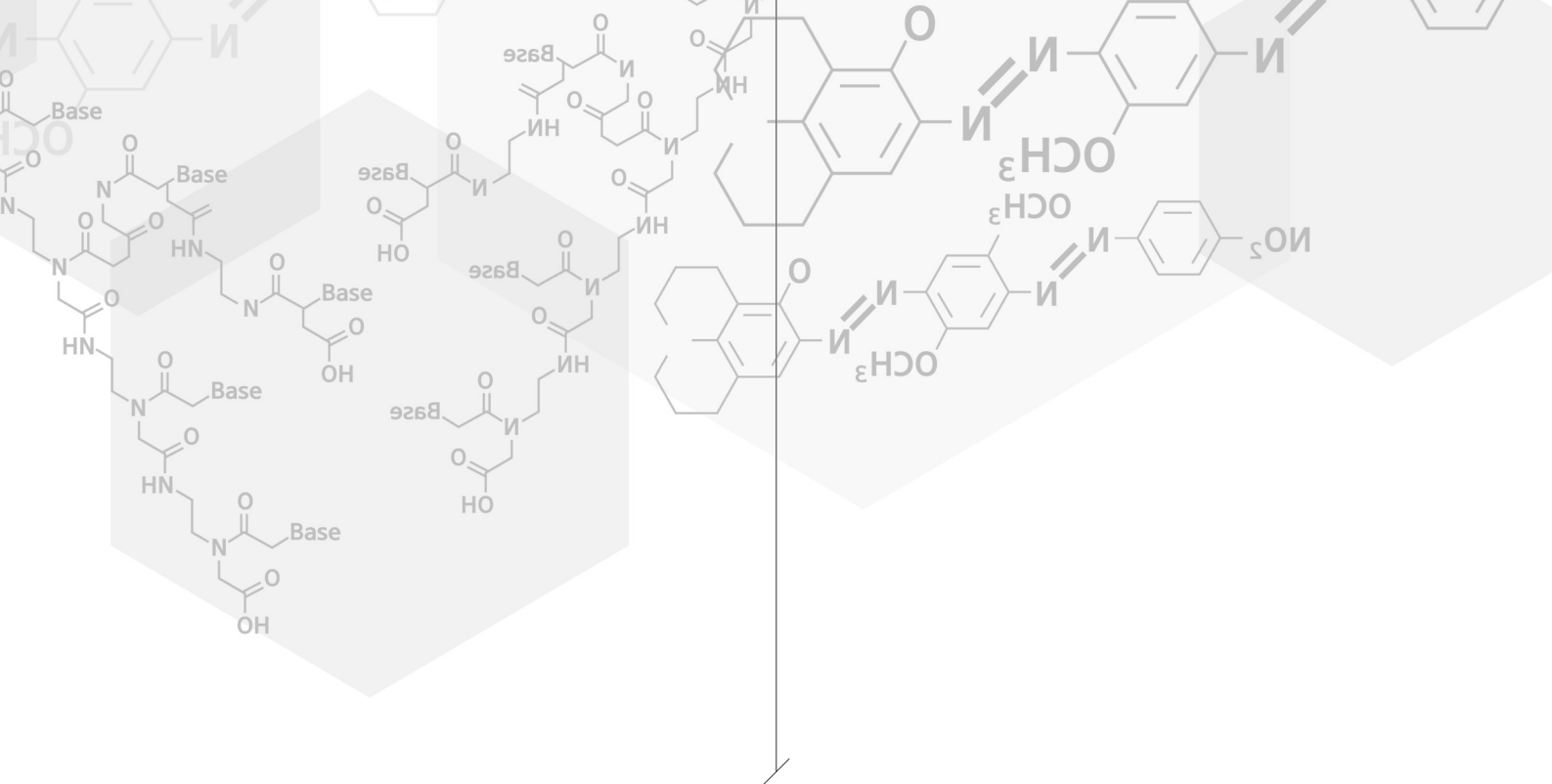
¹Department of Biological Science and Institute for Basic Science, Wonkwang university 460 Iksandae-ro, Iksan, Jeonbuk, Korea

²Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, USA

Tomato life adaptation in a year and sympodial determination fitness are the most important factors to increase yield for fresh market and commercial products. Here we show that tomato productivity can be fine-tuned and optimized by exploiting combinations of selected mutations in multiple florigen pathway components. By screening for chemically induced mutations that suppress the bushy, determinate growth habit of field tomatoes, we isolated a new weak allele of the florigen gene *SINGLE FLOWER TRUSS (SFT)* and two mutations affecting a bZIP transcription factor component of the 'florigen activation complex'. By combining heterozygous mutations, we pinpointed an optimal balance of flowering signals, resulting in a new partially determinate architecture that translated to maximum yields.

Additionally, we further show that loss of day-length-sensitive flowering in tomato was driven by the florigen paralog and flowering repressor *SELF-PRUNING 5G (SP5G)*. *SP5G* expression is induced to high levels during long days in wild species, but not in cultivated tomato because of cis-regulatory variation. CRISPR/Cas9-engineered mutations in *SP5G* cause rapid flowering and enhance the compact determinate growth habit of field tomatoes, resulting in a quick burst of flower production that translates to an early yield. We propose that harnessing mutations in the florigen pathway to customize plant architecture and flower production offers a broad toolkit to boost crop productivity.

*Corresponding Author: E-mail: sjpark75@wku.ac.kr



농생물게놈활용연구사업단

주요작물의 GWAS 분석을 통한 후보유전자 선발과 기능연구 콘서트

일시 2017년 7월 7일(금), 09:00 ~ 10:40

장소 대구 엑스코

주관 농생물게놈활용연구사업단



Concurrent Session(17.07.07) : 농생물게놈활용연구사업단

주요작물의 GWAS 분석을 통한 후보유전자 선별과 기능연구 콘서트

시간	발표제목 (가제)	발표자 (소속)
09:00~09:25	벼의 오믹스 정보육종: 새로운 시도와 경험	박용진(공주대학교)
	Utilizing multi-omic information in rice breeding: experience from new trials	Yong-Jin Park (Kongju National University)
09:25~09:50	SNP 분석을 통한 유전자형에 따른 재배콩 및 야생콩 핵심집단 구축	최만수(국립식량과학원)
	Construction of core collection using single nucleotide polymorphism analysis in cultivated soybeans (<i>Glycine max</i> L. Merr) and wild soybeans <i>Glycine soja</i> Siebold & Zucc.) germplasm	Man-Soo Choi (National Institute of Crop Science)
09:50~10:15	고추 핵심집단을 이용한 주요농업형질의 게놈전체연관분석	권진경(서울대학교)
	GWAS of primary agronomic characters in <i>Capsicum</i> core collection	Jin-Kyung Kwon (Seoul National University)
10:15~10:40	콩에서 NAM 집단 개발과 GWAS 분석결과 활용	강성택(단국대학교)
	Soybean nested association mapping(NAM) population for novel gene/QTL mass screening)	Sungtaeg Kang (Dankook University)

※ 각 발표는 20분, 질의응답 5분씩 배정

Utilizing multi-omic information in rice breeding: experience from new trials

Kyu-Won Kim¹, Qiang He², Win Htet Oo², Ji-Min Yoo², Phitaktansakul Rungrana², Dong-Hee Kim¹, Jung-Rye Nam¹, Sang-Ho Chu¹, Wei-Guo Zhao³, Sang-Won Park⁴, Il-Pyung Ahn⁵, Yong-Soo Choi⁶, Yoo-Hyun Cho⁷, Young-Sang Lee⁸, Jung-Kyung Moon⁹, Yong-Jin Park^{1,2*}

¹Center for crop genetic resource and breeding (CCGRB), Kongju National University, Yesan 32439, Korea

²Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 32439, Korea

³School of Biology and Technology, Jiangsu University of Science and Technology, Sibaidu, Zhenjiang, Jiangsu 212018, PR China

⁴Chemical Safety Division, National Institute of Agriculture Science (NAIS), Wanju 55365, Korea

⁵National Institute of Agricultural Science, Rural Development Administration, Jeonju 54874, Korea

⁶National Medicine Center, Korea Institute of Science and Technology, Gangneung 02792, Korea

⁷Seedpia, 85 Maesil-ro, Kwonsun-ku, Suwon 16395, Korea

⁸Department of Medical Biotechnology, Soonchunhyang University, Asan 31538 Korea

⁹National Institute of Crop Science, Rural Development Administration, Wanju 55365, Korea

The development of high-throughput technology has led to a boost in omic-wide studies on organisms, and it is now actively applied to crop breeding. For domestic rice, we have produced and analyzed genome, transcriptome, and proteome from the Korean rice core collection (KRICE_CORE). Using genomic data, we characterized the ecotypes of Korean wild rice and identified the evolutionary characteristics of weed rice to evaluate the values of Korean wild and weed rice as genetic resources. We also carried out genome-, transcriptome-, proteome-wide association studies on major agricultural traits of rice. We applied a set of bioinformatics techniques for precise identification of candidate genes from the omic data. Our study showed the possibilities for using omic data in rice breeding.

*Corresponding Author: yjpark@kongju.ac.kr

Construction of core collection using single nucleotide polymorphism analysis in cultivated soybeans (*Glycine max* L. Merr) and wild soybeans (*Glycine soja* Siebold & Zucc.) germplasm.

Man-Soo Choi

National Institute of Crop Science, Rural Development Administration

A core collection is small population to represent the genetic diversity of the entire collection in plant germplasm resources, and is important strategy available as a small part of a germplasm collection to represent of the entire collection. Especially, developing of the core collection in soybean is also important and valuable task as one of the most important crop resources worldwide. Here, we developed the core collection consisting of 816 accessions by using approximately 180,000 (180K) single nucleotide polymorphisms (SNPs) developed in previous study. In addition, we performed genetic diversity and population structure analysis to construct the core collection from entire 4,400 collections. A good core collection has to conserve as much variation, such as phenotypic or genotypic, has no redundant accession included in the core, and is small enough to be easily manageable size. Therefore, there were excluded sample call rates less than 97% and also were removed duplicate samples more than 99.9% according to genotype analysis using 180K SNPs from total collections. Furthermore, we were also excluded natural hybridization resources of *Glycine max* and *Glycine soja* through population structure analysis. As a result, we are constructed the core collection of genetic diversity that reflects 99% of the entire collections, including 430 cultivated soybeans (*Glycine max*) and 386 wild soybeans (*Glycine soja*). The core collection developed in this study should be to provide useful materials for both soybean breeding programs and genome-wide association studies.

Corresponding Author: Tel. +82-63-238-5324, E-mail: mschoi73@korea.kr

GWAS of primary agronomic characters in *Capsicum* core collection

Jin-Kyung Kwon¹, Hea-Young Lee¹, Koeun Han¹, Na Young Ro², On-Sook Hur², Ho-Cheol Go² and Byoung-Cheorl Kang^{1*}

¹Department of Plant Science and Vegetable Breeding Research Center CALS, Seoul National University, Seoul 08826, Korea

²National Academy of Agricultural Science, National Agrobiodiversity Center, Rural Development Administration, Jeonju 54874, Korea

Pepper (*Capsicum* spp.) is one of the most popular vegetable that has medicinal and health benefits due to contain secondary metabolites such as capsaicinoid and carotenoid. In order to improve the power of the beneficial effects, many breeders and scientist were effort to figure out related genes or loci to control the diverse phytochemicals. Since the advance of genomics techniques, GWAS (Genome-wide association study) has become the most effective approach for identifying genetic variants associated to interested traits. For *Capsicum* GWAS, we have constructed a core collection as a natural population which can show the huge genetic diversity in reasonable size to control. From 2015, 19 quantitative traits and 4 kinds of secondary metabolites responsible for pungency were evaluated for 2 years. A genotyping-by-sequencing (GBS) approach was used to provide dense genome-wide marker (>9M SNPs) for a 355 pepper core collection. Population structure estimation (PCA and Kinship matrixes), and genome-wide association study (GWAS) based on the compressed mixed linear model were conducted using the R package of Genomic Association and Prediction Integrated Tool (GAPIT). As a result, average 26 SNPs distributed over 12 *Capsicum* chromosomes was identified that have association in each trait. For a validation, the associations were compared with well-known genes and the location of known QTLs which were surveyed from bi-parental population. It showed that, some QTL positions detected by GWAS were overlapped with previously detected QTLs in a parental population. These results will help to understand associations between phenotype and genotype and also will give more power to validate the candidate genes or quantitative trait loci.

*Corresponding Author: Tel. +82-2-880-4563, E-mail: sweettin@snu.ac.kr, bk54@snu.ac.kr

Soybean nested association mapping(NAM) population for novel gene/QTL mass screening

Sung-Taeg Kang^{1*}, Ju-Seok Lee¹, Jung-Kyung Moon², Soo-Kwon Park², Man-Soo Choi², Soon-Chun Jeong³, Namshin Kim⁴, Bo-Keun Ha⁵

¹Department of Crop Science & Biotechnology, Dankook University, Cheonan, 31116, Korea

²National Institute of Crop Science, Rural Development Administration, Jeonju, 54875, Korea;

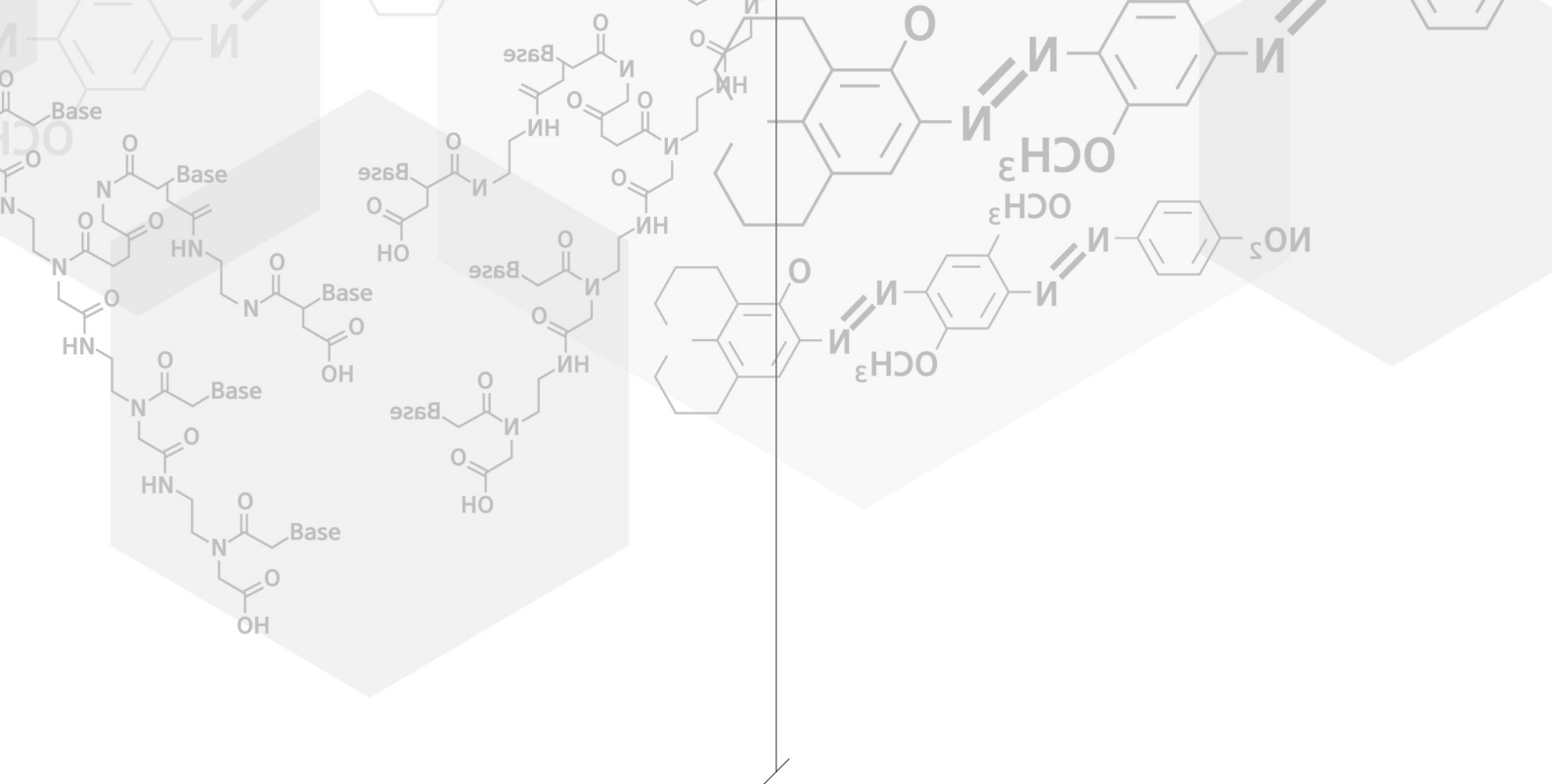
³Bio-Evaluation Center, Korea Research Institute of Bioscience and Biotechnology, Cheongju 28116, Korea

⁴Korean Bioinformation Center, Korea Research Institute of Bioscience and Biotechnology, Daejeon 34141, Korea,

⁵Division of Plant Biotechnology, Chonnam National University, Gwangju 61186, Korea

Recent achievements in plant genomics by the development of high throughput sequencing technology have produced large amount of genomic data in soybean [*Glycine max* (Merr.) L.] and therefore, new gene identification strategies were employed to identify the quantitative/qualitative traits loci. A number of soybean cultivars for wide-range of purpose have been traditionally developed in Korea using broad range of germplasm including wild soybeans, since Korea is a center of origin in soybean. We developed Nest Associated Mapping (NAM) population to identify the useful genes and QTLs through fast and accurate high throughput procedure with Korean cultivars and germplasm. To develop the NAM population, the elite variety, Daepoong, was used as Hub parents and total 27 cultivars and lines were selected as parents in considering application-specific characteristics, such as physiological characteristics, polymorphism in DNA markers, cross combination, and desired characteristics for specific utilities. The selected parents and Hub parent were artificially crossed, and total about 3,000 lines of F₇ (or F₆) were developed using single seed descent. The genotyping for parents and NAM lines was conducted using the state-of-the-art Axiom® 180K SoyaSNP array which is selected from more than four million high-quality SNPs identified from genome re-sequencing of 47 soybean accessions. The result showed that gene architecture can be disclosed with identification of the entire major and minor QTLs for flowering. The proposed NAM population could be very useful for further identification of agronomically important QTLs and genes. NAM population in soybean genomics could provide opportunity to discover the novel genes/QTLs for various traits for sustainable crop breeding.

*Corresponding Author: kangst@dankook.ac.kr



GSP 채소종자사업단 & GSP 원예종자사업단

일시 2017년 7월 7일(금), 09:00 ~ 10:40

장소 대구 엑스코

주관 GSP채소종자사업단 & GSP원예종자사업단



하늘초 품종 육성

박용주*, 이문호

경기도 안성시 미양면 갈전리 바이오통육종연구소

하늘초 고추(erect type)는 강신미 고추로 주로 아시아지역에서 재배되는 품종 군에 속한다. 재배면적은 80만ha~100만ha이며 아시아 고추재배면적의 약 40%에 달하는 주요 segment이다. 하늘초 품종 군에는 단화방하늘초, 복화방하늘초, 탄두형(볼)하늘초 등 크게 3개의 subgroup로 나뉘며 이 중 단화방하늘초와 복화방하늘초는 CGMS를 이용하여 F1품종이 보급되어 재배되고 있으나 탄두형(ball)하늘초는 아직 일반종(재래종)으로 재배되고 있어서 내병성이 약하고 수량성이 낮다. 탄두형하늘초는 주로 중국남부지역 및 동남아시아에서 주로 재배되며 이 들 지역은 온도가 높고 강수량이 많아 바이러스 및 역병 발생이 심하여 병저항성 품종 요구가 높은 실정이다. 탄두형하늘초의 과는 가공용(염장) 및 건과용의 과 형태로 유통되어 매운소스 등으로 이용되고 있다. 본 연구과제에서는 탄두형(ball) 일반종 소재(유전자원)를 이용하여 최초로 CGMS F1탄두(ball)형 신품종 육성연구를 수행하였다. 수집된 육종 소재는 MAS와 재배시험을 통하여 원예적인 형질과 내병성(역병, 바이러스) 평가를 수행하였으며 교배를 통하여 유전분석을 실시하고 이들 재료들을 활용하여 다양한 B-line(유지친:maintainer)계통과 이를 이용한 음성불임(MS) A-line 계통, C-line(임성 회복친:Rf) 계통을 육성하였다. 육성된 계통들은 F1예비조합능력 평가를 통하여 엘리트계통을 선발하였으며 선발된 F1조합은 현지 연락시험을 통해 최종 상품화 하였다.

*주저자: E-mail: yjpark0226@hanmail.net

고추 나출 소포자 배양을 이용한 정상 자엽배 생산 및 반수체와 배가반수체의 배수성 검증

박은준*, 양은영, 채수영, 문지혜, 박태성, 김옥례, 김대영, 이선이, 김상규

농촌진흥청 국립원예특작과학원 원예작물부 채소과

종자 수출시장 확대 및 수출액 증대를 위해서는 각 목표 시장 별 우수한 형질을 가진 자원의 보유 여부가 매우 중요하다. 우리나라에서 고추 육종에 활용되어온 유전자원은 변이의 폭이 제한적이며, 수출시장이 다원화 되면서 다양한 형질의 계통이 필요한 실정이다. 우수 유전자원을 고정시키고, 육종연한 단축을 위해서는 배가반수체 생산 기술이 요구된다. 본 연구는 실용적인 고추 소포자 배양기술을 확립하기 위해 모식물의 생육 시 광도 및 생육기간이 소포자배 발생 및 발달에 미치는 영향과, 원예적 특성 분석을 통해 반수체/배가반수체의 배수성을 검증하였다. 그 결과 모식물은 저광도에서 단기간 생육 시 소포자배 발생 효율이 높았고 정상자엽배의 발생이 가장 많았다. 모식물 생육 환경을 완전하게 제어할 수 없는 조건에서 광도조절과 생육 기간을 달리하는 간단한 방법을 통해 소포자 배발생을 크게 증가시킬 수 있었다. 소포자 유래의 배를 완전한 식물체로 생육 후 배수성 검증을 실시하였다. 총 208개의 식물체를 분석한 결과 반수체는 89개체, 배가반수체는 119개체로 재분화된 식물체는 반수체 또는 배가반수체이었다. 정확한 분석을 위해 잎조직의 염색체 유동분석과 식물체의 원예적 특성분석을 실시하였다. 반수체와 배가반수체의 특성을 조사한 결과 배가반수체는 모식물과 유사한 경향이었고, 반수체의 경우에는 모든 항목에서 왜소한 특성을 보였으며, 특히 잎과 열매의 크기는 유의성 있게 작았다. 표현형에 따른 반수체와 배가반수체 분석은 염색체 유동분석방법과 동일한 결과를 나타냈다. 반수체/배가반수체 발생 비율은 밀양재래 품종의 경우 35.6%, LV2319 품종의 경우 72.7%로 두 배 이상 차이가 났다. 소포자 유래의 배가반수체의 효율이 높은 품종의 경우에는 직접적으로 육종에 이용할 수 있으나, 효율이 낮은 품종은 콜히친 처리 후 이용할 수 있다. 이와 같은 결과들은 고추의 소포자 배양시스템을 확립하는데 기초자료가 될 것이며, 향후 반수체 육종프로그램에 활용하는데 유용하게 이용될 수 있을 것이다.

*주저자: Tel. 063-238-6613, E-mail: ejpark97@korea.kr

아시아 시장 공략을 위한 오리엔탈 백합 품종 개발

최강준

강원도 춘천시 충열로 83, 강원도농업기술원 원예연구과

나리(백합)는 *Lilium*속의 화훼 식물로 북반구에 130여종이 자생하고 있는 세계 4대 화훼 작목중 하나이다. 꽃의 형태는 6장의 꽃잎으로 이루어져 있고 종자와 구근으로 번식하는 영년생의 구근 화훼 식물이다. 대부분의 원종이 한국, 중국, 일본 등 동아시아를 원산지라고 있으나 상업적으로 유통되는 품종은 네덜란드를 중심으로 개발되어 세계적으로 유통되고 있다. 과거 백합의 세계적인 시장은 유럽, 미국, 일본이 주요 시장이었으나 최근 중국, 베트남에서 화훼 소비가 급격히 증가하고 있어 아시아에서의 백합 화훼 시장이 확대되고 있다. 오리엔탈 나리는 꽃의 크기가 가장 크고 화려하며 꽃의 향기와 절화 수명이 길어 화훼 시장에서 가장 많이 유통되고 있다. 이러한 흐름에 맞추어 강원도농업기술원에서는 2001년부터 동아시아 시장을 목표로 Oriental hybrid 품종 개발에 집중하여 추진하고 있으며 2013년부터는 수입되는 백합 품종 대체와 수출 확대를 위해 골든씨드 프로젝트에 참여하고 있으며 특히 아시아 시장 공략을 위한 오리엔탈 품종 개발을 위해 프로젝트를 수행하고 있다.

강원도농업기술원에서는 아시아 시장 공략을 위한 백합 품종 개발을 위해 4가지 전략을 갖고 품종 육성을 추진하고 있다. 첫번째는 동아시아의 기후에 적합한 품종 개발을 목표로 추진하고 있다. 기존 품종이 해양성 기후의 네덜란드에서 개발되어 유럽의 기후에는 적합하지만 동아시아에서는 기후적인 차이로 인해 품질 저하 문제가 발생하고 있어 동아시아 기후에 적합한 품종 개발을 목표로 품종 육성을 추진하고 있다. 두번째는 유럽인과 아시아인의 미적 감각이 다른 점에 착안을 두어 아시아인의 미학적 관점으로 화색과 화형의 품종 개발을 추진하고 있다. 세번째는 품종 개발 기간을 단축하여 신속한 품종 개발 시스템을 구축하여 시장의 트렌드 변화에 빨리 적응할 수 있도록 하였다. 마지막으로 네덜란드는 적절한 환경제어가 되는 온실을 이용 상자재배로 절화 생산이 이루어지고 있지만 일본을 비롯한 아시아는 대부분 토경 재배로 생산되고 있다. 아시아 지역의 토경 재배에 보다 적응할 수 있고 그러한 환경에서도 일정한 품질을 유지하는 품종 개발을 추진하고 있다. 현재 160여 계통과 7품종이 개발되었으며 아시아 시장 현지 적응을 위해 중국, 베트남, 몽골 등 아시아 지역에서의 개발 품종의 특성을 검토하고 있으며 아시아 시장 구근 수출을 위한 수출 루트를 개발하고 있다.

주저자: Tel. 033-248-6078, E-mail: biockj87@korea.kr

원예작물의 분자마커 개발 및 통합 지원체계 구축

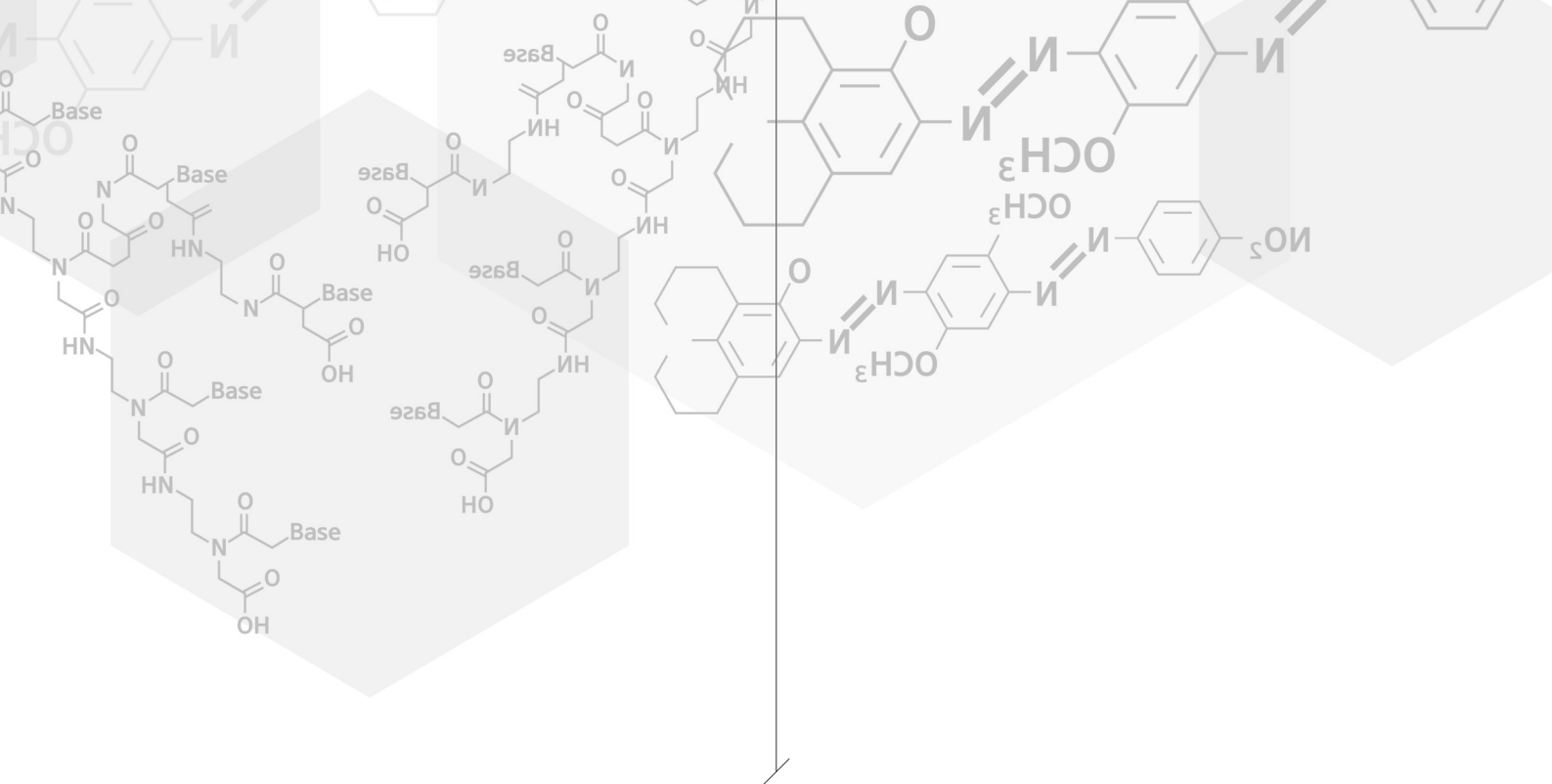
박종인, 김희택, 노일섭*

순천대학교 원예학과

최근 종자 생산에 있어서 교잡, 선발 등을 이용한 전통육종뿐만 아니라 분자유종 기술의 중요성이 급격히 커지고 있는 실정이다. MAS (Marker-assisted selection) 기술은 목표형질의 유전자를 기반으로 개체를 선발함으로써 전통육종의 단점을 보완하여 우량개체 선발효율을 극대화시킴과 동시에 육종연한과 투자비용을 현저히 감소시키므로 종자산업계에서는 우위 경쟁력 확보를 위해서는 필수적인 기술로 인식되고 있다. 그러나 현재 국내 종묘회사들 중 마커를 자체적으로 개발하여 활용할 수 있는 회사는 극히 일부 회사를 제외하고는 없는 실정이다. 또한 육종가들은 분자마커에 대한 필요성은 인식하고 있으나 국내에서 적용 가능한 분자마커들의 종류, 선발 효율성, 특성 등이 객관적으로 파악되고 정리되지 않아 그 활용은 극히 미미한 실정이다. 따라서, 국내 원예작물의 MAS 기술 지원을 가속화하기 위해서는 종묘회사들에서 필요로 하는 형질별 요구도를 명확히 분석 한 후, 빠른 시간내에 종묘회사들에서 요구하는 형질별 분자마커 서비스가 이루어져야 한다. 그러기 위해서는 신규로 개발이 필요한 분자마커 개발 연구와 더불어 전 세계 연구자들이 이미 개발하여 발표한 다수의 원예작물 분자마커들의 정보들을 수집하여 실용성을 검토한 후 실용성이 확인된 분자마커들은 즉시 종묘회사들에 분자마커 서비스가 이루어져야 한다.

본 발표에서는 수집된 정보들을 이용한 분자마커 개발 및 새롭게 개발되고 있는 양배추의 뿌리혹병(CR), 검은썩음병(BR), EP1 system을 이용한 자가불화합성 S-genotype 구분용 chip 개발, 양파의 순도검정용 마커개발, 토마토의 MABC (Marker-assisted backcrossing)용 chip개발 등의 현재 개발하고 있는 연구내용들에 대하여 소개하고, 본 연구실에서 수행하고 있는 분자마커 서비스 현황에 대하여 발표하고자 한다.

*교신저자: T. 061-750-3249, E-mail: nis@sunchon.ac.kr



2017년 한국육종학회 학회상 시상



2017년 한국육종학회 학회상 시상

○ 일시 및 장소 : 2017년 7월 6일(목), 17:40

○ 시상내용

1. 농우육종학회상

- 수상자 최봉호(전 충남대학교 교수)
- 선정사유 국내 재래종 찰옥수수를 다수 수집하고 적극적으로 개량하여 대한민국 찰옥수수 품질육종의 지평을 연 찰옥수수 「연농1호(일명 대학찰)」을 육성·보급하고, 교단에서는 작물육종의 중요성 일깨우고 젊은 육종가를 배출하는 등 농가 소득증대와 인재양성에 크게 공헌

2. 한국육종학회-연구상

- 수상자 1 이정동(경북대학교 농업생명과학대학)
- 논문제목 Reaction of Soybean Cyst Nematode Resistant Plant Introductions to Root-Knot and Reniform Nematodes (Plant Breeding and Biotechnology 2015, 3: 346-354)
- 수상자 2 이종열(국립농업과학원 농업생명자원부 생물소재공학과)
- 논문제목 국내 밀 품종의 오메가5-글리아딘 (Gli-B1) 유전자좌 분석 (한국육종학회지, 2016, 48: 159-167)
국내 밀 품종의 글리아딘 및 Spa 유전자 평가 (한국육종학회지, 2016, 48: 206-216)

3. 코레곤품종상

- 수상자 류수노(한국방송통신대학교)
- 품종명 슈퍼자미 [벼 품종 품종보호 제4151호 (2012. 10. 17)]

4. 한국육종학회-품종상

- 수상자 이준설 (국립식량과학원 바이오에너지작물연구소)
- 품종명 풍원미(Pungwonmi) 품종등록번호: 6428
(고구마(*Ipomoea batatas* (L.) Lam.))

5. 우수논문상 다피인용부문

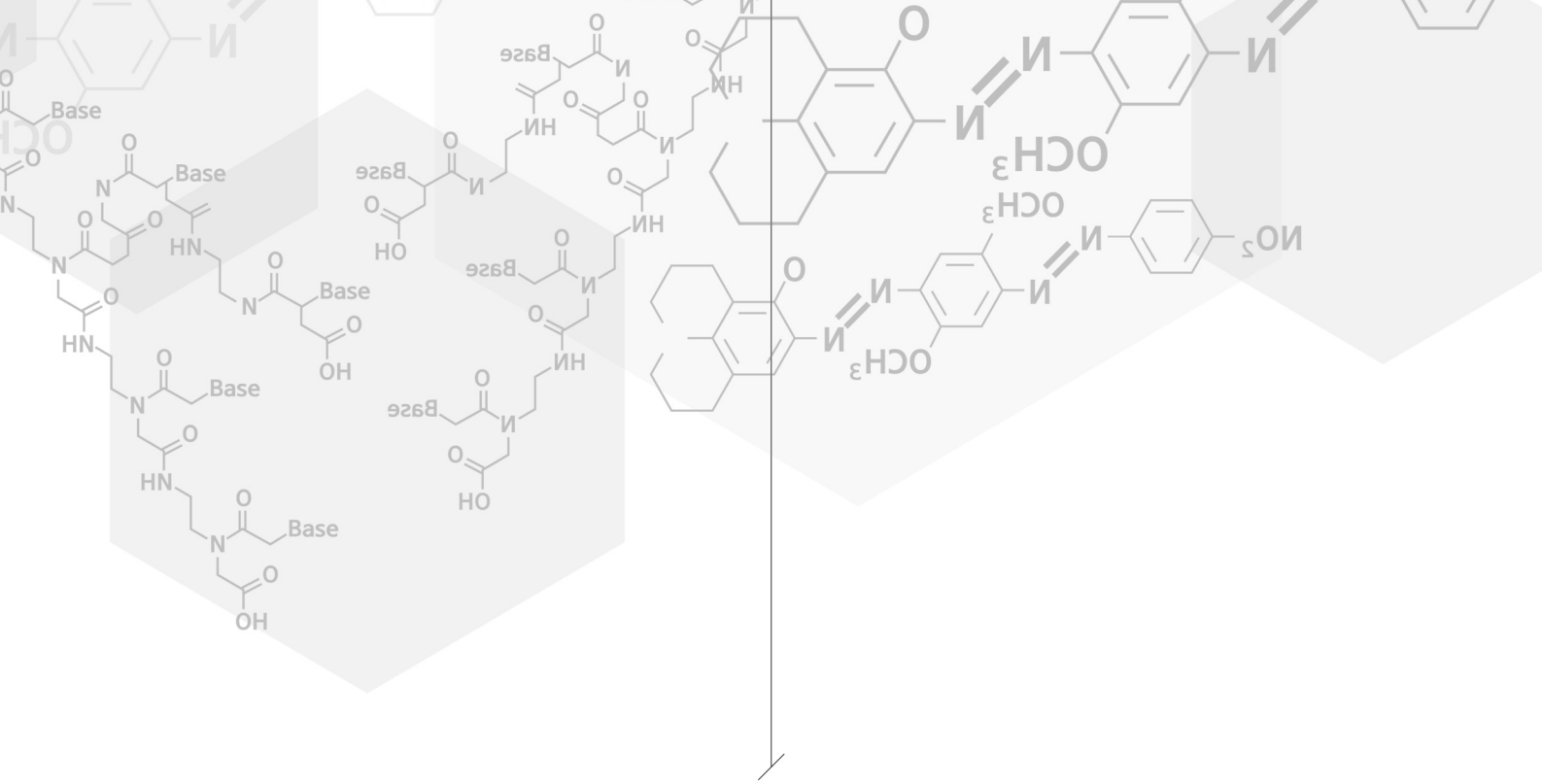
- 수상자(1) 박동수 (국립식량과학원 남부작물부)
- 논문제목 기능성 흑찰거대배아미 조생종 벼 품종 ‘눈큰흑찰’ (한국육종학회지, 2015, 47(1): 68-74)
- 수상자(2) 최홍규 (동아대학교 생명자원과학대학)
- 논문제목 Soybean [*Glycine max* (L.) Merrill]: Importance as A Crop and Pedigree Reconstruction of Korean Varieties (Plant Breeding and Biotechnology 2015, 3(3), 179-196)

6. 우수논문상 다수논문게재부문

- 수상자(1) 정지웅 (국립식량과학원 답작과)
- 수상자(2) 노일섭 (순천대학교 생명산업과학대학)

7. 한국육종학회 공로상

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인쇄처 교보문고 (070-8854-5572)

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