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2021년 한국육종학회 공동학술발표회

디지털 농업 시대에 직면한
식물 육종의 현재와 미래

Current status and future prospects of plant breeding confronting the era of digital agriculture

일시	2021년 6월 30일(수)~7월 2일(금)
장소	라마다플라자 제주호텔, www.breeding.or.kr
주최	사단법인 한국육종학회
공동주관	GSP 식량종자사업단, 신육종기술실용화사업단, 농촌진흥청 포스트게놈다부처유전체사업단, 농업기술실용화재단 종자산업진흥센터, 국립산림과학원, 서울대학교 식물유전체육종연구소
후원	농촌진흥청, 한국농식품생명과학협회, 한국과학기술단체총연합회, 제주컨벤션뷰로

한국육종학회
The Korean Society of Breeding Science

사단법인 한국육종학회 The Korean Society of Breeding Science

2021년 한국육종학회 조직위원회

위 원 장	**총괄**	이주경(강원대학교)
	학회장	양태진(서울대학교)
	공동	정진철(GSP 식량종자사업단), 정영희(신육종기술실용화사업단), 안병옥(농촌진흥청 포스트게놈다부처유전체사업단)
총괄총무	**위원**	이정동(경북대학교)
기획분과	**위원장**	최익영(강원대학교)
	위원	진중현(세종대학교), 김창수(충남대학교)
재무분과	**위원장**	이강섭(국립농업과학원)
	위원	정종욱(충북대학교), 조영일(농업기술실용화재단), 이종렬(국립농업과학원)
국제협력분과	**위원장**	강병철(서울대학교)
	위원	성동렬(LG화학), 조영득(한국원자력연구원)
홍보분과	**위원장**	강성택(단국대학교)
	위원	심성철(세종대학교), 이성우(충남대학교), 김경도(명지대학교)
대외협력분과	**위원장**	문중경(국립농업과학원)
	위원	강규석(서울대학교), 이만규(㈜월드그린), 서상현(한국농어민신문), 김종택(㈜윕스)
산학협력분과	**위원장**	윤재복(㈜고추와 육종)
	위원	조유현(㈜시드피아), 정운화(㈜코레곤종묘), 조성환(㈜씨더스)
학술분과	**위원장**	김성길 (전남대학교)
유전체분과	**위원**	강양제(경상대학교), 전태환(부산대학교)
분자육종분과	**위원**	김혜란(강원대학교), 정기홍(경희대학교)
작물육종분과	**위원**	모영준(국립식량과학원), 김재윤(공주대학교)
원예육종분과	**위원**	이준대(전북대학교), 김도선(국립원예특작과학원)
특용, 산림육종분과	**위원**	심동환(충남대학교), 조광수(국립식량과학원 남부작물부)
표현체분과	**위원**	정용석(제주대학교), 김경환(국립농업과학원)
분자표지분과	**위원**	하보근(전남대학교), 이주석(서울대학교 생명공학공동연구원)
신진연구자	**위원**	장철성(강원대학교), 유수철(한경대학교)

2021년 한국육종학회 임원

회장	양태진(서울대학교)		
차기회장	이주경(강원대학교)		
부회장	강병철(서울대학교), 강성택(단국대학교), 김성길(전남대학교), 김인식(국립산림과학원 산림생명자원연구부),		
	문중경(국립식량과학원), 박철수(전북대학교), 안경구(농업기술실용화재단), 윤재복((주)고추와 육종),		
	이강섭(국립농업과학원), 이우문(국립원예특작과학원 원예작물부), 이점호(국립식량과학원 작물육종과),		
	이효연(제주대학교), 최익영(강원대학교), 하선화(경희대학교)		
KJBS 편집위원장	권순욱(부산대학교)	**KJBS 편집위원**	김재윤(공주대학교)
PBB 편집위원장	이주현(건국대학교)	**PBB 편집위원**	박순주(원광대학교)
감 사	노재환(국립식량과학원 바이오에너지작물연구소), 김진백(한국원자력연구원)		
사무총장	이정동(경북대학교)		

한국육종학회지 사무국

경기도 수원시 권선구 수인로 126 국립식량과학원 중부작물부 내 (16429)
전화 031-296-6898, 팩스 031-292-0804, koreabreed@hotmail.com

- 한국육종학회지 홈페이지 www.koreabreedjournal.org에서 논문검색 및 파일다운로드를 할 수 있습니다.
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- 본 학회사무와 학회지에 관련되는 모든 문서는 학회사무국으로 등기우송바랍니다.

“이 학술지는 정부재원(과학기술진흥기금 및 복권기금)으로 한국과학기술단체총연합회의 지원을 받아 출판되었음.”
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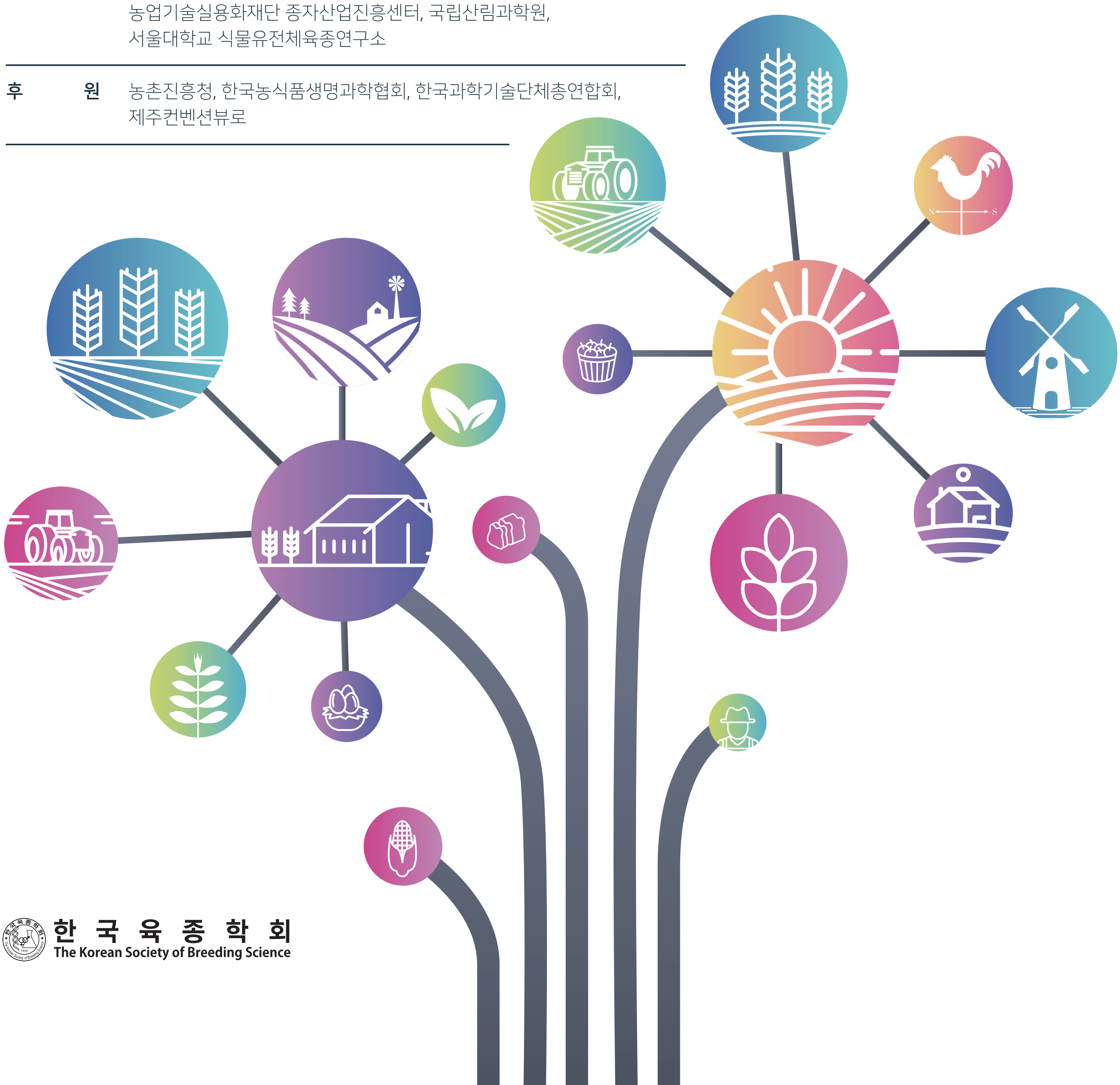
주최	사단법인 한국육종학회
공동주관	GSP 식량종자사업단, 신육종기술실용화사업단, 농촌진흥청 포스트게놈다부처유전체사업단, 농업기술실용화재단 종자산업진흥센터, 국립산림과학원, 서울대학교 식물유전체육종연구소
후원	농촌진흥청, 한국농식품생명과학협회, 한국과학기술단체총연합회, 제주컨벤션뷰로



한 국 육 종 학 회
The Korean Society of Breeding Science

[개 회 사]

(사)한국육종학회는 2021년 정기 학술대회를 6월 30일부터 7월 2일까지 제주시 라마다호텔에서 농촌진흥청과 공동으로 “디지털 농업 시대에 직면한 식물 육종의 현재와 미래”라는 주제로 개최하고자 합니다.

이번 학술대회는 Plenary Session 6분의 연자 그리고 Concurrent Session 8개 분과(Genome Sequence & Genomics, Gwas and Allele Mining, High Throughput Genotyping & Phenotyping, New Breeding Technology, Breeding for Major Crops, Breeding for Horticultural Crops, Genetic Resources & Special Crops, Young Breeding Scientist) 32분의 국내 및 국외 연자 그리고 5 minute talks와 poster 발표를 통해 디지털 농업시대에서 우리나라 육종 산업의 발전 방향을 찾아가는 계기를 마련해 보고자 합니다.

적극적인 참여와 질문을 통해 성공적인 학술대회가 되고 앞으로 더욱 발전하는 한국육종학회가 되기를 기원합니다.

지난해부터 시작된 코로나19 장기화로 회원 여러분의 건강과 안전을 위하여 2021 한국육종학회 학술발표회를 오프라인과 온라인 방식으로 병행하여 개최하기로 하였습니다. 회원 여러분의 많은 관심과 참여를 부탁드립니다.

조직위원장 이주경 드림

[환 영 사]

안녕하세요. 한국육종학회장 양태진입니다.

2년째 지속되는 코로나 팬데믹 터널을 뚫고 새로운 희망의 씨앗이 피어나고 있습니다. 2021년 한국육종학회 학술발표회를 통해 디지털농업시대에 직면한 식물육종의 미래를 설계하고 한국육종학회의 발전을 도모하고자 합니다. 48명의 초청연자님들께 감사합니다. 어려운 여건에서도 약 500명의 회원이 대면/비대면으로 참여하시고 404개의 구두 및 포스터 발표를 해주십니다. 디지털 육종은 미래를 위한 분명한 방향이지만 올바른 방향정립을 위해서는 학계의 지속적인 관심과 노력이 필요할 것이라 생각합니다.

학회 발전을 위해 물심양면 도와주신 회원님들과 공동주관 및 후원 기관에 감사드립니다. 축사를 해주신 허태웅 농촌진흥청장님 감사합니다. 이번 육종학회의 주제가 디지털농업과 디지털육종을 논하고 있는데, 농촌진흥청에서도 디지털육종 TF 팀을 운영하며 미래 10년의 디지털육종 기반 구축을 기획하고 있는데 이에 대해서도 응원을 보냅니다.

명예로운 한국육종학회상을 수상하시는 회원님들 진심으로 축하드리며 학회 발전에 애써주셔서 감사합니다. 특히 학회의 발전을 위해 큰 상금을 제공해주신 시드피아, 월드그린, 농우종묘, 코레곤종묘 대표님들께 진심으로 감사드립니다.

한국육종학회의 발전을 위해 지속적인 관심과 응원 부탁드리며 한국육종학회지와 Plant Breeding and Biotechnology 에도 좋은 논문 게재 및 인용 부탁드립니다.

한국육종학회장 양태진 드림

[축 사]

(2021. 7. 1(목), 한국육종학회 학술발표회)

반갑습니다. 농촌진흥청장 허태웅 입니다.

먼저, 2021년 한국육종학회 학술발표대회 개최를 진심으로 축하드립니다. 또한 어려운 여건에서도 학술대회 개최를 위해 헌신하신 양태진 회장님을 비롯한 한국육종학회 회원 관계자 여러분의 노고에 감사 말씀을 드립니다.

최근 우리나라 농업을 둘러싼 상황은 녹록하지 않습니다. 농경지 감소를 비롯해 농촌인구가 줄어들고 고령화됨에 따라 농업 생산력 저하가 우려되고 있습니다. 최근에는 이상기상, 돌발 병해충 발생 및 코로나19 장기화로 안정적 식량 확보가 위협받고 있습니다.

농업은 우리 국민들의 먹을거리를 책임져온 전통산업이자, 국가 성장 동력이 될 미래산업입니다. 이러한 식량안보 산업인 농업의 핵심 열쇠는 우수한 종자의 개발과 확보에 있다고 생각합니다.

과거 녹색혁명을 통한 주곡의 자급자족 달성과 백색혁명을 통한 사계절 신선한 농산물 생산 성공도 결국 종자의 개발로 가능했습니다. 현재는 기능성 식품, 의약품, 바이오 산업소재 산업으로 종자의 활용 범위가 확대되고 있습니다. 이러한 트렌드를 반영하듯 세계 종자 시장을 두고 다국적 기업, 중국, 네덜란드 등 주변 국가들은 사활을 건 경쟁을 벌이고 있습니다.

우리나라도 글로벌 차원의 종자주권 확보를 통한 식량안보 기반을 마련하기 위해서 다각적인 노력을 기울이고 있습니다. 기존 전통육종 및 생명공학기술에 빅데이터, 인공지능 등의 4차 산업혁명 기술이 융・복합된 디지털 육종기술을 개발하여 실용적이며 효율적인 품종개발 전략을 세워야 할 시점입니다.

이에 농촌진흥청에서는 지난 3월 데이터를 기반으로 한 과학영농의 실현, 지속가능한 농업의 구현을 위해 ‘디지털농업 촉진 기본계획’을 수립하였습니다.

디지털 육종 기반기술을 강화하기 위해 다양한 농생명 자원에 대한 정보를 디지털화하고, 원하는 육종형질에 대한 예측모델 개발, 인공지능(AI)을 이용한 우수한 계통을 선발할 수 있는 디지털 육종 지원 플랫폼을 구축해 신품종 개발에 활용할 계획입니다.

이러한 디지털 육종기술의 발전 및 생태계 조성을 위해서는 정부와 민간 등 종자관련 산・학・연의 적극적인 협업이 요구됩니다. 또한 디지털 육종 기술의 확산은 기후변화, 포스트 코로나, 디지털 농업 등을 대비하며 미래 지속 가능한 농업을 만드는 핵심 역할을 하리라고 확신합니다.

이런 점에서 한국육종학회 학술발표 주제인 ‘디지털 농업 시대에 직면한 식물 육종의 현재와 미래’는 시의적절하며 매우 의미 있다고 생각합니다.

아무쪼록 이번 학술대회가 많은 과학자분들의 연구개발 결과를 공유하는 자리가 되고, 이를 토대로 우리나라 육종연구가 전환점을 맞는 계기가 되길 기대합니다.

끝으로 한국 농업 연구의 정통성을 잇는 한국육종학회 학술발표회 개최를 다시 한 번 진심으로 축하드리며, 학회의 무궁한 발전을 기원합니다.

농촌진흥청장 허 태 웅

2021 공동학술발표회 일정

행사 진행방식에 따라 일정이 변경될 수 있습니다.

2021년 6월 30일(수)	
17:00~18:00	확대이사회 및 조직위원회의

2021년 7월 1일(목)	그랜드 볼룸 홀
10:00~10:30	대면등록
10:30~12:00	1. 한국육종학회 정기총회 * 현장&생중계 발표 2. 한국육종학회 학회상 시상 - 농우육종학회상, 한국육종학회-연구상, 코레곤품종상, 한국육종학회-품종상 - 월드그린시드피아 육종상(2020년, 2021년), - 월드그린시드피아 젊은육종가상(2020년, 2021년)
13:00~13:10	개회식 * 현장&생중계 발표 사회 : 이정동 교수 (사무총장, 경북대학교) 개회사 - 이주경 교수 (조직위원장, 강원대학교) 환영사 - 양태진 교수 (회장, 서울대학교) 축 사 - 허태웅 농촌진흥청 청장
	기조발표 [Plenary Session]
	좌장: 강시용 (공주대학교)
13:10~13:50	PS-01 고희종 (서울대학교) Plant breeding strategies for modern digital agriculture
13:50~14:30	PS-02 문중경 (국립식량과학원) 유전체육종을 넘어서 디지털육종 시대를 촉진하기 위한 계획
14:30~15:10	PS-03 조승호 (국립식량과학원) 디지털세대가 꿈꾸는 한국종자산업의 미래 (The future of our seed industry and agriculture revolutionized by digital technologies: A key to make it real)
15:10~15:30	휴 식
	좌장: 서용원 (고려대학교)
15:30~16:10	PS-04 이정동 (경북대학교) Breeding strategy for improvement of omega-3 fatty acid in soybean
16:10~16:50	PS-05 최규하 (포항공과대학교) Control of meiotic crossovers for plant breeding
16:50~17:20	PS-06 윤재복 ((주)고추와 육종) 전통육종과 분자육종 접목을 통한 고추 탄저병 저항성 및 복합내병성 품종 육성
17:20~17:50	PS-07 최근진 (국립종자원) 육종가 권리보호는 종자산업과 농업발전의 원동력
on-line 발표	1. 구두 발표 (Oral & Poster presentation 5분 talk 발표) * on-line 홈페이지 게시 2. 포스터 발표 (Poster presentation)

2021년 7월 2일(금)

	분과발표 [Concurrent Session] 1부	* 현장&생중계 발표
09:30~11:40	A. Genome Sequence & Genomics H. Young Breeding Scientist	그랜드볼룸1 & zoom1
	C. High Throughput Genotyping & Phenotyping D. New Breeding Technology	그랜드볼룸2 & zoom2
	E. Breeding for Major Crops F. Breeding for Horticultural Crops	그랜드볼룸3 & zoom3
	G. Genetic Resources & Special Crops	그랜드볼룸4 & zoom4

	특별발표 [Special Session]	* 현장발표
10:00~11:40	SA. Breeding for Woody Plants	그랜드볼룸 4
11:10~12:40	SB. 「디지털육종 전환지원사업」을 통한 첨단육종기술 확산	그랜드볼룸 2

	분과발표 [Concurrent Session] 2부	* 녹화방송 on-line 발표
13:00~15:00	A. Genome Sequence & Genomics	
	B. Gwas and Allele Mining	
	C. High Throughput Genotyping & Phenotyping	
	D. New Breeding Technology	
	E. Breeding for Major Crops	
	F. Breeding for Horticultural Crops	
	G. Genetic Resources & Special Crops	
	H. Young Breeding Scientist	
15:00	폐회식	

2021년 7월 5일(월)

10:00	우수발표상 발표	* on-line 홈페이지 게시

2021년 공동학술발표회 분과발표 (Concurrent Session)

분과발표 [Concurrent Session] 1부

* 현장&생중계 발표

	CS-A. Genome Sequence & Genomics	그랜드볼룸 1 & zoom 1
		좌장: 강양제(경상대학교), 전태환(부산대학교)
09:30~10:00	CA-01 하정민 (강릉원주대학교) Identification of genetic and epigenetic factors associated with synchronous pod maturity in mungbean using a near-complete reference genome sequence	
10:00~10:30	CA-02 이세현 (서울대학교) Draft genomes of three Apocynaceae and proposals for customized functional plant breeding	

	CS-H. Young Breeding Scientist	그랜드볼룸 1 & zoom 1
		좌장: 장철성(강원대학교), 유수철(한경대학교)
10:40~11:10	CH-01 윤진석 (고려대학교) Functional analysis of wheat ASR gene under environmental stresses	
11:10~11:40	CH-02 고윤실 (경희대학교) Optimization of crop yield using root-preferred promoter by improving Phosphate use of efficiency in rice	

	CS-C. High Throughput Genotyping & Phenotyping	그랜드볼룸 2 & zoom 2
		좌장: 정용석(제주대학교), 김경환(국립농업과학원)
09:30~10:00	CC-01 강병철 (서울대학교) High-throughput SNP marker set for genomic selection	

	CS-D. New Breeding Technology	그랜드볼룸 2 & zoom 2
		좌장: 김혜란(강원대학교), 정기홍(경희대학교)
10:00~10:30	CD-01 김유진 (부산대학교) Revealing key factors for rice pollen tube growth by CRISPR-Cas9	
10:30~11:00	CD-02 윤재영 (서울대학교) C-to-G Base Editing Induces Enhancement of Oleic Acid Production by Generating Novel Alleles of *FATTY ACID DESATURASE 2* in Plants	

분과발표 [Concurrent Session] 1부

* 현장&생중계 발표

	CS-E. Breeding for Major Crops	그랜드볼룸 3 & zoom 3
		좌장: 모영준(국립식량과학원), 김재윤(공주대학교)
09:30~10:00	CE-01 이종렬 (국립농업과학원) Precision Breeding Strategy for Development of Hypo-allergenic Wheat Through Multi-omics Study of Gluten Genomic Region	
10:00~10:30	CE-02 박현수 (국립식량과학원) 국내 최대재배 신동진 벼 형질 개선을 위한 육종사업	

	CS-F. Breeding for Horticultural Crops	그랜드볼룸 3 & zoom 3
		좌장: 이준대(전북대학교), 김도선(국립원예특작과학원)
10:40~11:10	CF-01 이상협 (세종대학교) QTL-seq analysis of disease resistance in a Korean cucumber inbred	
11:10~11:40	CF-02 임선형 (한경대학교) Deciphering the Anthocyanin Biosynthetic Mechanism in Horticultural Crops	

	CS-G. Genetic Resources & Special Crops	그랜드볼룸 4 & zoom 4
		좌장: 심동환(충남대학교), 조광수(국립식량과학원)
09:30~10:00	CG-01 김성업 (국립식량과학원) Identification of Candidate Genes for Non-dehiscent Capsule in Sesame(*Sesamum indicum* L.) via cross-population association analysis with whole genome re-sequencing	

분과발표 [Concurrent Session] 2부

* 녹화방송 on-line 발표

	CS-A. Genome Sequence & Genomics
13:00~13:30	CA-03 이태호 (국립농업과학원) 새로운 육종 패러다임 디지털육종, 도전과 응전
13:30~14:00	CA-04 유의수 (DNACARE) Integrated breeding platform for the data driven crop improvement
14:00~14:30	CA-05 김봉성 (QTLmax Global, USA) QTLmax: a genomic analytical pipeline for digital breeding

	CS-B. Gwas and Allele Mining
13:00~13:30	CB-01 선호근 (부산대학교) New statistical selection method to identify pleiotropic variants associated with both quantitative and qualitative traits
13:30~14:00	CB-02 이상범 (국립농업과학원) QTLs identification for arsenic in rice using genome-scale profiling and high-throughput analyses
14:00~14:30	CB-03 오상근 (충남대학교) Development of molecular marker sets associated with disease resistance in grapes
14:30~15:00	CB-04 송종태 (경북대학교) A component of post-transcriptional gene silencing in soybean affects seed coat color variation

	CS-C. High Throughput Genotyping & Phenotyping
13:00~13:30	CC-02 장성율 (한국원자력연구원) Forecasting biomass of plant with high throughput phenotyping platform (HTPP) and beyond
13:30~14:00	CC-03 김창수 (충남대학교) Genotype-by-Sequencing and its application to crop breeding
14:00~14:30	CC-04 Marcus Jansen (Lemnatec) Digital assistants for breeders' eyes: AI-based technologies for phenotypic analyses

분과발표 [Concurrent Session] 2부

* 녹화방송 on-line 발표

	CS-D. New Breeding Technology
14:00~14:30	CD-03 이양석 (University of Warwick, England) Crop yield improvement via manipulation of meristem initiation in wheat and rice
14:30~15:00	CD-04 배상수 (한양대학교) Current Status and Challenges of Genome Editing Tools in Plants

	CS-E. Breeding for Major Crops
13:00~13:30	CE-03 임성돈 (상지대학교) Engineering crassulacean acid metabolism to improve water-use efficiency.
13:30~14:00	CE-04 조성우 (경남과학기술대학교) Development of perennial wheat through wide hybridization mediated chromosome engineering

	CS-F. Breeding for Horticultural Crops
14:00~14:30	CF-03 안세웅 (국립원예특작과학원) 이미지 기반 채소 모종 생육 정보 수집과 육종 연구 활용 방안
14:30~15:00	CF-04 이혜은 (국립원예특작과학원) 채소 유전체 정보 기반의 초고속 대량 분자마커세트 개발 및 활용

	CS-G. Genetic Resources & Special Crops
13:00~13:30	CG-02 Linhai Wang (Chinese Academy of Agricultural Sciences) Genomic study showed insight to molecular basis of the high oil content and black sesame
13:30~14:00	CG-03 김창수 (충남대학교) Analysis of genes associated with salinity using trascriptomic information in *Sorghum bicolor*

	CS-H. Young Breeding Scientist
14:30~15:00	CH-03 김주희 (강원대학교) A rice really interesting new gene H2-type E3 ligase, OsRFPH2-23, contributes to salt tolerance
15:00~15:30	CH-04 장수 (서울대학교) Detection of QTLs controlling adaxial leaf rolling to achieve ideal plant type in rice

2021년 공동학술발표회 특별발표 (Special Session)

A. Breeding for Woody Plants

* 현장발표, 그랜드 볼룸 4

좌장: 어수형(공주대학교)

10:00~10:40	SA-01	강규석 (서울대학교) Forest Reclamation integrated with Tree Breeding in the Republic of Korea
10:40~11:10	SA-02	심동환 (충남대학교) Development of SNP chip for Genomic Selection of Korean Red Pine (*Pinus densiflora*) Trees
11:10~11:40	SA-03	최명석 (국립경상대학교) 국내 조림 권장 7수종의 복합내재해성 검정

좌장: 이현석(안동대학교)

11:40~12:10	SA-04	이경미 (국립산림과학원) Tree Improvement Research Using Information and Communication Technology
12:10-12:40	SA-05	정은주 (강원대학교) Analysis of genetic relationships of Pyrus pyrifolia native to Korea using SSR markers
12:40-13:10	SA-06	강준원 (경북대학교) 휘발성 유기화합물(VOCs) 저감 기능성 임목 개발을 위한 식물내생 미생물의 이용

B. 「디지털육종 전환지원사업」을 통한 첨단육종기술 확산

* 현장발표, 그랜드 볼룸 2

좌장: 정기홍 (경희대학교)

11:10-11:40	SB-01	정영민 (농업기술실용화재단) 디지털육종 전환지원사업 개요 및 운영방향
11:40-12:10	SB-02	조성환 (씨더스) 디지털육종전환지원사업에서 생물정보기업의 역할 및 제공 서비스
12:10-12:40	SB-03	이상춘 (파이젠) 디지털육종을 위한 생물정보분석 서비스 소개

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(G) Genetic Resources & Special Crops

(H) Young Breeding Scientist

Special Session A Breeding for Woody Plants

Special Session B 「디지털육종 전환지원사업」을 통한 첨단육종기술 확산

2021 한국육종학회 학회상 시상

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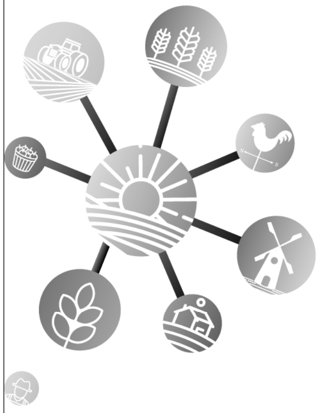
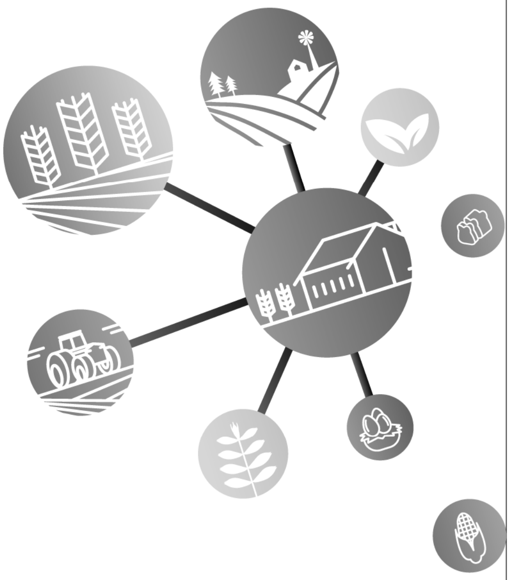
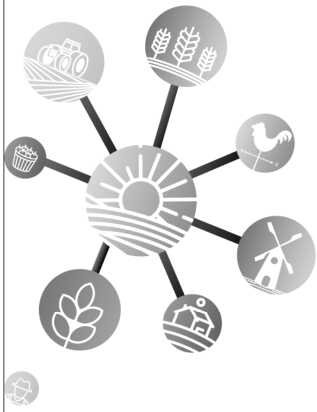


Plenary Session





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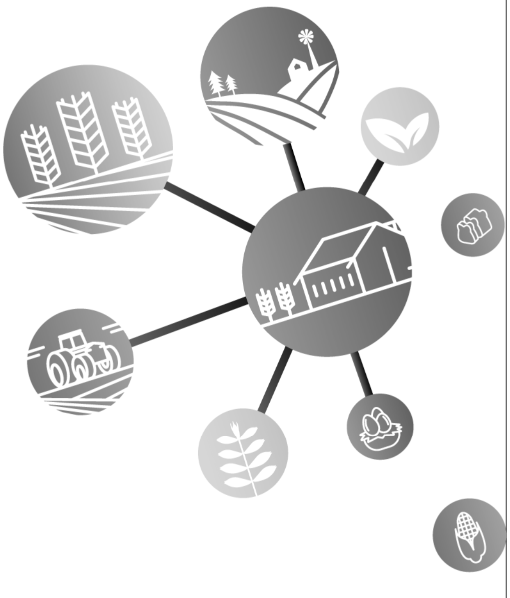

고희종(Hee-Jong Koh)

Position: Professor
Institution: Seoul National University, College of Agriculture and Life Sciences
Address: Seoul
Phone: 02-880-4541
E-mail: heejkoh@snu.ac.kr

<Research Interests>

1. Rice breeding and genetics
2. Plant molecular breeding

<Education>

1. 1980. Seoul National University, BSc
2. 1990. Seoul National University, PhD

<Professional Experience>

1. 1992~present: Professor, Seoul National University
2. 2011~2020: Director, Plant Molecular Breeding Center
3. 2010: President, Korean Society of Breeding Science

<Selected Publications> (Up to 10)

1. Z. Jin, J. Seo, B. Kim, S. Y. Lee, H.J. Koh (2021) Identification of a Candidate Gene for the Novel Cytoplasmic Male Sterility Derived from Inter-Subspecific Crosses in Rice (*Oryza sativa* L.). Genes 12(4):590. doi: 10.3390/genes12040590
2. B. Kim, R. Piao, G. Lee, E. Koh et al. (2021) *OsCOP1* regulates embryo development and flavonoid biosynthesis in rice (Oryza sativa L.) TAG, doi: 10.1007/s00122-021-03844-9
3. S. Jang, S. Shim, Y.K. Lee, D. Lee, H.J. Koh (2021) Major QTLs, *qARO1* and *qARO9*, Additively Regulate Adaxial Leaf Rolling in Rice. Front Plant Sci. doi: 10.3389/fpls.2021.626523
4. C. Lee, W.J. Hong, K.H. Jung, H.C. Hong et al. (2021) Arachis hypogaea resveratrol synthase 3 alters the expression pattern of UDP-glycosyltransferase genes in developing rice seeds. PLoS One 16(1):e0245446. doi: 10.1371/journal.pone.0245446.
5. S. Zhao, S. Jang, Y.K. Lee, D.G. Kim et al (2020) Genetic Basis of Tiller Dynamics of Rice Revealed by Genome-Wide Association Studies. Plants 9: 1695; doi:10.3390/plants9121695
6. S. Jang, Y.S. Kang, Y.K. Lee, H.J. Koh (2020) Evaluating Multiple Allelic Combination to Determine Tiller Angle Variation in Rice. http://dx.doi.org/10.3390/agriculture10100428
7. J. Seo, S.M. Lee, J.H. Han, N.H. Shin, Y.K. Lee et al. (2020) Characterization of the Common Japonica-Originated Genomic Regions in the High-Yielding Varieties Developed from Inter-Subspecific Crosses in Temperate Rice (Oryza sativa L.). http://dx.doi.org/10.3390/genes11050562
8. Y. Yu, M.O. Woo, R. Piao, H.J Koh (2020) The *DROOPING LEAF* (*DR*) gene encoding GDSL esterase is involved in silica deposition in rice. PLoS One 15(9): e0238887, https://doi.org/10.1371/journal.pone.0238887
9. J. Seo, G. Lee, Z. Jin, B. Kim et al (2020) Development and application of indica-japonica SNP assays using the Fluidigm platform for rice genetic analysis and molecular breeding. Mol Breeding 40:39
10. D.S. Kishor, J. Seo, J.H Chin, H.J. Koh (2020). Evaluation of Whole-Genome Sequence, Genetic Diversity, and Agronomic Traits of Basmati Rice (*Oryza sativa* L.). Trends in Genetics https://doi.org/10.3389/fgene.2020.00086

PS-0001

Plant breeding strategies for modern digital agriculture

Hee-Jong Koh*

College of Agriculture and Life Sciences, Seoul National University 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Republic of Korea

Digital agriculture refers to the use of digital technologies to integrate agricultural production from the paddock to the consumer, for which diverse types of varieties are required. To meet the varietal demands for digital agriculture, both precision and speed in plant breeding are fundamental needs. Plant breeding is currently facing a new era with innovative developments in biotechnology, genomics and phenomics. Under a new paradigm of plant breeding in the 21st century, breeders try to create new variations through direct manipulation of target genes and/or alleles instead of hybridization and phenotypic selection. Genetic resources are extended to the unrelated species through transgenic technologies overcoming the sexual limit for gene transfer. Selection and genetic fixation in the progeny can be performed by monitoring genes and genomic information by which modern breeders can develop new varieties precisely and quickly. Recent progress in understanding of meiosis and genetic recombination may facilitate for breeders to harmoniously recombine desirable genes/alleles into a target genotype. All of these technologies can be summed up into 'Digital breeding'. However, in order to routinely apply the state-of-the-art technologies to plant breeding, some points should be considered: 1) Genes and genomic information for target traits should be clearly understood. 2) Data for genomics and phenomics should be largely shared among breeders. 3) Legal restrictions against biotechnological tools for plant genetic improvement should be mitigated to accommodate modern technologies. Advancement and limitations of modern technologies and its application to actual plant breeding will be discussed.

***Corresponding Author:** Tel. 02-880-4541, E-mail: heejkoh@snu.ac.kr

문중경(Jung-Kyung Moon)

Position: 국립식량과학원 작물기초기반과장
Institution: 농촌진흥청 국립식량과학원
Address: 전북 완주군 이서면 혁신로 181
Phone: 063-238-5300
E-mail: moonjk2@korea.kr

<Research Interests>

1. 콩, 팥, 녹두 육종 (Legume breeding)
2. 콩 유전체육종 (Soybean breeding by genomics)

<Education>

1. 서울대학교 농생명과학대학 농학과 박사 (2005)
2. 서울대학교 농생명과학대학 농학과 석사 (1998)

<Professional Experience>

1. 차세대바이오그린21사업 농생물게놈활용연구사업단장 (2016~2021)
2. 국립식량과학원 작물기초기반과장 (2021~현재)

<Selected Publications> (Up to 10)

1. The patterns of deleterius mutations during the domesticaton of soybean. Narure Comm. 2021. 12(9): 1-14
2. High Throughput Phenotyping for Various Traits on Soybean Seeds Using Image Analysis. Sensors 2020. 14(10): 1-16.
3. Genetic diversity patterns and domestication origin of soybean. TAG. 2019. 132(4: 1179-1193.
4. GmBRC1 is a Candidate Gene for Branching in Soybean [*Glycine max* (L.) Merr.] Intern. of Mol. Sci. 2019. 20(1): 135-149.
5. Korean soybean core collection: Genotypic and phenotypic diversity population structure and genome-wide association study. Plos One 2019. 14(10): 1-16.

PS-0002

유전체육종을 넘어서 디지털육종 시대를 촉진하기 위한 계획

박수철[1], 조우석[1], 권수진[2], 이우문[3], 김도선[3], 윤호백[4], 최태정[4], 최만수[5], 문중경[5*]

[1]전북 전주시 덕진구 농생명로 370 국립농업과학원 농업생명자원부
[2]전북 전주시 완산구 농생명로 300 농촌진흥청 연구정책국
[3]전북 완주군 이서면 농생명로 100 국립원예특작과학원
[4]충남 천안시 서북구 성환읍 신방1길 국립축산과학원
[5]전북 완주군 이서면 혁신로 181 국립식량과학원

NGS 기술의 작물 및 가축 집단유전학으로의 도입과 IT 기술에 의한 빅데이터 분석을 위한 다양한 알고리즘의 개발 및 응용은 농축산 육종 및 개량에서 전통육종 및 가축개량의 육종효율 증가가 가능해지고 있다. 또한 작물 및 가축의 이미지 및 센서 장치의 도입은 환경 변이 및 표현형의 정확한 측정방법은 그동안 환경분산의 잔차를 최소화하는 기술적 진보를 이룩하고 있어서 이제는 유전체, 전사체, 단백체, 이온체, 표현체 등의 모든 정보가 디지털화하여 육종 프로그램에서 활용이 가능한 시대에 도달해 있다.

따라서, 유전체 육종 연구결과를 리뷰하고, 그 결과를 바탕삼아서 우리나라 작물 및 가축의 디지털 육종의 시대를 준비하기 위한 국가적 종합전략을 마련하는 것이 매우 시의 적절하다고 판단된다.

이에, 식량작물, 원예작물, 가축개량 및 디지털 육종을 지원할 수 있는 기반 연구에 대해서 농촌진흥청이 준비하고 있는 디지턱육종 추진계획에 대해서 논의를 하고자 한다.

***Corresponding Author:** Tel. 063-238-5300, E-mail: moonjk2@korea.kr

조승호(Seungho Cho)

Position: 부장
Institution: 국립식량과학원 중부작물부
Address: 경기도 수원시 권선구 수인로126
Phone: 010-9653-2530
E-mail: seunghocho@korea.kr

<Research Interests>

1. 식량작물 유전/육종 기술
2. 종자생산체계 및 품질관리 기술
3. 농업데이터과학의 실용화
4. 연구사업 전략 및 연구관리 최적화 기술

<Education>

1. 고려대학교 산림자원학과, 학사
2. 고려대학교 산림유전 및 생태학, 석사
3. 고려대학교 산림유전 및 생태학 박사과정수료
4. Washington State University Genetics & Cell Biology, 박사

<Professional Experience>

1. 국립식량과학원 중부작물부 부장 (2019년 4월 ~ 현재)
2. 국립식량과학원 고령지농업연구소 전문연구원 (2018년 7월 ~ 2019년 4월)
3. Monsanto Company 목화분자육종 연구사업총괄 (2010년 10월 ~ 2017년 10월)
4. BASF DNA Analysis 연구실장 (2006년 10월 ~ 2010년 9월)
5. Department of Agronomy and Plant Genetics, University of Minnesota. Post-doc (2003년 9월 ~ 2006년 9월)
6. 한솔제지기술원 환경육종연구소 연구원 (1995년 7월 ~ 1998년 12월)

<Selected Publications>

1. 이유영, 강문석, 김진숙, 조승호, 이병원, 김미향, 김현주, 이진영 디지털랩 연구데이터 관리 시스템(수확소재분야) 2020년 10월 13일 저작권 등록 제 C-2020-034973호
2. 강인정, 정건호, 노태환, 이석기, 강문석, 조승호, 최종서, 이대우, 양운호, 연구정보 이력 및 데이터 관리시스템「디지털데이터북」 2021년 04월 05일 저작권 등록 제 C-2021-015212호
3. 전원태, 조승호, 신명나, 이지현, 심강보, 구본일, 가압 마찰식 방법을 이용한 인공지능형 논 잡초 관리 로봇 2021.03.30. 특허출원번호 10-2021-0041239
4. 전원태, 조승호, 이지현, 신명나, 심강보, 수송형 드론과 멀티콥터의 협업을 이용한 저공비행 전용 살포기 2021.03.30. 특허출원번호 10-2021-0041241
5. 전원태, 조승호, 이지현, 신명나, 심강보, 밭작물 잡초관리를 위한 인공지능 가변 복합형 경운 로봇 2021.03.30. 특허출원번호 10-2021-0041240

PS-0003

디지털세대가 꿈꾸는 한국종자산업의 미래

조승호*

경기도 수원시 권선구 수인로 125 국립식량과학원 중부작물부

다양한 식량작물의 안정적인 생산과 보급유통의 체계화를 통해서 지난 반세기동안 우리가 달성한 식량안보와 국가발전과정은 국제사회에서도 매우 중요한 성공사례로 높이 평가받고 있다. 혁신적인 농업과학 기술체계의 개발과 보급을 통해서 관행농업을 디지털데이터산업으로 탈바꿈시키려는 우리의 노력이 결실을 맺기 위해서 과학적 논리에 근거한 새로운 규칙의 발견과 기존에 없었던 창의적 관계 구축이 필요하다. 종자산업을 포함한 농업전반에 걸친 디지털화는 농업과학의 고도화를 촉진할 뿐만 아니라 농촌경제의 안정화를 가속화할 것이다. 민관협력을 통해서 신기술의 농업현장 확대적용을 가속화하고 있으며, 이를 통해서 제2의 녹색혁명의 초석이 마련될 것으로 기대한다.

***교신저자:** Tel. 031-695-4001, E-mail: seunghocho@korea.kr

이정동(Jeong-Dong Lee)

Position: Professor
Institution: Dept. of Applied Biosciences, Kyungpook National Univeristy
Address: Daehakro 80, Bukgu, Daegue 41566
Phone: 053-95-05709
E-mail: jdlee@knu.ac.kr

<Research Interests>

1. Development of soybean varieties for application in various industry
2. Improving genetic potential of soybean by mapping, combining QTLs or genes, and genome data analysis

<Education>

1. Ph.D. Kyungpook Nat'l Univ., Daegu, Republic of Korea (1998-2002)
2. M.S. Kyungpook Nat'l Univ., Daegu, Republic of Korea (1996-1998)

<Professional Experience>

1. Professor; Kyungpook National University (10/01/2018 to present)
2. Assistant and Associate Professor; Kyungpook National University (09/01/2009 to 09/30/2018)
3. Post Doc. and Research Scientist; University of Missouri-Columbia (02/01/05 to 08/31/2009)

<Selected Publications> (Up to 10)

1. Hyun Jo, Minsu Kim, Hyeontae Cho, Bo-Keun Ha, Sungtaeg Kang, Jong Tae Song, and Jeong-Dong Lee. 2021. Identification of a Potential Gene for Elevating ω-3 Concentration and Its Efficiency for Improving the ω-6/ω-3 Ratio in Soybean. J. Agric. Food Chem. 69:3836-3847.
2. Hyun Jo, Ji Yun Lee, Hyeontae Cho, Hong Jib Choi, Chang Ki Son, Jeong Suk Bae, Kristin Bilyeu, Jong Tae Song and Jeong-Dong Lee. 2021. Genetic Diversity of Soybeans [*Glycine max* (L.) Merr.] with Black Seed Coats and Green Cotyledons in Korean Germplasm. Agronomy, 11:581.
3. Liakat Ali 1,2, Hyun Jo 1, Jong Tae Song 1 and Jeong-Dong Lee. 2021. The Prospect of Bentazone-Tolerant Soybean for Conventional Cultivation. Agronomy, 10:1650
4. Rupesh T, Kulkarni KP, Jo H, Song JT, Lee JD. 2019. Insight into the Prospects for the Improvement of Seed Starch in Legume—A Review. Front. Plant Sci. 10:1213.
5. Jo H, Kim M, Ali L, Tayade R, Jo D, Thao D, Phommalth S, Ha B-K, Kang S, Song JT, Lee JD. 2020. Environmental Stability of Elevated α-Linolenic Acid Derived from a Wild Soybean in Three Asian Countries. Agriculture. 10:70.
6. Lee DH, Kulkarni KP, Kim BO, Seok YM, Song JT, Lee JD. 2019. Comparative assessment of quality characteristics of Chungkookjang made from soybean seeds differing in oleic acid concentration. J. Functional Foods 52:529-536.
7. Park CW, Kulkarni KP, Kim M, Mukaiyama K, Tsukamoto C, Chung G, Song JT, Lee JD. 2018. Characterization of an EMS-induced soybean mutant with an increased content of Af saponin and a new component Ab-δ in the seed hypocotyl. Euphytica. 214:163.
8. Kulkarni KP, Tayade R, Asekova S, Song JT, Shannon JG, Lee JD. 2018. Harnessing the Potential of Forage Legumes, Alfalfa, Soybean, and Cowpea for Sustainable Agriculture and Global Food Security. Frontiers in Plant Sci. 9:1314.
9. Kulkarni, KP, Patil G, Valliyodan B, Vuong TD, Shannon JG, Nguyen HT, Lee JD. 2018. Comparative genome analysis to identify SNPs associated with high oleic acid and elevated protein content in soybean. Genome. 61: 217-222.
10. Jeong JE, Kulkarni KP, Chang JH, Ha BK, Kang ST, Bilyeu K, Jo H, Song JT, Lee JD. 2018. A Novel Allele of GmSACPD-C Associated with High Seed Stearic Acid Concentration in an EMS-Induced Mutant PE980 in Soybean. Crop Sci. 58:192-203.

PS-0004

Breeding strategy for improvement of omega-3 fatty acid in soybean

Jeong-Dong Lee*

Dept. of Appliec Biosciences, Kyungpook National Univeristy, Daegu 41566, Republic of Korea

Increasing alpha-linolenic acid (ALA, omega-3) in soybean [Glycine max (L.) Merr] seed oil is an important breeding goal in soybean because of its beneficial effects on human health. Commodity soybean oil generally has 8-9% omega-3 in contrast, wild soybeans have almost twice (15%) the omega-3 concentration. Although wild soybean has more genetic diversity than cultivated soybean, it is difficult to use wild soybean as a genetic resource because of several poor agronomic traits, and studies revealed that wild soybeans have multiple genes for regulation high omega-3 concentration. We identify a novel candidate gene that contributes to the elevated omega-3 concentration in a EMS mutant. Through fine mapping, NGS analysis and recombinant analysis a potential gene, Glyma.05g221500, controlling elevated omega-3 concentration was identified. Glyma.05g221500 is a homeodomain-like transcriptional regulator (HD) that may regulate the expression level of FAD3 genes responsible for the conversion of linoleic acid into ALA in the fatty acid biosynthetic pathway. In addition, we hypothesized that a combination of mutant alleles, and either of microsomal delta-12 fatty acid desaturase 2-1 (FAD2-1) could reduce the ω-6/ω-3 ratio. In populations where HD, FAD2-1A, and FAD2-1B genes were segregated, a combination of a hd allele from mutant and either of the variant FAD2-1 alleles was sufficient to reduce the ω-6/ω-3 ratio in seeds ratio in seeds. The discovery of this new mutant allele contributes to both increased ω-3 and a reduced ω-6/ω-3 ratio in soybean seed oil.

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

최규하(Kyuha Choi)

Position: Associate Professor
Institution: Pohang University of Science and Technology
Address: 77 Cheongam-Ro, Nam-Gu, Pohang, Gyeongbuk, 37673, Republic of Korea
Phone: 054-279-2361
E-mail: kyuha@postech.ac.kr

<Research Interests>

1. Control of meiotic crossover recombination in plants
2. Mechanism of meiotic DSB formation in plants

<Education>

1. Ph.D. Plant developmental genetics, Seoul National University, Korea (2007)
2. M.S. Plant molecular physiology, Seoul National University, Korea (2002)
3. B.S. Crop sciences, Seoul National University, Korea (1988)

<Professional Experience>

1. 2021-Present: Associate Professor, Department of Life Sciences, POSTECH
2. 2017-2021: Assistant Professor, Department of Life Sciences, POSTECH
3. 2016-2017: Research Professor, Gyeongsang National University
4. 2010-2016: Postdoctoral Researcher, University of Cambridge, UK

<Selected Publications> (Up to 10)

1. Divyashree C. Nageswaran*, Jaeil Kim*, Christophe Lambing, Juhyun Kim, Jihye Park, Eun-Jung Kim, Hyun Seob Cho, Heejin Kim, Dohwan Byun, Yeong Mi Park, Pallas Kuo, Seungchul Lee, Andrew J. Tock, Xiaohui Zhao, Ildoo Hwang, **Kyuha Choi*** and Ian R. Henderson* (**2021**) *HIGH CROSSOVER RATE1* encodes PROTEIN PHOSPHATASE X1 and restricts meiotic crossovers in Arabidopsis. ***Nature Plants 7, 452-467***
2. Eun-Cheon Lim, Jaeil Kim, Jihye Park, Eun-Jung Kim, Juhyun Kim, Yeong Mi Park, Hyun Seob Cho, Dohwan Byun, Ian R Henderson, Gregory P Copenhaver, Ildoo Hwang and **Kyuha Choi** (**2020**) DeepTetrad: high-throughput image analysis of meiotic tetrads by deep learning in Arabidopsis thaliana. ***Plant Journal*** 101, 473-483
3. **Kyuha Choi**, Xiaohui Zhao, Andrew J. Tock, Christophe Lambing, Charles J. Underwood, Thomas J. Hardcastle, Heïdi Serra, Juhyun Kim, Hyun Seob Cho, Jaeil Kim, Piotr A. Ziolkowski, Nataliya E. Yelina, Ildoo Hwang, Robert A. Martienssen and Ian R. Henderson (**2018**) Nucleosomes and DNA methylation shape meiotic DSB frequency in Arabidopsis transposons and gene regulatory regions. ***Genome Research 28, 532-546***
4. **Kyuha Choi***, Xiaohui Zhao*, Krystyna A Kelly, Oliver Venn, James D Higgins, Nataliya E Yelina, Thomas J Hardcastle, Piotr A Ziolkowski, Gregory P Copenhaver, F Chris H Franklin, Gil McVean and Ian R Henderson (**2013**) *Arabidopsis* meiotic crossover hot spots overlap with H2A.Z nucleosomes at gene promoters. ***Nature Genetics* 45, 1327-1336**

PS-0005

Control of meiotic crossovers for plant breeding

Kyuha Choi*

Department of Life Sciences, Pohang University of Science and Technology, Pohang, Gyeongbuk, Republic of Korea

During meiosis, homologous chromosomes pair and undergo reciprocal genetic exchange, called crossover. Crossovers have a profound effect on genetic diversity and are a critical process during crop improvement, generating new allele combinations. Meiotic crossovers are tightly restricted between one and three along chromosomes in most eukaryotes, which is a main bottleneck for plant breeding. The majority of plant crossovers are dependent on class I interfering repair pathway, with a minority formed via the class II non-interfering pathway. Class II crossover is limited by three anti-recombination pathways; however, similar pathways repressing class I crossovers have not been identified. We performed a forward genetic screen in *Arabidopsis* using fluorescent crossover reporters to identify *high crossover rate* (*hcr*) mutants. We identified new anti-crossover factors HCR1, HCR2 and HCR3 as repressing class I crossovers. Using genetic, cytological analyses, genome wide crossover mapping and high-throughput fluorescence reporter assays we revealed that HCR1 and HCR3 restrict crossover number by controlling protein phosphorylation and protein interactions with pro-crossover factors in class I pathway while HCR2 represses transcription of *HEI10* encoding a meiotic E3 ligase that promotes crossover formation in a dosage dependent manner. Our findings provide insights into how HCR anti-crossover factors limit class I interfering crossovers. In addition, genetic disruption of *HCR* genes will help to accelerate diverse plant breeding and mapping of desirable quantitative trait loci.

***Corresponding Author:** Tel. 054-279-2361, E-mail: kyuha@postech.ac.kr

윤재복(Jae-Bok Yoon)

Position: President & CEO
Institution: Pepper & Breeding Institute
Address: 196-15, Hajeong-ro, Gimje-si 54324, Republic of Korea
Phone: +82-10-2120-5797
E-mail: jaebokyoon@hanmail.net

<Research Interests>

1. Conventional and molecular breeding
2. Genetic resources and interspecific cross
3. Breeding for horticultural crops including chili pepper

<Education>

1. Ph.D. in Horticultural Science, Seoul National University (2003)
2. M.S. in Horticultural Science, Seoul National University (1999)
3. B.S. in Horticulture, Kangneung National University (1996)

<Professional Experience>

1. Director of R & D Unit in Pepper & Breeding Institute (2005-2007)
2. Post-doctoral fellow in the Center for Plant Molecular Genetic and Breeding Research of Seoul National University (2003-2005)

<Selected Publications> (Up to 10)

1. Park D, Barka GD, Yang EY, Cho MC, Yoon JB, Lee J (2020) Identification of QTLs controlling α-glucosidase inhibitory activity in pepper (*Capsicum annuum* L.) leaf and fruit using genotyping-by-sequencing analysis. *Genes* 11:1116.
2. Kim H, Yoon JB, Lee J (2017) Development of Fluidigm SNP type genotyping assays for marker-assisted breeding of chili pepper (*Capsicum annuum* L.). *Hort Sci Technol* 35:465-479.
3. Eun MH, Han JH, Yoon JB, Lee J (2016) QTL mapping of resistance to the *Cucumber mosaic virus* P1 strain in pepper using a genotyping-by-sequencing analysis. *Hort Environ Biotechnol* 57:589-597.
4. Lee J, Park SJ, Hong SC, Han JH, Choi D, Yoon JB (2016) QTL mapping for capsaicin and dihydrocapsaicin content in a population of *Capsicum annuum* ‘NB1’ × *Capsicum chinense* ‘Bhut Jolokia’. *Plant Breeding* 135:376-383.
5. Lee YR, Yoon JB, Lee J (2016) A SNP-based genetic linkage map of *Capsicum baccatum* and its comparison to the *Capsicum annuum* reference physical map. *Mol Breeding* 36:61.
6. Park HS, Lee J, Lee SC, Yang TJ, Yoon JB (2016) The complete chloroplast genome sequence of *Capsicum chinense* Jacq. (Solanaceae). *Mitochondrial DNA Part B* 1:164-165.
7. S.C. Hong, J-H. Han, J. Lee, Y.K Ahn, E-Y. Yang, S.Y. Chae, S. Kim and J.B. Yoon. (2013) A simple and fast microplate method for analysis of carotenoids contents in chili pepper. Kor. J. Hort. Sci. Technol. 31:807-811.
8. J. Lee, S.J. Park, J.W. Do, J.-H. Han, D. Choi, and J.B. Yoon. (2013) Development of a genetic map of chili pepper using single nucleotide polymorphism markers generated from next generation resequencing of parents. Kor. J. Hort. Sci. Technol. 31(4):473-482.
9. J. Lee, J.-H. Han, and J.B. Yoon. (2012) A set of allele-specific markers linked to *L* locus resistant to *Tobamovirus* in *Capsicum* spp. Kor. J. Hort. Sci. Tecnol. 30(3):286-293.
10. S.H. Soh, A.R. Park, S. Park, K. Back, J.B. Yoon, H.G. Park, and Y.S. Kim. (2012) Comparative analysis of pathogenesis-related protein 10 (PR10) gene between fungal resistant and susceptible peppers. Eur J Plant Pathol. 132:37-48.

PS-0006

전통육종과 분자육종 접목을 통한 고추 탄저병 저항성 및 복합내병성 품종 육성

도재왕[1], 이강현[1], 이준대[2], 윤재복[1*]

[1]전라북도 김제시 백산면 하정로 196-15 ㈜고추와 육종
[2]전라북도 전주시 덕진구 백제대로 567 전북대학교

고추 탄저병은 우리나라 고추 재배에 있어서 가장 심각한 피해를 주고 있는 병해 중에 하나로 매년 1천억 원 이상의 손실을 주고 있으며, 최근에는 CMV와 TSWV(일명 칼라병) 등에 의한 바이러스병 피해와 중복되어 때에 따라서는 50% 이상의 수량 손실을 일으키고 있다. 고추 탄저병 저항성 품종 개발을 위해 우리는 1) 탄저병 저항성 검정 방법 개발 및 유전자원 선발을 위해 지난 1996년부터 세계 각지로부터 1,000여 점 이상의 고추 유전자원을 수집하여 기내 접종을 통해 근연종인 Capsicum baccatum에 존재하는 저항성 자원을 선발하였고 2) 근연종의 저항성을 재배종인 C. annuum으로 도입하기 위한 종간교잡을 수행하였으며 3) 저항성이 도입된 분리집단으로부터 탄저병 주동유전자와 연관된 분자표지를 개발할 수 있었다. 최종 단계로 4) 농가에 보급하기 위한 상용 F1 품종을 개발을 위해 웅성불임을 이용한 모계와 부계를 개발한 후 이들간의 교배조합을 작성하여 탄저병 저항성이면서 원예적 특성이 우수한 조합을 선발하여 농가 실증시험을 통해 세계 최초 고추 탄저병 저항성 품종을 출시하였다. 육종 과정에서 가장 중요한 선발 과정에 있어서 우리는 ㈜고추와 육종에서 개발한 병 저항성(탄저병, 역병, CMV, TSWV 등) 및 웅성불임성 연관 분자표지들을 사용하여 정식 전에 1차 선발하였고 포장에 정식된 수많은 후보 식물체들의 원예적 특성과 병 저항성 정도를 평가하면서 매년 새로운 탄저병 저항성 및 복합내병성 계통들을 선발하고 있다. 또한 개발된 탄저병 저항성 분자표지 및 저항성 계통들을 다른 종자회사에 기술이전 함으로써, 최근에는 다수의 종자회사에서 우수한 탄저병 저항성 및 복합내병성 품종을 농가에 보급하고 있으며 이는 우리나라 종자산업을 한 단계 발전시키는 계기가 되었다고 생각한다.

***교신저자:** Tel. 063-543-0586, E-mail: jaebokyoon@hanmail.net

최근진(Keun-Jin Choi)

Phone: 010-8878-8599
E-mail: kjchoi1001@gmail.com

<Research Interests>

1. 품종보호, 종자산업, 생명산업
2. 신품종육성(옥수수, 고추, 토마토, 메론, 마늘 등)

<Education>

1. 전남대학교 농학과 학사
2. 서울대학교 농학과 석사
3. 서울대학교 농학과 박사

<Professional Experience>

1. 국립종자원 재배시험과장, 서부지원장, 동부지원장
2. 농식품부 종자생명산업과장
3. 농촌진흥청 국립원예특작과학원 채소과장, 국립식량원 전작과

<Selected Publications> (Up to10)

1. 품종보호와 유래품종에 대한 규정. 최근진. 한국육종학회지 30(3) : 317~324
2. 식물신품종 보호권의 효력범위. 한국종자연구회지 5권4호: 57-63. 2008년 12월호. 한국종자연구회.
3. Microsatellilte 마커를 이용한 한국 보리 품종의 유전적 다양성. 한국육종학회지. 43(4): 254-261(2011)
4. 양친품종의 품종보호권 효력범위. 한국종자연구회지 제11(1): 10~14. 2014. 4. 한국종자연구회
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PS-0007

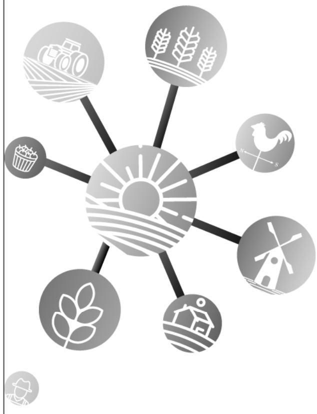
육종가 권리보호는 종자산업과 농업발전의 원동력

최근진*

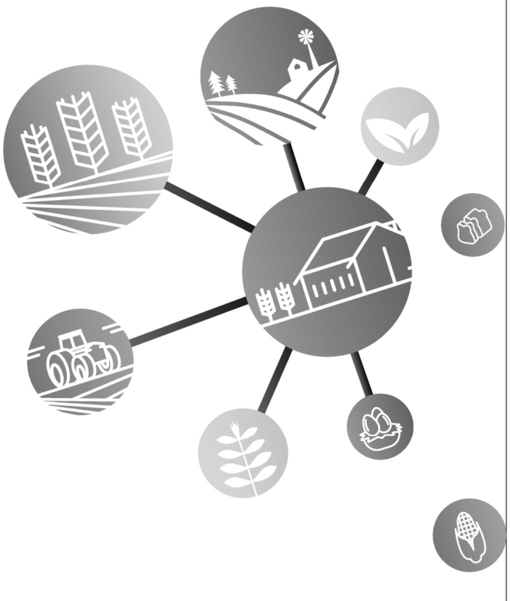
전 국립종자원

종자산업은 영향력이 큰 산업으로 종자수요가 1억원 증가하면 농림수산식품분야에서 1억9280만원 가량의 생산유발효과가 있으며 반대로 종자수요가 1억원 감소하면 전반에 걸쳐 약 4억원의 생산 감소효과가 있는 것으로 나타났다. 이는 종자가 다른 산업의 기초원료로 이용되었고 다른 산업을 견인하고 있다는 의미이다. 종자산업은 품종육성으로부터 시작된다. 우수 품종육성은 육종가의 노력의 산물이다. 육종가의 지속적인 품종육성은 국가나 소속된 조직의 투자와 제도운영에 의해 영향을 받는다. 육종가의 권리보호는 품종육성을 장려하는 제도로 일찍이 유럽에서 시작되었지만 국내에도 1998년에 시작되어 이미 23년째 접어들고 있다. 육종가 권리보호를 위해 실시권, 임시보호권, 육종가의 예외인정(육종재료 이용, 연구 및 실험)을 규정하고 있다. 관련 국제기구인 국제식물신품종보호연맹(UPOV)에 가입한지 20년에 이르고 있고 회원국 중 품종보호출원수로 보면 7~8위에 위치해 있다. 제도도입과 UPOV가입에 따라 국내에는 여러 가지 긍정적인 영향이 나타나고 있다. 우선 국내에는 국외 및 국내육종가로부터 많은 품종이 출원되었다(12,160품종, ‘20.12월말 현재). 이 품종들은 재배하는 농민이나 재배자의 선택권 확장과 함께 소득향상으로 이어졌다. 또 국내 육종가에게는 우수한 육종재료가 되었고 다양한 유전자원 이용을 통해 조기에 우수품종을 육성할 수 있게 된 것이다. 둘째는 국내 육종의 생태계 변화를 들 수 있다. 우수품종 육성에 대한 육성자 간의 경쟁체제가 확립되어 육종수준이 향상되었으며 육성품종의 상업화에 대한 경쟁을 통해 기존 품종들과는 차별성이 있고 독특한 특성을 가진 품종육성, 비슷한 품종개발에 대한 중복투자를 막는 효율적인 육성체계가 확립되었다. 셋째는 국제경쟁력의 향상이다. 국내에서 개발된 우수품종은 다른 나라에도 출원・등록함으로써 활발한 해외시장 진출이 촉진되어 로얄티 수입과 함께 국제 경쟁력이 향상된 점을 들 수 있다. 그러나 제도도입에 따른 부정적인 영향도 있다. 예를 들면, 일부 국내 육종이 열악한 작물에서의 종자가격상승, 국내 진출 외국 종자업체와의 경쟁력 미흡, 제도에 대한 인식미흡으로 인한 권리침해문제 등은 앞으로 규모화 등을 통해 도전해야할 과제이기도 하다.

***교신저자:** E-mail: kjchoi1001@gmail.com



Concurrent Session



CA-0001

Identification of genetic and epigenetic factors associated with synchronous pod maturity in mungbean using a near-complete reference genome sequence

Jungmin Ha[1], Suk-Ha Lee[2*]

[1]Department of Plant Science, Gangneung-Wonju National University, Gangneung, 25457, Republic of Korea
[2]Department of Agriculture, Forestry and Bioresources and Research Institute of Agriculture and Life Science, Seoul National University, Seoul, 08826, Republic of Korea

Mungbean (*Vigna radiata* L.), a fast-growing legume species, is an important source of carbohydrates and proteins in developing countries of Asia. Here, we constructed a near-complete genome sequence of mungbean with a scaffold N50 value of 5.2 Mb and only a 0.4% gap, with a total scaffold size of 475 Mb. We identified several misassembled pseudomolecules (Chr03, Chr04, Chr05 and Chr08) in the previous draft assembly, thus providing more accurate linkage information to breeders. Additionally, using an ultra-high-resolution linkage map constructed based on resequencing data, we identified several quantitative trait loci (QTLs) and the underlying candidate genes affecting synchronous pod maturity (SPM). Mungbean homologs of two soybean flowering genes, *E3* (*Phytochrome A*) and *J* (*Early flowering 3*), were identified as candidate genes for the QTLs, and the candidate genes for plant height, node number and SPM showed critical nucleotide substitutions between the reference cultivar and other genotypes (landraces and wild accessions). To elucidate the epigenetic influences on synchronous pod maturity (SPM) in mungbean, we determined the genome-wide DNA methylation profiles of eight mungbean recombinant inbred lines (RILs) and their parental genotypes, and compared DNA methylation profiles between high SPM and low SPM RILs, thus revealing differentially methylated regions (DMRs). Analysis of these genome-wide DNA methylation profiles suggests that SPM is mediated through gibberellin-mediated hormone signaling pathways. The genetic, genomic and epigenetic information represents an important resource for genome-assisted improvement in the mungbean breeding program.

***Corresponding Author:** Tel. 033-640-2352, E-mail: j.ha@gwnu.ac.kr

CA-0002

Draft genomes of three Apocynaceae and proposals for customized functional plant breeding

Sae Hyun Lee, Jiseok Kim, Eunbi Kim, Padmanaban Mohanan, Yonghyeok Jeong, Seonheui Jeong, Minyoung Lee, Jee Young Park, Tae-Jin Yang*

Department of Agriculture, Forestry and Bioresources, Plant Genomics & Breeding Institute, College of Agriculture & Life Sciences, Seoul National University, 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Korea

Apocynaceae family have diverse functional effects, and many studies have been conducted on pharmaceutical efficiency, metabolic analysis and metabolite biosynthesis pathways. *Cynanchum wilfordii* (Cw), *C. auriculatum* (Ca) and *Metaplexis japonica* (Mj) belonging to the Apocynaceae have long been used as traditional medicines. Many studies of pharmaceutical efficacy have been conducted on these plants as well, but diversity and genomic research are insufficient. We collected Cw germplasm from local farms in Korea and conducted research of morphological and pharmacological diversity of them. As a result of HPLC, concentrations of eight standard compounds were all different within Cw population. In bioassay for testing anti-inflammatory and anti-Alzheimers effect, efficacy of them were all different within individuals and the weight of roots differed by up to five times. Also, we identified 11 pairs of basic chromosome structure including juxtaposition of ribosomal RNA coding genes and 250 Mbp approximate genome sizes of three species. Through the hybrid assembly strategy using Illumina short read and Nanopore long read sequence, we obtained 107, 124, and 333 scaffolds from Cw, Ca, and Mj, respectively, with 99% BUSCO values. Additionally, the scaffolds were organized into 37 groups through scaffold flanking with each other species. Our pharmaceutical and morphological diversity research will provide the potentiality of Cw as the material for the elite cultivar breeding. Also, the draft genomes of three species in the highest quality among the Apocynaceae family will provide basic data for genome research and breeding for undomesticated plants.

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

CA-0003

새로운 육종 패러다임 디지털육종, 도전과 응전

이태호*, 이동준, 함서현

전라북도 전주시 국립농업과학원 농업생명자원부 유전체과, 54874

다양한 기술 발달과 함께 신품종 육종 기술도 관행육종을 시작으로 분자육종을 거쳐 유전체 데이터를 기반으로 하는 유전체 육종에 이르고 있다. 더 나가 인공지능 기술의 발달은 유전체, 대사체, 표현체 등 다양한 농생명 다차원 빅데이터와 함께 차세대 육종 패러다임인 디지털육종 시대를 열어가고 있다. 디지털 육종은 최근 각광을 받고 있는 딥러닝 기술을 바탕으로 개발된 인공지능 모델을 대량의 데이터를 이용하여 훈련, 전문가 시스템을 개발함으로서 인간의 경험이나 이전의 인공지능 기술로는 해결이 어려운 다중형질, 복잡한 양적형질 및 환경 요인을 고려한 선발을 가능케 하고자 한다. 성공적인 디지털육종 시대 개막을 위해서는 크게 3가지 전제 조건(디지털육종 기술 개발, 초고성능 인프라 확보, 다차원 데이터 구축)이 충족되어야 한다. 이에 본 발표에서는 다차원 데이터를 중심으로 성공적인 디지털 육종 실용화를 위해 필요한 내용에 대해 고찰한 내용을 공유하고자 한다.

사사: 본 성과물(구두발표)은 농촌진흥청 연구사업(과제번호 PJ01347301)의 지원에 의해 이루어진 것임

***교신저자:** Tel. 063-238-4558, E-mail: thlee0@korea.kr

CA-0004

Integrated breeding platform for the data driven crop improvement

SeungWook Lee, Sol-Ah Kim, Rachel Park, Yeisoo Yu*

DNACARE, #401 Gangnam-daero 43 gil 17, Seoul, 06730, Republic of Korea

Currently about 200 plant genomes have been sequenced and many more genomes are under way. With those sequenced genome, resequencing or GBS approach allows efficiently collecting sequence information from hundreds of individuals to identify and characterize genetic variations in populations. Coupled with high-throughput phenotyping data, the genetic variations in populations will be used to predict genomic regions where traits of interest are strongly associated. The genetic variation in multiparental population also will be served to identify minor QTLs and even predict genomic estimated breeding value to practice precision breeding using genomic selection (GS) approach. We have kin interests in developing an integrated breeding platform, which breeder can easily use database, analyses pipeline, visualization tools and breeder’s toolbox to perform precision breeding. The platform includes raw data processes, variant analysis pipelines, visualization, GWAS, and all other genome information are interactively worked together in the web-based application along with various handy tools. Five major components (raw data management, variants analysis, SNP browser, GWAS display and marker design) have been designed and modulated. Each of the modules works independently or together in the system in order to make interactive connection between data and analysis results. Therefore this developed platform will take care of vast majority of variants analysis from raw data to GWAS and marker design. The conventional molecular breeding is evolving to genomics assisted molecular breeding and this effort contributes to effectively develop new and better crops. The function and potentials of the interactive analysis platform will be presented in detail

***Corresponding Author:** Tel. 02-2055-2011, E-mail: yeisooyu@dnacare.co.kr

CA-0005

QTLmax: a genomic analytical pipeline for digital breeding

김봉성*

QTLmax Global, Webster, Texas 77598

미국의 다국적 종자기업들의 데이터활용 로드맵은 다음과 같습니다. (1) descriptive analytics, (2) diagnostic analytics, (3) predictive analytics, (4) prescriptive analytics. 이 로드맵은 운영비를 절감하면서 최적의 의사결정 시스템구축을 목표로 합니다. 현재 글로벌 종자기업들은predictive analytics 단계의 구현에 돌입하였습니다. 이 로드맵의 실천과 관련하여 기업들은 반복적으로 수행되는 분석들을 자동화시켜서 운영비를 절감하고, 막대한 돈으로 우수한 기술을 가진 생물정보업체들과 연합하여 predictive analytics시스템을 도입하면서, 최적의 의사결정 시스템을 구축하고 있습니다. 이와 관련하여 육종학계도 그동안의 연구관행에 관해 돌아볼 필요가 있습니다. 획일적 분석업무에 과도한 인건비를 지출하지는 않는지, 혹은 현재의 위치가 위의4단계중 어디에 해당하는지 점검할 때입니다. 최근 화두가 된 디지털육종은 축적된 데이터를 이용하여 의사결정에 이용하기 위한 작업이며, 또한 predictive analytics를 구현하겠다는 의지를 반영합니다.

이에 대한 해법을 위해 저희는 QTLmax라는 지노믹스분석파이프라인을 개발하였고 이미 출시하였습니다. QTLmax는 현재 30가지 이상의 분석 및 그래프 기능을 지원하며, 다음기능들을 포함합니다: imputation, GWAS, genomic prediction, genome browse, interactive plotting. QTLmax는 산업계와 학계의 요구를 충족하며, 이를 위한 세가지 중점은 정밀성, 표준성, 일관성입니다. 정밀성을 위해서 QTLmax는 국제학술지를 통해 검증된 분석방법들을 채용하였습니다. 표준성을 위해서는 표준화된 데이터의 입력형식을 지원하며, 표준화된 통계모델을 채용합니다. 일관성을 위해서는 여러 분석들 간에 원활한 연결을 위해서 하나의 분석결과가 다음분석에 바로 입력될 수 있도록 설계하였습니다. 위의 세가지를 통해 QTLmax는 쉬운 사용자환경과 정확한 결과를 보장합니다. QTLmax의 또 하나의 자랑은 자체 알고리즘인 GBLUP+를 이용한 genomic prediction 기능입니다. GBLUP+는 육종기업들에서 박차를 가하는 predictive analytics 구현을 앞당겨 줄 수 있을 것입니다.

저의 세미나에서는QTLmax 가 어떻게 연구실운영비용의 절감에 도움을 주고, 또한 앞서 설명한 4단계 로드맵 중 3단계인 predictive analytics에 도달하는데 도움을 줄 수 있는지 설명하겠습니다.

***교신저자:** Tel. +1 832-985-2884, E-mail: admin@qtlmax.com

CB-0001

New statistical selection method to identify pleiotropic variants associated with both quantitative and qualitative traits

Kipoong Kim, Hokeun Sun*

Department of Statistics, Pusan National University, Busandaehak-ro, 63beon-gil, GeumJeong-gu, Busan 46241 Republic of Korea

In recent genetic association studies, statistical methods to identify pleiotropic variants associated with multiple phenotypic traits have been developed, since susceptible variants with small or moderate effects are rarely detected by association methods based on a single trait. However, most of the existing methods to identify pleiotropic variants are designed for only quantitative traits even though pleiotropic variants are often associated with both quantitative and qualitative traits. There are some meta-analysis methods which basically integrate summary statistics of individual variants associated with either a quantitative or qualitative trait. However, these methods cannot account for correlations between genetic variants. In this article, we propose new selection method to prioritize individual variants associated with both quantitative and qualitative traits. For individual traits, regression coefficients of elastic-net regularization are first estimated and then they are additively combined to compute selection probability of individual variants. In our extensive simulation studies where either homogeneous or heterogeneous variant effects on both quantitative and qualitative traits were considered, we demonstrated that the proposed method outperforms the existing meta-analysis methods in terms of true positive selection. We also applied the proposed method to peanut data with 4 quantitative traits (leaf chlorophyll, leaf aspect ratio, seed area, and seed sucrose) and 2 qualitative traits (flowering date and fungi quantity grade), and cowpea data with 2 quantitative traits (pod length and seed numbers per pod) and 4 qualitative traits (mature pod color, mature pod curve, seed density, and shattering) traits.

***Corresponding Author:** Tel. 051-510-2258, E-mail: hsun@pusan.ac.kr

CB-0002

QTLs identification for arsenic in rice using genome-scale profiling and high-throughput analyses

Sang-Beom Lee[1], Gyeong-Jin Kim[2], Jung-Du Shin[3], Man-Soo Choi[1*], Yong-Jin Park[4*]

[1]National Institute of Crop Science, RDA, Wanju 55365, Republic of Korea
[2]Chemical Safety Division, National Institute of Agriculture Science (NIAS), Wanju 55365, Korea
[3]Department of Climate Change and Agro-Ecology, National Institute of Agriculture Science (NIAS), Wanju 55365, Korea
[4]Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 32439, Korea

Ionomics is defined as the composition of mineral nutrients and trace elements in organisms, and inorganic components in cells and organism tissue. Recently, its subjects have expanded not only to rice and maize, but also to mouse and human cells. Currently, there have been many studies to elucidate the interaction between arsenic (As) and functional minerals, but the mechanism for interaction between As and minerals by genotypic differences has not yet been explained. Therefore, this study attempted the first transcriptome-wide association studies (TWAS) for As in rice core collection, taking into account environmental (E) and genetic factors (G).

The correlation between As and essential elements was affected by both genetic and environmental factors, and it was confirmed that 6 As-genes were up-regulated in rice core collection. In addition, essential genes were identified by using the expression network to verify the effect size of individual genes in *Japonica* and *Indica lines*. The cluster coefficient of *Japonica lines* was 0.428, which was higher than that of *Indica lines* (0.414). Four essential genes involved in the As transporter were identified in *Japonica lines*, whereas two essential genes involved in As detoxification were identified in *Indica lines*.

We suggested from genetic evidence that *Japonica lines* could accumulate more As than *Indica lines* through the expression network and phylogeny analyses. In addition, a number of significant associated As loci were identified by genome-scale profiling, and these results are expected to be utilized in future research to reduce toxic elements and breeding of high-quality varieties.

***Corresponding Author:** Tel. 063-238-5059, E-mail: cldst81@korea.kr

CB-0003

Development of molecular marker sets associated with disease resistance in grapes

Sang-Keun Oh*

College of Agriculture and Life Sciences, Chungnaml National University, Daejeon 34134, Republic of Korea

Grapes (*Vitis* spp. L.) are the third most-produced fruit in the world. Grape ripe rot is a fungal disease, which is almost inextinguishable, particularly before and after harvest in most vineyards. The management of this disease largely depends on the breeding of resistant varieties. Thus, the search for resistant varieties should parallel the molecular analysis of the markers associated with disease resistance. Here, I applied a genome-wide association study (GWAS) by combining phenotyping and genotyping-by-sequencing (GBS) for the development of a single nucleotide polymorphism (SNP) marker set related to ripe rot disease by *Colletotrichum* spp. using 350 grapevine varieties. As a result of the phenotypes common to both species, 119 varieties (34%) were classified as resistant. Consequently, I discovered the locus with nucleotide-binding sites and carboxy-terminal leucine-rich repeat regions (NBS-LRR) associated with grape ripe rot resistance through GBS and GWAS. Ultimately, we identified the *Colletotrichum* R protein markers from chromosome 3, which belongs to the CC-NBS-LRR type, as disease-resistant proteins. These markers were verified as the melting peak, and their chromatograms of nucleotide sequences were visualized in each SNP loci. All the SNP markers successfully differentiated the resistant from the susceptible cultivars. Interestingly, I also found that a resistant cultivar named Bailey Alicante A has a heterozygous genotype, substantiating its potential usefulness for crops such as grapevine with many hybrids. Altogether, these results indicate that R gene markers can be utilized to distinguish grape ripe rot-resistant cultivars, particularly in crossbreeding populations.

***Corresponding Author:** Tel. 042-821-5762, E-mail: sangkeun@cnu.ac.kr

CB-0004

A component of post-transcriptional gene silencing in soybean affects seed coat color variation

Jinwon Lee[1], Gyu Tae Park[1], Hyun Jo[1], Jeongyun Ko[1], Junbeom Park[1], Jeong-Dong Lee[1], Hak Soo Seo[2], Jong Tae Song[1*]

[1]Department of Applied Biosciences, Kyungpook National University, Daegu, Korea
[2]Department of Agriculture, Forestry and Bioresources, Seoul National University, Seoul 08826, Korea

Soybean seed coat color pigmentation is mainly controlled by post-transcriptional gene silencing (PTGS) of *chalcone synthase* (*CHS*) genes. To understand thPTGS in seed coat pigmentation, we screened the EMS mutant population derived from the Pungsannamul (*I, r, t*) with yellow seed coat color, and isolated three mutant lines (PE63, PE407, PE631) with brown seed coat color. To study the genetic inheritance and co-segregation analysis, we crossed three mutants with two cultivars, Pungsannamul and Jinpung, respectively. Segregation analysis showed that all the three brown seed phenotypes are controlled by a single recessive gene. Allelism test by crossing the mutants each other revealed that the brown seed coat color is caused by mutation in the same gene. Using the single nucleotide polymorphism (SNP) array and Next Generation Sequencing, we identified a single nucleotide polymorphism in Glyma.11G190900 encoding ARGONAUTE 5a (AGO5a) in PE63 (G5369A), PE407 (G3707A), and PE63 (G37979A), respectively. dCAPS analysis of three mutants revealed that the brown seed phenotype was co-segregated with AGO5a mutation. In addition, qRT-PCR analysis in PE63 showed that the expression of *CHS7* gene is significantly upregulated in the seed coat, thus changing the seed coat color from yellow to brown. Our results demonstrated that soybean AGO5a plays roles in seed color pigmentation by regulating the *chalcone synthase* (*CHS*) genes.

***Corresponding Author:** Tel. 053-950-7753, E-mail: jtsong68@knu.ac.kr

CC-0001

High-throughput SNP marker set for genomic selection

Geno Woo Kim[1], Ju-Pyo Hong[1], Hea-Young Lee[1], Jinkwan Jo[1], Jin-Kyung Kwon[1], Dong-Am Kim[2], Byoung-Cheorl Kang[1*]

[1]Department of Agriculture, Forestry and Bioresources, Research Institute, College of Agriculture and Life Sciences, Seoul National University, 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Republic of Korea
[2]HANA Seed. Co., Ltd., R&D Center, Anseong 17601, Republic of Korea

The last decade has witnessed tremendous progress in genome sequencing and explosion of genome sequence information. This remarkable advancement in genomics provides unprecedented opportunities for crop improvement. Pepper (*Capsicum* spp.) is an important vegetable crop worldwide. Developing cultivars harnessing useful traits including disease resistance and consumer oriented-traits are ever increasing. Molecular markers linked to these traits will expedite developing new cultivars. Our group has identified novel traits and developed molecular markers linked to major traits using various genomics tools. For QTL mapping of quantitatively inherited traits, RILs and CC were developed and genotyped by the genotype-by-sequencing methods. Another approach, genome-wide association study (GWAS), has also applied for identifying genes controlling quantitative traits including *Phytophthora* resistance and capsaicinoid content. Genomic selection (GS) is a method of predicting the plant phenotypes in a breeding population using genome-wide markers and statistical models to achieve more reliable selection. There are many genes controlling the capsaicinoid content, which makes it difficult to develop pepper cultivars with various capsaicinoid content. For GS of capsaicinoid content, a core collection consisted of 351 accessions and 96 elite lines from a seed company were used as a training set and a testing set, respectively. The genome-wide SNPs or SNPs selected from GWAS were used in the modeling process. SNPs obtained from the genome-wide association study (GWAS) were used in the modeling process of GS to improve the power of GS. For practical application of GS, we are developing customized SNP chips. These results will presented in the seminar.

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

CC-0002

Forecasting biomass of plant with high throughput phenotyping platform (HTPP) and beyond

Sungyul Chang[1], Unseok Lee[2], Min JeongHong[1], Yeong Deuk Jo[1], Jin-Beak Kim[1*]

[1]Radiation Breeding Research Team, Advanced Radiation Technology Institute (ARTI), Korea Atomic Energy Research Institute (KAERI), 29 Geumgu-gil, Jeongeup-si, Jeollabuk-do 56212, Republic of Korea

[2]Smart Farm Research Center, Korea Institute of Science and Technology (KIST), 679 Saimdang-ro, Gangneung, Gangwon-do 210-340, Republic of Korea

Crop productivity is one of the most important factors in agriculture and can be predicted through plant biomass. Integrating biomass in digital agriculture challenging since the digital transformation required non-destructive data to check health or performance of plant. To meet the requirement, predict biomass from high-throughput phenotyping platforms (HTPPs) data. First, HTPP data with model plant (*Arabidopsis*) were obtained and analyzed with up-to-date U-Net deep learning (DL) network. Later, time series phenotyping data divided into pre-defined developmental stages and then search essential time intervals for predict target trait with machine learning algorithm. Established phenotyping data and biomass were validated in additional biological replication. The result indicated that a partial time series data were required to predict biomass in the end of developmental stage of *Arabidopsis.* In conclusion, phenotyping data not only predict projected area (PA) in different developmental stage but also it could reduce time intervals for interesting traits in crops. This study is a basic research to predict the growth of plant through HTPP acquisition data and apply it to digital agriculture in the future.

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

CC-0003

Genotype-by-Sequencing and its application to crop breeding

Changsoo Kim[1,2*]

[1]Department of Crop Science, Chungnam National University, Daejeon 34134, Republic of Korea
[2]Department of Smart Agriculture Systems, Chungnam National University, Daejeon 34134, Republic of Korea

Plant genetic study and breeding need to capture many genetic variations caused by DNA polymorphisms. Since molecular marker was used, a plethora of different molecular maker types have been introduced to plant genetic study to detect such variations. The advent of next-generation sequencing (NGS) technologies has conferred noble opportunities for high-throughput genotyping in various plant species. Recent improvements in high throughput sequencing enable sequences to be used to detect and score single nucleotide polymorphisms (SNPs), bypassing the entire marker development stage. This enables more powerful analyses of integrated SNP sets in a particular species, although high costs hinder the wider use of SNPs. However, genotype-by-sequencing (GBS), a series of genetic analyses that includes molecular marker discovery and genotyping using NGS technologies, has opened a new era for plant breeding and plant genetics. It offers cost-effective genome-wide scanning and multiplexed sequencing platforms. The GBS methodology uses enzyme cutting coupled with DNA barcoded adapters to provide a great degree of complexity reduction. GBS can simultaneously perform SNP discovery and genotyping with or without reference genome sequences. Consequently, GBS can be applied to various approaches for plant breeding and plant genetic studies, including linkage maps, genome-wide association studies, genomic selection, and genomic diversity. These features make GBS an ideal tool for studies ranging from single gene markers to whole genome profiling. GBS already becomes a major tool to detect numerous SNPs in a cost-effective and flexible manner for plant breeding and plant genetics.

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***Corresponding Author:** Tel. 042-821-5729, E-mail: changsookim@cnu.ac.kr

CC-0004

Title Digital assistants for breeders' eyes: AI-based image processing for phenotype analyses

Marcus Jansen*

LemnaTec GmbH, Aachen, Germany

In plant breeding, visual inspection is a frequent task. Breeders inspect seeds, seedlings, plants, or fields on a regular basis and draw conclusions from the visual impression. In the 21st century, we need to digitize such inspections and provide technology that assists breeders in their work so that breeding becomes more effective and keeps pace with challenges resulting from climate change.

Already image recording has advantages, as it provides a consistent documentation of the samples. However, once images are stored, image processing can deliver many parameters that provide information going far beyond the capabilities in visual scoring. Applying artificial intelligence, we count, measure, and determine quality of the samples. All data are provided in a numerical way. In an application case, seed germination was analyzed using imaging and machine learning based image analysis. The data show substantial differences among the tested cultivars, not only for germination rates but also for seedling sizes. One-step root- and shoot- measurements of large numbers of seedlings are the key added value provided by the technology.

Application cases for AI-based measurements are numerous and comprise growing plants, germinating seeds, or the monitoring of pests and pathogen spores. For instance, with similar methods we can monitor nematode infestation in soil samples, or pathogenic fungal spores in air. Together with classical plant phenotyping these methods provide valuable data for many kinds of visual inspections.

***Corresponding Author:** Tel. +492408 9818571, E-mail: marcus.jansen@lemnatec.com

CD-0001

Revealing key factors for rice pollen tube growth by CRISPR-Cas9

Yu-Jin Kim[1], Myung-Hee Kim[2], Woo-Jong Hong[3], Sunok Moon[3], Soon Ki Park[2], Ki-Hong Jung[3*]

[1]Department of Life Science and Environmental Biochemistry, and Life and Industry Convergence Research Institute, Pusan National University, Miryang, 50463, Republic of Korea
[2]School of Applied Biosciences, Kyungpook National University, Daegu 41566, Republic of Korea
[3]Graduate School of Biotechnology & Crop Biotech Institute, Kyung Hee University, Yongin 17104, Republic of Korea

The highly specialized haploid male gametophyte—pollen consist of two sperm cells and a large vegetative cell. Successful fertilization requires proper growth timing and rupture of the pollen tube until it delivers sperm cells, which occur immediately after a pollen grain hydrates. Although, a tight regulation on polar cell wall expansion of the pollen tube is fundamentally important, the underlying molecular mechanism remains largely unknown, especially in crop plants. Here, we characterized the function of male-gene transfer defective 2 (OsMTD2) gene in rice (*Oryza sativa*), which belongs to the plant-specific receptor-like kinase, the CrRLK1L family. We demonstrated that OsMTD2 is an essential male factor participating in pollen-tube elongation based on genetic evidence and physiological observations. Because unavailability of homozygous mutant via conventional methods, we used CRISPR-Cas9 system to obtain homozygous knock-out mutant of OsMTD2. We were able to identify phenotypic changes including male sterility due to early pollen-tube rupture in the mutant. We observed that the production of reactive oxygen species (ROS) was dramatically reduced in mutants of OsMTD2 pollen grain and tubes with defective pectin distribution. Transcriptome analysis of osmtd2-2 vs wild type anthers revealed that genes involved in defense responses, metabolic alteration, transcriptional, and protein modification were highly up-regulated in the osmtd2-2 mutant. Through yeast two-hybrid screening, we found that OsMTD2 kinase interacts with E3 ligase SPL11. Taken together, we propose that OsMTD2 has crucial functions in promoting pollen-tube elongation through cell-wall modification, possibly by modulating ROS homeostasis during pollen-tube growth.

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

CD-0002

C-to-G Base Editing Induces Enhancement of Oleic Acid Production by Generating Novel Alleles of *FATTY ACID DESATURASE 2* in Plants

Mid-Eum Park[1], Jae-Young Yun[2*], Hyun Uk Kim[1,3*]

[1]Department of Molecular Biology, Graduate School, Sejong University, Seoul, South Korea
[2]Institutes of Green Bio Science & Technology, Seoul National University, Pyeongchang, South Korea
[3]Department of Bioindustry and Bioresource Engineering, Plant Engineering Research Institute, Sejong University, Seoul, South Korea

The demand for vegetable oil, which is mainly used for dietary purposes, is steadily increasing worldwide. It is often desirable to reduce unsaturation levels of fatty acids in order to increase storage stability and prevent vegetable oils turning rancid and to reduce the amount of trans-fat generation during cooking. Functional disruption of Fatty acid desaturase 2 (FAD2) prevents the conversion of oleic acid to linoleic acid, thereby enhancing the production of the desirable monounsaturated oleic acid. However, *FAD2* null alleles are impractical for agronomical purposes due to their growth defects. Here, we aimed to attenuate FAD2 activity *in planta* while avoiding adverse growth effects by introducing amino-acid substitutions using CRISPR base editors. In *Arabidopsis* we applied the adenine base editor (ABE) and cytosine base editor (CBE) to induce random base substitutions within selected *FAD2* coding regions. Isolation of base-edited *fad2* alleles with higher oleic acid revealed that the CBE application induced C-to-T and C-to-G base substitutions within the targeted sequences, resulting in an alteration of the FAD2 enzyme activities. Among such base-edited missense alleles that showed significant increases in the oleic acid, C-to-G base-edited alleles showed the most dramatic increases in the oleic acids by ~3 fold higher than wild type often with less noticeable growth defects. Our "proof-of-concept" approach suggests that the equivalent alleles may be generated in vegetable oil crop via precision genome editing for practical cultivation and that our targeted semi-random strategy may serve as a new complementary platform for *in planta* engineering of useful agronomic traits.

***Corresponding Author:** Tel. 033-339-5824, E-mail: jae0yun@snu.ac.kr

CD-0003

Crop yield improvement via manipulation of meristem initiation in wheat and rice

Yang-Seok Lee*, Cathal Meehan, Jose Gutierrez-Marcos*

School of Life Sciences, University of Warwick, Coventry, West Midlands, CV4 7AL, United Kingdom

Plant meristems are centres of mitotic cell division and are composed of a group of undifferentiated self-renewing stem cells from which most plant structures arise. Axillary meristems and inflorescence meristems determine numbers of tillers and spike branches in grass species, respectively. Since numbers of tillers and spikes are closely connected with crop yield potential, many breeders and researchers have been interested in regulations of numbers of tillers or spike branches. Here, we found a Tauschii 1 (TAU1) was able to induce initiations of meristems in wheat. Upon ectopic expression of TaTAU1, numbers of meristems were significantly increased in axils and inflorescences. These result in increases of numbers of tiller and spikelet, and grain yield was finally increased. Tiller number of rice was increased by ectopic expression of OsTAU1 and AtTAU1, which are orthologues of TaTAU1 in rice and Arabidopsis, and grain yield was increased. Through transcriptomic analyses, we found several histone modification marker and cell cycle factors as putative targets of TaTAU1. These demonstrate that TAU1 induces meristem initiations via controlling histone modifications and cell cycle, and these result in increases of tillers and spikes. Identifying genes implicated in meristem formation could be a useful strategy to enhance seed productivity in various crop species.

***Corresponding Author:** Tel. +44-24-76-151904, E-mail: Y.Lee.6@warwick.ac.uk

CD-0004

유전체교정 기술의 최신 동향 및 미래 전망

배상수*

서울시 성동구 왕십리로 222, 한양대학교 자연과학대학 화학과

생명체의 모든 유전정보를 담고 있는 DNA를 자유자재로 바꾸거나 고칠 수 있는 유전자가위는 기초연구뿐 아니라, 동식물 품종 개량, 유전자 치료 등의 응용 분야에 필수적인 매우 핵심적인 도구이다. 유전자가위는 1세대인 징크핑거뉴클레아제(ZFNs), 2세대인 탈렌(TALENs)을 거쳐 3세대인 크리스퍼(CRISPR) 유전자가위가 개발되었는데, 크리스퍼 유전자가위는 가이드RNA만 바꾸어 줌으로써 타겟 DNA를 특이적으로 절단할 수 있기 때문에, 사용하기가 매우 쉽고 가격 또한 저렴하다. 크리스퍼 유전자가위 기술은 2013년 초, 처음으로 인간세포 교정에 이용된 이후로, 미생물, 동물 및 식물 등 다양한 종에 적용될 수 있다는 것이 밝혀졌고, 현재 유전공학, 의학, 약학, 농업 등 생명과학/공학 거의 전 분야에 걸쳐 매우 폭넓게 사용되고 있다. 이러한 공로로 2020년 노벨화학상은 '크리스퍼 유전자가위 기술의 개발' 분야에 주어졌다. 이제는 바야흐로 크리스퍼 유전자가위의 시대가 되었다고 할 수 있다. 유전자가위 기술은 계속해서 발전하고 있는데, 최근에는 DNA를 절단하지 않으면서도 단일 염기를 정교하게 교정해낼 수 있는 염기교정 기술과 수십개의 염기를 교정할 수 있는 프라임 에디팅 기술이 개발되기도 했다. 본 발표에서는 다재다능한 크리스퍼 유전자가위의 최신 동향에 대해 간단히 살펴보고, 현재 본 연구실에서 진행되고 있는 연구를 소개하고자 한다.

***교신저자:** Tel. 02-2220-2618, E-mail: sangsubae@hanyang.ac.kr

CE-0001

Precision Breeding Strategy for Development of Hypo-allergenic Wheat Through Multi-omics Study of Gluten Genomic Region

Jong-Yeol Lee*

National Institute of Agricultural Science, RDA, Jeonju, 54874, South Korea

The gluten proteins include several complex families of proteins that are difficult to separate, identify and quantify, and there is considerable allelic diversity among wheat cultivars in the genes that encode them. The primary goal of this study is to understand how the composition and quantity of gluten proteins from Korean cultivars related to end-use quality and immunogenic potential. To this end, there is a critical need to sequence the entire set of gluten genes expressed in individual wheat cultivars and to relate those sequences to individual flour proteins. Targeted gene capture methods and PacBio long-read sequencing were used to obtain the complete set of gluten genes from Korean elite cultivar “Keumkang”. A total of 100 genes were identified as gluten genes. Of these, 53 genes encode full-length gluten proteins. To elucidate the complexities of wheat flour proteome in same cultivar, Total flour proteins were separated by 2-DE and 160 proteins were identified by MS/MS. Genomic and proteomic information of gluten region within a single wheat cultivar made it possible to link individual protein to specific gene sequence. Individual spots of 2-DE were associated with 40 of 53 full length gluten genes. Based on this basic research, some efforts and latest results to reduce the immunogenic potential of wheat by breeding strategies or genome editing will be described.

***Corresponding Author:** Tel. 063-238-4616, E-mail: jy0820@korea.kr

CE-0002

국내 최대재배 신동진 벼 형질 개선을 위한 육종사업

박현수*, 백만기, 이창민, 고종철, 정오영, 조영찬, 이점호

전라북도 완주군 이서면 혁신로 181 농촌진흥청 국립식량과학원

‘신동진’은 1999년 농촌진흥청 국립식량과학원에서 개발된 벼 품종으로 재배면적이 지속적으로 증가하여 2018년부터는 우리나라에서 가장 많이 재배되고 있는 국내 최대재배 품종이다. ‘신동진’은 기존 밥쌀용 쌀에 비해 1.3배 정도 무거운 중대립 입형을 가지고 있어 육안으로도 다른 품종들과 구별된다. 이러한 차별성과 함께 ‘신동진’의 우수한 밥맛은 단일품종 브랜드 형성에 기여하였고, ‘신동진’은 전라북도를 중심으로 한 국내 대표 브랜드 품종으로 자리매김하였다. 하지만 재배기간과 면적이 늘어남에 따라 ‘신동진’ 재배의 문제점이 발생하고 있다. 기후변화에 의한 도복과 수발아 발생, 장기재배에 따른 병해충 저항성 붕괴, 품질고급화 정책의 일환인 다수확 품종의 보급종 축소 등으로 ‘신동진’을 대체할 품종 개발이 시급히 요구되고 있다. ‘신동진’ 대체품종이 갖추어야 할 조건으로는 차별성(중대립 입형), 안정성(도복, 병해충 등 단점 개선), 우수성(밥맛 유지 또는 향상)을 들 수 있다. 국립식량과학원은 ‘신동진’ 대체품종 개발을 위한 육종사업을 수행하고 있으며 2020년에 ‘참동진’을 개발하였다. ‘참동진’은 ‘신동진’의 내병성과 밥맛을 향상시키고자 여교배 육종법과 분자표지 선발법을 이용하여 ‘신동진’ 유전배경을 96.3% 회복한 유래품종이다. ‘참동진’은 중대립 입형(차별성) 등 ‘신동진’과 대부분 특성이 같으며, 벼흰잎마름병과 목도열병에 대한 내병성이 강화되었고(안정성), 밥맛이 향상된(우수성) ‘신동진’ 대체품종이다. ‘참동진’은 육종연구 분야 뿐만 아니라 보급 및 생산 분야의 협업과 소비자인 국민의 참여로 함께 개발된 품종으로 ‘신동진’을 보완할 수 있을 것으로 생각한다. ‘참동진’ 이외에도 ‘신동진’의 도복(‘전주665호’ 등), 내병성(*qFfR1* 도입 등), 저장성(*LOX-3* 결핍), 수발아・밥맛(‘참동진/영호진미’ RIL 등 유전분석) 등 형질 개선을 위한 육종사업이 수행되고 있어 향후 ‘신동진’을 대체할 우수한 벼 품종이 개발되어 보급될 것으로 기대된다.

***Corresponding Author:** Tel. 063-238-5214, E-mail: mayoe@korea.kr

CE-0003

Engineering crassulacean acid metabolism to improve water-use efficiency

Sung Don Lim[1*], John C. Cushman[2]

[1]Department of Plant Life & Resource Science, Sangji University, 83 Sangjidae-gil, Wonju-si, 26339, Republic of Korea

[2]Department of Biochemistry and Molecular Biology, University of Nevada, Reno, NV89557-300, USA

Global demand for crop production has increased, while the arable land in agriculture has been declining for decades due to water scarcity driven by global climate change. To overcome this major limitation in crop productivity, engineering crassulacean acid metabolism (CAM) into C_3 crops to enhance their water-use efficiency (WUE) might allow C_3 crops to be grown in arid and semi-arid regions with reduced freshwater inputs. CAM is a photosynthetic adaptation that enables plants to survive under water-limiting conditions by maximizing WUE. Thus, bioengineering CAM into C_3 plants enabling greater WUE is a potential solution to global food production. However, engineering a complex metabolic pathway like CAM requires a deep understanding of the precise regulation of the gene expression patterns and enzymatic and transporter activities orchestrating the pathway. Here, we summarize current progress in C_3-to-CAM Biodesign including tissue succulence engineering, the Multigene Circuit Assembly in Plant (MCAP) toolkit, and phenotypic analysis of several engineered CAM modules in the C_3 model *Arabidopsis thaliana*.

***Corresponding Author:** Tel. 033-250-0513, E-mail: sdlim@sangji.ac.kr

CE-0004

Development of perennial wheat through wide hybridization mediated chromosome engineering

Seong-Woo Cho*

Department of Smart Agro-Industry, Gyeongsang National University, 33 Dongjin-Ro, Jinju, Gyeongnam 52725, KOREA

Wide hybridization with *Leymus mollis* was performed to develop a perennial wheat line based on genetic analysis of *L. mollis* in this study. In chromosome observation. *L. mollis* had four chromosomes with satellites and two supernumerary chromosomes. In protein expression, *L. mollis* had major protein spots between ~50 kDa and 75 kDa. Also, it had the protein spots related to dough strength over 150 kDa and granule bound starch synthase I near 75 kDa. By RP-UPLC, three major high molecular weight glutenin subunits of *L. mollis* were identified. Through wide hybridization between common wheat and *L. mollis*, ten seeds were obtained with seed color of *L. mollis*. Among ten F_1 hybrids, five hybrids were with two coleoptiles. The coleoptiles of the hybrids showed either the same growth time or different growth time. The hybrids showed new shoots by rhizome like *L. mollis*, hence spikes of them showed different heading time each other. The new shoots by rhizome showed thin stem with adventitious roots like prop roots. Also, the other type of new shoots emerged from the side of main shoots like sprouting. The spike shape of the hybrids was similar to that of common wheat, but length and compactness were different. Finally, the hybrids were fertile. Seeds of the hybrids showed intermediate seed color between common wheat and *L. mollis*. Conclusionally, those hybrids might be useful to improve wheat breeding program. However, it is necessary to study more genetic information related to perennial and rhizome with F_2 genetic population for development of more efficient breeding material.

***Corresponding Author:** Tel. 055-772-3225, E-mail: chsw78@gnu.ac.kr

CF-0001

QTL-seq analysis of disease resistance in a Korean cucumber inbred

Mahdi Badri Anarjan[1], Shahida Begum[1], Sanghyeob Lee[1,2*]

[1]Sejong University, Neungdong-ro, Gwangjin-gu, Seoul 05006, Republic of Korea
[2]PERI, Sejong University, Neungdong-ro, Gwangjin-gu, Seoul 05006, Republic of Korea

Cucumber (Cucumis sativus L.) is an economically important and widely cultivated vegetable crop worldwide. Powdery mildew (PM), which is primarily caused by the obligate biotrophic ectoparasite *Podosphaera xanthii* (formerly known as Sphaerotheca fuliginea Schlech ex Fr. Poll.), is one of the most common, conspicuous, and widespread fungal disease of cucurbits, including cucumber, and affects cucumber production worldwide through causing serious losses in yield and quality. In addition, downy mildew (DM) caused by the obligate oomycete *Pseudoperonospora cubensis* (Berk. and Curt.) Rostovzev also one of the most economically important foliage diseases of all cucurbits worldwide. The development of PM- and DM-resistant inbred lines is thus of considerable significance for cucumber breeding programs. In this study, we applied bulked segregant analysis combined with QTL-seq to identify PM and DM resistance loci using F2 population derived from a crosses between Korean cucumber inbred lines, Genome-wide SNP profling using bulks of the two extreme phenotypes (for PM and DM) identified the loci responsible for PM and DM resistance. Our results provide new genetic insights for gaining a better understanding of the genetic basis of PM and DM resistance in cucumber, and pave the way for further utilization in cucumber PM and DM resistance breeding programs.

***Corresponding Author:** Tel. 02-3408-4375, E-mail: sanglee@sejong.ac.kr

CF-0002

Deciphering the Anthocyanin Biosynthetic Mechanism in Horticultural Crops

Sun-Hyung Lim*

Division of Horticultural Biotechnology, Hankyong National University, Anseong, 17579, Korea

Anthocyanins belong to flavonoid-derived secondary metabolic compounds ubiquitously found in the plant kingdom. They play an important role in coloring flowers and fruits and contributing to plant adaptation to environmental conditions such as cold or UV stresses. In addition, these compounds possess health-promoting properties extremely attractive for human health. Therefore, they have been an interesting target for breeders and consumers, due to affect the quality of flowers, fruits, and vegetables.

For the past decades, many researchers tried to elucidate the anthocyanin biosynthetic mechanism and to approach enhancing and modifying anthocyanins via metabolic engineering. However, it is still needed to elucidate and understand the structural and regulatory genes for anthocyanin biosynthesis. Here, I will present our recent results; (I) anthocyanin biosynthetic mechanism in chrysanthemum; and (II) elucidation of the regulator role on anthocyanin biosynthesis in radish. Through a better knowledge of anthocyanin biosynthetic mechanisms, it will contribute to the development of the generation of value-added horticultural crops with desired anthocyanin content.

***Corresponding Author:** Tel. 031-670-5105, E-mail: limsh2@hknu.ac.kr

CF-0003

이미지 기반 채소 모종 생육 정보 수집과 육종 연구 활용 방안

안세웅*, 유인호, 이희주, 최학순, 여경환, 위승환

전라북도 완주군 이서면 농생명로 100 국립원예특작과학원 채소과

채소 육묘는 일반적으로 30-60일의 기간 동안 종자 발아부터 정식 작업 이전까지의 어린 식물을 키우는 과정으로 정의 되며, 이러한 짧은 육묘 기간 동안 환경 조절 기술, 시비 및 관수 관리, 병해충 관리 등 재배 관련 모든 기술이 집약되어 정밀하게 작물을 관리하고 있다. 우리나라는 현대화된 공정육묘를 1990년대 초반 도인한 후 산업적 및 기술적으로 괄목할 만한 발전을 이루어 왔다. 한국형 육묘 온실 설계, 대목 품종 개발, 접목 방법, 접목 활착 관리, 각 생산 단계별 육묘 트레이 및 파종기 등의 국산화의 성과를 도출하였다. 그러나, 최근 들어 기후 변화와 증가하는 육묘 생산비로 인하여 육묘 산업의 지속가능한 발전을 저해하고 있으며, 육묘 품질 및 생산성 증대를 위해서 정밀 육묘 관리 기술에 대한 요구가 높아지고 있다. 육묘 관리의 정밀성 향상을 위한 기술적인 요구에 맞춰서, 각 육묘 단계의 모종 생육 및 환경 정보의 수집과 분석을 위해 스마트 육묘 기술에 대한 연구가 진행되고 있다. 모종 생육 정보의 비파괴적인 수집을 위해 영상 기술이 적용되고 있으며, 초장 및 엽면적 등 외적인 정보 수집을 위해서는 RGB 및 LiDar 센서가 적용되어 파종 후 발아율 판단, 육묘 기간의 모종의 초장, 엽면적을 수집하였다. 또한, 모종 품질 관리를 위해 VNIR 및 초분광 영상 센서를 이용하여 육묘 기간 동안에는 식생지수 판별과 출하 전 모종의 병해 감염 여부 확인을 위한 토마토 세균성점무늬병을 대상으로 이미지 기반 병해 판단 기술 연구도 수행되고 있다. 이러한 영상 기반의 채소 모종 생육 정보 수집 기술은 채소 육묘 기간 동안의 정밀한 관리를 통해 육묘 생산성 향상을 위한 기술 적용뿐만 아니라, 디지털 육종 시대를 맞이하는 채소 육종 분야의 페노믹스 시스템 적용에 적합할 것으로 판단하고 있다. 다양한 채소 육종 소재의 유묘기 동안에 비파괴적인 영상기술을 적용하여 각 작물의 외적인 특성과 더불어 환경내성과 병 저항성과 같은 내적인 특성 등 원예적 형질에 대한 신속한 판별과 객관화된 데이터의 수집이 가능하여 디지털 기반의 채소 육종 효율을 증진 시킬 수 있을 것이다.

***교신저자:** Tel. 063-238-6652, E-mail: woong0911@korea.kr

CF-0004

채소 유전체 정보 기반의 초고속 대량 분자마커세트 개발 및 활용

이혜은*, 김진희, 이은수, 한고은, 김도선

전라북도 완주군 이서면 농생명로 100 국립원예특작과학원 채소과

최근 차세대 염기서열분석(Next-Generation Sequencing, NGS) 기술의 발전으로 빠른 분석 속도와 저렴한 비용으로 표준유전체 서열정보를 구축함으로써, 다양한 유전체 분석기술이 보편적인 분자육종의 수단으로 자리매김하고 있다. 즉 육종기술은 기존 아날로그식 관행육종 방법을 벗어나 유전체 정보와 다중 오믹스 정보수집, 분석, 인공지능을 기반으로 육종 효율성 및 품질 고도화를 위한 첨단 육종기술로 발전하고 있는 것이다. 다국적 종자회사는 육종연한을 단축하기 위해 자체적으로 high-throughtput 유전자형 분석 플랫폼으로 시스템을 구축하고 있으나, 국내 종자회사는 아가로스겔을 이용한 PCR-based marker를 주로 활용하고 있어 유전자형 분석 효율이 낮은 실정이다. 현재 종자시장을 선도하는 고부가가치 품종들은 분자표지를 활용한 목표 유전자 보유 개체 선발과 세대진전 등을 통한 여교배 육종법을 통해서 대부분 만들어졌으며, 여교배(Marker-Assisted Backcross, MAB)는 우수친에 목표형질을 도입하기 위해 가장 일반적으로 사용되는 육종방법으로, 최소 5~6 세대진전이 필요하다. 단일염기다형성(Single Nucleotide Polymorphisms, SNP)는 유전체 내 빈도수가 많고 분석 방법이 간편하며, 무엇보다 최근에 다양한 high-throughput 기술로 SNP 분석의 자동화가 가능한 장점을 가지고 있어 육종조합에 적용이 가능한 마커세트를 구성할 수 있다. 따라서 본 연구에서는 주요 채소작물인 배추, 무, 오이, 호박 및 수박의 유전체 정보 기반의 초고속 대량 분자마커세트를 개발하기 위해 작물별 대표형질을 고려한 핵심계통을 선정하여 염기서열 분석(Transcriptome sequencing, Resequencing 등)을 수행하였다. 염기서열 정보로부터 SNP 선발은 depth 10 이상, 동협접합성 대립유전자(homozygous diallele), 다형성지수(PIC) 값이 0.5에 근접한 것, 인접한 SNP 제외(60bp 간격) 등을 기준으로 염색체 위치별로 고르게 분포된 SNP 프라이머 조합을 선발하였다. 선발한 SNP는 품종 분류, 분자마커를 이용한 여교배, 형질 마커 개발, 유전자지도 작성 등 다양한 목적에 따라 고속대용량 유전자형 분석기기를 활용한 초고속 대량 마커세트로 개발하였다. 특히 배추에서는 총 468개의 SNP를 선발하여 Fluidigm사의 Biomark 플랫폼 시스템에 맞는 마커세트의 MAB 적용 가능성을 확인한 결과, BC_1F_1에서 양친의 유전자형과 90.3%, BC_2F_1에서 93.3% 이상의 회복률을 나타내면서 최소 2세대 이내로 배추 여교배의 세대진전을 단축시킬 수 있음을 보여주었다. 그동안 개발한 주요 채소의 초고속 대량 마커세트는 농업기술실용화재단 종자산업진흥센터 등으로 기술이전되어 민간 종자기업의 high throughtput 분자마커 분석서비스에 활용되면서 종자산업 R&D 경쟁력 강화에 기여하고 있다. 이러한 채소 유전체 정보기반 종자기업 맞춤형 초고속 대량 마커세트 개발로 첨단 육종기술 기반 구축을 통해 다수의 양적 형질 조기 선발을 가능하게 하였으며, 추후 SNP 마커세트를 이용해 내병성 및 고품질 관련 다양한 육종 조합 및 육종 목표에 활용할 수 있을 것으로 기대한다.

***교신저자:** Tel. 063-238-6674, E-mail: helee72@korea.kr

CG-0001

Identification of Candidate Genes for Non-dehiscent Capsule in Sesame (*Sesamum indicum* L.) via cross-population association analysis with whole genome re-sequencing

Sung Up Kim[1], Jeongeun Lee[1], Keunpyo Lee[2], Eunyoung Oh[1], Jung In Kim[1], Min Young Kim[1], Sang Woo Kim[1], Myoung Hee Lee[1], Chan-sik Jung[1], Kwang-Soo Cho[1*]

[1]Department of Southern Area Crop Science, National Institute of Agricultural Science, RDA, Miryang, Geongnam-do, 50424, Republic of Korea
[2]Genomics Division, National Institute of Agricultural Sciences, Jeonju, Korea

Non-dehiscent capsule is the most important trait for reducing yield loss during harvesting sesame by machinery combine. In this study, we carried out whole genome re-sequencing of the 100 individuals of Suwon195 X IT030100 F_8 RIL population to identify quantitative trait loci (QTL) and candidate genes associated with non-dehiscent capsule characteristics. We detected five significant QTLs for non-dehiscent capsule on chromosome 9, explaining range from 5.26% to 25.01% of phenotypic variations, and scanned these regions to identify candidate genes. This region contained 17 non-synoymous SNP with one early stop codon and InDel. Two candidate genes associated with capsule non-shattering are found. One of them, SIG_09g13830 confers a determinant of cell adhesion, cell wall porosity and elasticity. Another gene SIG_09g14070(SiNAC) is NAC (NAM, ATAF and CUC) trancsription factor, this gene was known to mediate pod shattering resistancs in soybean. Based on this results, we designed KASP and InDel markers and applied to Suwon195 X IT030100 F_8 RIL population and germplasm. These marker will be useful to develop marker-assisted selection in sesame breeding program.

***Corresponding Author:** Tel. 055-350-1227, E-mail: sesameup@korea.kr

CG-0002

Genomic study showed insight to molecular basis of the high oil content and black sesame

Linhai Wang*, Senouwa Segla Koffi Dossou

Oil Crops Research Institute of the Chinese Academy of Agricultural Sciences, Key Laboratory of Biology and Genetic Improvement of Oil Crops of the Ministry of Agriculture, Wuhan, 430062, China

Sesame is high in oil content and quality. sesame seed coat color is is strongly linked to seed oil, proteins, and lignan content, and also influences consumer preferences. Sesame genome was predicted to contain 708 lipid-related genes. The number was lower than other oil crops such as soybean, in spite of the higher oil content, but it has more lipid transfer protein genes. Whole genome screening identified 54, 42, 35, 44 and 34 LTP genes in cultivars Zhongzhi 13, Baizhima, Mishuozhima, Swetha and Yuzhi11 respectively. They shared 19 LTP genes, and Swetha, Yuzhi11, Zhongzhi13 have 2, 1, 6 special LTP respectively. It suggested LTP genes are active in evolution and varied in different sesames. Genome-wide association study located 13 significant associated peaks including 4 LTP genes. Comparative transcriptome profiling of developing sesame seeds and capsules showed a list of lipid-related genes including 11 encoding LTP. By comparing of the developing seeds transcriptome of two varieties of sesame “Zhongfengzhi No.1” (white seed) and “Zhongzhi No.33” (black seed), it showed the black sesame seed turned to yellow between 9 and 11 DPA and then black between 12 and 14 DPA. Annotation of the DEGs between the black and white sesame showed flavonoid biosynthesis and biosynthesis of secondary metabolites were dominants in shaping black sesame. Furthermore, we identified 20 candidate genes associated with pigment biosynthesis in black sesame seed. The study showed molecular basis of the high oil content and black sesame.

***Corresponding Author:** Tel. 86-027-86711856, E-mail: wanglinhai@caas.cn

CG-0003

Analysis of genes associated with salinity using trascriptomic information in *Sorghum bicolor*

Changsoo Kim[1,2*], Donghyun Jeon[1,2]

[1]Department of Crop Science, Chungnam National University, Daejeon 34134, Republic of Korea
[2]Department of Smart Agriculture Systems, Chungnam National University, Daejeon 34134, Republic of Korea

One of the abiotic stresses, salt stress has an impact on the production and development of crops around the world. Sorghum is a functional genomics model crop of C4 plants and ‘Saccharinae’ due to its small genome size, and is a clue to the mechanism associated with salt tolerance at the transcriptomic level. However, the mechanism of salt tolerance-related genes in sorghum has not been well reported. The RNA sequencing analysis in the ‘Sodamchal’ and ‘Nampungchal’ genotypes between control and high salinity treatment in a time-course was performed using next generation sequencing (NGS) technology through Illumina. In addition, physiological responses such as proline, anthocyanin, chlorophyll, and reducing sugar were identified under salt stress treatment between two sorghum genotypes.We obtained about 42 million pairs of short reads with 96.7 % and 96.5 % concordant pair alignment rate respectively in Nampungchal and Sodamchal genotypes. In addition, 1270 and 1643 DEGs between Nampungchal and Sodamchal were identified in leaves and roots respectively. Comparative analysis of two sorghum genotypes provides candidate genes involved in salt stress response and may offer a better understanding of the salt tolerance mechanism in sorghum.

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***Corresponding Author:** Tel. 042-821-5729, E-mail: changsookim@cnu.ac.kr

CH-0001

Functional analysis of wheat ASR gene under environmental stresses

Jin Seok Yoon[1], Yong Weon Seo[1,2*]

[1]Department of Plant Biotechnology, Korea University, Seoul 02841, Korea
[2]Department of Biotechnology, Korea University, Seoul 02841, Korea

Environmental stresses such as drought, salinity, heat and cold adversely affect plant growth and crop productivity. Wheat is a major food crop, consuming about 34.2 kg per person per year in Korea. Recently, the problem of crop production stability has arisen due to the climate change by global warming. We performed genome-wide analysis using wheat genome database. We identified wheat *ASR* gene family though genome wide analysis using the wheat genome database. The sequence alignment and phylogenetic analysis were performed compare with ASR genes of other crops. Expression levels of *TaASR* genes were investigated in respond to abiotic stresses and hormones. Transgenic plants of *ASR* gene were evaluated phenotypic analysis as well as physiological analysis under drought and salinity stress. Transgenic plants of *TaASR* affected expression levels of ABA biosynthesis and stress-associated genes under drought and salinity stress condition. Moreover, we examined stomatal aperture in transgenic plants and WT plants under drought stress condition. In addition, we identified that *TaASR* interacts with ABA biosynthesis and stress-related protein. This study could help to develop wheats against abiotic stresses.

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***Corresponding Author:** Tel. 02-3290-3005, E-mail: seoag@korea.ac.kr

CH-0002

Optimization of crop yield using root-preferred promoter by improving phosphate use of efficiency in rice

Yun-Shil Gho[1], Heebak Choi[1], Sunok Moon[1], Sung-Ryul Kim[2], Doh-Hoon Kim[3], Sun-Hwa Ha[1], Ki-Hong Jung[1*]

[1]Graduate School of Biotechnology & Crop Biotech Institute, Kyung Hee University, Yongin 17104, Republic of Korea
[2]Strategic Innovation Platform, International Rice Research Institute, Metro Manila, Philippines
[3]Department of Life Science, College of Life Science and Natural Resources, Dong-A University, Busan, South Korea

Phosphate (Pi) is one of the essential macro-nutrients of maintaining growth and a pivotal component of major organic molecules such as RNA, DNA, and ATP in all organisms. The fine-tuning of phosphate utilization efficiency (PUE) has been a challenging topic for long agricultural history in rice. Although several studies have been conducted for improving PUE in rice, most of the studies have focused on the phosphate absorption rate using constitute promoters, but have shown the results as impaired growth or reduced biomass. In this study, we reported that the Pi-starvation-induced *RNase T2* (*RNS*) genes are involved in Pi recycling by RNA catabolic process under Pi starvation. Among the *OsRNS* gene family, *OsRNS1* has root-preferred expression and *osrns1* mutants have shown severely impaired root growth. To optimize the function of the *OsRNS1* gene, which functions primarily in the root, we generated the *OsRNS1*-overexpression plants by expressing its coding sequence under two different promoters: *ubiquitin 1* promoter (*Ubi*) for whole-plant expression and *Os1-CysPrxB* (*Per*) promoter for root-preferred expression. Compared to WT, *OsRNS1*-overexpression plants using the *Per* promoter showed an increase of root length, plant height, and grain yield by more than 35%, 19%, and 42 %, respectively. Meanwhile, the root length and grain yield of *OsRNS1*-overexpression plants using the *Ubi* promoter were smaller than those of WT. Our results suggest that this strategy has a great potential to optimize the function of root-preferred genes and contributed to developing the high PUE rice.

***Corresponding Author:** Tel. 031-201-3470, E-mail: khjung2010@khu.ac.kr

CH-0003

A rice really interesting new gene H2-type E3 ligase, OsRFPH2-23, contributes to salt tolerance

Ju Hee Kim[1*], Ki-Hong Jung[2], Cheol Seong Jang[3]

[1]Agriculture and Life Sciences Research Institute, Kangwon National University, Chuncheon 24341, Korea
[2]Graduate School of Biotechnology, Kyung Hee University, Yongin 17104, Korea
[3]Plant Genomics Laboratory, Interdisciplinary program in Smart Agriculture, Graduate School, Kangwon National University, Chuncheon 24341, Korea

Environmental stress, including salt stress, seriously threatens plant growth and development. In previous work, we examined OsRFPH2-23, a positive regulator of salt insensitivity in *Arabidopsis*. However, the exact mechanism by which OsRFPH2-23 regulates the interacting protein remains unknown. In the present study, we demonstrated that OsSalT acts as an interacting protein of OsRFPH2-23 using yeast two-hybrid and bimolecular fluorescence assays. An *in vitro* ubiquitination assay showed that OsRFPH2-23 ubiquitinated the OsSalT protein. Additionally, under salinity stress, *OsRFPH2-23*-overexpressing plants displayed better salt tolerance than WT and *osrfph2-23* plants. The *OsRFPH2-23*-overexpressing plants had a lower Na^+/K^+ ratio and higher accumulation of proline and chlorophyll contents than WT and *osrfph2-23* plants. Furthermore, the expression of some rice transporters (*OsHKT1;5*, *OsHKT2;1*, *OsSOS1*, and *OsNHX1*) involved in Na^+/K^+ homeostasis and salt-induced genes (*OsDREB2A* and *OsNAC1*) were analyzed in the *OsRFPH2-23*-overexpressing plants under salinity. qRT-PCR data suggested that the expression levels of these genes enhanced the salt tolerance of *OsRFPH2-23*-overexpressing plants. Thus, these results provide experimental evidence that *OsRFPH2-23* is an important regulator of Na^+ and K^+ regulation and plays a critical role in salt tolerance, possibly by modulating the expression of transporters and salt-responsive genes.

***Corresponding Author:** Tel. +82-70-7135-9637, E-mail: juheekim@kangwon.ac.kr

CH-0004

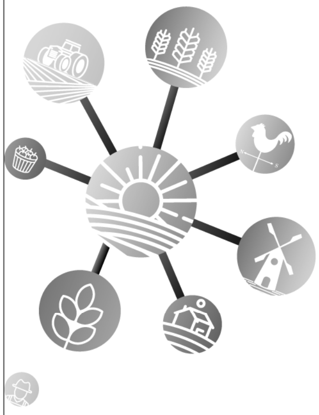
Detection of QTLs controlling adaxial leaf rolling to achieve ideal plant type in rice

Su Jang, Hee-Jong Koh*

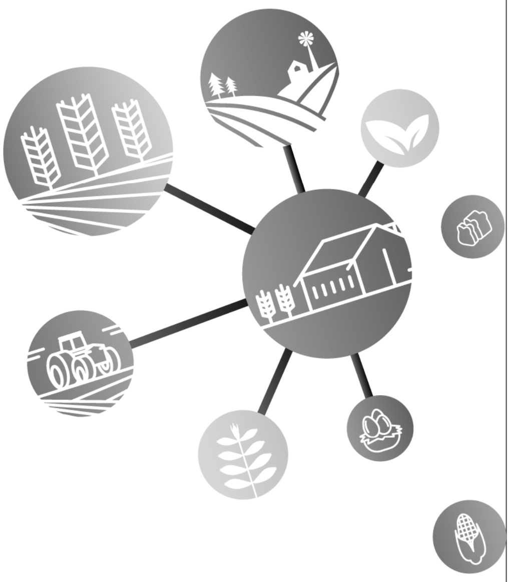
Department of Agriculture, Forestry and Bioresources, Plant Genomics and Breeding Institute, Research Institute for Agriculture and Life Sciences, Seoul National University, Seoul, 08826, Republic of Korea

Moderate leaf rolling is considered optimal for the ideal plant type in rice (*Oryza sativa* L.), as it improves photosynthetic efficiency and consequently grain yield. In this study, we identified three stable QTLs, *qARO1*, *qARO5*, and *qARO9*, which control adaxial leaf rolling in a recombinant inbred line (RIL) population derived from a cross between Tong 88-7 (T887) and Milyang 23 (M23). These QTLs controlled the rolling phenotype of both the flag leaf and secondary leaf, and different allelic combinations of these QTLs led to a wide variation in the degree of leaf rolling. Additive gene actions of *qARO1* and *qARO9* on leaf rolling were observed in a backcross population. In addition, *qARO1* and *qARO9* were successfully fine-mapped to approximately 60 and 90 kb intervals on chromosomes 1 and 9, respectively. Histological analysis of near-isogenic lines (NILs) revealed that *qARO1* influences leaf thickness across the small vein, and *qARO9* affects leaf thickness in the entire leaf and bulliform cell area, thus leading to adaxial leaf rolling. The results of this study advance our understanding of the genetic and molecular bases of adaxial leaf rolling, and this information can be used for the development of rice varieties with the ideal plant type.

***Corresponding Author:** Tel. 02-880-4541, E-mail: heejkoh@snu.ac.kr



Poster Session



PA-0001

PCR-based markers to distinguish *Solanum cardiophyllum* from other *Solanum* relatives were developed by comparison of complete chloroplast genome sequences of *Solanum* species

Tae-Ho Park*

Department of Horticulture, Daegu University, Gyeongsan 38453, Republic of Korea

The diploid *Solanum cardiophyllum*, a wild tuber-bearing species from Mexico is a relative to potato, *S. tuberosum*. It was identified as a source of resistance to crucial pathogens and insects such as *Phytophthora infestans*, Potato virus Y, Colorado potato beetle, etc. and used for potato breeding. However, sexual hybrid between *S. cardiophyllum* and *S. tuberosum* is limited due to their sexual incompatibility. Therefore, somatic hybridization can be used to introduce various traits from this wild species into potato. After somatic hybridization, it is essential to select fusion products with the aid of molecular markers. In this study, the chloroplast genome sequence of *S. cardiophyllum* was obtained by next-generation sequencing technology and compared with those of other *Solanum* species to develop specific markers for *S. cardiophyllum*. The chloroplast genome has a total sequence length of 155,570 bp. Its size, gene content, order and orientation are similar to those of the other *Solanum* species. Phylogenic analysis with 14 other Solanaceae species revealed that *S. cardiophyllum* is most closely located to *S. bulbocastanum*. After detailed comparisons of the chloroplast genome sequences of the eight *Solanum* species, we identified 13 SNPs specific to *S. cardiophyllum*. Based on the information, four allele-specific PCR markers were developed for discriminating *S. cardiophyllum* from other *Solanum* species. The results obtained in this study will aid in exploring the evolutionary aspects of *Solanum* species and accelerating breeding using *S. cardiophyllum*.

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***Corresponding Author:** Tel. 053-850-6711, E-mail: thzoo@daegu.ac.kr

PA-0002

The defense response of sweetpotato resistance to root-knot nematode Meloidogyne incognita: comparison of root transcriptomes of resistant and susceptible sweetpotato cultivars

Yun-Hee Kim[1*], Jung-Wook Yang[2], Jeung Joo Lee[3], Donghwan Shim[4]

[1]Department of Biology Education, IALS, Gyeongsang National University, Jinju, 52828, Republic of Korea
[2]Department of Crop cultivation & Environment, Research National Institute of Crop Science, Rural Development Administration, Suwon, 16429, Republic of Korea
[3]Department of Plant Medicine, IALS, Gyeongsang National University, Jinju, 52828, Republic of Korea
[4]Department of Biological Sciences, Chungnam National University, Daejeon, 34134, Republic of Korea

Sweetpotato (*Ipomoea batatas* [L.] Lam) is an economically important, nutrient- and pigment-rich root vegetable used as both food and feed. Root-knot nematode (RKN), *Meloidogyne incognita,* causes major yield losses in sweetpotato and other crops worldwide. The identification of genes and mechanisms responsible for resistance to RKN will facilitate the development of RKN resistant cultivars not only in sweetpotato but also in other crops. In this study, we performed RNA-seq analysis of RKN resistant cultivars (RCs; Danjami, Pungwonmi and Juhwangmi) and susceptible cultivars (SCs; Dahomi, Shinhwangmi and Yulmi) of sweetpotato infected with *M. incognita* to examine the induced and constitutive defense response-related transcriptional changes. During induced defense, genes related to defense and secondary metabolites were induced in SCs, whereas those related to receptor protein kinase signaling and protein phosphorylation were induced in RCs. In the uninfected control, genes involved in proteolysis and biotic stimuli showed differential expression levels between RCs and SCs during constitutive defense. Additionally, genes related to redox regulation, lipid and cell wall metabolism, protease inhibitor and proteases were putatively identified as RKN resistance genes. The root transcriptome of SCs was also analyzed under uninfected conditions, and several potential candidate genes were identified. Overall, our data provide key insights into the transcriptional changes in sweetpotato genes that occur during induced and constitutive defense responses against RKN infection.

***Corresponding Author:** Tel. 055-772-2237, E-mail: cefle@gnu.ac.kr

PA-0003

Characterization of complete chloroplast genome of *Atractylodes ovata*

Jinhyuk Kim[1], Heesu Yun[1], Hwayong An[1], Hyang Sook Chun[2], Sang-Il Han[3], Gyoungju Nah[1*]

[1]Genome Analysis Center at National Instrumentation Center for Environmental Management, Seoul National University, Seoul, Korea
[2]Department of Food Science and Technology, Chung-Ang University, Ahnsung, Korea
[3]Medicinal Herb Garden, College of Pharmacy, Seoul National University, Goyang, Korea

We generated the complete chloroplast genome sequence of *Atractylodes ovata*, a species of the Asteraceae family, and characterized from the *de novo* assembly of Illumina HiSeq paired-end sequencing data. The total length of the chloroplast genome of *Atractylodes ovata* was 153,170 bp with a large single-copy (LSC) region of 84,256 bp, a small single-copy (SSC) region of 18,622 bp, and a pair of identical inverted repeat regions (IRs) of 25,146 bp. The total of 110 genes were annotated in the chloroplast genome of *Atractylodes ovata*, including 76 protein-coding genes, 30 transfer RNA (tRNA) genes, and 4 ribosomal RNA (rRNA) genes. The phylogenetic analysis of *Atractylodes ovata* with related species revealed the closest taxonomical relationship with *Atractylodes lancea* in the *Asteraceae* family.

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***Corresponding Author:** Tel. 02-880-4971, E-mail: gnah.nicem@snu.ac.kr

PA-0004

Comparative FISH karyotype and genome size analyses in cultivars and root cultures of *Panax ginseng*

Eliazar Alumbro Peniton Jr., Nomar Espinosa Waminal, Hyun Hee Kim*

Bioscience Research Institute, Department of Life Science, Sahmyook University, Seoul, 139-742, Korea

The conservation of the genome integrity in plants is crucial for their survival and adaptation. Genome instability can be observed in the variations of genome size (GS), chromosome number (CN) and physical genome organization between *in vitro* culture and their mother plant, and even between cultivars of the same species. Despite the high economic and pharmaceutical importance of *Panax ginseng*, there has been no comparative study on the genomic integrity between its cultivars and *in vitro* root cultures. Here, we measured the GS and CN in nine cultivars and four *in vitro* cultures of *P. ginseng,* 2 hairy roots (HR) and 2 adventitious root lines (AR). We performed seven-color fluorescence *in situ* hybridization (FISH) using 5S and 45S rDNAs, *Arabidopsis*-type telomere, Pg167TRa, Pg167TRb, Pg*Del1* and Pg*Del2* to identify each chromosome. There was negligible variation in GS and CN between ginseng cultivars and AR ($1C_{\bar{x}}$ = 4.1 Gb, $2n$ = 48). However, clear distinct GS peaks were observed between one HR line (TYP-1) and the rest of the samples. CN analysis verified a loss of four chromosomes (8, 13,16 and 17) in TYP-1 (1C = 3.69 Gb, $2n$ = 44; -8,13,16,17). TYP-1 was used for nanopore sequencing to validate the ginseng genome assembly before knowing its fundamental genomic features. These results highlight the role of cytogenetics analysis prior to genome sequencing. Nevertheless, this information will facilitate the on-going ginseng genome validation.

Keywords: Cell cycle synchronization, cytogenetics, fluorescence *in situ* hybridization, genome size, *Panax ginseng*

***Corresponding Author:** Tel. +82-2-3399-1715, Fax. +82-2-3399-1729, E-mail: kimhh@syu.ac.kr

PA-0005

The Complete Plastid Genome Sequence of a Medicinal Citrus Landrace 'Jinkyool' (*Citrus sunki* Hort. ex Tanaka) in Korea

Ho Bang Kim[1*], Chang Jae Oh[1], Yun Ji Choi[1], Hee-Jung Jung[1], Seung Chul Shin[2], Minju Kim[3], Su-Hyun Yun[3], Hyoungseok Lee[2,4]

[1]Life Sciences Research Institute, Biomedic Co., Ltd., Bucheon 14548, Korea
[2]Korea Polar Research Institute, Incheon 21990, Korea
[3]Citrus Research Institute, National Institute of Horticultural & Herbal Science, Seogwipo 63607, Korea
[4]Polar Science, University of Science & Technology, Incheon 21990, Korea

Citrus sunki (Jinkyool) is a medicinal landrace citrus belonging to the Rutaceae family. We determined the complete chloroplast genome (160,699 bp) of *C. sunki* CRS0085 in Jeju Island, Korea. The genome is composed of four distinct parts; a large single copy of 87,918 bp, a small single copy of 21,355 bp, and a pair of inverted repeat regions of 25,713 bp. A total of 134 genes including 89 protein-coding genes, 37 tRNA genes and 8 rRNA genes was identified. The phylogenetic tree showed that *C. sunki* CRS0085 has the closest relationship with *C. reticulata* within genus *Citrus*.

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***Corresponding Author:** Tel. 032-218-1515, E-mail: hobang@ibiomedic.co.kr

PA-0006

Re-annotation and comparative analyses of PHD-finger gene family in pepper

Ji Yoon Guk, Yeon Mi Lee, Seungill Kim*

Department of Environmental Horticulture, University of Seoul, Seoul 02504, Korea

The plant homeodomain (PHD) finger genes that belong to zinc-finger genes have an important role in regulating gene transcription by recognition of epigenetic mark in eukaryotes. However, inaccurate annotation of PHD-finger genes hinders their downstream comparative and evolutionary studies. Here, we conducted re-annotation and comparative analyses of the PHD-finger gene family in five plant genomes: *Arabidopsis*, rice, pepper, potato, and tomato. In total, we identified 875 PHD-finger genes in the five genomes including 225 genes (26%) that were missed in previous annotations. Domain architecture analysis revealed that PHD-finger genes had diverse integrated domains, suggesting that integration of diverse domains could contribute to the structural and functional diversification of PHD-finger gene family. Gene ontology analysis suggested that most of pepper PHD-finger genes (96%) might be involved in 'binding' function that was consistent with the previously known function of PHD-finger genes. Based on the phylogenetic analysis, PHD-finger genes were classified into 19 subgroups with distinct domain architectures (G1~G19). Specifically, G7, G16, and G18 were mainly consisted of PHD-finger genes having histone reader domains (PWWP, SAD_SRA, and Chromo, respectively) that could enhance the readout potential of PHD-finger genes by pairing with PHD-finger domain. Estimation of duplication time revealed that expansion of pepper PHD-finger genes in G12 might be the result of lineage-specific gene duplication. Our study provides fundamental genomic resources and a comprehensive evolutional relationship of PHD-finger gene family for accelerating further functional and breeding research.

***Corresponding Author:** Tel. 02-6490-5607, E-mail: mentorlg195@gmail.com

PA-0007

Genome-wide re-annotation and comparison provide insight into comprehensive diversification and adaptation of ZF-HD genes in plants

Min Jeong Jang, Jin Wook Choi, Geun Young Chae, Seungill Kim*

Department of Environmental Horticulture, University of Seoul, Seoul 02504, Korea

Zinc finger homeodomain (ZF-HD) is an important transcription factor family that plays significant roles in plant growth and responses to environmental stresses. However, comprehensive analyses of ZF-HD have not been conducted in plants based on accurate annotation. Here, we re-annotated ZF-HD genes in 90 plant species and performed a comparative analysis. We found 490 newly annotated genes which is equivalent to 37% of 1,342 previously annotated genes. In particular, 90% of total 1,650 genes had 2 main domain architectures: ZF-HD and ZF. We predicted conserved motif sequences of ZF-HD genes and determined motif positions. We found that motifs in ZF and HD regions were highly conserved compared with the other regions whereas motifs in regions encompassing ZF and HD were variable. Phylogenetic analyses revealed that ZF-HD genes were distinctly grouped into 16 subgroups with distinct domain architectures (G1~G16). Specifically, 8 and 5 subgroups were mainly consisted of ZF-HD and ZF respectively. Our analyses along with an improved annotation will serve as fundamental resources for accelerating functional and breeding studies in plants.

***Corresponding Author:** Tel. 02-6490-5607, E-mail: dedd502@naver.com

PA-0008

A proteomic approach to find modulators for PIN-FORMED (PIN) trafficking

Kwang-Ho Maeng[1], Hyodong Lee[1], Anindya Ganguly[2], Hyung-Taeg Cho[1*]

[1]Department of Biological Sciences, Seoul National University 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Republic of Korea

[2]Department of Biology and Center for Engineering Mechanobiology, Washington University in St. Louis, Missouri 63130

Auxin works as a morphogen to modulate the differentiation of cells, tissues, and organs by building local concentration gradients. The local auxin gradient can be formed by cell-to-cell movement of auxin in a directional way which is enabled by asymmetrical localization of auxin transporters, such as PIN-FORMEDS (PINs) in the plasma membrane (PM). Several proteins have been known to modulate intracellular PINs trafficking. To expand the scope of regulation of PIN polarity, we have searched for the interacting proteins with the hydrophilic loop (HL) domain of PINs. Bacteria-expressed PIN1-HL, PIN2-HL and PIN3-HL were used as baits to pull out their interacting proteins (PIPs for PIN-interacting proteins) from whole Arabidopsis seedling proteins. Isolated PIP proteins were analyzed by mass spectrometry to identify the proteins. This screening has identified several candidates for PIN trafficking-regulating factors, among which PIP1 shows a negative role in PIN trafficking to the PM and is thought to modulate the lytic pathway of PINs.

***Corresponding Author:** Tel. 02-880-6679, E-mail: htcho@snu.ac.kr

PA-0009

Calcium-dependent protein kinase 29 uses a unique phosphorylation code to modulate PIN-FORMED polarity and *Arabidopsis* development

Hyodong Lee[1], Anindya Ganguly[2], Song Baik[1], Hyung-Taeg Cho[1*]

[1]Department of Biological Sciences, Seoul National University 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Republic of Korea

[2]Department of Biology and Center for Engineering Mechanobiology, Washington University in St. Louis, Missouri 63130

PIN-FORMED (PIN)-mediated polar auxin transport is involved in key developmental processes in plants. Various internal and external cues influence plant development via the modulation of intracellular PIN polarity and, thus, the direction of polar auxin transport, but the mechanisms underlying these processes remain largely unknown. PIN proteins harbor a hydrophilic loop (HL) that has important regulatory functions, and was thus selected as bait in protein pulldown screening for modulators of intracellular PIN trafficking. CPK29, a Ca^{2+}-dependent protein kinase, was identified and shown to phosphorylate specific unique target residues on the PIN-HL that were not phosphorylated by other kinases. Furthermore, loss of CPK29 or mutations of the phospho-target residues in PIN-HLs significantly hampered intracellular PIN trafficking and polarity, causing defects in PIN-mediated auxin redistribution and biological processes such as lateral root formation, root twisting, hypocotyl gravitropism, phyllotaxis, and reproductive development. These findings indicate that CPK29 directly interprets Ca^{2+} signals from internal and external triggers, resulting in the modulation of PIN trafficking and auxin responses.

***Corresponding Author:** Tel. 02-880-6679, E-mail: htcho@snu.ac.kr

PA-0010

Oryza sativa, C3HC4-type E3 ligase, OsRFPHC-13 is positive a role to salt stress by regulating ABC transporter

Jong Ho Kim, Min Seok Choi, Yo Ram Uh, Cheol Seong Jang*

Plant Genomics Laboratory, Kangwon National University, Chuncheon 200-713, Republic of Korea

Salinity stress negatively affects plant growth, productivity, and metabolism. However, plants have evolved diversity strategies to survival upon high salinity condition. Among them, Ubiquitin-mediate E3 ligase is closely association for enhancing salt tolerance. So, we characterized molecular functions of rice C3HC4 RING-type E3-ligase gene. Oryza sativa RING finger protein HC-13 (OsRFPHC-13) was highly expressed upon 100 mM NaCl, 20% PEG8000 and 100 uM ABA. The GFP-OsRFPHC-13 protein was localized at cytosol in rice protoplasts. In vitro ubiquitin assay confirmed that OsRFPHC-13 possessed E3-ligase activity. Under salt stress, *OsRFPHC-13* overexpression plants (OE) has been measured higher Chlorophyll contents, enzyme activity (SOD, POD, CAT) and lower H_2O_2 contents. Additionally, *OsRFPHC-13* overexpression plants (OE) were identified low contents of Na^+, high K^+ both shoots and roots. In contrast, OsRFPHC-13 T-DNA knock-out plants (KO) have been measured low chlorophyll content, enzyme activity and higher H_2O_2. Also, knock-out plants were low absorbed Na^+, K^+ under salt stress. Growth of *OsRFPHC-13* overexpression plant was delayed under normal condition, but Knock-out plant growth not did. To identify OsRFPHC-13 salt tolerance mechanism, we conducted qRT-PCR for eight Na^+, K^+ transporter genes under 100 mM NaCl condition for 3, 6, 12h. Interestingly, various marker genes were shown significant diffident expression levels under salt stress in transgenic plants. Additionally, we conducted Y2H yeast hybrid system, confirmed to interaction gene (ABC transporter). Collectively, these results suggest that OsRFPHC-13 E3-ubiquitin ligase serves as a positive regulator of high salinity conditions via regulation of ABC transporter.

***Corresponding Author:** Tel. 070-7135-9637, E-mail: csjang@kangwon.ac.kr

PA-0011

Transcriptional regulation by receptor-like kinase Root Hair Specific 10 in *Arabidopsis thaliana*

Sang-So Lee, Song Baik, Hyung-Taeg Cho*

Department of Biological Sciences, Seoul National University 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Republic of Korea

Root hairs contribute to the survival and health of seedling plants as they provide physical support on soil and access to water and nutrition. Plants are equipped with toolkits to properly modulate root hair growth and development. ROOT HAIR SPECIFIC 10(RHS10)/PERK13, a receptor-like kinase specifically expressed on the root hair cell plasma membrane, is a negative regulator of root hair elongation. Although the function of RHS10 has been revealed, the downstream pathway leading RHS10 signal from plasma membrane to cellular response has yet to be uncovered. As part of an effort to identify RHS10-mediated signal transduction process, here we focused on identifying transcriptional targets of RHS10 (tTORs). RHS10-regulated transcriptome was acquired and analyzed from RHS10 inducible line *Arabidopsis thaliana* roots by RNA-seq. RHS10 regulates transcription of various genes. In particular, environmental stress-related genes were upregulated within a short period of time after RHS10 induction. Putative common *cis*-regulatory elements were screened from the promoter region of tTOR genes. Our findings suggest that RHS10 may also be involved in a different biological function other than root hair growth inhibition. Further experiments should characterize the transcriptional regulation mechanism by RHS10.

***Corresponding Author:** Tel. 02-880-6679, E-mail: htcho@snu.ac.kr

PA-0012

근적외선 분광분석법을 이용한 형질전환 콩 판별

손수인, 조우석, 오서윤, 신은경, 배재호, 조윤성*

전라북도 전주시 덕진구 농생명로 370 농업생명자원부

유전자변형 작물의 비의도적 혼입 또는 환경 방출 사고 등의 발생 가능성이 높아지는 상황에서 GMO 안전관리를 위한 신속하고 정확한 GMO 검출 기술이 필요하다. 현재 보편적으로 이용되는 DNA를 이용한 PCR 검사는 시료 준비부터 결과를 확인하기까지의 시간이 많이 걸리고 숙련된 인력을 필요로 하여 대량의 시료를 신속하게 검사하는데 어려움이 있으며, 단백질의 항원 항체 반응을 이용한 lateral flow strip은 사용이 간단하고 결과 확인에 걸리는 시간은 짧으나 비용 부담이 크다는 단점이 있다. 최근에는 기존 검사법에 대한 대안으로 근적외광 분광분석법을 이용한 판별기술 연구가 이루어지고 있는데 비파괴 검사로 시료의 준비가 간편하고 측정 방법이 간단하며 데이터 분석 및 결과 도출이 컴퓨터를 통해 이루어지기 때문에 데이터의 취급이 용이하다는 장점이 있다. 본 연구에서는 근적외선 분광분석법과 머신러닝을 이용하여 형질전환 콩인 카로티노이드 강화 콩과 그 모본인 광안 콩을 판별할 수 있을지 확인하고자 하였다. 분광 데이터는 콩잎을 이용하여 측정하였으며 자연광 하에서 325-1075nm 파장의 근적외선을 각 샘플 당 1,000회 이상 측정하여 수집하였다. 또한 다양한 환경에서 재배되더라도 구별이 가능할지 확인하기 위하여 봄과 가을에 각각 노지와 온실의 상이한 환경에서 재배된 두 집단에서 데이터를 측정하여 합산하였다. 측정된 데이터는 training set과 estimating set으로 나누어 training set을 대상으로 데이터마이닝을 수행하고 estimating set를 이용하여 평가하였다. 본 연구에서는 데이터의 전처리 없이 머신러닝을 수행하였을 때 Support Vector Machine(SVM) 적용 시 82%의 예측률을 보였다. 향후 데이터의 전처리를 적용하고 측정된 분광 데이터의 양이 더 많이 누적 될수록 더 높은 예측 정확도를 보일 것으로 기대된다.

***교신저자:** Tel. 063-238-4706, E-mail: younsung@korea.kr

PA-0013

A lipid kinase is identified by the proteomic approach to find PIN-FORMED trafficking modulators

Kyeonghoon Lee[1], Hyodong Lee[1], Anindya Ganguly[2], Kwang-Ho Maeng[1], Hyung-Taeg Cho[1*]

[1]Department of Biological Sciences, Seoul National University 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Republic of Korea

[2]Department of Biology and Center for Engineering Mechanobiology, Washington University in St. Louis, Missouri 63130

A local auxin gradient is an important cue for plant growth and organogenesis. The subcellular polarity of PIN-FORMED (PIN) auxin efflux carriers is achieved by intracellular vesicle trafficking and important to form local auxin gradients. The central hydrophilic loop (HL) of a PIN protein provides an interface for various interactions between PIN and its modulator proteins. Several direct interactions of PINs and their interacting proteins were revealed but whole interactome around PINs are still vague. To find other modulators of PIN-vesicle trafficking, we took advantage of proteomic approach. First, we used bacteria-expressed HL of 3 different PINs as baits to pull out their interacting proteins (PIPs) from Arabidopsis seedling proteome. Then, PIPs, segregated by SDS-PAGE and analyzed by mass spectrometry to identify the proteins. These putative PIPs include lipid kinases, GTPases, scaffolding protein, protein kinases, etc. To verify direct interactions and interaction sites between PIPs and PIN-HL in vitro, we used GST pull-down assays and confirmed that PIP3 interacts with PINs-HL. This approach reveals novel modulators that could be involved in regulation of intracellular PIN trafficking and auxin-mediated plant development.

***Corresponding Author:** Tel. 02-880-6679, E-mail: htcho@snu.ac.kr

PA-0014

Wheat (*Triticum aestivum* L.) gluten relative gene transcript variants are frequently expressed under heat stress during grain filling stage

Chan Seop Ko[1], Jin-Baek Kim[2], Min Jeong Hong[2], Yong Weon Seo[1*]

[1]Department of Plant Biotechnology, Korea University, 145 Anam-ro, Seongbuk-Gu, Seoul, Korea
[2]Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, 29 Geumgu, Jeongeup, Korea

Common wheat (*Triticum aestivum* L.) is frequently exposed to high temperature during anthesis and ripening period, which resulted in yield loss and detrimental end-use quality. Especially, high temperatures induce that glutenin and starch relative genes were decreased, which inhibits the rate of seed filling and size. To reveal the effect of high temperature stress on wheat grain development, wheat grain studies were conducted. Total seed storage proteins were extracted from grains of “Con” (nine days after flowering), “DAT6-T” (six days of treatment) and DAT10-T (ten days of treatment) were analyzed by SDS and 2DE-PAGE. Protein spots showing decreased level in stressed plants were shown to have strong similarities with a high-molecular glutenin gene (*TraesCS1D02G317301*). QRT-PCR results confirmed that high-molecular glutenin gene was expressed in its full form and in the form of four different transcript variants. These events always occurred between repetitive regions at specific deletion sites (5'-CAAGG/TG-3') in an exonic region. Specific deletion sites formed hairpin structures, which is required for “transcription slippage”, and provide cleavage starts to generate transcript variants. This structural form might support deletion between specific sites that are reside on both ends of the repetitive regions, which resulted in transcript variants. Our results proved that all transcript variants maintained the HMW-GS functions and shortened mRNA were formed without a non-mediated protein or truncated protein under heat stress during grain filling stage.

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***Corresponding Author:** Tel. 02-3290-3005, E-mail: seoag@korea.ac.kr

PA-0015

Genetic variations of the starch synthase gene family in rice (*Oryza sativa* L.)

Hongjia Zhang[1†], Seong-Gyu Jang[1†], San Mar Lar[1], Ah-Rim Lee[1], Fang-Yuan Cao[1], Junhee Hong[1,2], Jeonghwan Seo[1,2], Soon-Wook Kwon[1,2*]

[1]Department of Plant Bioscience, College of Natural Resources and Life Science, Pusan National University, Miryang 50463, Korea
[2]Life and Industry Convergence Research Institute, Pusan National University, Miryang 50463, Korea

Starch is a major ingredient in rice, and the amylose content significantly impacts the rice quality. *OsSS* is a gene family related to the synthesis of amylose and amylopectin, and 10 members have been reported. In the present study, a synteny analysis of a novel family member belonging to the *OsSSIV* subfamily that contained a starch synthase catalytic domain showed that three segmental duplications and multiple duplications were identified in rice and other species. Expression data showed that the *OsSS* gene family is involved in diverse expression patterns. The prediction of miRNA targets suggested that *OsSS* are possible widely regulated by miRNA functions, with miR156s targeted to *OsSSII-3*, especially. Haplotype analysis exhibited the relationship between amylose content and diverse genotypes. These results give new insight and a theoretical basis for the improved amylose content and eating quality of rice.

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[†] These authors contributed equally to the work.

***Corresponding Author:** Tel. 055-350-5506, E-mail: swkwon@pusan.ac.kr

PA-0016

Genomic and Evolutionary analysis of Triticain-α in Cultivated Wheat and Wild Barley

Sang Heon Kim, Yong Weon Seo*

Department of Plant Biotechnology, Korea University, Seoul, Korea

Prolamins are the major seed storage proteins in grain. Gluten proteins are major prolamins in the *Triticeae* crops such as wheat and barley. During seed germination and consecutive seedling growth, seed storage proteins are degraded and mobilized from endosperm by cysteine proteases. Triticain-α is a novel papain-type cysteine protease from wheat and hydrolyze gluten proteins. To find out genomic differences of Triticain-α between cultivated wheat and wild barley, coding DNA sequences (CDS) of Triticain-α were sequenced from durum wheat (*Triticum turgidum* ssp. *durum*, 2n = 4x = 28, genome AABB) cv. 'Cappelli', common wheat (*T. aestivum*, 2n = 6x = 42, genome AABBDD) cv. 'Baekgang', and wild barley (*Hordeum roshevitzii*, 2n = 2x = 14, genome II). The sequences of nucleotides and amino acids were analyzed and compared with the gene sequences of papain-type cysteine proteases from other species were obtained from NCBI (https://www.ncbi.clm.nih.gov/) and Uniprot (http://www.uniprot.org/). The phylogenetic relationship of the collected data was investigated. The results indicated that Triticain-α of wheat and barley were relatively close and their sequences were grouped by genome. The secured information will be helpful to understand evolutionary relationship of cysteine proteases between wheat and barley.

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***Corresponding Author:** Tel. 02-3290-3005, E-mail: seoag@korea.ac.kr

PA-0017

Comparative FISH analysis of *Senna tora* tandem repeats revealed insights into the chromosome dynamics in genus *Senna*

Ta Thanh Dat, Nomar Espinosa Waminal, Nguyen Thi Hong, Remnyl Joyce Pellerin, Hyun Hee Kim*

Department of Chemistry & Life Science, BioScience Institute, Sahmyook University, Seoul 01795, Republic of Korea

DNA tandem repeats (TRs) are often abundant and occupy discrete regions in eukaryotic genomes. Tracing the chromosomal distribution of TRs could therefore provide insights into the chromosome dynamics and speciation among closely related taxa. The basic chromosome number in the genus *Senna* is $2n = 28$, but dysploid species like *Senna tora* have also been observed. Derived on *Senna tora* genome, we have successfully identified 13 abundant TRs. To understand the dynamics of these TRs and their impact on *S. tora* dysploidization. We performed a comparative fluorescence *in situ* hybridization (FISH) analysis among nine closely related *Senna* species and compared the chromosomal distribution of these repeats from a cytotaxonomic perspective by using the ITS1-5.8S-ITS2 sequence to infer phylogenetic relationships. Of the nine *S. tora* TRs, two did not show any FISH signal whereas seven TRs showed similar and contrasting patterns to other *Senna* species. StoTR01_86, which was localized in the pericentromeric regions in all *S. tora*, but not at the nucleolar organizer region (NOR) site, was colocalized at the NOR site in all species except in *S. siamea*. StoTR02_7_tel was mostly localized at chromosome termini, but some species had an interstitial telomeric repeat in a few chromosomes. StoTR05_180 was distributed in the subtelomeric region in most species and was highly amplified in the pericentromeric region in some species. StoTR06_159 was either absent or colocalized in the NOR site in some species, and StoIGS_463, which was localized at the NOR site in *S. tora*, was either absent or localized at the subtelomeric or pericentromeric regions in other species. These data suggest that TRs play important roles in *S. tora* dysploidy and suggest the involvement of 45S rDNA intergenic spacers in “carrying” repeats during genome reshuffling.

Keywords: Chromosome rearrangement, dysploidy, FISH, tandem repeat, *Senna*

***Corresponding Author:** Tel. +82-2-3399-1715, E-mail: kimhh@syu.ac.kr

PA-0018

Comparative triple-color FISH-mapping in five *Senna* species using rDNA and telomeric repeat probes

Hong Nguyen, Nomar Espinosa Waminal, Do Sin Lee, Remnyl Joyce Pellerin, Ta Dat, Byung Yong Kang, Hyun Hee Kim*

BioScience Institute, Department of Chemistry and Life Science, Sahmyook University, Seoul 01795, Republic of Korea

Senna is a diverse and paraphyletic genus in the subfamily Caesalpinioideae (Fabaceae Lindl.) comprising various species of industrial and medical value. However, to date, the genome-based taxonomic relationship among several *Sena* species remains enigmatic. The insufficient chromosomal data in many *Senna* species impedes comparative cytotaxonomic analyses to decipher their phylogenetic relationship and genomic evolution. To provide additional *Senna*-related molecular cytogenetic information, we compared the karyotypes of five *Senna* species employing triple-color fluorescence *in situ* hybridization (FISH) of 5S rDNA, 45S rDNA and *Arabidopsis*-type $(TTTAGGG)_n$ telomeric pre-labeled oligonucleotide probes. The chromosome number $2n = 28$ was predominant but a $2n = 22$ was also observed. While all species revealed only one interstitial 5S rDNA locus, the 45S rDNA showed 1 to 3 loci and mostly localized at the terminal region of chromosomes. Additionally, we observed a hemizygous 45S rDNA locus in *S. auriculata*. Telomeric signals localized at the chromosome termini of all chromosomes in all species. Moreover, weak interstitial telomeric signals were also detected in two chromosome pairs in *S. alexandrina*. These cytogenetic data can be integrated with molecular phylogenetic data for more comprehensive *Senna* cytotaxonomic analyses.

Keywords: Cytogenetic markers, FISH, Genome, Karyotype, *Senna*

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***Corresponding Author:** Tel. +82-2-3399-1715, E-mail: kimhh@syu.ac.kr

PA-0019

Comprehensive transcriptome analysis and growth phase-specific profiling of gene expression in mungbean (*Vigna radiata* [L.] Wilczek)

Eunsoo Lee[1], Moon Young Kim[2], Hyoseob Seo[1], Hyun-Ju Jang[2], Suk-Ha Lee[1*]

[1]Department of Agriculture, Forestry and Bioresources and Research Institute of Agriculture and Life Sciences, Seoul National University, Seoul 08826, Republic of Korea

[2]Plant Genomics and Breeding Institute, Seoul National University, Seoul 08826, Republic of Korea

Understanding the stages of plant development is important for obtaining high yields and for managing environmental variations properly. In particular, the developmental transition from the vegetative to reproductive phase, accompanied by large physiological changes, has a critical influence on plant productivity. Mungbean (*Vigna radiata* [L.] Wilczek) belonging to legumes is consumed continuously worldwide, however, the genetic background related to the development process remains poorly understood. Here, we divided the development stages of mungbean into three categories: Vegetative stage (Veg), which produces only leaves, Reproductive 1 stage (R1), which forms leaves but also forms inflorescence, and Reproductive 2 stage (R2), which produces the only inflorescence without generating leaves. The overall gene expression patterns appearing during three stages through two genotypes, VC19573A and IT208075, showing different plant architecture were surveyed by RNA-seq analysis using shoot apical tissue and grouped from clustering analysis. A total of 1,890, 1,105, and 3,130 differentially expressed genes (DEGs) appearing between stages and common to genotypes were identified in Veg-R1, R1-R2, and Veg-R2, respectively. The most highly enriched Gene Ontology term for these DEGs was biological processes. This study suggests a standard model for the classification of plant architecture in mungbean. Our results also provide a comprehensive characterization of gene expression during transitioning of the plant phase and will serve as resource for unraveling the function underlying plant development.

***Corresponding Author:** Tel. 02-880-4555, E-mail: sukhalee@snu.ac.kr

PA-0020

Transcriptome analysis of red colored rice mutant at seed developmental stage

Gileung Lee, jae Wan Park, Jisu Park, Ah-Reum Han, Min Jeong Hong, Yeong Deuk Jo, Jin-Beak Kim, Hong-Il Choi*

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

Red colored rice seeds contain various bioactive ingredients such as phenolic compounds and tannins, which are known to have anti-oxidant, anti-cancer, and anti-inflammatory effect. In this study, comparative transcriptome analysis between red colored rice (MR1, a mutant induced by γ-ray irradiation) and non-colored rice (cv Dongan) was performed to investigate genetic basis of pigment biosynthesis at two different seed developmental stage. A total of 401 (150 up-regulated and 251 down-regulated genes) and 908 (342 up-regulated and 566 down-regulated genes) differentially expressed genes (DEGs) were identified at milky stage (14DAF) and mature stage (28DAF), respectively. The result of gene ontology (GO) classification revealed that metabolic process and catalytic activity terms included larger number of up-regulated DEGs compared to down-regulated DEGs, while the opposite was observed in response to stimulus, binding, and intracellular terms. Kyoto encyclopedia of genes and genomes (KEEG) pathway were significantly enriched in flavonoid biosynthesis, DNA replication, diterpenoid biosynthesis, biosynthesis of secondary metabolites, and protein processing in endoplasmic reticulum. Also, we found eight up-regulated DEGs, *CHS*, *F3H*, *F3'H*, *Rd*, *ANS*, *LAR*, *GSTU*, and *Rc* which were involved in biosynthesis pathway of proanthocyanidin (known as red pigment in rice), and the expression of the genes were further validated by using quantitative real time PCR. Our results provide comprehensive expression profiling data and foundation for further study on pigment biosynthesis in red colored rice.

***Corresponding Author:** Tel. 063-570-3298, E-mail: hichoi@kaeri.re.kr

PA-0021

Structure and Function of Rice Chloroplast Genome Based on the Comparison with Nuclear and Mitochondria Genomes

Luqi Hu[1], Sang-Ho Chu[2], Kyu-Won Kim[2], Yong-Jin Park[1,2]*

[1]Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 32439, Republic of Korea

[2]Center of Crop Breeding on Omics and Artificial Intelligence, Kongju National University, Yesan 32439, Republic of Korea

The chloroplast genome has played an extremely important role in photosynthesis, and cooperated with nuclear genes to regulate the expression of chloroplast genes and the formation of chlorophyll in rice, that is one of the major food crops in the world and the utilization of its functional genes has become a widespread subject. This review not only collects the latest research in the field of rice chloroplast genome research in recent years, but also counts the complete genetic information on the genomes of rice. We also excavated the genome data of 154 rice germplasms and analyzed the structural variation between the chloroplast genome and the mitochondrial genome. Our results proved that the chloroplast genome has higher stability. This has certain reference value for future research on plant domestication. This review paper focuses on the functional and structural genetic information of rice chloroplast genome, as well as the expression and transfer of functional genes, and further discusses the utility of chloroplast genome in phylogenetic research, functional genome research and rice breeding.

Keywords: chloroplast genome, rice, Oryza, gene sequence, functional genes, gene transfer

***Corresponding Author:** Tel. 041-330-1213, E-mail: yjpark@kongju.ac.kr

PA-0022

Identification of gene expression response to drought stress using RNA-seq analysis in maize

Kyung-Hee Kim[1], Jeong Min Park[1], Jae Yoon Kim[2], Byung-Moo Lee[1*]

[1]Department of Life Science, Dongguk University-Seoul, Seoul 04620, Republic of Korea
[2]Department of Plant Resources, College of Industrial Science, Kongju National University, Yesan 32439, Republic of Korea

Maize is often affected by drought stress, resulting in poor growth and reduced yields. This study aims to identify specific genes involved in vegetative and reproductive stages in maize under drought stress using network-based transcriptome analysis. To analyze stage-specific gene for drought stress, cluster analysis was conducted by using 144 RNA-seq data of B73 at seedling and development stage. We also analyzed using Weighted Gene Correlation Network Analysis (WGCNA) method to identify drought stress-related modules. A total of 38 modules were detected based on RNA-seq data. Of these, six modules (darkgrey, lightpink4, novajowhite2, red, salmon, salmon4) were associated with the characterization of drought stress according to the modules eigengene (ME) expression pattern. Among 6 modules, the expression level of the red module gradually decreased due to drought stress during seedling development, while the expression level of tassel and silk increased and decreased in the other modules. In addition, Salmon4 module showed a decreasing pattern due to drought stress in the ear, and relatively increased expression in the tassels. In Salmon4 module, 103 genes were identified, but 64 genes consistent with entrez IDs were identified. Twenty genes (GRMZM2G090262, GRMZM2G388915, GRMZM5G895064, GRMZM2G328988, GRMZM2G128877, GRMZM2G157462, GRMZM2G091143, GRMZM2G156320, GRMZM2G104833 GRMZM2G077844, GRMZM2G154366, GRMZM2G343588, GRMZM2G470556, GRMZM2G099160, GRMZM2G360455, GRMZM2G146386l, GRMZM2G102243, GRMZM2G118344, GRMZM2G416386, GRMZM2G075900) in Salmon4 module were related to phosphoprotein phosphatase activity, nucleotide excision repair, ubiquitin mediated proteolysis, oxidative phosphorylation, non-lysosomal glucosylceramidase, pgr5 protein, phosphatidate phosphatase PAH2, protein phosphatase 2C isoform gamma, putative aminodeoxychorismate synthase, and putative E3 ubiquitin-protein ligase RF298.

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

PA-0023

Screening and characterization of wheat lines missing omega-5 gliadins encoded by the 1D genome in 665 wheat germplasm

Sewon Kim, Jae-Ryeong Sim, Su-Bin Lee, Yu Jeong Yang, Jong-Yeol Lee*

National Institute of Agricultural Science, RDA, Jeonju, 54874, Republic of Korea

Omega-5 gliadins are a group of highly repetitive gluten proteins in wheat flour encoded on the 1B chromosome (ω-5B) of hexaploid wheat. These proteins are the major sensitizing allergens in a severe form of food allergy called wheat-dependent exercise-induced anaphylaxis (WDEIA). Furthermore, we confirmed that the omega-5 gliadins, encoded on the 1D chromosome (ω-D4), is minor allergens of WDEIA. Using a specific marker of omega-5 gliadin encoded on the 1D chromosome, we screened twelve ω-D4 missing lines from 665 wheat genotypes employed in breeding programs in South Korea. As a result of measuring the *ω-D4* gliadin gene copy number in twelve ω-D4 missing lines, there was a significant decrease in the *ω-D4* gliadin gene copy number in all twelve ω-D4 missing lines. Two-dimensional gel electrophoresis (2-DE) analysis and ω-5B monoclonal antibody immune response confirmed a decrease in ω-D4. In addition, reversed-phase ultra-performance liquid chromatography (RP-UPLC) and repeat junction primer (RJPrimer) were used to confirm the deficiency of the ARE-type omega-1,2 gliadin encoded in the 1D genome in seven of the twelve ω-D4 missing lines. Crossing the ω-D4 missing lines with the major ω-5 gliadins missing varieties could contribute to the development of safe varieties for WDEIA patients.

***Corresponding Author:** Tel. 063-238-4616, E-mail: jy0820@korea.kr

PA-0024

Characterization of mutated wax synthesis gene and improvement of drought insensitivity in rice

Seung Young Choi, Hyeonung Seo, Jong Ho Kim, Yea Dam Kim, Cheol Seong Jang*

Plant Genomics Laboratory, interdisciplinary Program in Smart Agriculture, Kangwon National University, Chuncheon 200-713, Republic of Korea

Drought stress greatly reduces rice productivity. Therefore, the development of new varieties with drought stress tolerance was a big challenge in rice breeding. Accordingly, 200-1034(36) mutant were selected among the rice line M12 irradiated with gamma rays. Through whole genome re-sequencing analysis, it was confirmed that a deletion occurred in the Os05g48260 gene, and this gene was named OsWSD1 as a gene related to wax synthase. It is thought that the mutation of OsWSD1 showed insensitivity to drought stress, and the experiment was carried out accordingly. Two-week plants showed no significant difference between WT and 200-1034(36) mutant and showed higher values in survival rate and fresh weight after dehydration for 8 hours for drought stress treatment and then water again for 5 days. SEM images were captured to confirm the differences in the leaf surfaces of the two plants. SEM images showed that many cuticular wax compounds were accumulated on the surface of adaxial leaves in 200-1034(36) mutant compared to WT. When the expression levels of wax synthesis-related genes were observed in 4th leaves of 2-week-old WT and 200-1034(36) through qRT-PCR, it was found that the expression levels of wax synthesis-related genes were generally increased. Also, we identified fatty acid contents in leaf of WT and 200-1034(36). Interestingly, free-fatty acid, aldehyde, alkane and alcohols contents of 200-1034(36) were higher identified than WT except for ester. And the difference in gene expression levels of WT and mutant plants was analyzed through RNA-seq DEG analysis.

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***Corresponding Author:** Tel. 070-7135-9637, E-mail: csjang@kangwon.ac.kr

PA-0025

Highly accurate long-read HiFi sequencing data in 12 doubled haploid lines of *Brassica rapa*

Jung Sun Kim*, Mi-Sun Moon, Hyun Woo Park

Department of Agricultural Biotechnology, National Institute of Agricultural Sciences, Rural Development Administration, Jeonju, 54874, Republic of Korea

We conducted 161 doubled haploid (DH) plants by microspore culture on the intercross F_1 with *Brassica rapa* ssp. *trilocularis* (yellow sarson) and *B. rapa* ssp. *chinensis* (pak choi). Phenotype traits are measured in the locule number, seed color, sinus, leaf width, leaf length, column length, leaf color, leaf angles and flowering time etc. in DH plants. We selected 12 DH lines which are distinguished on the locule numbers, seed color, and flowering time. The PacBio® HiFi sequencing method yields highly accurate long-read sequencing datasets with read lengths averaging 10~25kb and accuracies greater than 99.5%. The N50 average read lengths of row data, subread, and CCS are determined 188Kb, 13.7Kb and 13.1Kb, respectively. Assembly results, they reached 391.8 Mb in average and this size as the longest as *B. rapa* genome sequences. Average longest assemble size is 15Mb and the complete BUSCSO(v4.0) is 99.05%. These accurate long reads can be used to improve results for complex applications such as single macrolide and structural variant selection for our target traits.

Keywords: The PacBio® HiFi sequencing, *Brassica rapa* ssp. *trilocularis*, *B. rapa* ssp. *chinensis*, BUSCSO(v4.0)

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***Corresponding Author:** Tel. 063-238-4559, E-mail: jsnkim@korea.kr

PA-0026

Expression analysis of genes involved in isoflavone and astragalosides biosynthetic pathways in the mature roots of *Astragalus membranaceus*

Ji-Nam Kang[1], JongWon-Han[2], Tae-Ho Lee[1], Si Myung Lee[1*]

[1]Genomics Division, National Institute of Agricultural Sciences, 370 Nongsaengmyeong-ro, Jeonju-si, Jeollabuk-do, 54874, Republic of Korea
[2]Herbal Crop Research Division, Department of Herbal Crop Research, 92 Bisanro, Eumseong, Chunbuk, 27709, Republic of Korea

Astragalus membranaceus (*A. membranaceus*) belongs to the legume family and is a medicinal crop used as one of the most important herbal medicines in Korea. The roots of *A. membranaceus* have been used as a material for therapy of antiperspirant, antiviral, antibacterial, antioxidant, and anti-inflammatory. Isoflavones are secondary metabolites mainly found in legumes. Genistein and daidzein are well-known isoflavones and have reported benefits for human health, including relieving menopausal symptoms, improving blood cholesterol levels, reducing osteoporosis, and reducing the risk of heart disease. Isoflavones are synthesized via the phenylpropanoid pathway. Astragalosides are the major bioactive substances found in *Radix astragali* (*A. membranaceus* and Related Species), which belong to the cycloartane-type triterpene saponins. Astragalosides exhibit pharmacological functions such as anti-tumor, anti-viral, immune-boosting, anti-hypertensive, hepatoprotective, anti-diabetic, and anti-aging. In this study, the expression of genes involved in the biosynthesis of isoflavones and astragalosides during root maturation of *A. membranaceus* was analyzed. Isofrom and RNA sequencing were used to construct de novo transcripts. We investigated all genes involved in the biosynthesis of isoflavones and astragalosides along with their parologue genes. The expression of the gene encoding isoflavone synthase was significantly higher in 150 DAG (day after grown) roots than that of 90 DAG roots. The expression of genes involved in astragalosides biosynthesis was significantly lower in 150 DAG roots than that of 90 and 120 DAG roots. Our results suggest that the biosynthesis of isoflavones and astragalosides in *A. membranaceus* roots is regulated at different times, which may provide information on the collection timing of *A. membranaceus* roots for better pharmacological activity.

***Corresponding Author:** Tel. 063-238-4560, E-mail: tataby@korea.kr

PA-0027

New modulators for intracellular trafficking of PIN-FORMEDs (PINs)

Young Kim, Hyodong Lee, Anindya Ganguly, Kwang-Ho Maeng, Kyeonghoon Lee, Hyung-Taeg Cho*

Department of Biological Sciences, Seoul National University 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Republic of Korea

The polar distribution of auxin is essential for plant growth and development. This polar distribution of auxin is known to be regulated mainly by the polar localization of PIN-FORMED (PIN) auxin efflux carriers in the plasma membrane (PM). In addition, PIN polarity regulation is also known to be mediated through several protein kinases/phosphatases. To expand knowledge of PIN polarity regulation, we took advantage of the proteomic tool to find the modulators that directly interact with PINs and affect their trafficking and plant development. First, we used the bacteria-expressed central hydrophilic loops (HL) of 3 different PINs as baits to pull out their interacting proteins (PIPs) from whole Arabidopsis seedling proteins. Next, PIPs, differentially displayed on SDS-PAGE, were analyzed by mass spectrometry to identify the proteins and genes. These putative PIPs include protein kinases, GTPase, protein-interacting proteins, etc. PIP12, a protein kinase, interacted with PINs-HL in yeast 2-hybrid and in vitro pull-down assays. Although the in vivo functions of PIP12, for example, modulation of PIN phosphorylation and trafficking, has yet to be characterized, this approach reveals novel putative modulators that regulate intracellular PIN trafficking and auxin-mediated plant development.

***Corresponding Author:** Tel. 02-880-6679, E-mail: htcho@snu.ac.kr

PA-0028

Molecular characterization of *FAB2* genes in diploid and tetraploid perilla

Hye Ji Lee, Hyun Uk Kim*

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

Perilla is one of the oilseed crops cultivated mainly in Korea and East Asia. Perilla seed has 43% triacylglycerol (TAG), which composed of 64% of α-linolenic acid and 14 % of linoleic acid. This polyunsaturated fatty acids (PUFAs) have the advantage of helping metabolism and lowering cholesterol levels in humans. *Fatty acid biosynthesis 2* (*FAB2*) is responsible for forming a first double bond in catalyzing 18:0-acyl carrier protein (ACP) to 18:1-ACP in plastid and this 18:1 moiety is transported to endoplasmic reticulum and it is used for precursor to synthesize PUFAs. In this study, we identified the *FAB2* gene from the wild type diploid perilla (*Perilla citriodora*) and the cultivated tetraploid perilla (*Perilla frutescens* var. *frutescens*) genomes. Sequence analysis revealed that *P. citriodora* has two copies of *PfrFAB2A* and *PfrFAB2B,* which is different from Arabidopsis has one copy of *FAB2*. Current cultivated tetraploid perilla, *P.frutescens* exist four copies of *PfrFAB2A-1, PrFAB2A-2, PfrFAB2B-1,* and *PfrFAB2B-2,* which is indicating that tetraploid perilla came from natural crossing between *P.citrodora* and unidentified diploid perilla. To test functional activity of perilla *FAB2* genes, we are doing complementation test by transforming perilla *FAB2* genes to Arabidopsis *fab2* mutant.

***Corresponding Author:** Tel. 02-6935-2491, E-mail: hukim64@sejong.ac.kr

PA-0029

A transcriptomic analysis of the faba bean (*Vicia faba* L.) genome reveals the presence of novel cold stress-related genes through long-read isoform sequencing technology

Jae Il Lyu[1], Rahul Ramekar[2], Jung Min Kim[1], Nguyen Ngoc Hung[1], Ji Su Seo[1], Jin-Baek Kim[1], Ik-Young Choi[2], Kyong-Cheul Park[2], Soon-Jae Kwon[1*]

[1]Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongup 56212, Korea
[2]Department of Agriculture and Life Industry, Kangwon National University, Chuncheon, 24341, Korea

Faba bean can also adapt to diverse climate and soil conditions, providing it with another advantage over other legumes. However, similar to other major legumes, faba bean yield remains relatively unstable, which has limited its competitiveness as a commercial crop. The lack of draft genome annotations and the unclear structural information regarding mRNA transcripts have impeded the genetic improvement of faba bean. In this study, we sequenced and analyzed the total RNA using the PacBio single-molecule long-read isoform sequencing platform. We identified 28,569 non-redundant unigenes, ranging from 108 to 9,669 bp, with a total length of 94.5 Mb. Many of the unigenes (3,597, 12.5%) had 2-20 isoforms, indicative of a highly complex transcriptome. The predicted proteins and transcription factors encoded by the unigenes included NB-ARC, Myb_domain, C3H, bHLH, and heat shock protein family members, implying the faba bean genome carries a considerable abundance of stress resistance genes. To validate our results, we selected a few unigenes from the ICE-CBF-COR pathway to analyze their expression patterns in cold-treated samples via qRT-PCR assays. The expression of the dehydrin-related genes was induced by cold stress. The assembled data provide the first insights into the deep sequencing of full-length RNA from faba bean at the single-molecule level. The results of this study may be useful for future functional and comparative genomic studies. Moreover, our findings demonstrate the advantages of the SMRT Iso-seq method for identifying genes in non-model plants.

***Corresponding Author:** Tel. 063-570-3312, E-mail: soonjaekwon@kaeri.re.kr

PA-0030

Novel QTL associated with root radial oxygen loss (ROL) identified in double haploid rice

Dang van duyen[1*], Youngho Kwon[2], Nukulu Rolly Kabange[2], Ji-Yun Lee[1], Dongjin Shin[2], So-Myoeng Lee[2], Jin-Kyung Cha[2], Jun-Hyeon Cho[2], Jong-Hee Lee[2], Jong-Min Ko[2]

[1]Department of molecular biology, Agricultural genetic institute, Hanoi11917, Vietnam
[2]Department of southern area crop science, Paddy crop research division, NICS, RDA

According to Paris agreement Korea must reduce greenhouse gasses (GHG) to 37% to 2030. GHG from rice cultivation possesses 29.5% on agricultural area. In rice field, in anaerobic condition, methanogen makes methane and methanotrophs degrade methane in aerobic condition. So secreting amount of oxygen from rice root is important such as radial oxygen loss (ROL). Rice root ROL is considered as an important trait for low methane emission on rice plant. Methanotroph oxidize methane to dihydrogen oxide and carbon dioxide using oxygen from root. Likewise, methanotrophs well colonizes on rice variety which has high ROL ability. In this study, we evaluated ROL ability of double haploid population derived from a cross between 93-11 (P1, *indica*) and Milyang352 (P2, *japonica*), grown under FeS media. When rice root grew on FeS media, oxidized zone to be clear. The results of the phenotypic evaluation indicated that parental lines 93-11 (P1, low ROL ability *indica* cultivar) and Milyang352 (P2, high ROL ability *japonica* cultivar) showed different phenotype responses, also reflected in mapping population. Furthermore, the linkage mapping and quantitative trait loci (QTL) analysis detected one QTL associated with ROL on chromosome 2 which is *qROL2-1* and LOD score was 3.17. The *qROL2-1* having highest phenotypic variation explained, and being the only QTL associated with ROL on FeS media. Therefore, a novel *qROL2-1* can be promising trait to a new aspect of reduce GHG.

***Corresponding Author:** Tel. 055-350-1162, Email: dangvanduyen79@gmail.com

PA-0031

Transcriptome analysis by RNA-Seq reveals genes related to flower coloration in Kenaf (*Hibiscus cannabinus* L.) mutants

Jae Il Lyu[1], Jaihyunk Ryu[1], Jung Min Kim[1], Dong-Gun Kim[1], Nguyen Ngoc Hung[1], Ji Su Seo[1], Jin-Baek Kim[1], Joon-Woo Ahn[1], Si-Yong Kang[2], Soon-Jae Kwon[1*]

[1]Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongup 56212, Korea
[2]Department of Horticulture, College of Industrial Sciences, Kongju National University, Yesan, Chungnam Province 32439, Korea

The biochemical compounds of kenaf leaves and flowers have been analyzed and mainly consist of flavonoids, including flavonoid glycosides and floral anthocyanins. In this study, we performed RNA-sequencing to obtain comprehensive transcriptome analysis and identified putative genes involved in flower coloration according to different flower developmental stages in Baekma (white flower), Jangdae (ivory flower) and Bora (purple flower). A total of 36.1 Gb reads were generated for two kenaf accessions and finally yielded 38,601 representative transcripts having an average length of 1,350 bp, of which 33,057 (85.64%) were annotated against various databases. Expression profiling of the transcripts identified 1,044 and 472 differentially expressed genes (DEGs) among three mutants at young buds and full bloom stages, respectively. Those DEGs revealed that the representative pathway were "biosynthesis of secondary metabolites", including phenylpropanoid biosynthesis, flavonoid biosynthesis by KEGG enrichment analysis. Thus, we investigated genes related to phenylpropanoid pathway, which counted 140 DEGs from 1,150 annotated DEGs. Our results provide a resource for understanding gene functions and should also be useful in further studies of flower coloration in kenaf.

***Corresponding Author:** Tel. 063-570-3312, E-mail: soonjaekwon@kaeri.re.kr

PA-0032

Comparative genome analysis of two contrasting *Saltol* QTL introgressed lines under salinity stress during the vegetative growth stage

Jae-Hyuk Han, Na-Hyun Shin, Joong Hyoun Chin*

Department of Integrative Biological Sciences and Industry, Sejong University, Seoul, 05006, Korea

Soil salinity is a serious problem and adversely affects all aspects of plant development. Several studies have been reported to elucidate the molecular basis of salinity tolerance in rice. However, genetic information such as quantitative trait loci (QTL) and molecular markers from these studies has been rarely utilized in marker-assisted breeding. Two sisters backcrossed inbred lines (BILs) have been developed by marker-assisted backcrossing using the *Saltol* linked markers to improve the salinity tolerance of MS11 (a temperate japonica growing in tropical condition). The genomic similarity of the two BILs was 73%. Interestingly, the BILs showed very different phenotypes in seedling stage under salinity stress conditions, although both contained the *Saltol* QTL. The gene *OsHKT1;5* located in *Saltol* region showed higher expression levels at seven days after salinity treatment. Futher, genes of expression levels constituting the transcriptional complex regulating *OsHKT1;5* were analysed, but there were no significant differences among them. To identify the genetic differences between two lines, we performed whole genomes resequencing and generated a coverage of more than 13X using Illumina Hiseq2500. These were mapped to Nipponbare (*japonica* rice), Zhenshan 97 (*indica* rice), and N22 (*aus* rice) reference genomes. The distribution of single nucleotide polymorphisms (SNPs) were presented and SNPs analysis is being performed. Through this study, we will identify alleles related to *Saltol* and provide breeders with useful informations when breeders utilize *Saltol* QTL in molecular breeding.

***Corresponding Author:** Tel. 02-3408-3897, E-mail: jhchin@sejong.ac.kr

PA-0033

Transcriptome analysis to figure out the interplay of *Pup1* and *Sub1* under phosphorous -sufficient and -deficient conditions

Na-Hyun Shin[1], Jae-Hyuk Han[1], O New Lee[2], Joong Hyoun Chin[1*]

[1]Department of Integrative Biological Sciences and Industry, Sejong University, 209 Neungdong-ro, Gwangjin-gu, Seoul 05006, Korea
[2]Department of Bioindustry and Bioresource Engineering, Sejong University, 209 Neungdong-ro, Gwangjin-gu, Seoul 05006, Korea

In many countries, submergence is one of the devastating stress leads to severe yield reduce in rice production. The nutrients in soils dissolved in water during submergence arousing nutrients deficiency after drainage. Among the macronutrients, phosphorous deficiency is one of the most important issue from lack of phosphate rock. In this study, *Sub1* and *Pup1* which impart tolerance of submergence and phosphorous deficiency to plant are pyramided in IR64 and the QTL functions were tested under each stress conditions with IR64 and NILs (IR64-Pup1, IR64-Sub1, IR64-Pup1-Sub1 (IPS)). IPS showed IR64-allele of 99.3%. Under submergence stress, IPS showed tolerance phenotype and the expression of *Sub1A* was same as IR64-Sub1 and significantly higher than IR64 and IR64-Pup1. The high expression of *OsPSTOL1* was unexpectedly appeared in IR64-Pup1 and IPS under submergence. In phosphorous deficient screening, IPS didn't show negative phenotype in P100, however, IPS showed the largest phenotypic variation under P0 compared to that of P100. The *OsPSTOL1* expression in IPS was higher than those of IR64 and IR64-Sub1 in shoots, however, significant difference was not observed in roots compared to that of IR64-Sub1. IR64-Pup1 and IPS showed the highest P content in shoots and roots under both P conditions. To figure out the difference between IPS and NILs, transcriptome was performed with root samples of P100 and P0. About 47millions to 71millions of reads were generated. Mapping rate of IR64-Sub1 and IPS was lower as 87.8% and 87.6% than IR64 (98.1%) and IR64-Pup1 (98.6%) in P0. IR64-Sub1 showed the lowest mapping rate as 94.3% in P100. The mapping rate of IR64, IR64-Pup1 and IPS was 99.2%, 98.8% and 97% in P100. DEGs analysis is being conducting and we expect to figure out the functional difference of *Pup1* and *Sub1* among the NILs.

***Corresponding Author:** Tel. 02-3408-3897, E-mail: jhchin@sejong.ac.kr

PA-0034

Constructing a bioinformatic platform, LegCompara, for the comparative analyses across fully sequenced legume genomes

Jin Hyun Kim[2], Joo Seok Park[1], Yo Ram Choi[1], Min Gyun Jeong[1], Yeong Il Jeong[1], Hong Kyu Choi[3*]

[1]Department of Applied Bioscience, Dong-A University, Busan, Republic of Korea
[2]Department of Agricultural Biotechnology, National Institute of Agricultural Sciences, Rural Development Administration, Jeonju, Republic of Korea
[3]Department 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. arietinum*) and two model plants (*A. thaliana, O. sativa*). This genome browser, unlike other traditional genome browsers, was designed for researchers to dynamically interact with user interface, so it can navigate multiple chromosomes of different or same species simultaneously, resulting in genome-wide and/or regional comparisons by depicting corresponding syntenies with either blocks or lines between orthologous regions or genes. It is expected that LegCompara may provide researchers and breeders with useful resources for more efficient and user-friendly comparative genome analysis.

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

PA-0035

Development of a bioinformatic interface, LegExpress, for the transcriptome analysis in legumes

Joo Seok Park[1], Jin Hyun Kim[2], Yo Ram Choi[1], Min Gyun Jeong[1], Yeong Il Jeong[1], Hong Kyu Choi[3*]

[1]Department of Applied Bioscience, Dong-A University, Busan, Republic of Korea
[2]Department of Agricultural Biotechnology, National Institute of Agricultural Sciences, Rural Development Administration, Jeonju, Republic of Korea
[3]Department 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. 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

PA-0036

Characterization of the signaling component for RHS10-mediated inhibition of *Arabidopsis* root hair growth

Eunju Cheon, Song Baik, Hyung-Taeg Cho*

Department of Biological Sciences, Seoul National University 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Republic of Korea

Plant cell growth is restricted by the cell wall, and the cell-wall dynamics would play as signal for cytoplasmic and nuclear events for cell growth. Among diverse receptor kinases, ROOT HAIR SPECIFIC 10 (RHS10) belongs to the receptor kinase subfamily with the Pro-rich extracellular domain. RHS10 defines the root hair length of *Arabidopsis thaliana* by negatively regulating hair growth and modulates the duration of root hair growth rather than the growth rate. RHS10 showed strong association with the cell wall most likely through its extracellular Pro-rich domain (ECD). The cytoplasmic kinase domain of RHS10 showed autophosphorylation. RHS10 suppressed the accumulation of reactive oxygen species (ROS) in the root which is necessary for root hair growth. RHS10 is likely to inhibit root hair growth downstream of hormone signaling because auxin and ethylene precursor could not restore RHS10-inhibited hair growth. To characterize the signaling mechanism for RHS10-mediated root hair inhibition, a genetic screening approach has been taken, where EMS-mutagenized suppressors of RHS10ox (SORs) were screened. One of the candidates, SOR1 is expected to act as RHS10 downstream and interact with RHS10 as a receptor-like-kinase. Root hair phenotypes of *sor1-1 mutant* and SOR1 overexpression demonstrated a negative effect of SOR1 on root hair length consistently with the RHS10 function. Additional experiments are required to prove that SOR1, as a downstream of RHS10, negatively regulate root hair growth.

***Corresponding Author:** Tel. 02-880-6679, E-mail: htcho@snu.ac.kr

PA-0037

Identification of Quantitative Trait Loci Related to 100-Seed Weight in Korean Wild Soybean

Jae Ah Choi[1], Sewon Park[1], Hye Ji Han[1], Moon Young Kim[2], Suk-Ha Lee[1,2*]

[1]Department of Agriculture, Forestry and Bioresources and Research Institute of Agriculture and Life Sciences, Seoul National University, Seoul 08826, Republic of Korea
[2]Plant Genomics and Breeding Institute, Seoul National University, Seoul 08826, Republic of Korea

Soybean is a crop of great economic importance that substantial efforts were to increase yield. The 100-seed weight is one of the yield determinants of soybean and has been the primary target for genetic breeding. Researchers have identified several quantitative trait loci(QTL) associated with this trait, but long regions of linkage disequilibrium(LD) in cultivated soybeans resulted from the genetic bottleneck as human selection hinders the pinpointing of causal genes in QTLs. Fortunately, wild soybeans have allelic diversity throughout the genome and are promising resources of genetic diversity to break long LD and improve cultivated soybean traits by gene introgression from wild soybeans. Therefore, the objective of this study was to identify novel QTL using 220 recombinant inbred line population derived from a cross between landrace IT109098 and wild-type soybean K7-113. 100-Seed weight was about 11.6g and 6.2g for IT109098 and K7-113, respectively. 100-Seed weight of IT109098 was about 1.9 times larger than that of K7-113 and showed a significant difference between those two. Using a high-density genetic map mapped via 4,813 single nucleotide polymorphism markers, we identified two major QTLs related to 100-seed weight on Chromosomes8 and 18, in which the LOD scores were 3.5154 and 6.8058, respectively. In Chromosome8, the QTL region spanned 280.35kb, and in chromosome18, 581.5kb. Identification and verification of putative candidate genes in these QTLs at the prospect of further studies may contribute to the breeding programs of novel soybean cultivars with greater seed weight through molecular-assisted breeding; out-looking for the increased yield in soybean cultivars.

***Corresponding Author:** Tel. 02-880-4555, E-mail: sukhalee@snu.ac.kr

PA-0038

Comparative FISH karyotype analysis using rDNA and telomeric repeat probes in six *Senna* species

Do Sin Lee, Hong Nguyen, Remnyl Joyce Pellerin, Ta Dat, Nomar Espinosa Waminal, Hyun Hee Kim*

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

Several species in the genus *Senna* (Fabaceae) had been intensively studied owing to their diverse industrial and medicinal potential. However, there is limited chromosomal information essential for cytogenetics and genomics research in the genus. Here, we used fluorescence *in situ* hybridization (FISH) to perform a comparative FISH karyotype analysis of six *Senna* species. We detected differences in the distributions of rDNA gene clusters and *Arabidopsis*-type telomeric repeats (TTTAGGG)n. All species have $2n$ = 28 chromosomes except for *S. uniflora,* which has $2n$ = 24. Only one pair of 5S rDNA was detected on chromosome 13 in four species, except for *S. siamea* and *S. uniflora*, which has two pairs of signals on chromosomes7 and 9. The chromosomal distribution of 45S rDNA showed more interspecific variation than that of 5S rDNA. The telomeric repeat localized mostly in every chromosome terminus. However, in *S. corymbosa* and *S. hirsuta* var. *leptocarpa,* intense telomeric signals appeared in interstitial regions of three chromosome pairs, which suggests past chromosome fusion events. These preliminary data demonstrate interspecific karyotype variation that reveals clues of past chromosomal rearrangements in the genus *Senna*. Our results are useful to understand the dynamic role of the *Senna* species.

Additional key words: *Arabidopsis*-type telomeric repeats, Cytogenetic marker, Genome, Karyotype, 5S rDNA, 45S rDNA

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***Corresponding Author:** Tel. +82-2-3399-1715, E-mail: kimhh@syu.ac.kr

PA-0039

A chromosome-level reference genome assembly of *Panax ginseng*

Hyeonah Shim, Woohyeon Cho, Padmanaban Mohanan, Soomin Kim, Hyunjin Koo, Tae-Jin Yang*

Department of Agriculture, Forestry and Bioresources, College of Agriculture and Life Sciences, Seoul National University, Seoul, 08826, Republic of Korea

Panax ginseng is one of the most representative medicinal plants not only in Korea but also worldwide. Despite excellent pharmacological effects of ginseng, growth characteristics hinder breeding and overall ginseng research. We had previously reported a draft reference genome sequence of *P. ginseng*, which is in its draft level with room for improvement. In this study, we aimed to complete a high-quality chromosome-level assembly of ginseng with recent sequencing technologies such as Nanopore, Illumina, and Hi-C. Sequencing was performed with a single ginseng resource 'TYP1', which is maintained as hairy roots through tissue culture. We established an optimized assembly pipeline and obtained a 3.2 Gb pseudochromosome-level assembly with an N50 of 163 Mb. The longest scaffolds were representative of the 24 chromosomes of *P. ginseng*. The assembly was validated with different methods such as the construction of linkage groups using genotyping-by-sequencing data of F_2 populations and fluorescence in situ hybridization with oligoprobes designed from unique regions of the genome. Furthermore, comparative analysis was conducted with the recently reported diploid relative, *Panax notoginseng*. The high-quality pseudochromosome level assembly will provide fundamental information that can be utilized in further ginseng research and breeding.

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

PA-0040

Identification of C2 domain contain proteins and characterization of the genetic variations in rice (*Oryza sativa* L.)

Hongjia Zhang[1], Seong-Gyu Jang[1], San Mar Lar[1], Ah-Rim Lee[1], Fang-Yuan Cao[1], Junhee Hong[1,2], Jeonghwan Seo[1,2], Soon-Wook Kwon[1,2*]

[1]Department of Plant Bioscience, College of Natural Resources and Life Science, Pusan National University, Miryang 50463, Korea
[2]Life and Industry Convergence Research Institute, Pusan National University, Miryang 50463, Korea

C2DPs have been identified in different genomes that contain single or multiple C2 domains in their C or N-terminal, it possesses higher functional activity in the cell membrane between the cytoplasm and nucleus. In this study, we identified 82 C2DPs in the rice genome and divided them into seven groups through phylogenetic analysis. Synteny analysis revealed that duplication events were either exhibited within the genome of rice or between the genome of rice and other species. Through the analysis of *cis*-acting elements in promoters, expression profiles, and qRT-PCR results, the functions of *OsC2DPs* were found to be widely expressed in diverse tissues and were extensively involved in phytohormones. Prediction of the miRNA targets of *OsC2DPs* revealed that some of the homolog genes were regulated by consistent miRNAs and may carry out redundancy function. Notably, *OsC2DP50/51/52* as a co-tandem duplication exhibited similar expression variations and involved the coincident miRNA-regulation pathway. Moreover, the results of SNP genotyping and haplotype analysis revealed that *OsC2DP17*, *OsC2DP29*, and *OsC2DP49* possessed diverse haplotypes for impacted cold tolerance owing to genomic variations. These findings provide a comprehensive sight for characterized *OsC2DPs* in rice and their roles for abiotic stress. Further, the genetic variation supports the theoretical reference for molecular breeding in rice.

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***Corresponding Author:** Tel. 055-350-5506, E-mail: swkwon@pusan.ac.kr

PA-0041

Chloroplast Localized FIBRILLIN11 is Involved in Osmotic Stress Tolerance via ABA Signaling during *Arabidopsis* Seed Germination

Yu-Ri Choi[1], Hyun Uk Kim[1,2*]

[1]Department of Molecular Biology, Graduate School, Sejong university, Seoul, 05006, Republic of Korea
[2]Department of Bioindustry and Bioresource Engineering, Plant Engineering Research Institute, Sejong University, Seoul 05006, Republic of Korea

Plant live in ever-changing environments, facing adverse environmental conditions including pathogen infection, herbivore attack, drought, high temperature, low temperature, nutrient deficiency, toxic metal soil contamination, high salt, and osmotic imbalance that inhibit overall plant growth and development. Plants have evolved mechanisms to cope with these stresses. In this study, we found that the *FIBRILLIN11* (*FBN11*) gene in *Arabidopsis*, which has a lipid-binding FBN do-main and a kinase domain, is involved in the plant's response to abiotic stressors, including salt and osmotic stresses. FBN11 protein localizes to the chloroplast. *FBN11* gene expression significantly changed when plants were exposed to the abiotic stress response mediators such as abscisic acid (ABA), sodium chloride (NaCl), and mannitol. The seed germination rates of *fbn11* homozygous mutants in different concentrations of mannitol and NaCl were significantly reduced compared to wild type. ABA-dependent and -independent stress response regulatory genes were differentially expressed in the fbn11 mutant compared with wild type when grown in mannitol medium. These results suggest a clear role for chloroplast-localized FBN11 in mediating osmotic stress tolerance via the stress response regulatory signaling pathway in the nucleus.

***Corresponding Author:** Tel. 02-6935-2491, Email: hukim64@sejong.ac.kr

PA-0042

De novo whole genome assembly of *Panax vietnamensis*

Woohyeon Cho, Hyeonah Shim, Vo Ngoc Linh Giang, Tae-Jin Yang*

Department of Agriculture, Forestry and Bioresources, Plant Genomics & Breeding Institute, College of Agriculture & Life Sciences, Seoul National University 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Korea

Panax vietnamensis is a closely related species of *P. ginseng*, which is the most representative medicinal herb in Korea. Diploid *P. vietnamensis* (n=12) grow on high altitude mountains in warm, freeze-free area while tetraploid *P. ginseng* (n=24) can overcome freezing winters. In this study, 2nd and 3rd generation sequencing was performed with *P. vietnamensis* in the state of hairy roots to minimize the genome variations between multiple runs. Through the whole genome assembly processes, we assembled the genome into 1,391 scaffolds that sum up to about 2.1 Gb length with N50 of 4 Mb. By comparing 1,391 scaffolds with chromosome-level genome of *P. notoginseng* (n=12) and *P. ginseng,* we confirmed 1:1 and 1:2 genome structure correspondences respectively, as well as high completeness. We are looking forward to complete the chromosome-level genome assembly of *P. vietnamensis* through other latest technologies such as chromosome conformation capture (3C). This research may serve as fundamental information for downstream studies of *P. vietnamensis* and also reveal the evolutionary history of diploid and tetraploid *Panax* species in detail.

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

PA-0043

Identification of long terminal repeat retrotransposons (LTR-RTs) and DNA methylation dynamics in *Panax ginseng*

Hyunjin Koo, Soomin Kim, Hyeonah Shim, Padmanaban Mohanan, Tae-Jin Yang*

Department of Agriculture, Forestry and Bioresources, College of Agriculture and Life Sciences, Seoul National University, Seoul, 08826, Republic of Korea

Retrotransposons have been known to play a crucial role in the evolution of host genomes. Major LTR-RTs were identified as occupying 34% of the ginseng genome in previous study. In this study, we conducted *de-novo* LTR-RTs prediction in ginseng resource 'TYP1', which has been assembled as high-quality pseudochromosome level. LTR-RTs with a total of 7,156 conserved domain were identified; del (53.38%), athila (14.51%), tork (7.08%), sire (6.41%) and tat (5.04%). DNA methylation has been known to globally silence the activity of transposable elements for genome stability. We also confirmed that most of the LTR-RT body regions were hypermethylation through bisulfite-seq. In order to affirm the relationship between LTR having transpositional potential and DNA methylation, we performed ALE-seq (amplification of LTR of eclDNAs followed by sequencing) to predict the current transpositional potential in TYP1. LTR-RTs having transpositional potential were identified as hypomethylation. This result indicates that DNA methylation and LTR-RTs activity are antagonistic to each other. This study shows the interplay between LTR-RTs activity and DNA methylation level in *P. ginseng*.

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

PA-0044

Transcriptomic changes in responses to different types and doses of ionizing radiations in rice

Hong-Il Choi*, Jae-Wan Park, Gileung Lee, Jin-Baek Kim

Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongup 56212, Republic of Korea

Ionizing radiations (IRs) are regarded as abiotic stressors for plants, because they causes oxidative stress and change the expression of genes in living organism. In this study, we investigated the variations in gene expressions induced by three different types of IRs with different doses in rice. Rice seeds were irradiated with 100, 200, and 400 Gy gamma rays (GR), 20, 50, and 80 Gy ion beams (IB), 100, 200, and 400 Gy proton beams (PB) and RNA sequencing data were obtained from 3-week-old seedlings of the irradiated seeds. Averagely, 28,963.7 genes were expressed and 488.9 up- and 234.3 down-regulated differentially expressed genes (DEGs) were found per sample ($|\log2\ FC| \geq 1$ and p-value ≤ 0.01). Union sets of DEGs for each types of IRs were listed to simplify the comparison of the effects among different IRs, which resulted a total of 1,558 DEGs with 1,187 ups and 371 downs, 1,865 DEGs with 1,244 ups and 621 downs, and 1,347 genes with 769 ups and 578 downs for GR, IB, and PB, respectively. Gene ontology (GO) enrichment analysis of the union DEG sets revealed 69 and 12 commonly enriched GO terms for up- and down-regulated DEGs, many of which were closely related to oxidative stress response. KEGG pathway mapping and enrichment analysis of the union DEG sets also showed that most of DEGs were on common pathways related to oxidative stress and stress signaling. These results suggest that different types and doses of IRs can induce universal gene expression changes to respond to oxidative stress. This study will contribute to understanding the molecular response mechanism to ionizing irradiation in plants.

***Corresponding Author:** Tel. 063-570-3298, E-mail: hichoi@kaeri.re.kr

PB-0001

Identification of Novel Loci Conferring Salt Tolerance in a Korean Soybean Landrace [*Glycine max* (L.) Merr.]

Kang-Heum Cho[1], Hakyung Kwon[2], Moon Young Kim[1], Suk-Ha Lee[2*]

[1]Plant Genomics and Breeding Institute, Seoul National University, Seoul 08826, Republic of Korea
[2]Department of Agriculture, Forestry and Bioresources and Research Institute of Agriculture and Life Sciences, Seoul National University, Seoul 08826, Republic of Korea

Salt stress affects over 20% of the world's farmland and is regarded as one of the main abiotic stresses crops face. Soybean [*Glycine max* (L.) Merr.] is a glycophyte whose agronomic traits are negatively impacted by salt stress. The objective of this study was to identify quantitative trait loci (QTLs) controlling salt tolerance in soybean, using a recombinant inbred line (RIL) population made from a cross between a salt-sensitive cultivar Cheongja 3 and a salt-tolerant landrace IT162669. IT162669 was more tolerant than Cheongja 3 in six salt tolerance-related traits, all of which were significantly correlated with each other. Using a high-density genetic map constructed from 2,630 single nucleotide polymorphism (SNP) markers, we identified ten QTLs and found that two loci, *qST6* and *qST10* (loci for 'Salt Tolerance'), overlapped two and four major QTLs, respectively. *qST6*, *qST10* and their paralogous regions in soybean were co-localized with previously reported abiotic stress-associated QTLs, and these loci collectively enhanced salt tolerance-related traits in an additive manner. We further surveyed putative candidate genes in these regions based on functional annotations and expression level changes using quantitative real-time PCR, and found sequence variants in the candidate genes. These genes include a phosphoenolpyruvate carboxylase gene (*PEPC*, Glyma.06G277500), an ATP synthase I-related protein (*CGL160*, Glyma.06G277600), an ethylene response factor (*ERF*, Glyma.10G016500) and a universal stress protein gene (*USP*, Glyma.10G018700). This study will help extend our understanding on mechanisms upon salt stress and provide additional genetic resources to assist breeding soybean with enhanced salt tolerance.

***Corresponding Author:** Tel. 02-880-4555, E-mail: sukhalee@snu.ac.kr

PB-0002

Identification of QTLs controlling fruit firmness of octoploid strawberry (*Fragaria × ananassa*) by integrating GWAS and QTL analysis

Jinkwan Jo[1], Koeun Han[2], Jun-Geol Yeum[1], Abinaya Manivannan[2], Muhammad Irfan Siddique[2], Hye-Eun Lee[2], Eun Su Lee[2], Ye Rin Lee[2], Jin-Kyung Kwon[1], Byoung-Cheorl Kang[1], Do-Sun Kim[2*]

[1]Department of Agriculture, Forestry and Bioresources, Plant Genomics and Breeding Institute, College of Agriculture and Life Sciences, Seoul National University, Seoul-08826, Republic of Korea

[2]Vegetable Research Division, National Institute of Horticultural and Herbal Science, Rural Development Administration, Wanju 55365, Republic of Korea

Fruit firmness is one of the most important horticultural traits in octoploid strawberry (*Fragaria × ananassa*) for producer, traders and consumers. Molecular mechanism of fruit firmness has been studied and cascade of molecular events, cell wall degrading enzymes and multiple hormones are involved to control this trait. QTLs for strawberry fruit firmness have been identified in multiple populations. However, most of the reported QTLs are population-specific and are unable to use in candidate genes prediction. Therefore, in this study, we constructed strawberry core collection and one bi-parental F_2 population for genome-wide association study (GWAS) and QTL mapping, respectively. Single nucleotide polymorphism (SNP) maps of core collection were constructed using whole-genome resequencing and genotyping-by-sequencing (GBS) method based on 'Wongyo 3115' reference genome. In addition, genetic map of F_2 population was constructed by Axiom 35K chip. Fruit firmness were scored using non-destructed method to perform GWAS and QTL mapping. Five QTLs were detected on chromosome 3-3, 5-1, 6-1, and 6-4. One QTL on chromosome 6-1 was co-located with SNPs detected by GWAS and this locus was used to propose candidate genes. Our results will be useful to understand the molecular mechanism of fruit firmness.

***Corresponding Author:** Tel. 063-238-6670, E-mail: greenever@korea.kr

PB-0003

Genome-Wide Association Study of Salinity Tolerance Using 58K SNP Array in Peanut (*Arachis hypogaea* L.) accessions

Kunyan Zou, Tae-Hwan Jun*

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

Peanut (*Arachis hypogaea* L.) is considered as a moderately sensitive species to salinity stress, a few reports on salinity tolerance in peanut have been reported.

A total of 283 peanut accessions were used for the study, 73 Korean accessions and 210 core collections from the RDA-GenBank Information Center, South Korea and the US Department of Agriculture, respectively. The Axiom_Arachis array with 58K SNPs was used for genotyping. Six seeds per accession (three seeds for control and three seeds for salt treatment) was treated at a salt concentration of 200mM NaC1 when the third branch of peanut appeared. The difference in stem height between the control and treatment group was used to evaluate the salinity tolerance of different peanut varieties after 2 weeks.

The population structure was analyzed by ADMIXTURE software. The enriched compressed mixed linear model (ECMLM) of GAPIT package in R software were used to conduct GWAS for the association analysis. LD decay and LD block was calculated with PopLDdecay and HaploView 4.2.

A total of 10,426 SNPs were selected for GWAS analysis and six SNPs were significantly related to the phenotype. Pentatricopeptide repeat superfamily protein and WRKY family transcription factor were found among the twenty-seven genes within a linkage disequilibrium (LD) of the significant SNPs and could have a strong causal effect in salt tolerance. This study to identify genomic regions related to peanut seeding salinity tolerance by GWAS analysis provide a cornerstone of molecular breeding for salinity tolerance in peanut.

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

PB-0004

The Phenotype and Genotype Association Analysis Reveals Genetic Loci Related to Important Agronomic Traits of Wheat (*Triticum aestivum* L.)

Woo Joo Jung[1], Yong Jin Lee[2], Chon-Sik Kang[3], Yong Weon Seo[1,2*]

[1]Department of Plant Biotechnology, Korea University, Seoul 02841, Korea
[2]Department of Biotechnology, Korea University, Seoul 02841, Korea
[3]National Institute of Crop Science, Rural Development Administration, Wanju 55365, Republic of Korea

In spite of its importance as a major food source, investigating genome of bread wheat (*Triticum aestivum* L.) has been dragged due to its complex and huge genome. However, thanks to the development of next-generation sequencing as well as DNA chip technology, identification of genetic loci controlling quantitative traits has become possible. We performed phenotype-genotype association analysis using the iSelect 90K SNP chip. The observed agronomic traits were the winter survival rate (WSR), days to heading (DTH), days to maturity (DTM), stem length (SL), spike length (SPL), awn length (AL), liter weight (LW), thousand kernel weight (TKW), and the number of seeds per spike (SPS), of 287 wheat accessions from diverse country origins. The relationship between the observed traits was revealed via correlation analysis, and the wheat accessions were classified into three groups according to the population structure analysis and the principal component analysis. The best linear unbiased prediction (BLUP) values of the genotypic effect for each trait under different environments were predicted and used for GWA analysis based on a mixed linear model (MLM). Putative candidate genes closely located to the significant SNP markers were obtained following the linkage disequilibrium (LD) analysis, and the function of each candidate genes was predicted by gene expression analysis. Further, the effect of the favorable or unfavorable alleles on each trait was verified. Newly identified candidate genes and alleles from this study will help to develop wheats with superior agronomic traits.

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***Corresponding Author:** Tel. 02-3290-3005, E-mail: seoag@korea.ac.kr

PB-0005

Quantitative trait loci and candidate gene related to soyasaponin derivatives biosynthesis

Sang-Beom Lee, Hyun-Young Kim, Hyeon-Seon Park, Dool-Yi Kim, Mi-Suk Seo, Jung-Kyung Moon, Man-Soo Choi*

National Institute of Crop Science, RDA, Wanju 55365, Republic of Korea

Soyasaponin is a type of glycoside like steroids, steroid alkaloids, or triterpene. It is known as a component that enhances the human body's immunity. Soybeans are a major food crop and contain soyasaponin which serves as a source of protein and fat. Although there are studies showing that soyasaponin has anti-cancer effects, many studies are still needed to verify its safety and certainty of effect.

In this study, a genome-wide association study (GWAS) was conducted to select resources with high soyasaponin and develop functional varieties using the soybean core collection (individual number=430) and 180K chip data. Most of the soyasaponin derivatives showed a significant difference in the two years (Aa was excluded) of the study, and the total soyasaponin contents decreased in the second year. However, the correlation between the soyasaponin derivatives was not significantly affected by environmental factors.

Thus, as a result of the annual GWAS to investigate the genetic associations for soyasaponin derivatives, the SNPs associated with Aa and Ab were mapped on chromosome 7, and Glyma. 07g254600 (UDP-glycosyltransferase) was identified. Glyma. 07g254600 is a candidate gene related to the soyasaponin derivatives biosynthesis, and 6 bp InDels in 5' UTR and 19 variants in the coding region were found by its comparative analysis of nucleotide sequences, respectively.

The functional verification of Glyma. 07g254600 is required in the future, and it is also expected that these results will contribute to the development of soyasaponin-rich varieties and molecular markers.

***Corresponding Author:** Tel. 063-238-5059, E-mail: cldst81@korea.kr

PB-0006

A Genome-wide Association Study for the Identification of Powdery Mildew Resistance QTL in Tomato

Jiyeon Park, Siyoung Lee, Girim Park, Seungahn Kwon, Yunseo Choi, Seoyeon Park, Younghoon Park*

Department of Horticultural Bioscience, Pusan National University, Miryang 50463, South Korea

Powdery mildew (PM) is caused by *Oidium* spp. in tomato during the cultivation worldwide and results in greatly reduced yield. This study aimed to identify novel quantitative trait loci (QTL) for powdery mildew resistance (PMR) through a genome-wide association study (GWAS) in tomato. Sequencing analysis of the internal transcribed spacer (ITS) of powdery mildew strains (PNU_PM1) isolated from Miryang, Gyeongnam, identified it as *Oidium neolycopersici*. PM bioassay was conducted for a total of 348 tomato accessions, among which 24 accessions showed high levels of resistance to the PNU_PM1. A GWAS was performed using TASSEL and GAPIT software based on the phenotypic data of 290 accessions and 11,912 SNPs obtained from the Tomato Axiom SNP chip array. As a result, a total of nine significant SNPs were selected from chromosome (Chr.) 1, 4, 6, 8, and 12, and five novel QTL regions different from previously known PMR-QTL loci could be detected. From these QTL regions, three putative candidate genes for PMR were selected from Chr. 4 and 8, which include two NBS-LRR class genes and a receptor-like kinase gene known as causative genes for PMR in several crop species. The SNPs discovered from these genes provide useful information for understanding the molecular basis of PMR and developing DNA markers for MAS of PMR in tomato.

***Corresponding Author:** Tel. 055-350-5961, E-mail: ypark@pusan.ac.kr

PB-0007

A GWAS approach to finding SNPs associated with the grain shape of Rice (*Oryza sativa* L.)

Byeongyong Jeong, Yoonjung Lee, Tae-Ho Ham, Joohyun Lee*

Department of Crop Science, Sanghuh Collage of Life Sciences, Konkuk University, 120 Neungdong-ro, Gwangjin-gu, Seoul 05029, Republic of Korea

Rice (*Oryza sativa* L.) grain is evaluated by several traits such as color, length, chunkiness, and amylose contents. The grain Length-Width ratio (LWR) is one of the evaluation criteria for rice grain shape. We conducted Genome-Wide Association Study to reveal the associated genetic information of grain Length-Width ratio in Rice. For GWAS analysis to LWR in rice grain, a set of 966 rice accessions was used in this study. The length and width of 5 brown rice grains of each accession were measured using vernier calipers. The calculated Length/Width values of each grain strike a mean and the average Length-Width ratio were used for GWAS analysis. The range of LWR values is 1.36 - 3.84 and the average was 1.89. The GWAS analysis performed with a total of 183,477 SNPs with MAF > 0.05 and the *P*-value threshold at 2.73×10^{-7}. Total 10 lead SNPs associated with grain LWR were founded in chromosomes 1, 3, 4, 5, 6, 8, and 12. A 348.8kb range of region surrounding each lead SNPs were appointed according to the Linkage Disequilibrium (LD) analysis. The candidate genes will be used to identify candidate genes underlying rice grain LWR.

***Corresponding Author:** Tel. 02-450-3769, E-mail: edmund@konkuk.ac.kr

PB-0008

Genome-Wide Association Study for grain weight in Rice (*Oryza sativa* L.) through Axiom Oryza 580K Genotyping Array

Wondo Lee[1], Jahong Lee[1], Youhyun Cho[1], Joohyun Lee[2*]

[1]Seedpia INC., Hwaseong 18313, Republic of Korea
[2]Department of Crop Science, Sanghuh Collage of Life Sciences, Konkuk University, 120 Neungdong-ro, Gwangjin-gu, Seoul 05029, Republic of Korea

To improve rice yield, 1,000-grain weight (TGW) of rice grains have been studied to increase rice yield. We performed a Genome-Wide Association Study to find candidate genes associated with TGW. For GWAS, we used a set of 958 rice accessions (*Oryza sativa* L.). 1,000-grain of each rice accession were measured using an electronic microbalance and used as phenotypic data in GWAS. The range of TGW was 6.97g - 34.259g, and the average TWG of 958 rice accessions was 20.53g. A total of 183,705 out of a possible 280,802 SNPs was obtained after filtered, and the *P*-value threshold was set at 2.72×10^{-7} using a Bonferroni correction. GWAS was conducted using EMMA (the efficient mixed-model association) method. Chromosomes 2, and 11 showed associated SNPs with TGW. According to the LD decay analysis, a 348.8 kb region surrounding the SNPs will be used to find the candidate genes related to TWG trait in rice.

***Corresponding Author:** Tel. 02-450-3769, E-mail: edmund@konkuk.ac.kr

PB-0009

Searching for genomic loci and genes associated with the pigmentation of soybean seeds using 438 soybean accesssions

Jin Hyun Kim[2], Joo Seok Park[1], Yo Ram Choi[1], Min Gyun Jeong[1], Yeong Il Jeong[1], Hong Kyu Choi[3*]

[1]Department of Applied Bioscience, Dong-A University, Busan, Republic of Korea
[2]Department of Agricultural Biotechnology, National Institute of Agricultural Sciences, Rural Development Administration, Jeonju, Republic of Korea
[3]Department of Molecular Genetics, Dong-A University, Busan, Republic of Korea

Soybean (*Glycine max* [L.] Merr.) is the most important crop among all cultivated legume crops in the world. Seed coat has been significantly influenced during the period of domestication in that it is linked to seed dormancy, seed viability and cost factors in processing seeds for oil and soy foods. To identify loci linked with seed pigmentation, we collected the resequencing data of 438 accessions. A genome wide association study using all possible combinations of three traits revealed four loci (designated as SP1-SP4). More important, we identified a gain of function mutation affecting a CaaX-type endopeptidase gene (Glyma.01G198500), which was a chloroplast-targeted transmembrane protein, as a strong candidate for the green seed coat. Glyma.01G198500 gene was highly coexpressed with the genes associated with chloroplast development and shared CaaX protease self-immunity domain (PF02517) with SCO4 which is a chloroplast-targeted protein that plays important roles in development of chloroplast. Glyma.01G198500 protein of the green soybeans had all of the CaaX protease self-immunity domain and resembles alpha-helical bundle structure of major three transmembrane protein structures, whereas that of the yellow soybeans had a partial CaaX protease self-immunity domain and was far from the alpha-helical bundle structure. This study provides insights into how to effectively utilize the data accumulated in the public databases and the interaction of four loci controlling seed pigmentation.

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

PB-0010

Genetic divergence of integrated GWAS analysis pipeline between standard Korean tea plant (*Camellia sinensis L*) and the other tea plants

Dong-Jun Lee*, Myung-Eun Park, Da-Hye Jeon

Genomics Division, National Institute of Agricultural Sciences(NAS), Jeonju 54874, South Korea

Tea is an important drink that is consumed worldwide. But the absence of reference genomes has hampered the use of useful tea plant gene resources for molecular breeding. We generated high-quality reference genomic data for a tea plant that produced 172 Gb short data and 246 Gb long read data using Illumina and PacBio sequencing technology with standard Korean (Sangmok var.) tea plants.

To compare Sangmok var. with other tea plants, there was an inconvenience of analyzing the data obtained from the process by Next generation sequence(NGS) data into the application at each stage in the existing GWAS analysis pipeline method and executing the program. Therefore, an advanced analysis pipeline is built to improve this inconvenience. Using this analysis pipeline, a test for genetic divergence was attempted by comparing varieties of tea plants compared to Sangmok var.

***Corresponding Author:** Tel. 063-238-4557, E-mail: leemoses1004@korea.kr

PB-0011

Identification of soybean germplasm with resistance to soybean cyst nematode in the Korean soybean core collection

Jiyong Song, Kyung Do Kim*

Department of Bioscience and Bioinformatics, Myongji University, 116 Myongji-ro, Cheoin-gu, Yongin, Geonggi-do, 17058, Republic of Korea

Soybean cyst nematode (SCN) is a soybean pathogen that occurs in all the soybean production areas worldwide, including United States, China, and Korea. SCN causes inhibition of rhizobium and nitrogen deficiency and can result in significant interference in the growth and quantity of soybeans, which leads to annual yield losses of more than 1.2 billion USD in the US. Two representative genotypes with SCN resistance are known as the Peking-type and PI88788-type, and *Rhg1* and *Rhg4* genes are responsible for this SCN resistance. For developing SCN resistant varieties, soybean germplasms resistant to SCN need to be determined. For soybean germplasms in Korea, however, little is known for SCN resistance and the genotypes of *Rhg1* and *Rhg4*. Here, we used whole-genome resequencing data of the Korean soybean core collection (430 accessions in total) from a previous study to identify single nucleotide polymorphisms (SNPs) located at *Rhg1* and *Rhg4*. Three SNPs at *Rhg1* were selected (Glyma18g022500; Glyma.Wm82.a2.v1) to classify the types of SCN resistance *in silico*. A total of 430 accessions from the Korean soybean core collection was classified into the different SCN resistance types by only using three SNPs.

***Corresponding Author:** Tel. 031-330-6192, E-mail: kyungdokim@mju.ac.kr

PB-0012

Genome-Wide Association Study of Resveratrol Content Using 58K SNP Array in Peanut Sprout

DongWoo kang, Yu-Hyeon Park, Tae-Hwan Jun*

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

Resveratrol (trans- 3,5,4'-trihydroxystilbene) is one of the major stilbene phytoalexins, and the content of resveratrol in peanut sprouts is significantly higher than in peanut seed. Few studies have been reported on the genes controlling the resveratrol content of peanut sprouts using the peanut accessions. A total of 150 peanut accessions were used for the present study, 42 Korean accessions and 108 core collections from the RDA-GenBank Information Center, South Korea and the US Department of Agriculture, respectively. The Axiom_Arachis array with 58K SNPs was used for genotyping. Peanut sprouts were grown with 27 ℃ and 2 min every 2 h irrigation for 9 days in sprout growth chamber. After drying at 50℃ for 20 h, 1 g sample is mixed with 20 ml of 80% methanol (v/v) and ultrasonicated for 1 h to extract resveratrol from peanut sprouts. Resveratrol content was analyzed by high resolution LC/MSMS spectrometer. A genome wide association study (GWAS) was performed with 15444 SNPs using Fixed and random model Circulating Probability Unification (FarmCPU) model over 2 years. A total of 20 significant SNP markers were found. Among them, a significant marker AX-147252023 was simultaneously identified in GWAS results with a fairly low p-value. Through this study, finding genes and high-content resources related to resveratrol content will provide useful information for molecular breeding programs in peanut.

***Corresponding Author:** Tel. 055-350-5507, E-mail: thjun76@pusan.ac.kr

PC-0001

Discrimination of Geographical Origin and Variety for Soybean using AS(Allele-Specific)-PCR

Myoung-Jin Kim, Bo-Young Kim, Nam-Kuk Kim, Jeong-A Choi, Ji-Won Kim, Youn-Ju Choi, Seong-Hun Lee, Kie-Chul Jung*

Experiment Research Institute of National Agricultural Products Quality Management Service, 141, Yongjeon-ro, Gimcheon-si, Gyeongsangbuk-do, 740-220, Korea

Recently, due to continuous decline in domestic soybean cultivation area and production, the import of soybean is being increased and some local vendors deliberate mislabeled cultivation of origin for economic purposes. Therefore, the discrimination study of domestic and import products was performed for prevent illegal distribution of soybean based on varieties distinction by analysing genetic variation. First, we select 17 insertions/deletions(Indels) from 16 soybean varieties including major domestic and import. AS(Allele-Specific)-PCR method was developed with 17 selected indel sequences and genotyping test was performed to identify whether the varieties of soybeans could be distinguished. Through this process, 11 markers to distinguish 16 soybean varieties were finally selected. In addition, validation of the selected markers has been conducted by using AS-PCR on the 20 soybean samples from 7 countries including Korea, China, U.S. ect. The result showed that the selected 11 markers can be used for the origin discrimination and variety identification of soybean. Therefore, the soybean AS-PCR analysis gives reliable information to discriminate the geographical origin and some varieties of soybeans.

***Corresponding Author:** Tel. 054-429-7870, E-mail: gumdung3@korea.kr

PC-0002

Utilization of vegetation index for evaluation of soybean germplasms under waterlogging condition

Se-Hun Kim, Pooja Tripathi, Hyun Jo, Jeong-Dong Lee, Yoonha Kim*

Department of Applied Life Science, Kyungpook National University, Daegu 41566, South Korea

A vegetation index (VI) is calculated by reflectance of two or more wavelengths in the leaf surface thus, it’s value reflects chlorophyll content, photochemical reflectance, anthocyanin content etc. For this reason, we used VI normalized difference vegetation index (NDVI) for evaluation of waterlogging tolerance and susceptible. First of all, we selected two waterlogging tolerance accessions (WTA) and two waterlogging susceptible accessions (WSA) among 798 soybeans (*Glycine max*. L). Using pre-selected 4 soybean accessions, we supplied waterlogging condition and then, we measured hyper-spectral data from 400 nm to 1000 nm for 7 days after waterlogging (DAW). According to our result, two WTA did not show statistically different NDVI between treatments however, two WSA revealed significantly decreased NDVI in the waterlogging treatment as compared to that of control. In particular, different NDVI between control and waterlogging treatment was detected from 4DAW. Moreover, NDVI was continuously revealed below 0.55 in WSA from 4DAW. Consequently, in the viewpoint of VI, our result indicated that the soybean showed susceptible symptom from 4DAW and the symptom could be evaluated by the NDVI which showed below 0.55. Therefore, we anticipated that acquired information (4DAW and 0.55 NDVI) could be applied for evaluation or screening of soybeans under waterlogging.

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***Corresponding Author:** Tel. 053-950-5710, E-mail: kyh1229@knu.ac.kr

PC-0003

Genetic identification of tartary buckwheat resources using 50 InDel-based barcode system

Yul-Ho Kim[1*], Hwang-Bae Sohn[2], Su-Jeong Kim[2]

[1]Department of Central Area, NICS, RDA, Suwon 16429, Korea
[2]Highland Agriculture Research Institute, NICS, RDA, Pyeongchang 25342, Korea

Tartary buckwheat (*Fagopyrum tataricum* Gartn.) is poised to be the target of many future breeding efforts to take advantage of its nutritional values and medicinal properties. The reliable *ex situ* conservation of various genetic resources is essential for the modern breeding of tartary buckwheat varieties. We developed PCR-based co-dominant insertion/deletion (InDel) markers to discriminate tartary buckwheat genetic resources. First, we obtained the whole genome from 26 accessions across a superscaffold-scale reference genome of 569.37 Mb for tartary buckwheat cv. “Daegwan 3-7.” Next, 171,926 homogeneous and 53,755 heterogeneous InDels were detected by comparing 26 accessions with the “Daegwan 3-7” reference sequence. Of these, 100 candidate InDels ranging from 5-20 bp in length were chosen for validation, and 50 of them revealed polymorphisms between the 26 accessions and “Daegwan 3-7.” The validated InDels were further tested through the assessment of their likelihood to give rise to a single or a few PCR products in 50 other accessions, covering most tartary buckwheat genome types. The major allele frequencies ranged from 0.5616 at the TB42 locus to 0.9863 at the TB48 locus, with the average PIC value of 0.1532 with a range of 0.0267-0.3712. To create a user-friendly system, the homology of the genotypes between and among the accessions were visualized in both one- (1D) and two-dimensional (2D) barcode types by comparing amplicon polymorphisms with the reference variety, “Daegwan 3-7.” A phylogenetic tree and population structure of the 76 accessions according to amplicon polymorphisms for the 50 InDel markers corresponded to those using non-synonymous single nucleotide polymorphism variants, indicating that the barcode system based on the 50 InDels was a useful tool to improve the reliability of identification of tartary buckwheat accessions in the germplasm stocks.

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***Corresponding Author:** Tel. 031-695-4029, E-mail: kimyuh77@korea.kr

PC-0004

Optimizing the method for stomata-profiling automation of soybean leaves based on deep learning

Syada Nizer Sultana[1], Halim Park[2], Sung Hoon Choi[2], Hyun Jo[1], Jong Tae Song[1], Yang Jae Kang[2,3], Jeong-Dong Lee[1*]

[1]Department of Applied Biosciences, Kyungpook National University, Daegu 41566, Republic of Korea
[2]Division of Bio & Medical Big data Department (BK4 Program), Gyeongsang National University, Jinju 52828, Republic of Korea
[3]Division of Life Science Department, Gyeongsang National University, Jinju 52828, Republic of Korea

Stomata is a main functional attribute of interest among researchers working across different plant biology sectors, because of its role in regulating plant productivity and response to the environment. Stomata observation and automatic stomata detection are useful stomata analyses for taxonomic, biological, physiological, and ecophysiological aspects of science. This study suggested a new clearing method for providing better microscopic images of stomata in soybean and automated stomata detection by deep learning. We developed modified leaf-clearing procedures for analyzing the stomata of soybean by showing the details of epidermal cells. There are three steps for clearing procedures, which are fixation, dehydration, and transparency in leaves. We tested eight combinations of clear agents based on different ethanol and sodium hypochlorite (NaOCl) concentrations to develop a new clearing agent for the transparency in leaves step. A new clearing agent-a 1:1 (v/v) mixture of 95% ethanol and NaOCl (6%-14%)-produced better stomata quality in microscopic images for soybean. To develop an automatic stomata detector using deep learning, we used micrographs taken from leaf imprints of 386 soybean accessions according to a new clearing method. We also improved a deep-learning algorithm that automatically analyzes stomata through an object detection model using YOLO v.3. The YOLO v.3 deep-learning model successfully recognized stomata with high mAP (0.9507). A web page was provided to use the model of stomata detection when users have stomatal images.

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

PC-0005

Genome-specific microsatellite markers enabled detection of parental genomes and genomic rearrangement in *Brassica* hybrids

Nicole Bon Campomayor[1], Nomar Espinosa Waminal[1], Remnyl Joyce Pellerin[1], Soo-Seong Lee[2], Jin Hoe Huh[3], Hyun Hee Kim[1*]

[1]Department of Life Sciences, Chromosome Research Institute, Sahmyook University, Seoul 01795, Republic of Korea
[2]BioBreeding Institute, Ansung, Republic of Korea
[3]Department of Plant Science, Plant Genomics and Breeding Institute and Research Institute for Agriculture and Life Sciences, Seoul National University, Seoul 08826, Republic of Korea

Genome-wide microsatellite characterization and marker development has been conducted to discriminate genomes of the sequenced *Brassica* crops: several cabbage (*Brassica*) species and radish (*Raphanus sativus* L.). Several breeding programs including intergeneric crosses have been performed to improve their productivity and utility. New synthetic hybrids are often genetically unstable and one way to evaluate genome stability in hybrids is through karyotype analysis. However, because of close genetic relationship between the commercial *Brassica* genomes, it has been difficult to distinguish subgenomes in allopolyploids through conventional cytogenetic analysis methods. To ensure easy, rapid, and efficient identification of subgenomes, we performed *in silico* mining for A, C, B, and R genome-specific microsatellite repeats and validated their genome specificity using sequential rapid FISH. Three microsatellites, ACBR_msat1, ACBR_msat14, and ACBR_msat20 were identified as B/R, A, and C genome specific in terms of abundance and chromosomal distribution. ACBR_msat14, and ACBR_msat20 were detected exclusively in A and C chromosomes, respectively, in hybrid species, whereas ACBR_msat1 was detected in both B and R genomes, albeit with different distributions. Moreover, detection of ACBR_msat20 in the tri-genome × *Brassicoraphanus* line 977 supports the frequently observed involvement of 45S rDNA array in genome rearrangement. The plant telomeric repeat $(TTTAGGG)_n$ was also detected as very intense signals in C genome chromosomes. These data demonstrate the utility of microsatellites as FISH probes in identifying subgenomes and revealing genome rearrangement within closely related *Brassica* and *Raphanus* species. A similar system may also be applicable in other plants.

Keywords: *Brassica*, microsatellite, *Raphanus sativus*, rapid FISH, subgenome, tandem repeat marker

***Corresponding Author:** Tel. +82-2-3399-1715, Fax: +82-2-3399-1729, E-mail: kimhh@syu.ac.kr

PC-0006

Detection of physiological response and phenotype of rice under the elevated temperature condition using the thermal image

Hoejeong Jeong, Eun-Ji Kim, Wan-gyu Sang, Jaekyeong Baek, Jun-Hwan Kim, Pyeong Shin, Dongwon Kwon, Myung-Chul Seo, Jung-Il Cho*

National Institute of Crop Science, RDA, Wanju 55365, Republic of Korea

Recently, many researches about early detection of crop conditions are demonstrated as the crop sensing technique has been developed. There are studies about figure out the crop conditions using non-distructive observations such as spectral analysis, fluorescence, and leaf temperature and based on this information various indices are suggested. Various indices have been proposed or supplemented to figure out crop conditions or responses under different treatments. For example, Crop Water Stress Index (CWSI) is suggested in 1980s to detect the water stress of crops based on the leaf temperature. As the thermal imaging or infrared thermometer technology has been developed, recently CWSI is used not only detect the water stress but also detect biotic, abiotic stress using leaf temperature. Because CWSI is calculated using leaf temperature and the leaf temperature is regulated by stomatal conductance, CWSI is closely related to stomatal conductance. Based on the relationship between stomata conductance and the leaf temperature, estimated stomatal conductance using CWSI can be observed more easily and earlier than before. Likewise, monitoring crop responses and growth using remotely sensed data can give more information to understand the physiological responses. In this study we will investigate the responses under elevated temperature and its effect on yield using rapid and accurate identification method such as thermal image to understand about the anabolic metabolism of paddy rice.

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***Corresponding Author:** Tel. +82-63-238-5286, E-mail: jungilcho@korea.kr

PC-0007

Analysis of phytohormone related DEGs in Korean wheat (*Triticum aestivum*) under PHS conditions and ABA response according to gene expression

Sang Yong Park[1], Yong Jin Lee[2], Jae Yoon Kim[1*]

[1]Department of Plant Resources, College of Industrial Science, Kongju National University, Yesan 32439, Republic of Korea

[2]Division of Biotechnology, College of Life Sciences and Biotechnology, Korea University, Seoul 02841, Repub-lic of Korea

PHS (Pre-Harvest Sprouting) is a representative phenomenon of excessive moisture stress that damages wheat seeds worldwide, including in Korea. As the harvest season frequently overlaps during the rainy season in Korea, premature seed germination is a problem that causes enormous damage to the quality of the final product of grain production. Because PHS during grain filling lead drastic reduction of the quality and economic value of wheat grain, the PHS resistance wheat is one of the most important breeding goal in Korean wheat breeding system. RNA-seq analysis was performed in PHS-resistant Korean wheat cultivar ‘Woori’ and sensitive Korean wheat cultivar ‘Keumgang’. The transcriptome analysis was conducted by exploring differentially expressed genes (DEGs) affected by PHS and ABA processing in both cultivars. A total of 123 unigenes are hormone-related and 1,862 DEG were found in the metabolic and signaling pathways of abscisic acid (ABA), gibberellic acid (GA), indole-3-acetic acid (IAA), and cytokinin. In addition, the specific gene ontology (GO) of DEG, which showed higher expression in “Woori,” compared to “Keumgang” was confirmed through network analysis of each DEG group. DEG analysis showed the majority of genes were categorized in sugar-related processes, which interact with ABA signaling in PHS tolerant cultivar under PHS-induction. The selected key DEGs were validated their expression by qRT-PCR with PHS and ABA-treated wheat spikes. Several DEGs were suggested key genes in the role of each phytohormone under PHS conditions in schematic diagram. Eventually, ABI5 and ABI3 were identified as key regulators during PHS mechanism and these would be a valuable information in Korean wheat PHS resistant breeding.

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***Corresponding Author:** Tel. 041-330-1203, E-mail: jaeyoonkim@kongju.ac.kr

PC-0008

Genome Wide Association Study on Preharvest Sprouting Resistance in Rice

Myeong-Hyeon Min[1], Do Hyun Kim[1], Jungrye Nam[2], Sang-Ho Chu[2], Yong-Jin Park[1,2*]

[1]Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 32439, Korea

[2]Center of Crop Breeding on Omics and Artificial Intelligence, Kongju National University, Yesan 32439, Korea

Preharvest sprouting (PHS) has been a problem threatening to rice production in very near future. The available genetic resources conferring the PHS resistance should be explored as much as possible. We conducted Genome Wide Association Study (GWAS) on PHS in rice was performed using genome wide resequencing data of the diverse 127 rice germplasm to identify the new candidate genes associated with the PHS and related traits as well as to confirm the previously identified dormancy and PHS associated genes. ERF genes were found to be most significantly associated with PHS, D7, D14, and GI. 3 candidate genes which have potential implication in improving the PHS resistance in rice were also detected. The result showed an evidence that points out physiological aspects of germination considerably and will provide very valuable information of the associated candidate genes for further studies on the PHS resistance in rice.

Key words: GWAS, PHS, ERF genes, stress related genes, rice germplasms

***Corresponding Author:** Tel. 041-330-1213, E-mail: yjpark@kongju.ac.kr

PC-0009

Development of Orange Flesh Color Discrimination Marker from Watermelon (*Citrullus lanatus*)

Hayoung Song, Kayoun Lee, Geung-Joo Lee*

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

Carotenoids are one of the most widely distributed pigments in plant, and their excellent antioxidant activity reduces the risk of various cancers and cardiovascular diseases and aids in visual function. Watermelon (*Citrullus lanatus*) is one of the fruit vegetables with high commodity demand worldwide. The flesh color is determined by the type and content of carotenoids. The flesh color of watermelon is considered to be an important trait because it is not only a factor providing diversity in color but also a major motivation for consumer choice from a nutritional point of view. Molecular markers are a rapid and accurate screening technique, and the development of useful markers in breeding is very important. In a previous study, we obtained genome-wide SNP identification data by performing whole genome resequencing (WGRS) on 24 inbred watermelon lines with different flesh color traits (PRJNA516776). In this study, we propose candidate genes that are judged to be related to orange flesh color based on SNPs that occur specifically for orange flesh among the identified genome-wide SNPs. And we found that an allelic at 445bp of phytoene synthase (PSY), which mediates the first step of carotenoid biosynthesis, is associated with the orange flesh color of watermelon. Based on the mutation, a molecular marker specificity resided on the ClPSY1 gene was developed and verified for discrimination of orange flesh watermelon. This marker, along with several previously reported markers derived from different genes, could be usefully used for selective breeding of functional carotenoid-containing watermelons.

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***Corresponding Author:** Tel. 042-821-5734, E-mail: gjlee@cnu.ac.kr

PC-0010

콩 식미저해인자 결여 품종 판별용 SNP기반의 분자마커 개발

이인혜[1*], 김남걸[1], 박명렬[1], 서민정[2], 윤홍태[1]

[1]경기도 수원시 권선구 수인로 126, 국립식량과학원 중부작물과
[2]전라북도 완주군 이서면 혁신로 181, 국립식량과학원 기획조정과

고단백질 등 풍부한 영양성분을 포함하고 있는 두유는 소비자들에게 기호도가 높고 친숙한 콩 가공식품 중 하나이다. 생콩이 가지고 있는 비린 향미, 알러지 유발, 소화가 어려움 등과 같은 식미저해인자로 인해 두유를 제조할 때 이를 제거하기 위한 열을 처리한다. 이 과정에서 유용 타영양성분도 함께 변형 및 소실되는 문제가 발생한다. 이를 보완하고자 육종적 방법으로 식미저해인자가 제거된 고기능성 콩 개발 연구를 진행 중이며, 식미저해인자 결여 계통 선발의 효율성 증대 및 대량 분석할 수 있는 분자마커 세트를 개발하였다. 식미저해인자 중 비린내 관련 인자 *Lipoxygenase1(Lx1), Lx2* 결여 품종과 소화억제효소인 *KTI* 결여 품종을 선별할 수 있는 SNP 기반의 대량 분석용 TaqMan genotyping 마커와 비린내 관련 인자 *Lx3* 결여 품종, 알러지 유발 인자 *P34, CG-1* 결여 품종을 선별할 수 있는 전기영동 기반의 분자마커를 개발하였다. 개발된 분자마커는 식미저해인자의 exon에 위치한 중요 변위 부위를 타겟으로 하여 고효율 검정이 용이하고, 분석 개체로부터 추출한 gDNA만으로 5종의 식미저해인자 결여 품종을 판별할 수 있어 신속한 대량 분석이 가능하다는 장점이 있다.

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***교신저자:** Tel. 031-695-4049, E-mail: ih22@korea.kr

PC-0011

쓴메밀 유전자원의 자원 정보 구축 및 종자신분증 개발

김수정[1*], 손황배[1], 김율호[2], 남정환[1], 이종남[1], 서종택[1]

[1]강원도 평창군 대관령면 경강로 5481 고령지농업연구소 국립식량과학원
[2]경기도 수원시 권선구 수인로 125 중부작물과 국립식량과학원

우리 품종과 유전자원의 특성에 대한 유전정보를 표준화해 효율적으로 관리할 수 있는 농작물 ‘종자신분증’ 모델 개발이 필요하다. ‘종자신분증’ 에는 각 작물의 품종명이 주민등록증의 이름처럼 사용된다. 사람의 얼굴 사진은 식물체의 꽃이나 종자 사진으로, 개개인을 식별하는 지문은 각각의 유전자원 또는 품종에 대한 유전형을 바코드화하여 표시하였다. 대상작물로 콩 품종 147종 및 메밀 국・내외 자원 74종에 대하여 품종 인식 프로그램(MyCrops_soybean, MyCrops_buckwheat)을 개발했으며, 이를 QR 코드에 적용하였다. 종자신분증’의 정보는 각각의 작물 유전형을 분석하고, 종자의 표현형, 유용성분을 표준화한 후, 시각화를 통해 일반인들도 알기 쉽게 표현했다. 콩과 메밀의 주요 품종과 유전자원의 종자특성 및 각각의 유용성분인 이소플라본과 루틴을 분석해 데이터베이스(DB)를 구축했다. 이를 통해 유전형, 표현형, 유용성분을 한눈에 알기 쉽게 검색할 수 있는 융합 플랫폼 프로그램 모델을 구축하였다. ‘종자신분증’ 제도가 도입되면 품종과 유전자원의 관리 효율을 높일 수 있고 소비자들은 농산물 가공제품의 ‘종자신분증’ QR코드를 이용해 제품 원료의 정보를 한눈에 볼 수 있게 될 것이다. 또한, 소비자들은 해당 종자의 생산지, 가공업체 등의 생산이력 정보를 확인할 수 있으므로 안심하고 안전한 먹거리를 구입할 수 있다. 현재 콩・메밀에서 ‘종자신분증’ 모델이 개발 단계이며, 다른 식량작물로 확대 적용할 계획이다.

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***교신저자:** Tel. 033-330-1820, E-mail: sjkim@korea.kr

PC-0012

Accelerate kenaf (*Hibiscus cannabinus* L.) breeding using its germplasm by vegetation index (VI) from RGB image obtained from drone

Jae Young Kim, Ki Bon Ku, Gyung Deok Han, Yong Suk Chung*

Department of Plant Resource and Environment, Jeju National University, Jeju, 63243, Republic of Korea

Fast and efficient crop breeding is required for the demand for the various uses of crops and the sufficient food supply of the rapidly growing population on the earth. Even the growing population is concentrated in the urban area, not a rural area that produces crops. Recently, the rural area is suffered by reducing the workforce, and this phenomenon is expected to continue and expanded to the related industry like breeding. Also, climate change is one of the urgent problems that needed new breeding cultivars to adapt. Breeders started to apply drones, cameras, and sensors for breeding selection to solve this problem because the selection process is labor-intensive and time-consuming. In this study, the kenaf field RGB image was captured by a camera in the drone. The six vegetation indices and the area of kenaf are confirmed, and the height of kenaf is predicted. At the same time, the stem diameter and number of the node of kenaf were measured. Those traits are known as tightly connected with the production of biomass or fiber production. As a result of correlation analysis, a significant and strong positive or negative correlation between traits is found that could be applied to predict the final kenaf yield. Because getting an RGB image from a drone is efficient, inexpensive, simple, fast, and does not need much workforce, it would accelerate kenaf breeding if applied to the breeding selection process.

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***Corresponding Author:** Tel. 82-64-754-3318, E-mail: yschung@jejunu.ac.kr

PC-0013

Development of Mask-RCNN model for detecting greenhouses based on satellite image

Yun Seok Kim, Seong Uk Yoon, Anh Tuan Le, Ji Eun Park, Ji Hyeon Jung, Yong Suk Chung*

Department of Plant Resources and Environment, Jeju National University, Jeju, 63243, Republic of Korea

The number of greenhouses is expanding with funding sources from government, positively impacting on saving labors and enhancing production quality. Meanwhile, the number of illegal greenhouses is also increasing as well, which is serious issues for local governments in Republic of Korea. Thus, in the current study, we developed Mask-RCNN model for detecting greenhouses based on satellite images obtained by using Kakaomap API. Greenhouses in the satellite images were labeled to be used for inferring the following data test. For distinguishing between existing greenhouses and new one, Detectron2 which is framework based on Mask-RCNN is used. As a result, greenhouses could be detected in the image. This method can be utilized for detecting newly built greenhouses with periodical image data screening. This method could be applied to detecting disease symptoms in the field.

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***Corresponding Author:** Tel. 82-64-754-3318, E-mail: yschung@jejunu.ac.kr

PC-0014

Optimization of fast and reliable RP-UPLC method for HMW-GS allelic variation analysis in large bread wheat germplasm

Su Bin Lee, Sewon Kim, Jae-Ryeong Sim, Jong-Yeol Lee*

National Institute of Agricultural Science, RDA, Jeonju, 54874, Republic of Korea

High molecular weight glutenin subunits (HMW-GS) account for only 10% of the total wheat storage protein, but play an important role in end-use quality. In this study, we established an optimized RP-UPLC method to identify HMW-GS more quickly, accurately and reproducibly. The separation parameters were optimized by adopting an ACQUITY UPLC Protein BEH C4 column and a step-wise ACN gradient. With the optimized RP-UPLC method, HMW-GS of Chines Spring (CS) was well separated within about 5.5 min, and all analyzes were completed within 12 min. The separation patterns and retention times (RT) of 22 HMW-GS in 16 standard wheat cultivars were analyzed by an optimized RP-UPLC method. As a result, 16 HMW-GS could be distinguished by differences in RT, but three of 1Bx (1Bx7, 1Bx7^{OE} and 1Bx14) or three of 1By (1By8*, 1By9 and 1By15) had very similar of RT and were indistinguishable. 1Bx7/1Bx7^{OE} and 1Bx14 or 1By8*, 1By9 and 1By15, which were difficult to distinguish due to RT overlap, were separated by SDS-PAGE. To distinguish between 1Bx7 and 1Bx7^{OE}, the 7^{OE} DNA junction marker was used. The optimized method was successfully applied to the determination of HMW-GS alleles in large bread wheat germplasm (1787 lineage), and identified the frequency of HMW-GS allele variation. In addition, wheat lines with 1Dx null, 1Dx null and 1Dy null were identified.

***Corresponding Author:** Tel. 063-238-4616, E-mail: jy0820@korea.kr

PC-0015

Influence of high temperature on growth and metabolic process of rice and potatoes

Eun-Ji Kim, Wan-gyu Sang, Jaekyeong Baek, Jun-Hwan Kim, Pyeong Shin, Dongwon Kwon, Hoejeong Jeong, Myeng-Chul Seo, Jung-Il Cho*

National Institute of Crop Science, RDA, Jeollabuk-do, Korea

Recently, the atmospheric temperature has been continuously rising due to global warming. In Korea, the average temperature has risen by 1.5℃ for the past 100 years. High temperature affects the metabolic mechanism of crops and causes changes in seed nutrient content and quality. Therefore, in this study, the effect of high temperature during the growing season on the growth response and metabolic process of rice and potatoes was analyzed using SPAR (Soil-Plant-Atmosphere-Research) chambers and temperature gradient field chambers (TGFC).

It was confirmed that the high temperature during the vegetative growth stage of rice and potatoes affects growth, flowering time and tuber formation, and the high temperature during the reproductive growth stage causes changes in nutritional components such as starch. In the case of rice, high temperature causes infertility or changes in nutritional components such as starch, which is a threat to the quality and productivity of rice. On the other hand, in the case of spring potatoes, high temperature promotes early vegetative growth, but acts as an inhibitor in tuber formation and bulking, resulting in decreased yield.

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***Corresponding Author:** Tel. +82-63-238-5286, E-mail: jungilcho@korea.kr

PC-0016

Characterization of *GBSSII* Haplotypes and Its Domestication Signals in KRICE_CORE (Korean World Rice Collection)

Thant Zin Maung[1], Sang-Ho Chu[2], Kyu-Won Kim[2], Yong-Jin Park[1,2*]

[1]Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 32439, Republic of Korea

[2]Center of Crop Breeding on Omics and Artificial Intelligence, Kongju National University, Yesan 32439, Republic of Korea

The granule-bound starch synthase II (*GBSSII*), one of the GBSS proteins (*GBSSI* and *GBSSII*) which is mainly expressed in non-storage tissues like leaves, is responsible to synthesize amylose in starch biosynthesis of rice. To characterize the identified haplotypes and its domestication signals in 475 accessions in KRICE_CORE (Korean World Rice Collection), haplotyping and evolutionary analyses were performed using classified collections into 421 cultivated and 54 wild rice and the cultivated rice were subdivided into temperate japonica, tropical japonica, indica, aus, aromatic and admixture according to their geographical location. After a series of analyses, we observed a total of 45 haplotypes representing 58 SNP, of which 38 SNPs were nonsynonymous representing different functional substitutions in different respective exons of chromosome 7. Cultivated rice showed both the highest and lowest diversity (π) values, representing the highest by temperate japonica (0.0036) and the lowest by tropical japonica (0.0015). Positive values of Tajima's D were observed in all the cultivated ecotypes suggesting the balancing selection, whereas negative value (-0.6207) observed in wild rice meaning excess of rare alleles suggesting domestication. High interbreeding level was found between temperate and tropical japonica, indicated by lowest F_{ST} value (0.0498), compared to its greatest differentiation observed in tropical japonica-aroma (F_{ST} =0.8318). Our observations on haplotype diversity and on selective sweep will provide a cue to understand nucleotide changes and their contribution to the function of *GBSSII* during domestication and be used for the genetic improvement of grain quality involving *GBSSII*.

Keywords: Granule-bound starch synthase II (*GBSSII*), SNP, Domestication, cultivated rice, wild rice

***Corresponding Author:** Tel. +82 41-330-1201, E-mail: yjpark@kongju.ac.kr

PC-0017

Anticipated polymorphic SSRs and its application based on high-throughput sequences in four cultivars of *Prunus persica*

Jung Sun Kim[1*], Yun Suk Ku[1], Sin-Gi Park[2], Se Hee Kim[3], Prabhakaran Soundararajan[1], Hyun Woo Park[1], So Youn Won[1]

[1]Department of Agricultural Biotechnology, National Institute of Agricultural Sciences, Rural Development Administration, Jeonju, 54874, Republic of Korea
[2]Bioinformatics Team of Theragene Etex Institute, Suwon 16229, Republic of Korea
[3]Fruit Research Division, National Institute of Horticultural & Herbal Science, Rural Development Administration, Wanju-gun, 55365, Republic of Korea

Prunus persica 'Mihong', is a domesticated white peach that was generated from the crossing between 'Yumyeong' and 'Chiyomaru' in 1995, Republic of Korea. RDA launched the genome sequencing of 'Mihong' since 2018. 'Mihong' reached to 200 scaffold and 241Mb sequences using long-read sequencing and Hi-C technology. F1 populations of 'Kawanakajima Hakuto' and 'Mihong' and, 'Changhowon Hwangdo' and 'Yumi' were developed in NIHHS. These four cultivars of parents were sequenced and assembled using SOAPdenovo version 2.04. At the first, we surveyed the SSRs in 'Mihong' assembly sequences and extracted the ±300bp flanking sequences, containing SSRs. The second, three cultivar assemble sequences were aligned and mapped against to 'Mihong' flanking sequences using BLASTn (version 2.2.29+). The SSRs were extracted differential length in SSR region among four cultivars. The primer pairs were designed to generate amplicon of 160-200 bp in polymorphic SSR regions using primer3 (version 3-2.2.3). We selected 260 SSR markers with genetic distance and standard deviation in four cultivars (STEV >4.5). These anticipated polymorphic SSR markers could take 74% polymorphism in four genotypes. Finally, a F1 population of 'Kawanakajima Hakuto' and 'Mihong' was covered 884.5 cM with 465 SNPs and 86 SSRs and this genetic map matched correctly to HI-C pseudomolecule of *P. persica.*

Keywords: NGS, Peach, SSRs, genetic map

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***Corresponding Author:** Tel. 063-238-4559, E-mail: jsnkim@korea.kr

PC-0018

Mining SNPs linked to flower-related traits in Chrysanthemum using genotyping-by-sequencing

Ye-Ji Lee[1], Jae-A Jung[2], Jung Sun Kim[1], So Youn Won[1*]

[1]National Institute of Agricultural Sciences, RDA, Jeonju, 54874, Republic of Korea
[2]National Institute of Horticultural and Herbal Sciences, RDA, Wanju, 55365, Republic of Korea

Chrysanthemum (*Chrysanthemum morifolium* Ramat.) is a leading ornamental species worldwide with valuable floral diversity such as flower type, color, and size. Here, we investigated genetic basis of two representative inflorescence shapes, anemone-type and single-type in chrysanthemum. For this, we performed a genome-wide association study (GWAS) using 182 F_1 progenies derived from a cross between two cultivars, 'Puma white' (anemone-type) and 'Dancer' (single-type). The results showed that the phenotypic values in anemone-type flowers were significantly higher than single-type flowers in flower diameter (FD), number of ray flower (NRF) and disk flower diameter (DFD) traits. Genotyping-by-sequencing (GBS) analysis identified 1,287 single nucleotide polymorphisms (SNPs) in the population. GWAS analysis revealed that a total of 17 SNPs were significantly associated with flower type (FT), NRF and DFD traits. Of them, five potential candidate genes were identified to be linked with FT traits, and their expression patterns were analyzed using RNA-seq data of *Chrysanthemum nankingense* (a diploid species close to *C. morifolium*). Finally, three genes showed high expression values in flower bud tissues and predicted to regulate the flower growth and development in chrysanthemum. These results will provide for analyzing the genetic information with important horticultural traits, and reveal insights for further research in chrysanthemum breeding.

***Corresponding Author:** Tel. 063-238-4561, E-mail: soyounwon@korea.kr

PC-0019

표현체 분석장비(3D Scanalyzer)의 영상 분석 최적 조건 설정

김년희, 김송림, 안은숙, 이채원, 김민수, 김영욱, 백정호, 지현소, 윤인선, 김경환*

전라북도 전주시 덕진구 농생명로 370, 국립농업과학원 유전자공학과

급격한 기후변화로 인해 우수 품종의 고속, 대량 선발이 필요하며, 사람의 경험 중심 전통적인 육종에서 데이터 기반의 디지털 육종으로 농업의 패러다임이 변화하고 있다. 국립농업과학원에서는 디지털 육종 기술의 활용도를 증대시키기 위해 표현체 분석 인프라를 구축하여 농업 형질 디지털 특성 분석에 이용하고 있다. LemnaTec의 3Dscanalyzer를 이용하여 작물 생육 영상을 수집, 분석하고 있으며 영상분석 조건은 형질 특성 분석에 중요한 요인이다. 기존 형광등과 흰색 배경의 촬영 조건을 LED, 파란색 배경으로 변경하여 영상 획득 효율을 증대하였다. 변경된 조건에서 촬영 식물체의 바이오매스 수치값은 10%이상 증대되었으며 색상 분석도 기존 3개 채널에서 LAB 색차공간 중 B 채널(blueyellow) 한 개로 분석할 수 있었다. 한편, 작물이 일정 크기 이상인 경우 지지대를 설치하여 영상을 수집하고 분석시 LAB 색차공간 중 B 채널(blueyellow)과 LUV 색차공간 중 V 채널(greenmagenta)을 복합적으로 적용해 지지대를 제거하여 분석할 수 있었다. 변경된 영상 수집 조건을 이용하여 작물의 영상 촬영 환경설정 최적화와 색상 분석 방법의 표준 매뉴얼을 구축하였으며 생육특성 분석의 정확성과 효율성을 높일 수 있었다.

***교신저자:** Tel. 063-238-4658, E-mail: biopiakim@korea.kr

PC-0020

디지털 영상분석 기술을 통한 벼 생육기 농업 특성 연구

김송림, 안은숙, 김민수, 김재호, 김경환*

전주시 덕진구 농생명로 370 국립농업과학원 농업생명자원부 유전자공학과

기후변화와 인구증가는 농업 분야의 큰 도전이며, 급변하는 환경변화로 인해 신속, 정확한 농업형질 분석 기법들이 연구되고 있다. 그 중 표현체(phenomics) 기술은 작물의 영상을 수치로 변환하여 농업 특성을 파악하는 디지털 신 육종 기술로 발전하고 있지만, 정밀 재배 기술 및 영상지표개발 등의 미비로 농업적 활용도는 아직 미흡하였다. 이로 인해 본 연구에서는 조생종(오대), 중생종(화영), 중만생종(동진, 신동진) 4품종을 기초로 파종, 정식, 컨베이어 이송, 인프라 제어, 물공급, 비료시비 등의 일련의 과정을 거치며 벼 생육기 영상을 획득하였다. 획득된 영상은 벼 특이적 알고리즘과 영사면적(projected plant area), 관심영역의 Y축 최대길이(object extent Y), 관심영역의 X축 최대길이(object extent X), 볼록선체 면적(convexhull area), 밀집도(compactness) 등의 기하학적 영상지표에서 디지털 품종 특성을 산출하였다. 재배시스템, 인프라 스케줄링, 영상획득 및 분석과정은 벼 생육기 동안 표현체 획득의 표준화 구축에 사용되었으며, 바이오매스, 키, 폭 등의 농업형질에 대한 영상지표 활용성을 높였다. 본 연구의 표현체 분석 기반 기술들은 향후 다양한 벼 품종의 농업적 특성을 신속하게 대량 분석해 낼 것으로 보이며, 이를 바탕으로 옥수수, 수수 등과 같은 단자엽 작물로 확대 가능할 것으로 보인다.

***교신저자:** Tel. 063-238-4658, E-mail: biopiakim@korea.kr

PC-0021

영상기반 팥 종자 GWAS분석 시스템 구축

김영욱[1], 김년희[1], 이혜경[1], 김송림[1], 지현소[1], 이창우[2], 이홍로[2], 백정호[1], 김경환[1*]

[1]전라북도 전주시 완산구 농생명로 370, 농촌진흥청 국립농업과학원
[2]전라북도 군산시 대학로 558, 군산대학교

최근 새로운 품종개발 및 종자를 개량하기 위해 유전체와 표현체를 이용한 통합 분석 연구가 많이 진행되고 있다. 식물 육종에서 유전체정보와 연계하여 종자 형질 선별을 촉진하려면 효율적이고 신뢰할 수 있는 High-Throughput 방식의 표현형 분석 방법이 필요하다. 본 연구에서는 팥 종자 200품종 20,000립의 이미지를 처리하고 분석할 수 있는 웹 기반 GWAS 시스템을 구축하였다. 해당 시스템은 영상 데이터의 LAB색차정보를 활용하여 종자와 배경을 분리하여 Area, Perimeter, Circulation 등 10개의 형태 관련 특성 정보와 HSV 색상 히스토그램으로 디지털정보를 추출하는 영상처리 기능, 검색 및 데이터 정렬을 수행하기 위해 추출된 디지털정보를 실시간으로 데이터베이스로 구축하는 기능, 디지털 종자 특성 정보들을 유전체데이터와 연계하여 농업적 형질과 연관된 유전자를 탐색하기 위한 GWAS분석 기능으로 이루어져 있다. 향후 종자 영상으로 추출된 특성 정보와 GWAS분석 결과로 고부가가치를 갖는 신품종 및 종자개량 연구에 활용될 것으로 기대한다.

***교신저자:** Tel. 063-238-4658, E-mail: biopiakim@korea.kr

PC-0022

High-throughput authentication system of Korean wheat cultivars by digital genotyping

Woohyeon Cho[1], Jee Young Park[1], Jin-Kee Jung[2], Min-Young Kang[2], Tae-Jin Yang[1*]

[1]Department of Agriculture, Forestry and Bioresources, Plant Genomics & Breeding Institute, College of Agriculture & Life Sciences, Seoul National University 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Korea
[2]Seed Testing & Research Center, Korea Seed & Variety Service, Gimcheon, 39660, Republic of Korea

The common wheat, *Triticum aestivum*, is one of the world's most frequently consumed grain. However, cultivation level is still low in Korea. In this study, we developed Korean wheat cultivar identification markers. We sequenced and completed chloroplast genome of seven major Korean cultivars and found variations through comparative analysis. Also, we utilized web database CerealsDB to obtain nuclear genome derived single nucleotide polymorphisms (SNP). As wheat has large (17Gbp) and complex nuclear genome (2n = 6x = 42), we tried to identify single copy region locating SNPs for accurate genotyping. Ten SNPs were developed into allele specific PCR marker and 2 chloroplast, 6 nuclear SNPs were developed into high-throughput TaqMan assay. The genetic distance and relationship of 35 cultivars were analyzed with genotyping results. With this high-throughput molecular marker set, high-efficient and cost, labor effective analyze will be possible at the farm and industrial scene.

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

PC-0023

Evaluation of agricultural trait using high-throughput phenotyping in soybean

Minsu Kim, Chaewon Lee, Nyunhee Kim, Subin Hong, Song Lim Kim, JeongHo Back, In Sun Yoon, Hyeonso Ji, Kyung-Hwan Kim*

National Institute of Agricultural Science, RDA, Wanju 54874, Republic of Korea

Global crop production should be increased to meet rising demand for food due to rapid population growth, while crop yields are not growing at sufficient rate. To resolve this issue, it is important to cultivate varieties with high yields, but breeding takes long time due to growth cycle of plants. Understanding characteristics of each growth cycle and revealing the correlation with yield can contribute to reduce breeding period through rapid selection. RGB (red green blue) images can be processed to estimate projected plant area and high-throughput phenotyping (HTP) technology can do this process faster and more accurately. In this study, various types of soybean varieties were analyzed from seedling to reproductive (R) stage using LemnaTec 3D Scanalyzer system (LenmaTec GmbH, Aachen, Germany). Three side images (120 ° apart) and one top image were acquired at 1-day intervals. We developed twelve parameters to measure the growth characteristics of soybean. Through this, from vegetable (V) stage 1 to 3 were distinguished, and determinant/in-determinant growth types were discriminated.

***Corresponding Author:** Tel. 063-238-4658, E-mail: biopiakim@kroea.kr

PC-0024

스마트폰을 이용한 종자 개수 측정 프로그램 개발

김영욱, 이혜경, 김송림, 백정호*

전라북도 전주시 완산구 농생명로 370, 농촌진흥청 국립농업과학원

현대생활에서 종자는 풍요로운 인간의 삶을 유지하기 위해 식량, 의료, 제약, 화장품 등 다양한 산업에 활용되고 있어 이를 관리하고 개량하기 위해 많은 연구들이 진행되고 있다. 종자관련 연구를 수행하는데 가장 기본적인 것은 수량을 파악하여 수확량, 충실도 등 우수형질을 확인하는 작업이다. 종자 수량을 측정하는데 활용되는 방법은 자동화 장치를 이용하는 방법과 사람이 직접 확인하는 방법이 많이 이용된다. 하지만 자동화 장치는 매우 비싸며 측정하는데 시간이 오래 걸려 소규모 작업하는 기업과 연구실에서 활용하기에 비효율적이다. 사람이 직접 종자의 개수를 확인하는 작업 역시 많은 시간과 노동력이 필요하여 연구를 수행하는데 어려움이 있다. 본 연구에서는 장치의 비용문제, 작업시간, 노동력 문제를 개선하고자 누구나 가지고 있는 스마트폰을 활용하여 즉각적으로 종자의 개수를 확인 할 수 있게 다음과 같이 3단계로 이루어지는 프로그램 개발 연구를 진행하였다. 1단계, 종자와 배경의 분리를 위해 파란색 배경판에서 스마트폰을 이용하여 촬영. 2단계, 종자 영상이 서버로 전송되어 영상 처리를 수행. 3단계, 처리된 결과를 디지털화 하여 다시 스마트폰으로 전송하여 사용자가 확인. 향후 딥러닝 방법으로 연구데이터의 정확성 향상하여 연구현장에서 편리하게 사용할 수 있는 시스템을 구축하고자 한다.

***교신저자:** Tel. 063-238-4670, E-mail: firstleon@korea.kr

PC-0025

Water absorption evaluation in germination process using high-throughput phenotyping

김민수[1], 김영욱[1], 김년희[1], 이채원[1], 김송림[1], 지현소[1], 백정호[1], 문중경[2], 김경환[1*]

[1]National Institute of Agricultural Science, RDA, Wanju 54874, Republic of Korea
[2]National Institute of Crop Science, RDA, Wanju 55365, Republic of Korea

식물의 생장에 있어 가장 우선적으로 수행 되어야하는 과정이 발아이다. 종자의 발아는 수분 흡수 특성에 따라 1) 빠르게 물을 흡수, 2) 충분한 수분 흡수 후 안정기, 3) 저장 조직의 에너지 활성을 통한 뿌리 출현 등 보통 3단계로 진행 된다. 따라서 종자 발아에서 수분 흡수는 가장 기초적인 단계이지만 이후 과정을 위한 필수적인 단계라고 할 수 있다. 본 연구에서는 콩 핵심집단 430계통별 수분함량의 변화를 실시간 이미지 시스템을 활용하여 분석하고 군집화 하였다. RGB 기반 이미지로 획득한 면적의 변화는 실제 종자의 수분함량 변화와 비교하여 $R > 0.99$ 유의한 상관관계를 나타내었다. 이후 실시간 영상 분석을 이용해 수분 공급 시작부터 48시간 동안의 종자 발아를 관찰하다. 영상처리를 통해 면적(area), 둥근 정도(roundness), 밀집도(compactness), 둘레길이(circumference) 지표의 값을 산출하였고, 수분 흡수율과 발아를 동시에 조사하였다. 향후 확보된 데이터는 발아 초기 수분 흡수와 발아력의 연관성 검정 및 종자 특성 별 흡수 속도의 차이 분석에 활용할 수 있으며 발아와 관련된 다양한 대사작용과의 연관성 검정에 활용할 예정이다.

***교신저자:** Tel. 063-238-4658, E-mail: biopiakim@kroea.kr

PC-0026

Breeding of High Cooking and Eating Quality Lines based on Marker-Assisted Backcrossing (MABc) with KASP Markers in Rice

Me-Sun Kim[1], Ju-Young Yang[1], Sothea Ouk[1], Le Van Trang[1], Seo-Rin Ko[1], Kwon-Kyoo Kang[2], Yong-Gu Cho[1*]

[1]Department of Crop Science, Chungbuk National University, Cheongju 28644, Korea
[2]Department of Horticulture, Hankyong National University, Ansung 17579, Korea

The primary goals of rice breeding programs are grain quality and yield potential improvement. With the high demand for rice varieties of premium cooking and eating quality, we developed low-amylose content breeding lines from the cross between Samgwang and Milkyqueen through the marker-assisted backcross (MABc) breeding program. Trait markers of SSIIIa gene referring to low-amylose content were identified through a SNP mapping activity, and the markers were applied to select favorable lines for a foreground selection. To rapidly recover the genetic background of Samgwang (recurrent parent genome, RPG), 386 genome-wide KASP markers for a background selection were used in BC_1F_1 and BC_2F_1 generations. Seven BC_2F_1 lines with targeted traits were selected, and the genetic background recovery ranges were varied with 97.4~99.1% of RPG. The amylose content of selected BC_2F_2 grains was measured and the results showed a range of 12.4~16.8% showing the promising levels. We demonstrated the MABc using trait and genome-wide markers, allowing us to efficiently select lines of accurate genetic components and reduced the breeding cycle effectively. In addition, the BC_2F_2 lines confirmed by KASP markers in this study can be utilized as parental lines for subsequent breeding programs of high-quality rice for cooking and eating.

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***Corresponding Author:** Tel. +82-43-261-2514, E-mail: ygcho@cbnu.ac.kr

PC-0027

Identification of breeding lines related to eating and processing quality of brown rice using marker-assisted backcross breeding (MABC) with KASP markers in rice

Me-Sun Kim[1], Sothea Ouk[1], Le Van Trang[1], Ju-Young Yang[1], Seo-Rin Ko[1], Gi-Jo Kim[1], Kwon-Kyoo Kang[2], Yong-Gu Cho[1]*

[1]Department of Crop Science, Chungbuk National University, Cheongju 28644, Korea
[2]Department of Horticulture, Hankyong National University, Ansung 17579, Korea

Compared to white rice, brown rice is rich in nutrients such as protein, dietary fiber, and vitamins, so it is highly preferred by consumers as a dietary and health food. However, brown rice has a problem in which the texture is somewhat rough even after cooking because the bran layer is thicker than white rice and moisture absorption is not good due to differences in structural characteristics. This study used Seolgaeng, known as a high-quality brown rice cultivar among domestic cultivars as a donor in order to develop lines for a brown rice variety with improved taste and processing aptitude of Samgwang cultivar. In the BC_1F_1 and BC_2F_1 generations, the genes related to high-brown rice quality of Seolgang was selected in the foreground selection. Four lines, SS50-25, SS50-26, SS50-27 and SS50-28, having over 98.65% of genome recovery rate of the recurrent parent Samgwang were selected through the molecular backcrossing (MABc) method with KASP markers for a background selection. When the thickness of the seed coat and aleurone layer of seeds harvested from the selected brown rice lines were measured, the thickness of Samgwang was 30.91 ㎛, but the selected lines with the thickness of 11.7 to 21.7 ㎛ similar to those of Seolgang (11.93 ㎛) in BC_2F_2 generation were developed. In addition, it is believed that these lines can be used as breeding materials for developing varieties with high value-added brown rice.

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***Corresponding Author:** Tel. +82-43-261-2514, E-mail: ygcho@cbnu.ac.kr

PC-0028

Determine genetic resources specific variants by massive sorghum genotyping project

Tae-Ho Lee*, Myung-Eun Park, Yun-Ho Oh, Da-Hye Jeon, Seo-Hyeon Ham

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

Generic resource-specific variants are essential sources in genomic research and agricultural development, such as molecular marker development. Thus, many countries have been making various efforts to secure various genetic resources. NAC (National Agrobiodiversity Center) has secured more than 3,300 sorghum genetic resources as a part of the effort. For the efficient use of the sorghum as an agricultural resource, we developed a pipeline to determine genetic resources specific variants from massive sorghum genotyping data. The programs efficiently determined generic resource-specific variants In the test determination in 358 samples. Notably, we found many resource-specific variants which can be candidates of a good SNP marker. We will keep our effort to determine variants in over a thousand sorghum resources, and the data would be helpful in agricultural development such as breeding.

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***Corresponding Author:** Tel. 063-238-4558, E-mail: thlee0@korea.kr

PC-0029

The Correlation between Herbicide and 4-hydroxyphenylpyruvate Dioxygenase on Vitamin E Pathway in Rice

Aueangporn Somsri[1], Sang-Ho Chu[2], Kyu-Won Kim[2], Yong-Jin Park[1,2*]

[1]Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 32439, Korea

[2]Center of Crop Breeding on Omics and Artificial Intelligence, Kongju National University, Yesan 32439, Korea

Tocochromanols are lipophilic compounds which are chiefly produced by photosynthetic organisms including plants, algae, and cyanobacteria. It is also known as vitamin E, one of the most powerful antioxidants. Due to its capacity to interact with oxidative stress caused by scavenge lipid peroxyl radicals, polyunsaturated acyl groups and quench reactive oxygen species (ROS), which are abiotic stresses and responsible for severe damage to plant cells. Many plant studies exhibit evidence that elevated levels of vitamin E can confer tolerance upon several abiotic stresses. These include salinity, drought, metal toxicity, UV radiation, and herbicide. In rice cultivation systems, weeds lead to serious yield reduction issues; therefore, the application of herbicides is becoming the dominant approach for weed control. In contrast, the application of herbicide also effects crops by targeting 4-hydroxyphenylpyruvate dioxygenase (HPPD), a key enzyme in the plastoquinone and vitamin E biosynthesis. We also analyzed the correlation of vitamin E and herbicides with respect to 295 rice germplasms. Our results found the relationship between vitamin E and HPPDi to result in vitamin E content in rice. Therefore, this review will provide more information for our understanding to improve and develop rice breeding in the future.

Keywords: vitamin E biosynthesis, 4-hydroxyphenylpyruvate dioxygenase (HPPD), herbicide, homogentisate dioxygenase, *Oryza sativa.*

***Corresponding Author:** Tel. +82 41-330-1201, E-mail: yjpark@kongju.ac.kr

PC-0030

Integrative System of New Functional Haplotypes and DNA Markers in Aromatic Rice Breeding

Rungnapa Phitaktansakul[1], Sang-Ho Chu[2], Yong-Jin Park[1,2*]

[1]Department of Plant Resources, College of Industrial Science, Kongju National University, Yesan, 32439, Korea

[2]Center of Crop Breeding on Omics and Artificial Intelligence, Kongju National University, Yesan 32439, Korea

Fragrant rice (*Oryza sativa* L.) is attractive to consumers and is of great economic importance, providing a premium price in world trade. Fragrance was due to the betaine aldehyde dehydrogenase (*BADH2*) gene located on chromosome 8. We sequenced the whole genomes of 475 KRICE_CORE (Korean World Collection) and 3,000 rice accessions from the database and analyzed them for their nucleotide variation of *BADH2*. We detected a total of 26 non-synonymous alleles in *BADH2* coding sequences, belonging to 114 aromatic rice accessions. Of those, we identified sixteen alleles as novel alleles, representing *badh2*-E1-198G>C, *badh2*-E1-199C>T, *badh2*-E1-208T>A, *badh2*-E2-476C>A, *badh2*-E2-440C>G, *badh2*-E4-1771T>G, *badh2*-E4-1789A>C, *badh2*-E4-1810A>T, *badh2*-E5-2604T>C, *badh2*-E5-2658C>T, *badh2*-E9-4036delT, *badh2*-E10-4460G>A, *badh2*-E10-4550G>A, *badh2*-E12-5149A>C, *badh2*-E13-5433A>T, and *badh2*-E14-5768C>T. Furthermore, we developed a total of ten functional SNP markers, nine of which were distinguished by a tetra primer amplification refractory mutation system-polymerase chain reaction (ARMS-PCR) system, and one (*badh2*-E2-476C>A) that was discriminated by a TaqMan probe fluorescent assay using the CFX96 real-time system (Bio Rad). We selected 46 rice accessions to verify these markers, and ten molecular markers were reliable in distinguishing between the fragrant and other fragrant or non-fragrant rice accessions. The ARMS-PCR technique is cost-effective, reliable and simple to use. However, due to the very fast and precise results by the real-time PCR method, it is recommended to examine a large number of samples and markers in high GC contents. Both the ARMS-PCR and real-time PCR methods will be useful for the genotyping of *BADH2* and development of new fragrant rice by using a marker-assisted breeding program.

Keywords: fragrant rice, *BADH2*, SNP marker, tetra-primer amplification refractory mutation system-polymerase chain reaction (ARMS-PCR), allelic discrimination

***Corresponding Author:** Tel. +82-41-330-1201, E-mail: yjpark@kongju.ac.kr

PC-0031

High-Thoughput Phenotyping and Diversity Analysis of Korean Soybean Cultivars Seeds

Seong-Hoon Kim*, Xiaohan Wang, Bum-Soo Hahn, Myoung-Jae Shin, Ae Jin Hwang, On sook Hur, Bichaem Kim, IK Jang

National Agrobiodiversity Center, National Institute of Agricultural Sciences, Rural Development Administration, Jeonju 54874, Republic of Korea

Soybean (*Glycine max*) is a native crop in Northeast Asia including Korea and one of the representative food crops grown in fields. The National Agrobiodiversity Center (NAC) is conserving approximate 30,000 soybean germplasms and distributes them to related field researchers and scientists. The phenotype-traits data of soybean seeds were usually investigated during periodic multiplication. It was time-consuming work to collect a sufficient number of data, especially width and height. Due to these difficulties, NAC has been a consideration to include seed morphology in passport information. During a last decade, the fantastic development on phenomics could efficiently analysis high-throughput phenotying seed morphology. Here we collected and analyzed seed image (seed phenotype traits such as width and height) of fifty-nine germplsams (5,900 seeds) in Korean cultivars using digital camera and Python programs. In order to analysis the diversity of germplasms, we conducted principal component analysis (PCA) and cluster analysis using data of seed phenotypes. The characteristics (area vs perimeter and width vs height) were shown positive correlations, whereas circularity and roundness were shown negative correlations. Based on these results, we divided soybean cultivars into three groups (9, 16 and 34 germplasms). Our results strongly could be facilitating gene analysis as GWAS and elite germplasm breeding.

***Corresponding Author:** Tel. 063-238-4886, E-mail: shkim0819@korea.kr

PC-0032

Identification and validation of fatty acids and lipid content related gene based on transcriptomic study of *Perilla frutescens*

Rizwana B.Syed Nabi*, Myoung Hee Lee, Jung In Kim, Kwang-Soo Cho, Eunyoung Oh, Sungup Kim, Jae Eun Park

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

Perilla (*Perilla frutescens (L.)* var frutescens) is an annual herbaceous self-pollinating crop. The crop is widely distributed and mostly grown in East Asia. Perilla typically, used as a source of food and traditional medicine. For decades, perilla is used as a dietary oil seed crop in Korea, which contains a high level of α-linolenic acid (ALA) or omega (ω-3) fatty acids having great health and development benefit. Here, we interested to investigate genotypic variation in lipid content of the two species 'Daesil deulkkae (*Perilla frutescens*) and lemonegoma (*Perilla citriodora*)'. Based on transcriptome evaluation, two genes FAD5 (fatty acid desaturase 5) and MIPS5 (myo-inositol-1-phosphate synthase 2) were selected. Further, the expression of two genes evaluated and correlation with the lipid content were performed with four different stages (Stage 1- Seedling, Stage 2- Vegetative, Stage 3- Flowering, Stage 4- Maturing stage). We observed the strong positive correlation with the expression abundance measured in RNA-seq analysis. FAD5 gene expression showed highly significant difference between stage 1 (Seedling) and stage 4 (Mature stage) analysis. Similarly, MIPS gene expression also revealed the difference between 'Daesil and lemon' cultivars at stage 1 analysis. Moreover, we have validated the expression levels of both genes in advanced population. Besides, polymorphic markers were designed that can be used in Perilla breeding for screening high lipid content at early stages.

***Corresponding Author:** Tel. +82-8934-8199, E-mail: emhee@korea.kr / rizwananabi@korea.kr

PC-0033

Measuring meiotic recombination rates in barley pollen nuclei in high-throughput with Crystal Digital PCR

Yun-Jae Ahn*, Joerg Fuchs, Andreas Houben, Stefan Heckmann

Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), OT Gatersleben, Correnstraβe 3, 06466 Stadt Seeland, Germany

Diverse allelic combinations generated through meiotic recombination assure genetic variation that is harnessed during plant breeding. Measuring meiotic recombination rates directly in gametes before fertilization enables the screening of large sample numbers from single individuals independent of molecular marker analysis in segregating populations or time-consuming crossover (CO) detection based on cytological observations. Furthermore, it allows the measurement of CO frequencies in hybrid gametes without segregation distortion. Up to now, single pollen nucleus genotyping in barley (*Hordeum vulgare*) requires a Whole Genome Amplification (WGA) step before PCR-based genotyping or single-cell sequencing due to the limited pollen nucleus DNA content (≈ 5 pg per haploid nucleus) thus restricting the number of samples analyzed. We developed a Crystal Digital PCR-based single pollen nucleus genotyping assay to measure meiotic recombination rates within four selected chromosomal intervals (two centromeric and two distal) in high-throughput in pollen nuclei without WGA. We improved the genotyping assay efficiency through a restriction enzyme pre-treatment of pollen nuclei and genotyped more than 42,000 individual pollen nuclei. Measured rates of meiotic recombination in hybrid pollen nuclei corresponded to that in segregating populations. The throughput was further increased by multiplexing our assays allowing the simultaneous analysis within two chromosomal intervals. Additionally, nuclei from several crop plants with different nuclear sizes and amounts of DNA were shown to be compatible with the set-up, suggesting a broad application of Crystal Digital PCR-based single nuclei genotyping assays.

***Corresponding Author:** Tel. +49 (0)039482 5673, E-mail: yjahn0121@gmail.com

PC-0034

Haplotyping and evolutionary studies on Trehalose-6-Phosphate Phosphatase 7 (*TPP7*), Anaerobic Germination 1 (*AG1*) tolerance gene (Os09g0369400) in KRICE_CORE

Kyaw Myo Aung[1], Thant Zin Maung[1], Sang-Ho Chu[2], Kyu-Won Kim[2], Jungrye Nam[2], Yong-Jin Park[1,2*]

[1]Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 32439, Korea

[2]Center of Crop Breeding on Omics and Artificial Intelligence, Kongju National University, Yesan 32439, Korea

Among the trehalose-6-phosphate phosphatase (TPP) gene family, *TPP7* is responsible for the germination vigor under submergence. Anaerobic germination 1 (*AG1*), encoding *TPP7* enhanced the coleoptile elongation in seeds and AG plays an important role in submergence resistance, an important trait for rice production in flood-prone lowland areas. AG tolerance enables robust seedling establishment through the rapid and sustained coleoptile elongation under flooded situations. Here, we used 475 improved KRICE_CORE (Korean World Rice Collection) rice varieties and conducted haplotype and genetic variant analyses aiming to provide the comprehensive information of functional SNPs and InDels based on *TPP7* (Os09g0369400) gene. We classified 18 haplotype groups and we found 10 functional SNPs in exon 1,3,4,5,6, and 7. Among the 18 haplotypes, the functional SNP, C/A (exon-5) was observed in haplotype 3 (50 accessions) and the functional SNP C/T (exon-3) together with 25 bp deletions (intron-5) was found in haplotype 12 including 6 indica and 4 temperate japonica accessions. In the genetic diversity analysis of *TPP7* (Os09g0369400) gene, we found that indica group revealed the highest nucleotide diversity (pi) value and the fixation index (*Fst*) between Tropical japonica and Aus observed higher than that of other sub-groups. We also observed that japonica types show a higher tolerance in anaerobic germination than the other types of rice. Combining these findings related to *AG1* gene, encoding *TPP7* with their functional SNPs and their genetic diversities can promote future rice breeding programs.

Keywords: Trehalose-6-Phosphate Phosphatase 7 (*TPP7*), Anaerobic germination (AG), haplotype, SNP

***Corresponding Author:** Tel. +82-41-330-1201, E-mail: yjpark@kongju.ac.kr

PD-0001

간척농지 고부가 작물 재배를 위한 토양환경 개선 및 현장실증연구

박영준*, 엄한용

경기도 안산시 상록구 해안로 870 한국농어촌공사 농어촌연구원

본 연구는 간척지에서 밭작물 재배를 위한 재배환경 표준화 및 실증연구를 통한 간척지 기반의 고부가가치 농업활용기술 개발을 목표로 한다. 특히, 기존 간척 염류지에서의 벼재배 단일적 활용에 대해 간척지 활용 다각화 방안으로 밭작물 재배의 가능성을 제시함으로서 간척지에서의 타작물 재배확대, 수입대체 및 개선방안 마련을 위해 수행되었다. 주요 결과로는 1) 간척지 용수원에서 포장으로까지 물공급 체계화 및 포장내에서 물관리 기준을 설정하였고, 2) 간척지구별 배수여건에 대한 현장도출을 통해 현행 간척지의 배수개선 및 토양관리기술을 개발하였다. 또한, 3) 간척지구별 정상생육 가능 원예 및 약용작물 총 8종 선발 및 작부체계를 작성하였고, 간척지 토양수분함량 기반 알고리듬 활용 근권환경 모니터링 시스템 및 제어시스템 시제품을 개발하였다. 본 연구를 통해 적정 수량을 산정하고 토양관리 방법을 제시함으로써 간척농지에 투자되어야할 생산기반 시설비의 타당성 및 적정한 기준을 제시하여 투자에 대한 의사결정 시 기초적 자료로 활용이 가능할 것으로 판단된다.

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

PD-0002

노지스마트 관개모델 개발을 위한 테스트베드 개선 및 실증연구

박영준*

경기도 안산시 상록구 해안로 870 한국농어촌공사 농어촌연구원

본 연구는 농어촌연구원에서 기개발한 스마트 관수로 시스템의 Test-Bed 시스템 고도화를 통해 작물이 필요로 하는 실시간 관개수량을 적시에 최적으로 수원에서 취수ㆍ공급하는 스마트 농업용수공급시스템을 적용시키는 것을 목적으로 수행되었다. 특히, 공사의 농업용수공급시스템과 민간기술인 스마트 관수ㆍ관비시스템 등 연계ㆍ통합방안을 마련하였으며 현장실증을 통해 기술개발에 대한 검증을 실시하였다. 농업용 관수로에 SCADA(Supervisory Control And Data Aquisition;감시제어 및 데이터 취득) 시스템을 도입하여 관망을 모니터링하고 펌프, 밸브 제어가 가능한 스마트 관수로 시스템을 개선하고 농촌용수 논관개와 밭관개를 위한 스마트 관수로 운영관리 시스템을 구축하였다. 또한, AMI 연계 자동화관개시스템을 통해 논에서는 무동력 자동급수장치 및 자동수위계 활용, 밭에서는 토양수분(수분장력, 수분함량, 기상정보)을 고려한 밭관개자동화시스템을 도입하였다. 본 시스템의 기본계획은 노지스마트 시범사업 및 첨단 무인자동화 농업생산 시범단지에 도입될 예정이다.

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

PD-0003

기상재해 대비 간척지 논 범용화를 위한 암거 및 적용기술 개발

박영준[1*], 김현태[2], 박태웅[1]

[1]경기도 안산시 상록구 해안로 870 한국농어촌공사 농어촌연구원
[2]경기도 의왕시 내선로 57 미래농촌기술연구소

소비자 기호, 기후 등 주요 농업 환경변화에 대응하여, 농업생산의 대부분을 차지하는 논의 범용화 대책 마련 필요하다. 이에 농어촌연구원에서는 간척지 논 범용화를 위해 기상재해(습해, 가뭄, 염해)에 대비할 수 있는 저비용 고효율 지하암거공법을 개발을 수행하고 있다. 1차년 연구에서는 토양수분 이동 수치해석을 통한 모관공급수 저류 시트형 지하관수+배수암거 요소기술개발을 실시하였고, 실내 요소실험을 통한 지표잔류수 지하흡수공 + 지하배수기능 최적 조합을 도출하였다. 또한 간척지에 적합한 고효율의 저류시트형 지하관수+배수 암거공법 시공기술 개발을 통해 적정장비 선정 시공효율화 기술, 토성에 따른 공법 적용 가능성 분석, 최적화 및 표준화 연구를 수행하였다. 본 결과는 지표잔류수와 지하배수가 동시에 가능한 기술로서 간척지의 고질적 문제인 지하배수 및 지표배수 불량으로 인한 습해문제를 해결할 수 있는 대안으로 기대된다.

사사: 본 연구는 농림축산식품부의 재원으로 농림식품기술기획평가원의 농업기반 및 재해대응기술개발사업의 지원을 받아 연구되었음(320050-3).

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

PD-0004

Agrobacterium-Mediated *Capsicum annuum* Gene Editing in Two Cultivars, Hot Pepper CM334 and Bell Pepper Dempsey

Sung-il Park[1], Hyun-Bin Kim[2], Hyun-Ji Jeon[2], Hyeran Kim[1,2*]

[1]Interdisciplinary Graduate Program in BIT Medical Convergence, Kangwon National University, Chuncheon 24341, Republic of Korea

[2]Department of Biological Sciences, Kangwon National University, Chuncheon, 24341, Republic of Korea

Pepper (*Capsicum annuum, C. annuum*) is one of the most economically attractive vegetables of the *Solanaceae* family. *C. annuum* is the most widespread and cultivated species of *Solanaceae* in subtropical and temperature countries. Although the whole-genome sequences of peppers and genome-editing tools are available, we are still far from the pepper precision editing, due to the lack of a stable pepper transformation method. Here, we employed three *Agrobacterium tumefaciens* strains AGL1, EHA101, and GV3101 to investigate which *Agrobacterium* strain could be used for pepper transformation. We co-cultivated soil-grown sterilized pepper leaves together with the *Agrobacteria* each. We measured the callus induction efficiency of pepper leaves after *Agrobacteria* co-cultivation. We optimized a suitable concentration of phosphinothricin (PPT) to select a CRISPR/Cas9 binary vector (pBAtC) for both pepper types. Finally, we screened transformed calli for PPT resistance in cv. CM334 and Dempsey, respectively. These selected calli showed different indel frequencies from the non-transformed calli.

***Corresponding Author:** Tel. 033-250-8535, E-mail: ranny@kangwon.ac.kr

PD-0005

TRV-mediated genome editing with mobile single guide RNA in *Nicotiana benthamiana*

Hwa-Jeong Kang[1], Da-Yeon Park[2], Venkatesh Jelli[2], Byoung-Cheorl Kang[2*]

[1]Interdisciplinary Program in Agricultural Biotechnology, College of Agriculture and Life Sciences, Seoul National University 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Republic of Korea

[2]Department of Plant Science and Plant Genomics and Breeding Institute, College of Agriculture and Life Sciences, Seoul National University 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Republic of Korea

Genome editing (GE) with sequence-specific nucleases is an easy and quick targeted mutation method. Previously, GE via RNA virus to deliver single guide RNA (sgRNA) was developed to avoid time-consuming tissue culture. sgRNA targeting two *phytoene desaturase* (*PDS*) genes of *Nicotiana benthamiana* was cloned into *Tobacco rattle virus* (TRV) vector. The TRV vector (TRV2-PDS-sgRNA) together with TRV1 was inoculated to transgenic *N. benthamiana* plants overexpressing Cas9. GE efficiency was compared between two TRV constructs driving PDS-sgRNA expression under U6 and Pea early browning virus (PEBV) promoters. Mutations were detected in the inoculated and upper leaves in the *PDS* genes after TRV2-PDS-sgRNA inoculation, and shoots regenerated from upper leaves showed GE efficiencies of 91.7% and 31.3% for U6 and PEBV promoters. TRV2-PDS-sgRNA containing the U6 promoter resulted in photobleached shoots due to mutations in the *PDS* genes. However, no photobleaching phenotype was observed among the progeny of *N. benthamiana* plants that showed mutations in *PDS* after TRV inoculation. To improve GE efficiency, mobile sgRNA containing flowering locus T (FT) or tRNA-Isoleucine sequence was introduced to TRV2-PEBV-PDS-sgRNA vector at the 3' of the sgRNA scaffold. FT and tRNA sequences increased GE efficiency from 0.6 - 4.0% to 14.4 - 51.2% in the upper leaves. Furthermore, up to 5.8% of the progenies of *N. benthamiana* plants that showed mutations after mobile TRV2-PDS-sgRNA inoculation also showed mutations in *PDS*. About 73.4% and 90% of regenerated shoots from TRV-PDS-FT-sgRNA and TRV-PDS-tRNA-sgRNA inoculation, respectively, showed mutations, which were much higher than that (31.3%) of non-mobile sgRNA.

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

PD-0006

팝콘용 옥수수 알곡 재수화가 튀김부피에 미치는 영향

최재근[1*], 박종열[2], 장은하[3], 류시환[1], 최승출[1], 남궁민[1], 김문종[1], 한정헌[1], 용우식[1], 이승훈[1], 홍대기[1]

[1]강원도 홍천군 두촌면 장남길 26 강원도농업기술원 옥수수연구소
[2]강원도 춘천시 충열로 83 강원도농업기술원 작물연구과
[3]강원도 춘천시 신북읍 신북로 386-2 강원도농업기술원 농식품연구소

팝콘옥수수 국내 재배면적은 2017년에 11h에서 2020년에는 68ha로 재배면적이 증대되고 있는 작목으로 지역특화작목으로 육성가능하다. 옥수수연구소에서 개발한 Non-GMO 품종인 오륜팝콘, 오륜2호를 이용하여 국내에서 생산하고 가공하여 지역특화상품개발까지 꾸준히 늘어가고 있다. 또한, 농촌체험마을에서 체험용 상품으로도 널리 이용되고 있다. 팝콘옥수수에서 중요한 팝핑율은 원료인 알곡의 저장온도, 저장방법, 저장기간 등 환경적 요인에 의해 품질이 변한다. 알곡이 가지고 있는 적정 수분대는 11~13%내로 유지될 때 최상의 튀김부피(30~33㎝^{3}/g)을 보인다. 하지만 저장시 환경적 변화로 알곡의 수분이 10%이하로 저하될 때는 튀김부피는 정상적으로 보관한 알곡에 비해 50%이하 까지 떨어질 수 있다. 알곡수분함량이 10%이하로 떨어진 원료는 상품으로 사용할 수 없다. 따라서 본 연구는 10%이하로 떨어진 원료곡의 튀김부피를 회복시키는 방법을 찾고자 수행하였다. 옥수수연구소에서 개발한 품종인 오륜팝콘, 오륜2호, 지팝콘, 기찬팝콘의 알곡 수분 함량이 10%이하인 원료곡을 가지고 각각 25℃, 30℃로 유지시킨 물 상자에 망자루를 이용하여 30분 간격으로 5회에 걸쳐 침지 후 튀김부피를 조사하였다. 물 온도에 따른 튀김부피 회복은 오륜팝콘의 경우 30℃에서 25℃보다 0.7㎝^{3}/g 높게 나타났다. 나머지 3품종도 30℃ 침지방법에서 튀김부피가 높게 나타났다. 튀김부피 회복을 위한 적정 물 온도는 30℃로 설정하였다. 침지시간에 따른 튀김부피 회복에서는 침지전에 비해 30분 이상만 침지하면 튀김부피가 회복되는 것을 알 수 있었다. 오륜팝콘의 경우 침지전 20.2㎝^{3}/g에서 30.0㎝^{3}/g으로 회복되었다. 오륜2호는 20.4㎝^{3}/g에서 33.7㎝^{3}/g, 지팝콘은 19.1㎝^{3}/g에서 33.0㎝^{3}/g, 기찬팝콘은 21.3㎝^{3}/g에서 33.0㎝^{3}/g으로 회복되었다. 따라서 과건조된 팝콘 원료곡의 튀김부피를 회복시키기 위해서는 30℃온수에 30분간 침지하는 방법으로 회복시킬 수 있어 튀김부피 품질 회복방법으로 사용할 수 있을 것으로 기대된다.

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

PD-0007

배가반수체 기술을 이용한 옥수수 육성계통의 선발체계 확립

류시환*, 김문종, 한정헌, 최재근, 남궁민, 최승출, 용우식, 홍대기

강원도 홍천군 두촌면 장남길 26, 강원도농업기술원 옥수수연구소

옥수수 육종에서 배가반수체 기술의 활용으로 2~3작기의 단기간에 대량으로 순도 100%의 계통을 육종할 수 있게 되었다. 계통육종의 효율성도 높은 것으로 확인되면서 배가반수체 기술은 최근 국외 옥수수연구소 및 기업에서 필수적으로 활용하는 기술이다. 계통육종은 옥수수 품종육성을 위한 필수단계로서, 99% 이상의 순도를 가진 계통을 육종하기 위해서는 전통적인 방법에 의해 7회 이상의 인공교배를 실시하여야 한다. 많은 노동력과 시간이 소요되는 전통육종의 이러한 단점을 보완하고자 배가반수체(Doubled Haploid) 방법에 의한 계통육종이 실용화되고 있다. 국내에서는 옥수수 계통육종의 효율성을 향상시키고자 강원도농업기술원 옥수수연구소에서 국제옥수수・밀연구소(CIMMYT)와 협력하여 배가반수체 기술 이용에 필수적인 반수체 유기체(Inducer)의 사용 권리를 확보하였고, 2014년부터 이 기술을 국내 환경에 맞게 정착시켜오고 있다. 배가반수체 기술에 의해 대량으로 육성된 계통 중에서 우량한 계통의 선발은 매우 중요한 단계이다. 이를 위해 다음과 같이 2단계의 선발과정을 거쳐 계통을 선발하였다. 육성한 계통은 종자가 소량이므로 종자증식과 함께 특성평가를 실시하였다. 2019년 312계통을 시험하여 농업적 형질이 우수한 54계통을 1차 선발하였다. 2020년 선발된 계통 중 52계통 대하여 강원도 내 3개 지역(홍천, 평창, 철원)에서 계통의 적응성을 검토하였다. 대비 계통보다 10일 이상 빠른 조숙성 18계통, 계통의 수량성이 300kg/10a 이상인 다수성 12계통, 100립중이 30g 이상인 대립종 7계통, 이삭장이 14cm 이상 11계통, 착립률 90% 이상 14계통, 이삭폭 4cm 이상 15계통, 그리고 이삭열수 14열 이상 18계통을 선발하였다. 여러 농업적 형질을 고려하여 최종적으로 20DR06 등 12계통을 선발하였으며 지역 적응성이 양호하여 단교잡종 육성을 위한 교배친으로 활용성이 높을 것으로 기대된다.

사사: 본 연구는 기관고유사업(배가반수체 육종효율 증진연구, LP0034302021)의 지원에 의해 이루어진 것임

***교신저자:** Tel. 033-248-6911, E-mail: shr8921@korea.kr

PD-0008

농림축산업용 유전자변형생물체의 정성·정량 검정 시스템 확립

박태성*, 김영순, 이재인, 손수인, 임명호, 강현중

전라북도 전주시 덕진구 농생명로 370 국립농업과학원

1996년 첫 GM 작물이 도입된 지 24년이 되었다. 그 동안 재배되는 양은 112배가 증가하였으며, 총 누적 면적은 27억 헥타르에 이른다. 이는 세계에서 가장 빠르게 증가하는 작물 기술이다. 전세계적으로 29개 나라에서 식품용, 사료용 및 농업용으로 32작물 530개 품목이 승인되었고, 그중 국내에서는 식품용 4개 작물 187품목(미생물 포함), 농업용 5개 작물 169품목이 승인되어 유통됨에 따라 국가안전관리를 위한 검정시스템구축이 필요하다. 본 기관에서는 농림축산업용 LMO 의 국가간 이동에 따른 검정 및 검사방법을 확립하고자 한다.『유전자변형생물체의 국가간 이동 등에 관한 법률』에 의거 농림축산업용의 LMO 의 수입 승인을 얻고자 하는 연구자 및 개발자의 심의와 검정에 관한 심사서 작성요령을 돕기 위한 방법으로 심사 의뢰된 농림축산업용 LMO 검출 마커를 검정하기 위한 방법으로 유전자 증폭을 통한 전기영동 및 유전적 특이 마커 증폭을 확인 할 수 있는 자동화전기영동기기 방법을 제시하였다. 또한, 심사 의뢰된 농림축산업용 LMO 의 비의도적 혼입률을 검정하기 위해 심사 의뢰한 유전자변형생물체와 숙주생물체간의 정량분석을 위한 실시간 중합효소연쇄반응을 통하여 검정 방법을 확립하였다. 농림축산업용 LMO 표준품의 정성 및 정량을 통한 과학적인 분석과 검토를 하여 검사 방법을 표준화하여 승인과 관련된 전반에 관한 연구 및 지원 업무를 수행하고 있다.

***교신저자:** Tel. 063-238-4717, E-mail: jowon007@korea.kr

PD-0009

An unusual *Agrobacterium*-mediated transformation event whereby large deletions occurred in T_1 progenies after CRISPR/Cas9 editing

Yang Qin, Tae-Sung Park, Myung-Ho Lim*

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

The present study adapted a CRISPR/Cas9 system combined with *Agrobacterium*-mediated transformation method to generate targeted genomic deletions. On this basis, we attempted to knock out a selection marker *bar* gene in a fixed *Bt*- and herbicide-resistant transgenic line Bt-T07 (T_8 generation). We constructed three marker-free binary vectors which contain a CRISPR/Cas9 system using SpCas9 and each a gRNA respectively targeting on 108-130bp, 269-291bp and 394-415bp region of *bar* gene, and performed *Agrobacterium*-mediated transformation on rice callus. By using Cas9-specific primers, we selected 25 T_0 plants for further PCR and sequence analysis. As a result, four plants without T-DNA integrations but showed nucleotide deletions near targeting regions, indicating transient expressions of Cas9 system. However, a T_0 plant named as 130-4, targeting on 108-130bp region of *bar* gene, were confirmed a segregation on *bar* gene in its T_1 progenies with 16 *bar*-knockout lines and 7 normal expressed lines. In addition, long-PCR results indicated full-length nucleotide deletions of the pre-existing T-DNA (6037-nt) of all of *bar*-knockout T_1 plants. Interestingly, Illumina sequencing on one of *bar* knockout line 130-4-36 revealed full T-DNA removal with the exception of 33 reads of bar sequences. We speculate *Agrobacterium*-mediated transformation and Cas9/sgRNA-mediated site-specific targeting may cause several DNA double strand breaks (DSBs) of pre-existing T-DNA, followed large deletions through DNA repair processes. This rare phenomenon provides a possibility for T-DNA delivery without T-DNA integration on target site by using CRISPR/Cas9 editing system.

***Corresponding Author:** Tel. 063-238-4705, E-mail: mlim312@korea.kr

PD-0010

트리티케일의 스피드 브리딩 시스템 적용 시험

차진경[1*], 박명렬[2], 신동진[1], 권영호[1], 이소명[1], 고종민[1], 김경민[3], 이종희[1]

[1]농촌진흥청 국립식량과학원 논이용작물과
[2]농촌진흥청 국립식량과학원 중부작물과
[3]농촌진흥청 국립식량과학원 밀연구팀

트리티케일은 밀과 호밀의 속간 교잡을 통해 만들어진 동계 사료작물로, 단백질 함량이 높고 조사료로 이용했을 때 영양학적 가치가 높아 농가에서 선호되고 있다. 현재 트리티케일의 신품종 개발은 전통 육종방법을 통해 이루어지고 있으며, 평균 육성기간은 15년 정도로 긴 편이다. 따라서 본 시험에서는 트리티케일의 육종 연한을 단축하기 위해 최근 밀, 보리 등에서 개발된 스피드 브리딩 시스템을 적용하여 세대 단축 가능성을 검토하였다. 시험재료로 광영, 민풍, 세영, 신성, 신영, 신조성, 옹골진, 조성, 조영 등 국내 트리티케일 9 품종을 공시하였다. 각 품종의 종자를 72구 육묘상자(34mL/구)에 파종하여 식물생장용 LED 조명을 이용해 22시간 장일처리 하였다. 그 결과 9품종의 평균 출수일수는 38일이었고, 출수가 가장 빠른 품종은 신조성으로 파종 후 33일 만에 출수하였으며, 가장 느린 품종인 광영과 민풍도 42일 내외로 출수하였다. 출수일수를 비롯한 간장, 수장, 망장 등의 작물학적 특성은 본 시험에서 각 품종 별 유의한 차이가 나타났다. 반면 수수는 품종에 상관없이 모두 한 개의 유효분얼만 조사되었으나, 1수립수는 평균 11개 정도로 1개체 1계통법(Single seed descent)으로 세대를 전개하기에는 충분한 종자 양이 확보되었다. 출수 이후의 생육기간을 단축하기 위해 출수기로부터 14일, 17일, 20일 후 각 품종의 이삭을 수확하여 이삭 채로 35℃에서 4일간 건조시켰다. 그 후 탈곡한 종자를 페트리디쉬에 침종하여 4℃에서 3일 간 저온처리 하고, 상온에서 8일간 발아시켜 발아율을 조사하였다. 그 결과 평균 발아율은 각각 75.8%, 77.5%, 82.1%로 출수 20일 후 수확했을 때 발아율이 가장 높았으며, 본 연구 결과는 트리티케일의 육종 연한을 단축하는 데 활용할 수 있을 것으로 생각된다.

***교신저자:** Tel. +82-53-350-1182, E-mail: jknzz5@korea.kr

PD-0011

배추와 유채의 교배조합 이용 교잡종자의 수발아 특성 분석 및 수발아 관련 유전자클로닝

손수인[1*], 조윤성[1], 조우석[1], 박태성[1], 오영주[2], 신은경[1], 강현중[1]

[1]전라북도 전주시 덕진구 농생명로 370 국립농업과학원
[2]전라북도 전주시 덕진구 팔복 1길 ㈜ 미래환경생태연구소

형질 전환 카놀라 (*Brassica napus* L.)와 배추 (*B. rapa* L.) 사이의 교잡성에 대해서는 많은 연구가 수행 되어왔다. 본 연구에서는 *B. rapa*와 *B. napus*를 교배하여 얻은 F1 교잡종자의 수발아성(viviparacy)을 확인 하였다. *Brassica napus* L. (AACC, 2n = 38) 및 *B. rapa* L. (AA, 2n = 20) 종자는 한국 농업 유전자원 센터로부터 분양받았다. 교잡성(Interspecific crossability)은 꽃가루 공여자로 형질 전환 *B. napus*를 사용하고 종자 모체로 *B. rapa*를 사용하여 인공교배를 통해 결정되었다. F1 교잡 종자의 크기는 *B. rapa*와 형질 전환 *B. napus*의 중간 크기였고, PHS가 차지하는 비율은 배추 아종에 따라 다르지만 전반적으로 24,4 ~ 70.2 %로 분석되었다. 정상 종자와 수발아 종자의 지방산성분 분석결과 서로 간에 차이를 나타낸 지방산은 올레산, 리놀레산, 리놀렌산이었다. 수발아 종자에서는 C18 : 1의 함량이 감소하고 18 : 2와 18 : 3의 함량이 증가하는 경향이 있었다. 정상 발아 종자와 수발아 종자의 RNA sequencing을 통한 유전자 발현 비교 분석 결과 PHS 관련 후보군 중 3개 유전자를 선정하여 CRISPR-Cas9를 이용한 내성 유채 육종 소재 개발을 위해 형질전환을 수행중이다.

***교신저자:** Tel. 063-238-4712, E-mail: sisohn@korea.kr

PD-0012

Transgene introgression from genetically modified *Brassica napus* expressing *BrAGL20* to different subspecies of *B. rapa*

Soo-In Sohn[1*], Subramani Pandian[1], Young-Ju Oh[2], Woo-Suk Cho[1], Yoonsung Cho[1], Eun-Kyoung Shin[1], Young-Sun Ban[1], Tae Sung Park[1], Hyeon-jung Kang[1]

[1]National Institute of Agricultural Sciences, Jeonju, Republic of Korea
[2]Institute for Future Environmental Ecology Co., Ltd, Jeonju, Republic of Korea

A number of studies have been conducted on hybridization between transgenic *Brassica napus* and *B. rapa* or backcross of F1 hybrid to their parents. However, trait changes must be analyzed to evaluate hybrid sustainability in nature. In the present study, 7 subspecies of *B. rapa* and early flowering transgenic (*BrAGL20*) *B. napus* were hybridized to verify the early flowering phenomenon of F1 hybrids, and F1 hybrid traits were analyzed to predict their impact on sustainability. Early flowering transgenic *Brassica napus* L. ‘Youngsan’ (AACC, 2n = 38) was transformed with CAMV 35S-regulated bar and *BrAGL20*, and *B. napus* L. ‘Youngsan’ and *B. rapa* L. (AA, 2n = 20) seeds were obtained from the National Agrobiodiversity Center (Jeonju, Republic of Korea). Interspecific crossability was determined using transgenic *B. napus* as the pollen donor and 7 species of *B. rapa* as the seed parent, by means of artificial emasculation and crossing. F1 hybrids bloomed later than transgenic *B. napus*, but without vernalization, owing to the expression of the *BrAGL20* transgene. The size of F1 hybrid seeds was intermediate between those of *B. rapa* and transgenic *B. napus*. 20-50% of F1 hybrid seeds showed viviparacy, and fatty acid analyses result indicated that linoleic acid content of these seeds was higher than that of seed that develop normally without viviparacy. F1 hybrids were either fertile or infertile depending on the cross combination. In natural conditions, gene transfer from *B. napus* to *B. rapa* decreased the crossing rate according to the distance, and it was analyzed that there was an influence by wind.

***Corresponding Author:** Tel. 063-238-4712, E-mail: sisohn@korea.kr

PD-0013

Tomato image analysis for recognition of TYLCV symptom in early stage

Jinjeong Lee, HwangWeon Jeong, Su Jung Ra, Sung Mi Kim, Eunhee Kim, Hong-Il Ahn, Il Pyung Ahn, Hye-Jin Yoon, Young-Joo Seol*

Gene Engineering Div., National Institute of Agricultural Science, RDA, Jeonju-si, Jeollabuk-do, 54874, Korea

Tomato yellow leaf curl virus (TYLCV) is major problem especially in green house tomato farming. Under the greenhouse circumstance, there are chance to occurring whiteflies anytime. So tomato variety which has TYLCV resistance is important. And recognition of TYLCV symptom in early stage is also important too. Normally, Initial symptom of tomato which is affected by TYLCV is stunting on shoot and whole plant. In this study, we try to develop image analysis for recognition of TYLCV symptom in early stage. 9 sample were infected by TYLCV sap inoculation at 27 days after germination. RGB images were measured 3 times at 0, 120 240 degree of side view of the samples from day of TYLCV sap inoculation to 9 days. RGB image analysis of Healthy and infected tomatoes for comparing plant growth, was processed using ImageJ and house script. Extracting plant region of interest was processed by removing background. Real area, convex-hull area, height and width of each sample were calculated. Result shows growth rate difference between healthy and infected plant. In follow study, we try to comparing TYLCV resistance genes and phenotype of TYLCV infected tomato images.

***Corresponding Author:** Tel. 82-063-238-4665, E-mail: yjseol@korea.kr

PD-0014

Transient Expression in Rice Protoplast System for Cell-Based Functional Analysis of Cytokinin Signaling

Jaeeun Song, Eunji Ga, Myung Ki Min, Jihee Ha, Sangkyu Park, Hyo Lee, Saet Buyl Lee, Jong-Yeol Lee, Beom-Gi Kim*

Metabolic Engineering Division, Department of Agricultural Biotechnology, National Institute of Agricultural Sciences, Rural Development administration, Jeonju 54874, Republic of Korea

The major components of the cytokinin (CK) signaling pathway have been identified from the receptors to their downstream transcription factors. It is challenging to discover characterizing and quantifying the contribution of each component or their combinations to the signaling cascade. Here, we describe a transient gene expression system in rice (*Oryza sativa*) protoplasts suitable to reconstitute CK signaling branches using the CK reporter construct TCSn:fLUC, consisting of a synthetic CK-responsive promoter and the firefly luciferase gene, as a sensitive readout of signaling output. We used this system to systematically test the contributions of CK signaling components, either alone or in various combinations, with or without CK treatment. The type-B response regulators (RRs) *OsRR16, OsRR17, OsRR18,* and *OsRR19* all activated TCSn:fLUC strongly, with *OsRR18* and *OsRR19* showing the strongest induction by CK. Cotransfecting the reporter with *OsHP01, OsHP02, OsHP05,* or *OsHK03* alone resulted in much weaker effects relative to those of the type-B *OsRRs*. When we tested combinations of *OsHK03, OsHPs,* and *OsRRs,* each combination exhibited distinct CK signaling activities. This system thus allows the rapid and high-throughput exploration of CK signaling in rice.

***Corresponding Author:** Tel. 063-238-4614, E-mail: bgkimpeace@gmail.com

PD-0015

Efficient Isolation and Gene Transfer of Protoplast in Korean Soybean (*Glycine max* (L.) Merr.) Cultivars

Chuloh Cho, Dool-Yi Kim, Man-Soo Choi, Mina Jin, Mi-Suk Seo*

Crop Foundation Research Division, National Institute of Crop Science, 181, Hyeoksin-ro, Iseo-myeon, Wanju-gun, Jeollabuk-do 55365, Republic of Korea

Soybean (*Glycine max* (L.) Merr.) is one of the most important crop with economic value as a source of protein and vegetable oil for human food and animal feed. In recent years, the rapid developed genome editing techniques have shown widespread application prospects for gene function study and improving important agronomic traits in many crops. Therefore, it is important to establish a highly efficient method for protoplast isolation and transient expression systems in soybean. In this study, we established an efficient method for the protoplast isolation and its application to transient gene expression in Korean soybean cultivars such as Kwangan, Pungwon and Taekwang. The protoplasts were isolated from different developmental stages and tissues such as leaves, epicotyls, hypocotyls, cotyledons, and etiolated hypocotyls. We found that high-quality and large amounts of protoplasts were isolated from the etiolated hypocotyls when incubated for 8 hours under 0.5% cellulase, 0.5% pectinase and 1% viscozyme conditions. In addition, we observed a high protoplast transfection efficiency of the green fluorescent protein (GFP) in etiolated hypocotyls. Taken together, our protoplast isolation and transfection method is highly efficient and it can be used for gene function and molecular analysis to better understand the biological and physiological processes in soybean.

***Corresponding Author:** Tel. 063-238-5326, E-mail: sms1030@korea.kr

PD-0016

Molecular characterization and transformation by CRISPR/Cas9 of *GmCYP72A69* gene related to soyasaponins biosynthesis in soybean

Mi-Suk Seo*, Chuloh Cho, Kwang-Sik Lee, Hyunyoung Kim, Mina Jin, Man-Soo Choi, Dool-Yi Kim

Crop Foundation Research Division, National Institute of Crop Science, 181, Hyeoksin-ro, Iseo-myeon, Wanju-gun, Jeonbuk, 55365, Republic of Korea

Soybean (*Glycine max* L.) is one of the most economically valuable crops, because its seeds contain high-quality protein and abundant lipids. Soybean seeds contains various secondary metabolites, such as soyasaponins, lutein and isoflavone. Plants produce more than 200,000 secondary metabolites that are involved in traits such as taste, color, and scent. Furthermore, secondary metabolites have various benefits, such as natural medicines, flavors, insecticides and industrial materials. We analyzed various secondary metabolites with high agronomic value in 26 soybean cultivars. Three cultivars with black seed coat were detected at the high levels of total carotinoids. The PI90763 showed the highest total contents of soyasaponins and isoflavones. Soyasaponins have recently attracted attention because of their various health benefits, including the prevention of dietary hypercholesterolaemia, antioxidant and anticarcinogenic activity. Understanding the biosynthesis pathway of soyasaponins will provide new approaches to control the pathway for valuable seed production. The some CYP (Cytochrome P45) genes were known as a regulators related to soyasaponin biosynthesis pathway. We analyzed sequences and genetic relationship of the *GmCYP* genes related to soyasaponin biosynthesis in soybean. Furthermore, guide RNA of two *GmCYP72A69* genes related to of GroupA and GroupB saponins were selected in the genomic region and validated the efficiency of gene editing using protoplast. Guide RNA with high editing efficiency was inserted into a CRISPR/Cas9 vector containing a selectable glufosinate resistance marker gene. The CRISPR/Cas9 was transformed using *Agrobacterium* into half seed of soybean and were produced the transgenic shoots.

***Corresponding Author:** Tel. 063-238-5326, E-mail: sms1030@korea.kr

PD-0017

Overexpression of an ABA receptor, OsPYL/RCAR7, confers drought tolerance without growth inhibition of rice

Jihee Ha[1], Nikita Bhatnagar[1†], Rigyeong Kim[1†], Seungsu Han[2], Jaeeun Song[1], Gang Seob Lee[3], Sangho Lee[2], Myung Ki Min[1*], Beom-Gi Kim[1*]

[1]Metabolic Engineering Division, Nationla Institute of Agricultural Sciences, RDA, Jeonju, Jeollabuk-do 54874, Republic of Korea

[2]Department of Biological Sciences, Sungkyunkwan university, Suwon 16419, Republic of Korea

[3]Biosafety Division, National Institute of Agricultural Sciences, RDA, Jeonju, Jeollabuk-do 54874, Republic of Korea

Overexpression of abscisic acid (ABA) receptors has been reported to enhance drought tolerance, but also to cause stunted growth and decreased crop yield. Here, we constructed transgenic rice for all monomeric ABA receptors and observed that only transgenic rice over-expressing *OsPYL/RCAR7* showed similar phenotype with wild type, without total yield loss when grown under normal growth condition in a paddy field. Even though transgenic rice over-expressing *OsPYL/RCAR7* showed neither an ABA-sensitivity nor an osmotic stress tolerance in plate assay, it showed drought tolerance. We investigated the ABA-dependent interaction with OsPP2CAs and ABA signaling induction by OsPYL/RCAR7. In yeast two hybrid assay, OsPYL/RCAR7 required critically higher ABA concentrations to interact with OsPP2CAs than other ABA receptors, and co-immunoprecipitation assay showed strong interaction under ABA treatment. When ABA-responsive signaling activity was monitored using a transient expression system in rice protoplasts, OsPYL/RCAR7 had the lowest ABA-responsive signaling activity as compared with other ABA receptors. OsPYL/RCAR7 also showed weak suppression of phosphatase activity as compared with other ABA receptors in vitro. Transcriptome analysis of transgenic rice over-expressing *OsPYL/RCAR7* suggested that only a few genes were induced similar to control under without exogenous ABA, but a large number of genes was induced under ABA treatment compared with control. We conclude that OsPYL/RCAR7 is a novel functional ABA receptor that has low ABA signaling activity and exhibits high ABA dependence. These results lay the foundation for a new strategy to improve drought stress tolerance without compromising crop growth.

***Corresponding Author:** Tel. 063-238-4614, E-mail: bgkimpeace@gmail.com

PD-0018

OsPP2C09, inhibitor in ABA signaling, work as positive regulator in osmotic stress

Myung Ki Min[1], Rigyeong Kim[1], Woo-Jong Hong[2], Ki-Hong Jung[2], Jong-Yeol Lee[1], Beom-Gi Kim[1*]

[1]Metabolic Engineering Division, Department of Agricultural Biotechnology, National Institute of Agricultural Sciences, RDA, Jeonju, Jeollabuk-do 54874, Republic of Korea

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

Clade A Type 2C protein phosphatases (PP2CAs) negatively regulate abscisic acid (ABA) signaling and have diverse functions in plant development and in response to various stresses. In this study, we showed that overexpression of the rice ABA receptor *OsPYL/RCAR3* reduces the growth retardation observed in plants exposed to osmotic stress. By contrast, overexpression of the *OsPYL/RCAR3*-interacting protein *OsPP2C09* rendered plant growth more sensitive to osmotic stress. We tested whether *OsPP2CAs* activate an ABA-independent signaling cascade by transfecting rice protoplasts with luciferase reporters containing the drought-responsive element (DRE) or ABA responsive element (ABRE). We observed that OsPP2CAs activated gene expression via the *cis*-acting drought-responsive element. In agreement with this observation, transcriptome analysis of plants overexpressing *OsPP2C09* indicated that *OsPP2C09* induces the expression of genes whose promoters contain DREs. Further analysis showed that *OsPP2C09* interacts with DRE-binding (DREB) transcription factors and activates reporters containing DRE. We conclude that, through activating DRE-containing promoters, *OsPP2C09* positively regulates the drought response regulon and activates an ABA-independent signaling pathway.

***Corresponding Author:** Tel. 063-238-4614, E-mail: bgkimpeace@gmail.com

PD-0019

A trial image analysis method of Bacterial Wilt symptom in seedling stage

HwangWeon Jeong, Sung Mi Kim, Jinjeong Lee, Su Jung Ra, Eunhee Kim, Il Pyung Ahn, Hye-Jin Yoon, Young-Joo Seol*

Gene Engineering Div., National Institute of Agricultural Science, RDA, Jeonju-si, Jeollabuk-do, 54874, Korea

Bacterial wilts (BW) is a destructive disease, caused by Ralstonia solanacearum. The disease is one of major problem of planting tomatoes in green house. BW can normally infect through the root system from soil on tropical temperature. Symptom of bacterial wilt looks like lack of moisture on plant, determination of BW is not simple, neither evaluation of disease severity or virulence level is not simple. So developing detection method for symptom of BW is important. In this study we used trial image analysis method for early symptom stage detection. Seokwang used as sensitive tomato sample. 5 stains KACC No. 10698, 10707, 10715, 10717, 18644 used for inoculation. samples were infected 46 days after germination. RGB images were measured 10 days with multiple angle of side view. Determination of BW infection, was processed using ImageJ and house script. Extracting plant region of interest was processed then angles of base line, main stem and nodes were calculated. Comparing angle of nodes were used for BW infection. Results shows possibility of evaluation for disease severity or virulence level using image analysis.

***Corresponding Author:** Tel. 063-238-4665, E-mail: yjseol@rda.go.kr

PD-0020

PEP-associated protein 3 is required for chloroplast development in rice

Deok Hyun Seo, Geupil Jang*

School of Biological Sciences and Technology, Chonnam National University, Gwangju, 61186, Republic of Korea

Chloroplast development is one of the major factors determining plant growth and productivity, because chloroplast is the place where photosynthesis occurs. In chloroplast developmental processes, expression of chloroplast genes is a key step to controlling transcriptional activity of plastid-encoded RNA polymerase (PEP), and the PEP activity is dependent on PEP-associated proteins (PAPs). Thus, PAPs are a key regulators of chloroplast development. Recently, *PAP3* was identified as a key regulator of chloroplast development in Arabidopsis. In this study, we identified and characterized *PAP3* in rice (*OsPAP3*). Through analysis of expression pattern and subcellular localization of *OsPAP3*, we found *OsPAP3* is expressed predominantly in leaf, and *OsPAP3* expression is positively regulated by light, showing similar transcription pattern of *OsrbcL*, a light-responsive gene. Also, *OsPAP3* is localized at nucleoid where PEP transcribes chloroplast genes. To further functional characterize *OsPAP3* in chloroplast development in rice, we generated *Cas-ospap3E1* transgenic rices transformed with CRISPR/Cas9 system. In T_0 generation, the *Cas-ospap3E1* mutants with mutation in the target site of *OsPAP3* showed abnormal albino phenotype. Similarly, albino phenotype was shown in *Cas-ospap3E1* transgenic rice in T_1 generation. These results indicates mutation of *OsPAP3* is tightly linked with albino phenotype, suggesting *OsPAP3* is required for chloroplast development in rice.

***Corresponding Author:** Tel. 062-530-0513, E-mail: yk3@chonnam.ac.kr

PD-0021

OsFSD3 and chloroplast development in rice

Hoyoon Shin, Geupil Jang*

School of Biological Sciences and Technology, Chonnam National University, Gwangju, Republic of Korea

Transcription of chloroplast genes is a key step determining chloroplast development, and plastid-encoded RNA polymerase (PEP) is a major RNA polymerase governing the transcription of chloroplast genes. PEP establishes a complex through interaction with PEP-associated proteins (PAPs), and at least 12 PAP genes have been identified in Arabidopsis thaliana. FSD3 encodes iron superoxide dismutase, and FSD3 proteins localize at chloroplast nucleoids. Previous studies reported that FSD3, which regulates ROS homeostasis also functions as a PAP protein, and the results that a knock-out mutant of FSD3 is defective in chloroplast development supported this. To understand FSD3-mediated chloroplast development in rice, we attempted to identify a rice homologue (*OsFSD3*) of Arabidopsis *FSD3*. To analyze the function of *OsFSD3* in rice chloroplasts, transgenic rice transformed with Cas9-*OsFSD3* recombinant plasmids were generated through rice callus transformation. Unlike wild-type plants, Cas9-*OsFSD3* transgenic rice exhibited abnormal whitening phenotype. Together with the DNA sequencing result showing that the whitening phenotype is tightly linked to the mutation of *FSD3* gene, these findings suggested that OsFSD3 is deeply involved in chloroplast development in rice.

***Corresponding Author:** Tel. 062-530-0513, E-mail: 206737@jnu.ac.kr

PD-0022

GM rice discrimination using deep learning based VNIR spectroscopy

Woo-Suk Cho, Soo-In Sohn*, Younsung Cho, Eun-Kyoung, Seo Yoon Oh, Jae Ho Bae

National Institute of Agricultural Sciences, Jeonju, Republic of Korea

The purpose of this study is to select the optimal model of GM rice discrimination by applying various machine learning models to a large spectrum obtained from the leaves of transgenic rice and general varieties of rice. For the spectral acquisition, an integrated portable Near-infrared (NIR) spectral analyzer (FieldSpec Hand Held 2^{TM}, ASD Inc. Boulder, CO, USA), working in reflectance mode(log/R) in the range of 325-1075 nm with an interval of 3nm was used. Spectral measurement were performed directly upon the adaxial surfaces of the leaves. All the computations were carried out in Unscrambler® X software, version 10.5.1 (CAMO ASA, Oslo, Norway). In order to obtain the best discrimination model, four different types of spectral preprocessing were used. These included no treatment (RAW), normalization (mean, max, range), savitzky-golay derivatives (1st, 2nd), and standard normal variate (SNV) to find an optimal preprocessing method that removes noise from the spectral data and improves predictability of the classification. Results show that the high percentage values of GM and non GM rice leaves that were correctly classified according to each algorithm when preprocessing was applied. These results suggest that deep learning-based VNIR spectroscopy is effective in discriminating GMOs.

***Corresponding Author:** Tel. 063-238-4712, E-mail: sisohn@korea.kr

PD-0023

A study of CRISPR/Cas9-mediated knockout of *Caffeoyl shikimate esterase 2* in hybrid poplar

Hyun A Jang, Su Jin Park, Eun-Kyung Bae, Young-Im Choi*

Department of Forest Resources, National Institute of Forest Science, Suwon 16631, Republic of Korea

To cope with climate change, it is necessary to utilize the woody biomass as an eco-friendly alternative energy resource. The content of the non-degradable lignin occupying about 30% of the woody component is controlled and the lignocellulose biomass utilization ratio can be improved. In this study, we edited *Caffeoyl shikimate esterase 2* (*CSE2*) gene that acts on lignin biosynthesis pathway using CRISPR/Cas9 technology to create a transgenic hybrid poplar (*Populus alba* x *P. glandulosa*). To knock-out *CSE2* gene in hybrid poplar, we targeted a guide RNA in the second exon of *Populus trichocarpa CSE2*. As a result, total of 27 regenerated plants were obtained from stem of hybrid poplar introducing them (pHAtC:*PagCSE2-sg3*) using *Agrobacterium*-mediated transformation. Editing rate of *PagCSE2* gRNA is 96.3 %. Among edited 26 plants, we finally selected three lines of *PagCSE2-sg3*-4, -17, and -19, which are inserted and deleted of 1 bp to 3 bp in target sites. The expression level of *PagCSE2* genes in transgenic lines was significantly lower than that of the wild type, and the genes in the lignin biosynthesis process were also reduced. Interestingly, the growth phenotypes of transgenic lines did not show significant differences compared to wild-type. Therefore, our results suggested that *PagCSE2* gene editing by CRISPR/Cas9 can contribute to improved tree biomass for sustainable biofuels.

***Corresponding Author:** Tel. 031-290-1103, E-mail: yichoi99@korea.kr

PD-0024

Establishment of a stable transformation method in Korean wheat varieties

Jae-Ryeong Sim, Sewon Kim, Su Bin Lee, Jong-Yeol Lee*

National Institute of Agricultural Science, RDA, Jeonju, 54874, Korea

A wheat storage protein, gluten protein, plays an important role in end-use quality as a major component of wheat flour. However, it is also a major antigen of wheat-related diseases that occur when consuming wheat. Especially gliadin protein acts as a major antigen in wheat-related diseases. Since the gliadin genes are encoded in six loci and spread throughout the genome, it is difficult to develop hypo-allergen wheat through traditional breeding. Therefore, cutting edge technology such as gene editing is essential and the establishment of transformation method is inevitable. In this study, we established stable transformation by biolistic particle bombardment system in Keumkang and the DH20, which lacks the *Glu-B3* and *Gli-B1* loci, of Korean wheat varieties that have not yet successfully transformed. The vector harboring the enhanced green fluorescent protein (eGFP) gene was introduced into immature wheat embryos. We confirmed insertion *eGFP* transgene into genome of primary (T_0) transformants by genomic PCR, RT-qPCR, fluorescence imaging. In addition, we also validated the stable expression of the transgene in the T_1 generation. Through this study, there will be usefully utilized for transformation studies and it will allow the manipulation of gene expression via such techniques as RNA interference, overexpression, and genome editing using Korean wheat varieties in the future tasks.

***Corresponding Author:** Tel. 063-238-4616, E-mail: jy0820@korea.kr

PD-0025

The change in ginsenoside contents according to LED based light quality between the adventitious roots of two different *Panax ginseng* cultivars

Padmanaban Mohanan[1], Soo Min Kim[1], Giang Vo Ngoc Linh[1], Sung won Cho[2], Heun Sung Park[2], Jee Young Park[1], Young hun Song[2*], Tae Jin Yang[1*]

[1]Department of Agriculture, Forestry and Bioresources, College of Agriculture & Life Sciences, Seoul National University, 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Korea
[2]Department of Applied Life and Chemistry, College of Agriculture and Life Science, Seoul National University 1 Gwanak-ro, Gwnak-gu Seoul 08826, Republic of Korea

Ginsenoside, the most valuable and pharmacologically active triterpenoid saponin enriched in *Panax ginseng*. It has been known that ginsenosides are synthesized in the leaves and gets stored in the roots (source to sink transport). Recent boom in smart farming technology uses LED based light sources to enhance ginsenoside production in ginseng seedlings. However, not much known about the changes in ginsenoside genes as well as the responses of cultivars towards the light quality. Here we show the adventitious roots of two different ginseng cultivar *P. ginseng* cv. Yunpoong (YP) and *P. ginseng* cv. Sunhyang (SH) responds differently according to the quality of light. By using monochromatic LED lights for blue, red and far-red lights with specific intensity were used to treat adventitious roots of YP and SH cultivars for 1 week. Interestingly, the ginsenoside biosynthetic genes were highly expressed in SH than YP. The expression of genes such as *3-hydroxy-3-methylglutaryl-CoA reductase (HMGR), squalene synthase (SS), Dammarenediol synthase (DDS)* were altered according to the light quality. The transcripts of *PgHMGR*, *PgSS3*, *PgDDS1* genes were enhanced especially under red and far red light conditions. Similarly, the total ginsenoside contents as well, increased under red and far red condition, between SH and YP cultivars the contents were significantly high in SH than YP. The change is reflected in the composition of minor ginsenosides as well. Thus, based on our results we could suggest that ginseng cultivars could respond differently to the quality of light there by eventually reflects in the biosynthesis of ginsenosides.

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***Corresponding Author:** Young hun Song (Tel. 02-880-4649, E-mail: younghsong@snu.ac.kr)
Tae Jin Yang (Tel. 02-880-4547, E-mail: tjyang@snu.ac.kr)

PD-0026

Generation and characterization of null mutants with stress tolerances through CRISPR/Cas9-targeted knockout of *PUB* genes

Me-Sun Kim[1], Le Van Trang[1], Sothea Ouk[1], Seo-Rin Ko[1], Kwon-Kyoo Kang[2], Yong-Gu Cho[1*]

[1]Department of Crop Science, Chungbuk National University, Cheongju 28644, Korea
[2]Department of Horticulture, Hankyong National University, Ansung 17579, Korea

Ubiquitination of a target protein was carried out by attaching a three-step (E1 → E2 → E3) conjugation cascade that detects specific ubiquitin signals. The plant U-box (PUB) protein is the E3 ligase that plays roles in the degradation or post-translational modification of target proteins. In this study, we applied the CRISPR/Cas9 system to modify U-box genes to generate null mutants in rice. Binary vectors harboring expression cassettes of Cas9 nuclease, single guide RNA (sgRNA) targeting the U-box type E3 ubiquitin ligase (PUB) and bar as a selection 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 PCR products of the edited PUB genes using NGS analysis. The gene edited plants containing DNA mutations such as nucleotide substitutions, insertions and deletions of the target site, which varied depending on the different edited lines. In parallel, we performed RNA-sequencing of Donjin with and without drought stress. The results revealed that a total of five genes were selected: *OsPUB9*, *OsPUB10*, and *OsPUB11* genes, whose expression was decreased upon drought stress treatment, and *OsPUB13* and *OsPUB41* genes, whose expression increased upon drought stress treatment. We will proceed to conduct drought tolerant line selection with the null T_3 homo lines according to drought stress treatment system established in this study.

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***Corresponding Author:** Tel. +82-43-261-2514, E-mail: ygcho@cbnu.ac.kr

PD-0027

밀 수발아 관련 *TaQSD1* (alanine aminotransferase 1) 유전자 교정 효율 분석

이명희*, 최창현, 강천식, 김경훈, 김경민, 정한용, 김유림, 박진희, 손지영, 박태일

전라북도 완주군 이서면 혁신로 181 국립식량과학원 밀연구팀

밀은 크기가 크고 복잡한 게놈 구조를 가지고 있어서 유전체 기반 연구가 구축된 상태임에도 불구하고 6배체 모두의 동형접합체를 만들기는 쉽지 않다. 따라서 유전제 정보 기반 유전자 교정 기술(genome editing)이 작물 육종에 응용되기 시작했으며, 정밀 육종을 위한 하나의 새로운 육종기술(신육종기술)로 각광 받고 있다. 최근에 밀 유전자 교정 연구 중에서 수발아 감수성 유전자인 *TaQSD1*의 편집을 통해 수발아 내성 밀 개발이 구체화 되었다. 본 연구에서는 국내 밀 품종 중 '백강'의 *TaQSD1* 유전자 교정의 효율성을 제고하기 위하여 *TaQSD1*유전자 염기서열을 바탕으로 4지역에서 guide RNA를 제작하여 백강 밀의 원형질체에 RNP (ribonucleoprotein) 방법을 활용하고 Deep-Seq 분석을 통해 sgRNA (single guide RNA)에 의한 유전자 교정 효율을 비교하였다. *TaQSD1* 유전자의 15개 exon 중에서 2번(RG1), 4번(RG2), 8번(RG5), 14번 exon(RG8, RG9)에서 각각 1개 또는 2개의 sgRNA를 선정하여 분석하였으며, 기존에 알려진 RG8의 유전자 교정 효율과 비교하였다. *TaQSD1*의 A 게놈에서는 RG8이 가장 높은 효율을 보였으며, B 게놈에서는 RG9번에서 상대적으로 높은 효율을 보였다. 하지만 D게놈에서는 모든 sgRNA의 효율이 낮았다. 이 분석 결과를 토대로 sgRNA 타겟 염기서열 및 염색체 별 유전자 교정 효율 차이가 매우 다름을 확인하였다. 현재 '백강' 외에도 수발아에 약한 '금강', 수발아에 강한 '수강' 등 국내 품종에서 RG8과 RG9의 *TaQSD1* 유전자 교정 효율을 A, B, D 게놈 별로 분석하고 있으며, 본 결과를 토대로 밀 유전자 교정 효율성 제고를 위한 연구가 더욱 활발히 진행될 것으로 생각된다.

***교신저자:** Tel. 063-238-5460, E-mail: mhlee17@korea.kr

PD-0028

Populational Transcriptomic Study Targeting Complex Eating and Cooking Quality Traits in Rice

Kyu-Won Kim[1†], Weiguo Zhao[2,3†], Qiang He[4†], Sang-Kyu Lee[5], Feifei Xu[4,6], Rungnapa Phitaktansakul[4], Kyaw Myo Aung[4], Myeong-Hyeon Min[4], Ji-Min Yoo[4], Jee-Su Kang[4], Sang Beom-Lee[7], Min-Young Yoon[4], Jungrye Nam[1], Sang-Ho Chu[1], Sang-Won Park[7], Yoo-Hyun Cho[8], Jung-Kyung Moon[9], Young-Sang Lee[10*], Jong-Seong Jeon[5*], Ill-Min Chung[11*], Yong-Jin Park[1,4*]

[1]Center of Crop Breeding on Omics and Artificial Intelligence, Kongju National University, Yesan 32439, Korea
[2]School of Biotechnology, Jiangsu University of Science and Technology, Sibaidu, Zhenjiang, Jiangsu 212018, PR China
[3]National Key Facility for Crop Resources and Genetic Improvement, Institute of Crop Science, Chinese Academy of Agricultural Sciences, Beijing 100081, China
[4]Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan, 32439, Korea
[5]Graduate School of Biotechnology & Crop Biotech Institute, Kyung Hee University, Yongin 17104, Korea
[6]Center for Plant Biology, Tsinghua-Peking Joint Center for Life Sciences, School of Life Sciences, Tsinghua University, Beijing, 100084, China
[7]Chemical Safety Division, National Institute of Agriculture Science, Wanju 55365, Korea
[8]Seedpia, 85 Maesil-ro, Kwonsun-ku, Suwon 16395, Korea
[9]National Institute of Crop Science, Rural Development Administration, Wanju 55365, Korea
[10]Department of Medical Biotechnology, Soonchunhyang University, 22, Soonchunhyang-ro, Sinchang-myeon, Asan 31538, Korea
[11]Department of Applied Bioscience, Konkuk University, Seoul 05029, Korea

Rice improvement in eating and cooking quality (ECQ) is important in current breeding programs. Here, we used a transcriptome-wide association study as a new platform for linking genomes and transcripts related to ECQ traits and discovered new ECQ genes through a coexpression network. We identified ten significant ECQ traits using 84 *Japonica*, and 285 significant transcripts for ECQ traits (false discovery rate < 0.05) 58, 175, 19, 16, 6, and 52 for their respective contents of amylose, protein, peak viscosity, consistency, peak time, and pasting temperature, which were mainly involved in the secondary metabolic biosynthesis and peroxisome pathways. For the ECQ-associated genes analyzed for their expressions by the expression quantitative trait loci (eQTLs), there were 66,905 eQTLs for 285 e-traits ($p < 1e\text{-}16$), including 21, 747 *cis* eQTLs (32.5%) and 45,158 *trans* eQTLs (67.5%). The coexpression network for ECQ-associated traits was also constructed with 130 genes (45.6%). The granule-bound starch synthase I gene is required for amylose synthesis, and it was coexpressed closely with *glb1*, so we used the clustered regularly interspaced short palindromic repeats-associated protein 9 technology (the CRISPR/Cas9 system) for a loss-of-function mutation into the *glb* gene, as the *glb* gene-induced opaque trait has a role in the eating quality. Our results showcased the power of integrating the genotype, gene expression, and phenotype to gain insights into the genetic basis of ECQ traits, and they will provide an informative resource for studying molecular regulation mechanisms of rice ECQ traits in breeding programs of new varieties.

Keywords: rice, genome-wide association studies, transcriptome-wide association study, expression quantitative trait loci, eating and cooking quality, CRISPR/Cas9 system

[†] These authors contributed equally to this work.

***Corresponding Author:** Yong-Jin Park (Tel. +82 41-330-1201, E-mail: yjpark@kongju.ac.kr)
Ill-Min Chung (E-mail: imcim@konkuk.ac.kr)
Jong-Seong Jeon (E-mail: jjeon@khu.ac.kr)
Young-Sang Lee (E-mail: mariolee@sch.ac.kr)

PD-0029

High-Volume Data Analysis Provides Insight into Precise Fragrance Control of Rice Fragrance Gene, *BADH2*

Rungnapa Phitaktansakul[1§], Kyu-Won Kim[2§], Ji-Min Yoo[1], Jee-Su Kang[1], Kyaw Myo Aung[1], Myeong-Hyeon Min[1], Lin Cheng[1], Yuan Cao[1], Sang-Beom Lee[1], Seung-Hyun Kim[3], Joo-hyun Lee[3], Soon-Wook Kwon[4], Sang-Ho Chu[2], Jungrye Nam[2], Sang-Won Park[5], Hee-Jong Koh[6], Young-Sang Lee[7], Ill-Min Chung[3], Yong-Jin Park[1,2*]

[1]Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 32439, Korea
[2]Center of Crop Breeding on Omics and Artificial Intelligence, Kongju National University, Yesan 32439, Korea
[3]Department of Applied Bioscience, Konkuk University, Seoul 05029, Korea
[4]Department of Plant Bioscience, Pusan National University Pusan, 46241, Korea
[5]Chemical Safety Division, National Institute of Agriculture Science (NIAS), Wanju 55365, Korea
[6]Department of Agronomy, Seoul National University, Seoul 08826, Korea
[7]Department of Medical Biotechnology, Soonchunhyang University, Asan 31538, Korea

The many fragrant varieties of rice account for a substantial share of the world's vast rice trade. Fragrance in rice is mainly controlled by the betaine aldehyde dehydrogenase 2 (*BADH2*) gene, which is associated with the accumulation of 2-acetyl-1-pyrroline (2AP). We resequenced the whole genomes of 135 breeding varieties and 58 wild rice accessions, sequenced the transcriptomes (RNASeq) of 134 accessions, identified the proteomes of 64 accessions by LC-MS/MS, and profiled the volatile metabolic compounds of 475 accessions by HS-SPME/GC-MS. Finally, KRICE_CORE v3 consisting of 475 genomes, 297 transcriptomes, 64 proteomes, and 475 profiles of volatile metabolic compounds were made. The results focused on *BADH2* revealed an atlas of *BADH2* across the gene-to-metabolite flow. We identified 46 novel alleles containing 14 nonsynonymous SNPs/InDels. The homozygous progeny of transgenic lines using CRISPR/Cas9 predicted by 3D protein structure simulation from virtual mutants showed that nine transgenic lines produced fragrant rice with different degrees of fragrance. These combined high-throughput analyses provided the value of ome-wide high-volume data that could be extended to improvements of tailored breeding, and our analyses with high-volume data showed potential for digital breeding.

Keywords: rice, *BADH2*, genome, transcriptome, proteome, metabolome, CRISPR/Cas9

[§]These authors contributed equally to this work.

***Corresponding Author:** Tel. +82-41-330-1201, E-mail: yjpark@kongju.ac.kr

PD-0030

Novel *OsCOP1* alleles participate in embryo development and flavonoid biosynthesis in rice (*Oryza sativa* L.)

Backki Kim[1,6], Rihua Piao[1,2], Gileung Lee[1], Eunbyeol Koh[1], Yunjoo Lee[1], Sunmin Woo[3], Reflinur[1,4], Wenzhu Jiang[1,5], Endang M. Septiningsih[6], Michael J. Thomson[6], Hee-Jong Koh[1*]

[1]Department of Agriculture, Forestry and Bioresources, Plant Genomics and Breeding Institute, Research Institute for Agriculture and Life Sciences, Seoul National University, Seoul, South Korea
[2]Rice Research Institute, Jilin Academy of Agricultural Sciences, Gongzhuling 136100, Jilin, China
[3]College of Pharmacy and Research Institute of Pharmaceutical Science, Seoul National University, Seoul 08826, Republic of Korea
[4]Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development, IAARD, Bogor 16111, Indonesia
[5]Jilin Province Engineering Laboratory of Plant Genetic Improvement, College of Plant Science, Jilin University, Changchun 130062, China
[6]Department of Soil and Crop Sciences, Texas A&M University, College Station, TX 77483, USA

Successful production of viable seeds is a critical component of plant life-cycles, and seed development is a complex, highly regulated process that affects seed characteristics such as viability and color. In this study, three *yellowish-pericarp embryo lethal* (*yel*) mutants, *yel-hc*, *yel-sk*, and *yel-cc*, were isolated from three different *japonica* cultivars of rice (*Oryza sativa* L). Mutant seeds had yellowish pericarps and exhibited embryonic lethality, with significantly reduced grain size and weight. Morphological aberrations were apparent by five days after pollination, with abnormal embryo development and increased flavonoid accumulation observed in the *yel* mutants. Genetic analysis and mapping revealed that the phenotype of the three *yel* mutants was controlled by a single recessive gene, *LOC_Os02g53140*, an ortholog of *Arabidopsis thaliana CONSTITUTIVE PHOTOMORPHOGENIC 1* (*COP1*). The *yel-hc*, *yel-sk*, and *yel-cc* mutants carried mutations in the RING finger, coiled-coil, and WD40 repeat domains, respectively, of *OsCOP1*. CRISPR/Cas9-targeted mutagenesis was used to knock out *OsCOP1* by targeting its functional domains, and transgenic seed displayed the *yel* mutant phenotype. Overexpression of *OsCOP1* in a homozygous *yel-hc* mutant background restored pericarp color, and the aberrant flavonoid accumulation observed in *yel-hc* mutant was significantly reduced in the embryo and endosperm. These results demonstrate that *OsCOP1* is associated with embryo development and flavonoid biosynthesis in rice grains. This study will facilitate a better understanding of the functional roles of *OsCOP1* involved in early embryogenesis and flavonoid biosynthesis in rice seeds.

***Corresponding Author:** Tel. 02-880-4541, E-mail: heejkoh@snu.ac.kr

PD-0031

Effects on the chloroplast development of a rice microprotein family

Heebak Choi[1], Taegyu Yi[1], Yun-Shil Gho[1], Young Jin Park[2], Jae Kwang Kim[2], Ki-Hong Jung[1], Sun-Hwa Ha[1*]

[1]Department of Genetics and Biotechnology and Graduate School of Biotechnology, College of Life Sciences, Kyung Hee University, Yongin 17104, South Korea
[2]Division of Life Sciences and Bio-Resource and Environmental Center, Incheon National University, Incheon 22012, Republic of Korea

The interconversion of plastid development is a challenging subject to improve agronomic traits. Although there are diverse types of plastid interconversion, regulatory mechanisms are mainly studied about the chloroplast and the chromoplast. From the screening of the plastid development regulators, we found a family which showed the dominant negative function in the chloroplast development with small protein size and named *OsMicroprotein* (*OsMP*) family. From the ortholog search among 64 species, *OsMP* family was conserved with multiple copy in vascular plants, while the most ancient *OsMP* ortholog was found in *Ostreococcus lucimarinus* from *Mamiellophyceae*. In rice, the three *OsMP* genes redundantly expressed in green tissues while *OsMP2* preferentially expressed at seedling stage. From the subcellular localization analysis by *in vivo* and *in vitro* experiments, the three OsMP proteins share same subcellular localization in nucleus and cytosol. From the overexpression (OE) constructions of each *OsMP* family, the pale-green phenotype was observed, meanwhile, the single-CRISPR construction of each *OsMP* family didn't showed a significant phenotype. To overcome the redundancy of *OsMP* family to study its molecular functions, we generated multiple-CRISPR construction and found dark-green phenotype from triple knock-out lines (*triKO*) with increased the chlorophyll contents and the chloroplast development. The RNAseq analysis from *triKO* and OsMP1-OE lines compare to non-transgenic lines showed that the transcription level of carbon fixation and stress response genes are significantly changed. Taken together, these finding suggest that the *OsMP* family function as novel microprotein in the chloroplast development in rice.

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

PE-0001

Characterization of null waxy allele Wx-B1 in bread wheat DH185

Sumin Seo[1,2], Chul Soo Park[3], Changsoo Kim[1,2*]

[1]Department of Crop Science, Chungnam National University, Daejeon 34134, Republic of Korea
[2]Department of Smart Agriculture Systems, Chungnam National University, Daejeon 34134, Republic of Korea
[3]Department of Crop Science and Biotechnology, Chonbuk National University, Jeonju 54896, Republic of Korea

Despite the importance of seed storage proteins in wheat for food quality, wheat carbohydrate is still the key nutritional factor and feeding a plethora of population in the world with a total of 215.9 million hectares harvested. Wheat starch is composed of branched amylopectin and linear amylose, and 22-35% of total starch is composed of amylose, and 69-75% is composed of amylopectin. In the case of amylopectin, it is made from proteins such as starch synthase(SS) and starch branching enzyme(SBE), and in the case of amylose, it is made through the granule bound starch synthase (GBSS) protein, also known as Waxy(Wx). Wx genes are known to exist in 7AS, 4AS (translocation at 7BS), and 7DS, and are called Wx-A1, B1, and D1. We made DB185 by crossing Geumgang, and Shinmichal1. As a result of starch analysis, amylose content was 2.3% lower than Shinmichal1. Therefore, it was predicted that there was a mutation in the amylose-related gene. The Wx gene, which has the greatest influence on the amylose content, was cloned and analyzed. As a result of sequencing, Wx-A1 and Wx-D1 were identified as null allels, Wx-A1b and Wx-D1b, which are the characteristics of Shinmichal1. In the case of the Wx-b1 gene, it is different from Wx-B1b, and compared to Wx-b1a, two snps and one Indel were observed. In the case of the wx-b1 gene, we are designing a primer for sequencing because the front side of the gene is not completely sequenced. When sequencing is performed, analyze changes in sequence.

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***Corresponding Author:** Tel. 042-821-5729, E-mail: changsookim@cnu.ac.kr

PE-0002

The Suitable Soybean Varieties for Sprouts by Seeding Time in Paddy Cultivation in Northern Gyeonggi Province

Jung-Hee Jang*, Sang-Wook Han, Dong-Hyeon Cho, Eun-Kyu Jang, Jung-Soo Park, Chang-Hui Cho

Gyeonggi Agricultural Research & Extension Services, Hwaseong 18388, Republic of Korea

This experiment was conducted a two-year test from 2019 to 2020 to select a soybean variety for bean sprouts by seeding time suitable for paddy cultivation in northern Gyeonggi Province. The tested varieties were ‘Pungsannamulkong’, ‘Pungwon’, ‘Haewon’, ‘Haepum’ and ‘Aram’. The tested seeding times were June 5th, June 20th and July 5th. The tested varieties had a later flowering and maturity date as the seeding time was delayed. Plant height was the tallest at the seeding time on June 20th and the shortest at the seeding time on July 5th. There was no significant difference in number of branches among the seeding times. Number of nods was the lowest at seeding time on July 5th. The main stem diameter decreased as the seeding time was delayed. There was no significant difference in the degree of lodging among the seeding times. In the seeding time on July 5th, all tested varieties did not mature before the first frost day. The maturity date of ‘Aram’ in the seeding time on June 20th was also delayed to Oct. 28th. Number of pods and seeds per pod were the lowest in the seeding time on July 5th, respectively. One hundred seeds weight had no significant difference in the seeding time between June 20th and July 5th, and was the lightest in the seeding time on June 5th. Yield was higher in order of seeding time on June 20th, June 5th and July 5th, but there was no significant difference. One hundred seeds weights of all varieties, except ‘Haewon’, were within the range of 10 to 12 g, which is the appropriate for bean sprouts. The ratios of the seed diameter which was more than 6.3 mm were 9.7, 8.9 and 2.2% in the seeding time on June 5th, June 20th and July 5th of the ‘Pungwon’, respectively and 4.1% in the seeding time on June 20th of the ‘Pungsannamulkong’. That was exceeded the government’s purchasing standard which was not more than 2.0% of seed remains on the 6.30 mm frame, resulting in reducing the yield. The tested varieties had a slightly lower yield of bean sprouts as the seeding time was delayed. The yield of bean sprouts was the highest in ‘Pungwon’. In the seeding time on June 5th, ‘Pungsannamulkong’, ‘Haewon’ on June 20th, and ‘Pungwon’ on July 5th were selected as the best varieties considering the screening indexes. It is expected that the stable cultivation of soybean for bean sprouts in paddy cultivation in northern Gyeonggi Province will be possible by growing the suitable varieties for each seeding time.

***Corresponding Author:** Tel. 031-229-6192, E-mail: jjh7648@gg.go.kr

PE-0003

Correlation of saponarin content with biosynthesis-related gene expression in hulled and hulless barley (*Hordeum vulgare* L.) cultivars

Jae-Hyeok Park, Jeong Hwan Lee*

Division of Life Sciences, Jeonbuk National University, 567 Baekje-daero, Deokjin-gu, Jeonju, Jeollabuk-do 54896, Republic of Korea

Saponarin found in young barley sprouts has a variety of beneficial biological and pharmacological properties, including antioxidant, hypoglycemic, antimicrobial, and hepatoprotective activities. Our previous work demonstrated that saponarin content was correlated with the expression levels of three biosynthetic pathway genes [*chalcone synthase* (*HvCHS1*), *chalcone isomerase* (*HvCHI*), and *UDP-Glc:isovitexin 7-O-glucosyltransferase* (*HvOGT1*)] in young barley seedlings under various abiotic stress conditions. In this study, we investigated the saponarin content and expression levels of three saponarin biosynthetic pathway genes in hulled and hulless domestic barley cultivars. In the early developmental stages, some hulled barley cultivars (Kunalbori1 and Heukdahyang) had much higher saponarin contents than did the hulless barley cultivars. An RNA expression analysis showed that in most barley cultivars, decreased saponarin content correlated with reduced expression of *HvCHS1* and *HvCHI*, but not *HvOGT1*. Heat map analysis revealed both specific increases in *HvCHS1* expression in certain hulled and hulless barley cultivars, as well as general changes that occurred during the different developmental stages of each barley cultivar. In summary, our results provide a molecular genetic basis for the metabolic engineering of barley plants to enhance their saponarin content.

***Corresponding Author:** Tel. 063-270-3375, E-mail: jhwanlee90@jbnu.ac.kr

PE-0004

Molecular analysis of soyasaponin biosynthetic genes in two soybean (*Glycin max* L. Merr.) cultivars

Young Jae Yun, Young-Cheon Kim, Jeong Hwan Lee*

Division of Life Sciences, Jeonbuk National University, 567 Baekje-daero, Deokjin-gu, Jeonju, Jeollabuk-do 54896, Republic of Korea

Here, we identified sequence variations of *CYP72A69* and *UGT73F4* genes from the Sojeongja and Haepum cultivars, and revealed that accumulation patterns of soyasaponin Aa and Ab were different in the Sojeongja and Haepum cultivars. Several genes related in soyasaponin biosynthetic pathway showed significant changes in their expression patterns in two soybean cultivars and soyasaponin contents were also altered under several abiotic stress conditions, albeit no significant correlations between soyasaponin contents and biosynthetic gene expression were observed. We also demonstrated that *UGT73F4* gene could be responsible for biosynthesis of soyasaponin Aa in the Socheongja by investigating genes expression and soyasaponin accumulations. Our results provide a molecular basis to improve the commercial properties of soyasaponin in Korean domestic soybean cultivars.

***Corresponding Author:** Tel. 063-270-3375, E-mail: jhwanlee90@jbnu.ac.kr

PE-0005

쓰러짐에 강한 녹자엽 아주까리콩 ‘까리1호’

서정현*, 강범규, 백인열, 신상욱, 성정숙, 박지희, 김준회, 정찬식

경남 밀양시 점필재로20 국립식량과학원 밭작물개발과

유색콩은 당도가 높아 맛이 좋은 특성이 있어 주로 주식인 쌀에 넣어 먹는 용도로 사용되어 왔다. 이중에서 아주까리콩은 종피에 그물 무늬가 있는 콩으로 피마자(아주까리)를 닮았다 하여 아주까리콩 또는 아주까리밤콩으로 불린다. 예로부터 맛이 좋은 것으로 알려져 있어 현재도 지역에 따라 재래종 아주까리콩을 재배하고 있으나, 재래종은 쓰러짐과 각종 병에 취약하고, 수량성이 낮은 단점이 있다. 국립식량과학원에서는 이와 같은 재래종의 재배적 단점을 개선한 최초의 아주까리콩 품종을 개발하였다. ‘까리1호’은 내재해 녹자엽 아주까리콩 육성을 목표로 하여 ‘청자3호’을 모본으로, ‘아주까리콩’을 부본으로 209년에 인공교배 하였으며 계통육종법에 의해 ‘YS2202-2B-14-4-1-2-3-4’가 선발되었다. 2016~2017년도에 실시한 생산력검정시험에서는 내재해 아주까리콩 계통으로 유망시되어 ‘밀양350호’의 계통명을 부여하고 2018~2020년 3년 간 7개소에서 지역적응시험을 실시하였다. ‘까리1호’는 유한형으로 엽형이 둥근형, 꽃색이 자색, 모용색이 갈색, 종실은 구형으로 검은색 종피에 그물무늬가 있는 고유특성을 가지고 있다. ‘까리1호’의 주요 생육특성은 ‘청자3호’와 유사하나, 성숙기는 10월23일로 ‘청자3호’ 보다 2일 늦으며 100립중은 32.7g으로 ‘청자3호’ 대비 다소 작다. ‘까리1호’의 불마름병 저항성은 전국 7개소 시험포장에서 ‘1’로 평가되어 강하였고, 인공접종 시 ‘청자3호’ 보다 강하였다. 콩모자이크바이러스는 인공접종 시 괴저가 나타났으며, 검정포장에서도 ‘청자3호’와 대등하였다. 내도복성은 전국 시험포장 평균 ‘2’로 평가되어 ‘청자3호(3)’ 보다 강하였고, 40℃ 건조기에서 48시간 처리하여 조사한 협개열성은 81.7%로 다소 약하였다. ‘까리1호’는 ‘청자3호’ 대비 당 함량이 다소 낮고, 안토시아닌 함량이 종피g 당 10,671㎍/g으로 ‘청자3호(21,981㎍/g)’ 대비 낮았다. 12시간 후 경실 종자가 없었고, 2시간 후 경실률이 ‘청자3호’ 대비 낮아 초기 수분흡수율이 높았다. ‘까리1호’의 수량성은 지역적응시험 7개소 평균 252kg/10a로 ‘청자3호(242ka/10a)’ 보다 4% 증수하였다. 이처럼 ‘까리1호’는 최초로 개발된 아주까리콩으로 재래종에 비해 수량성과 내재해성이 개선되어 앞으로 밥밑용 콩으로서 사용이 확대될 것으로 기대된다.

***주저자:** Tel. 055-350-1236, E-mail: next0501@korea.kr

PE-0006

불마름병과 쓰러짐에 강한 선비잡이콩 ‘새들’

서정현*, 강범규, 백인열, 신상욱, 성정숙, 박지희, 김준회, 정찬식

경남 밀양시 점필재로20 국립식량과학원 밭작물개발과

유색콩은 당도가 높아 맛이 좋은 특성이 있어 주로 주식인 쌀에 넣어 먹는 용도로 사용되어 왔다. 이중에서 선비잡이콩은 종피의 테두리에 무늬가 있는 콩으로 선비의 갓 모양을 닮았다 하여 선비콩 또는 정승콩으로 불린다. 예로부터 맛이 좋은 것으로 알려져 있어 현재도 지역에 따라 재래종인 선비잡이콩을 재배하고 있다. 하지만 재래종은 쓰러짐과 각종 병에 취약하고, 수량성이 낮은 단점이 있다. 국립식량과학원에서는 이와 같은 재래종의 재배적 단점을 개선한 최초의 선비잡이콩 품종을 개발하였다. ‘새들’은 내재해 선비잡이콩 육성을 목표로 하여 ‘선비콩’을 모본으로, ‘대풍’을 부본으로 2010년에 인공교배 하였으며 계통육종법에 의해 ‘YS2297-2B-29-2-1-3-1’이 선발되었다. 2016~2017년도에 실시한 생산력검정시험에서는 내재해 선비잡이콩 계통으로 유망시되어 ‘밀양349호’의 계통명을 부여하고 2018~2020년 3년 간 7개소에서 지역적응시험을 실시하였다. ‘새들’은 유한형으로 엽형이 둥근형, 꽃색이 자색, 모용색이 갈색, 종실은 구형으로 갈색 종피에 황색 줄무늬가 있는 고유특성을 가지고 있다. 성숙기는 10월28일로 ‘청자3호’보다 7일 늦으며 100립중은 27.9g으로 대립인 특성이 있다. ‘새들’의 불마름병 저항성은 전국 7개소 시험포장에서 ‘1’로 평가되어 강하였고, 인공접종 시 ‘청자3호’ 보다 강하였다. 콩모자이크바이러스는 인공접종 시 괴저가 나타났으며, 검정포장에서도 ‘청자3호’ 대비 약하였다. 내도복성은 전국 시험포장 평균 ‘2’로 평가되어 ‘청자3호(3)’ 보다 강하였고, 40℃ 건조기에서 48시간 처리하여 조사한 협개열성은 67.9%로 ‘청자3호(98.7%)’에 비해 강하였다. ‘새들’은 ‘청자3호’ 대비 지방함량이 높고, 콩의 주요 기능성 성분인 이소플라본 함량이 4,668㎍/g으로 ‘청자3호(2,115㎍/g)’ 대비 높았다. ‘새들’의 수량성은 지역적응시험 7개소 평균 261kg/10a로 ‘청자3호(242ka/10a)’ 보다 8% 증수하였다. 이처럼 ‘새들’은 최초 개발된 선비잡이콩으로 재래종과 기존품종에 비해 수량성과 내재해성, 기능성이 개선되어 앞으로 가공용 및 밥밑용 콩으로서 사용이 확대될 것으로 기대된다.

***주저자:** Tel. 055-350-1236, E-mail: next0501@korea.kr

PE-0007

쓰러짐에 강한 소립 녹자엽 검정콩 ‘세움’

서정현*, 강범규, 백인열, 신상욱, 성정숙, 박지희, 김준회, 정찬식

경남 밀양시 점필재로20 국립식량과학원 밭작물개발과

검정콩은 주로 주식인 쌀에 넣어먹는 용도로 사용되어 왔으며, 최근에는 종피에 들어있는 기능성 물질들에 대한 연구가 활발히 진행되고 있다. 이중에서도 종실 크기가 작은 검정콩은 우리나라에서 ‘약콩’ 또는 ‘쥐눈이콩’으로 불리며, 대립종인 서리태에 비해 기능성이 높은 것으로 알려져 있다. 최근 소립 검정콩은 두유, 낫또 등 가공식품의 원료로서 사용량이 확대되고 있다. 기존 소립 검정콩 품종인 ‘소청자’는 재래종에 비해 수량성이 높은 특성이 있으나, 키가 크고 쓰러짐과 탈립에 약한 단점이 있었다. 이에 국립식량과학원에서는 기존 품종인 ‘소청자’에 비해 쓰러짐과 탈립에 강하여 재배특성이 우수한 특성을 나타내는 ‘세움’을 개발하였다. ‘세움’은 소립, 녹자엽, 검정콩 육성을 목표로 하여 ‘원광쥐눈이콩’을 모본으로, ‘원광’을 부본으로 2010년에 인공교배하였으며 계통육종법에 의해 ‘YS2293-2B-41-2-2-2-4’가 선발되었다. 2016~2017년도에 실시한 생산력검정시험에서는 소립 녹자엽 검정콩 계통으로 유망시되어 ‘밀양347호’의 계통명을 부여하고 2018~2020년 3년 간 7개소에서 지역적응시험을 실시하였다. ‘세움’은 유한형으로 엽형이 피침형, 꽃색이 자색, 모용색이 갈색, 종실은 구형으로 검은색 종피에 자엽색이 녹색인 고유특성을 가지고 있다. 성숙기는 10월21일로 ‘소청자’보다 6일 늦으며 100립중은 11.4g으로 ‘소청자’와 비슷한 소립 품종이다. 내도복성은 전국 시험포장 평균 ‘2’로 평가되어 ‘소청자(4)’ 보다 강하였고, 40℃ 건조기에서 48시간 처리하여 조사한 협개열성은 64.6%로 ‘소청자(100%)’에 비해 강하였다. ‘세움’의 수량성은 지역적응시험 7개소 평균 292kg/10a로 ‘소청자(252ka/10a)’ 보다 16% 증수하였다. 이처럼 ‘세움’은 종실특성이 기존 품종과 비슷하면서도 수량성과 내재해성이 개선되어 앞으로 가공용 및 밥밑용 콩으로서 널리 사용될 것으로 기대된다.

***주저자:** Tel. 055-350-1236, E-mail: next0501@korea.kr

PE-0008

황색 대립 내도복 장류 가공적성 우수 콩 품종 '대장'

강범규*, 서정현, 박지희, 김준회, 백인열, 신상욱, 성정숙, 정찬식

경상남도 밀양시 점필재로20 국립식량과학원 남부작물부 밭작물개발과

국내 장류 시장은 약 7천 2백억원 규모로 약 4천 5백억원인 두부류보다 더 큰 시장이다. 국산콩 사용 비율도 약 26% 수준으로 두부, 콩나물, 두유 시장과 비교 시 가장 높다(2018 가공식품세분시장현황). 장류 적성은 업체의 가공방법에 따라 달라지나, 원료 및 품종의 종류에 따라서도 발효 지표가 달라지기때문에 장류 가공적성에 적합한 콩 품종 개발이 필요하다. '대장'은 발효적성이 우수하며 알이 굵으면서도 내탈립 유전자를 보유하고 있어 가공과 재배성능이 우수한 품종이다. 2010년 '선유'를 모본으로, '대원콩'을 부본으로 인공교배하여 2011년~2012년 F1, F2집단을 양성하고, 2013년~2015년 F3~F5세대 계통을 전개하여 우수계통을 선발하고 2016년~2017년 생산력검성시험을 통해 '밀양344호'의 계통명을 부여하였다. 2018년~2020년 지역적응시험을 거쳐 재배안정성과 발효 가공적성이 우수하여 신품종심의위원회에 상정하고 알이 굵고 장류에 적합하다는 의미인 '대장'으로 명명하였다. '대장'은 개화기가 7월 31일, 성숙기가 10월 23일인 만생종이며, 경장 59cm, 착협고 14cm, 마디수 13개, 분지수 4개, 협수 45개로 '대원콩' 대비 경장은 작으나 착협고가 높아 기계수확 적응성이 높다. 100립중은 33.9g으로 '대원콩'보다 7.8g 무겁고 7.1mm 이상 립 비율이 98.1%로 종실의 크기가 굵고 균일도가 높다. 수량성은 290kg/10a로 '대원콩'의 96% 수준이나 두부수율이 231%, 발효물의 아미노태질소 함량이 424mg%로 '대원콩' 대비 각각 22%p, 24mg% 높아 가공적성이 우수하다. 알이 굵은 콩을 선호하는 순창 지역 등 장류용 국산 원료곡으로 활용될 수 있을 것으로 기대된다.

***교신저자:** Tel. 055-350-1233, E-mail: hellobk01@korea.kr

PE-0009

담적색 대립이며 성숙기가 빠른 팥 신품종 ‘홍미인’

송석보*, 이병원, 최명은, 추지호, 김지영, 한상익

경남 밀양시 점필재로20 국립식량과학원 남부작물부

‘홍미인’은 기계화적성이 우수하고 대립이면서 성숙기가 빠른 팥 품종을 육성하고자 2008년 하계에 국립식량과학원에서 담적색 대립인 K204656(Toyomidainagon)을 모본으로 하고 성숙기가 빠르고 쓰러짐에 강한 SA9905(SA9411/Suwon38)을 부본으로 인공교배하여 계통육종법으로 선발한 품종이다.
2015~2016년 생산력검정시험에서 쓰러짐에 강하고 수량성이 높 ‘밀양38호’로 계통명을 부여하였다. 2017~2020년 4년간 지역적응시험(밀양, 청원, 나주, 원주)을 실시한 결과, 가공적성이 우수하고 도복에 강한 품종으로 인정되어 2020년 농작물 직무육성 신품종 선정위원회에서 신규 등록품종으로 결정되었다.
‘홍미인’의 개화일수는 42일로 아라리보다 13일 빠르지만 생육일수는 99일로 비슷하여 대립종으로써는 성숙기가 빠른 품종이다. 경장은 58㎝로 ‘아라리’보다 4㎝크고, 협당 립수도 7.4개로 ‘아라리’보다 많았다. 100립중은 20.5g(아라리 16.1g)으로 밝은 적색의 종피색을 가진 대립 품종 이다. 또한 통팥 가공적성이 우수하고 앙금수율이 높아 팥 가공제품 제조시 품질면에서 유리하다. 수량성은 지역적응시험에서 평균수량이 2.09MT/ha로 다수성 품종이다. 적응지역은 강원도 산간 고랭지를 제외한 전국 팥 재배지역에서 재배가 가능하다. 기계수확이 가능한 ‘홍미인’은 노동력과 생산비절감으로 생력화와 농가소득 증대에 기여할 것으로 기대된다.

***교신저자:** Tel. 055-350-1243, E-mail: songsb1254@korea.kr

PE-0010

A new hybrid rice cultivar, ‘Weolhami’ adaptable to Northern Vietnam

Kuk Hyun Jung[1*], Eok Keun Ahn[1], Woong Jo Hyun[1], Hyang Mi Park[1], Yong Jae Won[2], Yong Gu Cho[3], Yu Han Song[3]

[1]Department of Central Area Crop Science, National Institute of Crop Science, RDA, Suwon 16429, Republic of Korea
[2]Cheorwon Substation, National Institute of Crop Science, RDA, Cheorwon 24010, Republic of Korea
[3]Chungbuk National University, 1 Chungdae-ro, Seowon-gu, Cheongju 28644, Republic of Korea

Since first commercial hybrid rice was cultivated in China in 1976, there has been more than 20% general yield increment compared to inbred rice. In order to develop new hybrid rice cultivar for seed export to Southeastern Asia especially Vietnam, we have bred hybrid rice lines in Cambodia since 2014 and as the result of our project, ‘Weolhami’ was developed in 2020. It demonstrated to be adapted to Northern Vietnam with major disease resistance and high yielding capacity; It has resistances against Vietnamese blast and bacterial blight and it has rough rice yield of 11.0 MT/ha in Vietnam, 10.5 MT/ha in Korea, 32% higher than that of ‘Dasan’, high yielding Korean inbred rice. Furthermore, its grain quality is better than that of ‘ⅡA838’, super yielding Chinese hybrid rice. It has 6.8% protein content and 23.3% amylose content lower than those of ‘ⅡA838’ indicating softer texture and better eating quality. As the results of ‘Golden Seed Project’, ‘Weolhami’, second hybrid rice cultivar, will play an important role in boosting Korean seed industry in Korea.

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***Corresponding Author:** Tel. 031-695-4025, E-mail: khjung@korea.kr

PE-0011

중만생 내병성 강화 다수성 저아밀로스 중간찰 벼 ‘정다미’

안억근[1*], 강경호[1], 박향미[1], 원용재[2], 정국현[1], 현웅조[1], 이윤승[1], 김미정[3], 곽지은[3], 김기영[1]

[1]국립식량과학원 중부작물과
[2]국립식량과학원 철원출장소
[3]국립식량과학원 수확후이용과

최근 지자체는 지역에 특화된 브랜드 개발을 위해 차별적으로 벼 신품종을 개발 보급하고 있다. 소비자의 다양한 기호를 반영하여 질감이 더 부드럽고 찰성이 있는 중간찰의 요구가 높다. 이를 반영하여 수원농협과 협력하여 저아밀로스 중간찰인 ‘정다미’를 개발하였다. ‘정다미’는 출수기가 중부평야지 4개소 평균 8월 15일로 중만생종이며 간장은 77㎝, 수장은 20㎝. 주당수수 16개, 수당립수 96개로 수수형에 가깝다. 수발아(1.7%)에 강하고 기존 중간찰벼인 ‘백진주’나 ‘진상’에 비해 도열병과 흰잎마름병(균계 K1, K2, K3)에 저항성이다. 수량성(547㎏/10a)이 ‘백진주(472)’에 비해 16% 향상된 안전 다수성 품종이다. 현미는 천립중이 20.0g인 단원형이며 쌀알은 불투명하지만 ‘백진주’보다는 맑은 편이며 아밀로스 함량은 11.5%이다. 이는 모본인 ‘월백’의 염색체 6번에 위치한 *Wx-mq* 유전자로부터 기인한 것으로 보인다. 제현율, 현백률 및 도정률은 82.8%, 90.4%, 74.8%로 ‘백진주’와 비슷하고 토요윤기치는 78.8로 ‘백진주’(81.6)보다는 낮고 ‘화성’(71.7)보다는 높다. ‘정다미’는 지역이 요구하는 브랜드쌀 원료곡 대체를 통한 농가 소득 창출에 기여할 뿐만 아니라 곡실의 특성을 다양화 할 수 있는 소재로도 활용 가능하다. 본 연구는 농촌진흥청 연구사업(공동연구과제명: 중부지역적응 고품질 벼 품종개발(3단계), 공동연구과제번호: PJ013150032021)의 지원에 의해 이루어진 것이다.

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

PE-0012

사일리지용 내재해 다수성 트리티케일 품종 '옹골진' 개발

박명렬*, 라경윤, 구자환, 김율호

경기도 수원시 권선구 수인로 126 국립식량과학원 중부작물과

트리티케일 품종 '옹골진'은 2020 년에 농촌진흥청 국립식량과학원에서 육성되었다. '옹골진'의 잎은 녹색이며 잎의 길이와 너비는 표준품종 '신영'에 비해 짧고 초형이 양호하다. 이삭 및 까락의 길이는 '신영'에 비해 길고, 종실은 '신영'에 비해 크다. 전국 시험지 평균 출수기는 4 월 23 일로 '신영'보다 2일 빠르고, 대비품종 '조성'보다 2일 늦고, 초장은 134cm로 '신영'과 '조성' 보다 8cm 길었다. 포장에서 보리위축병(BYDV), 흰가루병, 잎녹병은 '신영'과 비슷하게 발생하였으나, '조성'에 비해 적게 발생하였다. 포장 월동 고엽률은 '신영'과 비슷하고, '조성'보다 강하였으며 '신영'보다 도복에 강한 편이나, '조성'과는 비슷하였다. 생체수량은 10a 당 4,631kg 으로 '조성'보다 18%, '신영'에 비해 2% 많았으며 건물수량은 1,575kg 으로 '조성'보다 17%, '신영'에 비해 4% 많았다. 출수 후 30 일경의 식물체 조단백질 함량이 6.2%로 '신영', '조성'과 비슷하였으며, 가소화양분총함량(TDN)은 61.8%로 '신영', '조성'과 비슷하였다. 종실수량은 657kg/10a 로 '신영'과 같았다. 본 연구는 농촌진흥청 어젠다사업(사업번호: PJ016017012021)의 지원에 의해 이루어진 결과로 이에 감사드립니다.

***교신저자:** Tel. 031-695-4051, E-mail: park5260@korea.kr

PE-0013

Novel QTL associated with shoot branching identified in doubled haploid rice (*Oryza sativa* L.) under low nitrogen cultivation

Youngho Kwon†, Nkulu Rolly Kabange†, Ji-Yun Lee, So-Myeong Lee, Jin-Kyung Cha, Dongjin Shin, Jun-Hyeon Cho, Ju-Won Kang, Jong-Min Ko, Jong-Hee Lee*

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

Nitrogen (N) is an essential macronutrient required for the growth and development of plants, as well as their productivity. Excessive application of nitrogen in rice cultivation has been shown to contribute to greenhouse gases (GHG) emissions, such as methane (CH_4) and nitrous oxide (N_2O), especially in flooded paddy fields. In this study, we investigated quantitative trait loci (QTLs) associated with tiller number and panicle number using Kompetitive Allele-Specific PCR (KASP) and Fluidigm markers on a doubled haploid rice population (n=117, a cross between 93-11 (P1) and Milyang352 (P2), *indica* and *japonica,* respectively). One set of the mapping population was grown under normal nitrogen conditions (90 kg ha^{-1} N, 45 kg ha^{-1} P_2O_5, and 57 kg ha^{-1} K_2O), and the other set under low nitrogen conditions (45 kg ha^{-1} N, 22.5 kg ha^{-1} P_2O_5 and 28.5 kg ha^{-1} K_2O) until maturity.

We identified a novel QTL (*qTNL2*, 134 cM, LOD: 6.1, PVE: 20.5%) associated with tiller number under low nitrogen cultivation, mapped on chromosome 2. Similarly, *qPNL4* (154 cM, LOD: 2.95, PVE: 11.9%) associated with panicle number under low nitrogen cultivation, mapped on chromosome 4, was detected. The additive effects (1.81 and 1.18) indicate that alleles from 93-11 explained the observed phenotypic variance for tiller number and panicle number. The breakthrough is that the *qTNL2* harbors candidate genes proposed to be associated with shoot branching and stress response in rice. Therefore, this study suggests a possible crosstalk between plant growth and stress response in rice.

† These authors contributed equally to this work as first authors.

***Corresponding Author:** Tel. +82-53-350-1168, Fax. +82-55-352-3059, E-mail: ccriljh@korea.kr

PE-0014

옥수수 배가반수체 육성효율 증진을 위한 배가 처리시기 및 포장 정식 방법 구명

한정헌*, 류시환, 최승출, 최재근, 김희연, 남궁민, 김문종, 왕승현, 용우식, 이승훈, 심재남, 홍대기

강원도 홍천군 두촌면 장남길 26, 강원도농업기술원 옥수수연구소

강원도농업기술원 옥수수연구소에서는 국내 최초로 배가반수체 육종기술을 도입하여 옥수수 계통육성을 실시하고 있다. 배가반수체 계통육성은 반수체 유기 및 반수체 종자선별, 염색체 배가 및 인공교배를 통한 계통생산, 생산된 계통의 특성평가 및 종자증식 등 3단계로 이루어진다. 이 중 염색체 배가 및 인공교배를 통한 계통을 생산하는 단계는 배가반수체 육성 계통에 있어 가장 중요한 단계로 여겨지며 배가반수체 계통육성 효율성 증진과 밀접한 관련이 있다. 염색체 배가 및 인공교배 단계는 반수체 종자를 발아시키고 일정시기에 콜히친을 처리하여 염색체를 배가하는 단계와 포장에 정식하여 종자를 획득하는 단계로 이루어진다. 본 연구는 발아 종자의 콜히친 처리시기에 따른 배가반수체 계통육성 효율과 배가 처리 후 포장 정식 방법에 따른 배가반수체 계통육성 효율을 조사하였다. 시험은 2019년도부터 2년간 진행하였으며 종실옥수수 3개 집단과 찰옥수수 1개의 집단을 재료로 사용하였다. 처리시기에 따른 배가반수체 계통육성 효율을 조사한 결과 종실옥수수에서는 2.5엽기 이내 처리 시 사용된 반수체 종자수에 대해 육성된 배가반수체 계통수의 비율이 평균 24.4%로 나타났으며 3.5엽기 처리 시에는 평균 16.9% 비율로 나타나 종실옥수수에서 배가처리는 2.5엽기 이내 처리 시 더 높은 비율로 계통이 육성되는 것을 확인하였다. 하지만 찰옥수수 집단에서는 처리 시기 별 계통 육성 비율이 차이 없이 낮게 나타나 찰옥수수 집단에서는 처리시기에 따른 계통 육성 효율을 확인할 수 없었다. 포장 정식 방법에 따른 계통 육성 효율 비교시험은 2.5엽기에 배가 처리 후 포장으로 바로 정식 하는 방법과 배가 처리 후 2차 육묘를 거쳐 포장에 정식하는 방법으로 실시하였다. 시험결과 배가 처리 후 2차 육묘하여 포장에 정식하였을 시 4집단 평균 15.8%의 배가반수체 계통육성 효율이 나타났으며 처리 후 바로 정식 하였을 때에는 4집단 평균 6.8%로 나타나 2차 육묘 후 정식 하는 것이 계통 육성 효율을 증진시키는 방법으로 판단된다.

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***주저자:** Tel. 033-248-6922, E-mail: wjdgjs9908@korea.kr

PE-0015

대립 준조숙 내탈립 기계화 초형 콩 품종 '중모3015호'

강범규*, 서정현, 백인열, 신상욱, 박지희, 김준회, 성정숙, 정찬식

경상남도 밀양시 점필재로20 국립식량과학원 남부작물부 밭작물개발과

콩은 국내에서 다양한 식품의 원료로 활용되는 중요한 작목임에도 불구하고, 재배면적과 생산량은 감소 추세에 있다. 콩 자급률 향상 등 국산콩 생산 확대를 위해서는 콩 생산비를 낮추고 경지이용율을 높여 경제성을 높여야 한다. 콩 품종개발 측면에서는 기계수확 적응성과 이모작에 적합한 특성을 통해 경제성 향상에 기여할 수 있을 것이다. 국립식량과학원에서는 기계수확과 이모작 적응성, 내탈립성과 종자 품질 등 우수한 형질을 집적하여 재배 및 교배모본으로 활용하기 적합한 '중모3015호'를 개발하여 육성과정과 특성을 소개하고자 한다. '중모3015호'는 2012년 YS1862-2B-6-2-3(대망/중국도입자원)을 모본으로, '장올(밀양235호)'를 부본으로 인공교배하여 2013년 F1 집단양성 및 동계온실을 이용하여 F2~3 집단을 전개하였으며, 2014년~2015년 F4~5세대 계통을 전개하여 우량계통을 선발하였다. 2016년~2017년 생산력검정시험과 2018년~2020년 전국 4개 지역에서 지역적응시험을 거쳐 신품종심의위원회에 상정하고 '중모3015호'로 명명하였다. '중모3015호'는 반무한형 초형에 개화기가 7월 26일, 성숙기가 10월 4일로 준조숙형이며, 경장이 85cm, 착협고가 23cm, 마디수가 14개, 분지수가 1.1개, 협수가 38개로 표준품종인 '새올콩' 대비 경장이 크고 착협고가 높으며 분지수는 적은 단지형 초형으로 내도복성도 '1'로 쓰러짐에 강해 기계수확 적응성이 높았고, 생육일수는 111일로 '새올콩'보다 3일 늦은 특성을 나타내었으나, 양파 및 맥류와 이모작 가능하다. 종실은 황색 구형에 광택이 있으며 100립중이 24.5g으로 대립이다. 만파 시(7월 15일 파종)에도 경장이 크고 착협고가 높았으며, 수량성도 232kg/10a로 '대원콩' 대비 6% 많아 안정성이 높았다. 수량성은 전국 평균 260kg/10a로 '새올콩' 대비 24% 증수되었으나, 최근 개발 품종에 비해 낮은편이다. 하지만 내탈립 유전자를 포함하고 있어 내탈립성이 우수하고 두부 수율이 256%로 '새올콩' 대비 31%p 높은 특성을 나타내었다. '중모3015호'는 수량성을 제외한 중요한 농업형질을 다수 집적한 품종으로 우수한 신품종 개발을 위한 중간모본과 필요시 재배용으로 활용될 수 있을 것이다.

***교신저자:** Tel. 055-350-1233, E-mail: hellobk01@korea.kr

PE-0016

조숙, 다수성, 올레산 고함유 유채 1대잡종 ‘아름’

김광수*, 이지은, 차영록, 안다희, 신운철

농촌진흥청 국립식량과학원 바이오에너지작물연구소

유채(*Brassica napus* L.)는 주로 식물체를 채소로 이용하고 종실은 기름을 생산하는 목적으로 재배되어 왔다. 유채는 동계작물로 종실수량이 많고 기름함량도 매우 높아, 전 세계 기름작물 중 생산량이 콩 다음으로 많이 생산되며, 기름 생산량은 팜오일, 콩기름에 이어 세 번째로 생산량이 많은 작물이다. 우리나라에서는 유채가 주로 경관용으로 재배되고 있으며 최근 건강에 대한 관심이 증가함에 따라 국내산 유채유 생산을 위한 재배면적도 점진적으로 증가하고 있다. 유채의 대규모 재배를 위해서는 기계화가 가능한 논 재배가 필수적이며 이를 위해서는 벼와 작부가 가능한 조숙성 품종의 육성이 필요하고 식용유 생산에 적합한 양질의 지방산이 함유된 유채 품종육성이 필요하다. 이에 따라 국립식량과학원 바이오에너지작물연구소에서 논 재배에 적합한 조숙, 다수성이며 지방산 조성이 좋은 품종 육성을 목표로 2015년도에 웅성불임계통인 ‘목포CGMS (IT237834)’를 모본으로 하고 조숙, 다수성 계통인 ‘09003-B-126-2-1-3’[♂, 목포111호(IT2765170/영산유채(IT237769)]를 부본으로 인공교배하여 1대잡종(F1 hybrid) ‘단교80호’를 양성하였다. ‘단교80호’는 2016~2017(2년)에 걸친 생산력 검정시험과 2018~2020(3년)에 걸친 지역적응시험 결과, 이형주의 발생이 없고 대비품종인 ‘선망’에 비해 개화와 숙기가 빠르며 다수성이며 올레산 함유량이 높은 특성을 가져 ‘아름’(Areum)로 명명하였다. 유채 신품종 1대잡종 ‘아름’의 개화기는 4월 3일이었으며 종실 숙기는 6월 1일로 ‘선망’에 비해 2일 정도 빠르다. 종실수량은 269kg/10a로 ‘선망’에 비해 4%가 증수되었다. 종자 내 불포화지방산인 올레인산 함량이 65.1%로 ‘선망’의 60.7%에 비해 4.4% 높았으며, 에루신산은 전혀 검출되지 않았다.

***주저자:** Tel. 061-450-0133, E-mail: ajuga@korea.kr

PE-0017

국립식량과학원 육성 벼 품종의 내풍성 특성 분석

박현수[1], 백만기[1], 정오영[1], 전용희[2*]

[1]전라북도 완주군 이서면 혁신로 181 농촌진흥청 국립식량과학원
[2]경상북도 영덕군 병곡면 원황길 44 농촌진흥청 국립식량과학원 영덕출장소

최근 태풍의 강도와 쌀 생산에 미치는 피해가 증가하고 있다. 국립식량과학원 영덕출장소에서는 이러한 풍해에 대비하기 위해서 내풍성 육종사업을 수행해오고 있다. 본 연구는 영덕출장소에서 육성된 내풍성 품종에 대한 성능을 분석함으로써 그간의 내풍성 육종사업의 효과를 검토하고자 수행되었다. 국립식량과학원 육성 17품종과 영덕출장소 육성 20품종에 대해서 풍동 시설을 이용한 내풍성 검정을 실시하였다. 영덕출장소 육성품종이 국립식량과학원 육성품종에 비해 백화영 비율, 백수율, 풍해 지수가 낮았고, 대조구와 처리구의 등숙률이 높았으며 등숙 감소율이 낮아 전체적인 내풍성이 강한 것으로 나타났다. 주성분분석을 통해 내풍성 관련 형질과 공시품종들의 구조적 관계를 살펴본 결과, 영덕출장소 육성품종들은 주로 처리구 및 대조구 등숙률과 같은 방향성에 근접하여 분포하고 있어 국립식량과학원 육성품종들과 구분되는 것을 확인할 수 있었다. 풍동 시설을 이용하여 조사된 6개 형질과 풍해 상습지 시험포장 적응성 검정에서 조사된 수량 관련 8개 형질을 이용하여 내풍성 품종의 성능을 분석하였다. 대표형질로 백수율, 처리구 및 시험포장 등숙률, 수량을 선정하고 K-means 군집분석을 실시하여 내풍성 품종을 3개의 군집으로 분류하였다. 분류된 군집 중 YC2가 풍해가 적고 수량성이 높아 내풍성이 가장 강하였고, 그 다음으로 YC3가 중간의 내풍성정도를 나타냈으며, YC1이 내풍성이 가장 약하였다. 내풍성이 강한 YC2에 속한 ‘신보’는 공시된 품종들 중 내풍성이 가장 강하였고 수량성이 높아 유망한 품종으로 판단되었다. 신보와 같은 영덕출장소에서 육성된 내풍성 벼 품종은 풍해 상습지 피해 방지에 실질적으로 활용될 수 있으며, 국내 육성 벼 품종의 내풍성 향상을 위한 육종소재로 적극 이용될 것으로 기대된다.

***교신저자:** Tel. 054-732-0385, E-mail: jeonyhee@korea.kr

PE-0018

직무육성 벼 핵심품종 기반의 NAM 집단 변이다양성 분석 및 농업적 형질

박향미[1*], 현웅조[1], 안억근[1], 정국현[1], 이윤승[1], 강경호[1], 원용재[2], 김정주[3]

[1]경기도 수원시 권선구 수인로 125 국립식량과학원 중부작물과
[2]강원도 철원군 동송읍 태봉로 2346 철원출장소 국립식량과학원
[3]강원도 춘천시 충열로 251 춘천출장소 국립식량과학원

우리나라 직무육성 벼 핵심 품종 40종을 모본으로, 화영벼를 부본으로 NAM(nested association mapping) 집단을 구축(40 species * 200 RILs = 총 8,000 plants)하여 세대진전(F7)된 집단 대상으로 변이다양성을 분석하고 주요 농업형질을 비교하였다. 변이다양성 분석은 16조합 4개체 총 96샘플을 대상으로 GBS 기반의 NGS분석을 실시하고 structure, phylogenetic tree 등 비교분석하였다. 전체 NAM 집단의 전장유전체 연관분석 가능성을 분석한 결과 6개의 subset에서 SNP 개수가 540~12,745개로 다양하였고, 전 염색체별로 고르게 분포하여 전체 유전체를 커버할 수 있는 QTL 분석이 가능할 것으로 판단되었다. 또한, NAM 집단의 이질접합성 인자 비율이 0.007로 매우 낮아 동형접합성 유효성이 인정되어 집단이 충실하게 만들어지고 유지된 것으로 판단되었다. 한편, 본 집단을 대상으로 2018년~2020년 3년간 주요 농업형질(출수기, 수장, 수수 등)을 조사하여 연차 간 변이를 비교하였다. 2018년 대비 2019년 출수기의 연차변이는 16집단에서 ±1일 차이가 났으며, ±2~3일 차이난 집단이 17조합, +4~5일 차이난 집단이 5조합, 6일 이상 차이난 집단이 2조합이었다. 또한, 2018년 대비 2020년 출수기의 연차변이는 20집단에서 ±1일 차이가 났으며, ±2~3일 차이난 집단이 12조합, +4~5일 차이를 보였던 집단이 4조합, 6일 이상 차이를 보였던 집단이 4조합이었다. 특히, 3년간 출수기가 ±1일로 변이 폭이 적었던 조합은 10조합이었으며 수장, 수수 등 농업형질의 변이를 조사한 결과, 2018년에 비해 2019년에는 수장이 1.8% 길어지고, 수수가 5.9% 증가하는 경향이었던 반면, 2020년에는 수장이 1.8% 짧아지고, 수수가 27.5% 증가하는 경향이었다. 한편, 모본 대비 집단의 3년간 출수기가 ±6일 이상으로 변이 폭이 컸던 조합은 16조합이었으며 수장, 수수 등 농업형질의 변이를 조사한 결과, 2018년에 비해 2019년에는 수장은 2.2% 짧아지고, 수수가 5.9% 감소하는 경향이었던 반면, 2020년에는 수장이 4.5% 짧아지고, 수수가 14.5% 증가하는 경향이었다. 향후, 본 NAM 집단은 목표형질별, 조합별 표현형과 유전형 연관분석을 통해 정밀육종에 활용 가능할 것으로 기대된다.

사사: 본 연구는 농촌진흥청 연구사업(공동연구과제명: 형질개량 효율성 제고 위한 벼 품종 표현형-유전자형 병합 DB 구축, 공동연구과제번호: PJ013572012021)의 지원에 의해 이루어진 결과임.

***교신저자:** Tel. 031-695-4036, E-mail: parkhm2002@korea.kr

PE-0019

종자 품질이 우수하고 콩나물 수율이 높은 소립 나물용 콩 품종 '신바람'

강범규[1*], 서정현[1], 박지희[1], 김준회[1], 백인열[1], 신상욱[1], 성정숙[1], 백정호[2], 정찬식[1]

[1]경상남도 밀양시 점필재로20 국립식량과학원 남부작물부 밭작물개발과
[2]전라북도 전주시 완산구 농생명로 370 국립농업과학원 농생명자원부 유전자공학과

다양한 요리의 재료로 활용되는 콩나물은 한국의 식문화적인 요소이며, 시장규모는 약 3천억원 정도로 추정하고 있다. 국내 나물용 콩 원료곡 수요량은 약 3만 7천톤이며 국내 생산량은 6천 9백톤으로 18.7%의 자급률을 나타내고 있다('16~'20, 농촌경제연구원). 나물용 콩 원료곡은 일반 콩과 다르게 종자의 발아능력, 콩나물 가공적성이 매우 중요하다. 이는 콩나물 가공업체의 수익과 직결되기 때문이다. 또한, 원료곡의 특성이 바뀌면 가공업체에서 수용하기 어려운 점이 있어 신품종 보급에 어려움이 있다. 국립식량과학원에서는 이러한 문제를 해결하고 우수한 콩나물 품질을 가진 품종을 개발하기 위해 가공업체와 협력평가를 통해 우수계통을 선발하여 '신바람'을 육성하고 그 과정과 특성에 대해 소개하고자 한다. '신바람'은 2010년 '풍산나물콩'을 모본, 'HS1371-49-2-2-2-2'을 부본으로 인공교배하여 2011년~2012년 F1 및 F2 집단을 양성하였다. 2013년~2015년 F3~F5 세대를 계통육종법으로 전개하고, 2016년~2017년에는 선발된 우량계통에 대한 생산력검정시험을 수행하고 '밀양356호'의 계통명을 부여하였다. 2018년~2020년에는 전국 4지역(수원, 달성, 나주, 제주)에서 지역적응시험을 수행하여 균일성과 안정성이 인정되어 신품종선정위원회를 통해 '신바람'으로 명명하고 품종으로 육성하였다. '신바람'의 종실은 100립중 10.2g의 소립 구형이며 종피색과 제색이 황색, 이병립율 조사 결과 0.0% 수준으로 종실 외관 품질이 매우 우수했다. 성숙기는 10월 9일 경으로 '풍산나물콩' 대비 5일 빠르고 성숙이 일시적으로 나타나 성숙특성이 우수하였다. 경장은 46cm, 착협고는 10cm, 분지수는 3.5개, 협수는 82개로 '풍산나물콩'과 비슷한 타원형 초형이나 내도복성이 '2'로 '풍산나물콩(4)' 보다 개선되었다. 수량성은 적응지역 평균 318kg/10a로 '풍산나물콩' 대비 96% 수준이나, 콩나물 가공적성 평가 결과 물콩비율, 불완전발아율, 부패율 등 '풍산나물콩' 대비 각각 2%p, 3.2%p, 3.2%p 낮아 품질특성이 우수했으며, 콩나물 수율도 629%로 '풍산나물콩' 대비 83%p 높아 경제성이 향상되었다. 2019년~2020년 4개 가공업체에서 수행된 협력평가에서도 콩나물 수율이 높고 설문평가 결과 6.7점으로 '풍산나물콩(6.0점)' 대비 선호도가 높아 상품성이 우수했다. '신바람'은 기계수확 적응성과 수량성에 아쉬운 점이 있으나, 내륙지역(제주도가 나물콩 주산지임)에서 고품질 원료곡을 수요로 하는 가공업체의 계약재배용 품종으로 활용될 수 있을 것으로 기대된다.

***교신저자:** Tel. 055-350-1233, E-mail: hellobk01@korea.kr

PE-0020

Screening of Soybean Genotypes for Resistance to *Phytophthora sojae* isolates 3053 and 3617

Jihee Park[1*], Beom-Kyu Kang[1], Sanjeev Kumar Dhungana[1], Jeong-Hyun Seo[1], Junhoi Kim[1], Yun-woo Jang[2], Jung-Sook Sung[1], Sang-Ouk Shin[1], In-Youl Baek[1], Chan-Sik Jung[1]

[1]Upland Crop Breeding Research Division, Department of Southern Area Crop Science, National Institute of Crop Science, RDA, Miryang 50424, Korea

[2]Crop Production Technology Research Division, Department of Southern Area Crop Science, National Institute of Crop Science, RDA, Miryang 50424, Korea

Soybean growth and development are inhibited by different abiotic and biotic factors. Phytophthora root and stem rot (PRSR), one of the emerging threats to soybean production in Korea, well develops in wet soil conditions like poorly drained paddy fields. *Phytophthora sojae,* a soil-borne oomycete, is the causal agent of PRSR. Currently, as soybean cultivation in paddy fields increases, the PRSR in soybean is being more concerned than before. The objective of this study was to screen the Korean soybean genotypes for PRSR resistance using two *P. sojae* isolates 3053 and 3617 that were collected from two major soybean production areas Andong and Kimje, respectively, in 2019. We inoculated *P. sojae* isolates 3053 and 3617 into 195 genotypes using the hypocotyl inoculation technique and made a close observation on the resistance and sensitivity reactions of the genotypes. After two independent screenings, 14 out of 195 genotypes showed resistance and intermediate resistance to isolate 3053, 10 out of 195 genotypes to isolate 3617, and 6 out of 195 genotypes to isolates 3053 and 3617 both. Further experiments are undergoing to carry out the genetic studies and to develop resistant cultivars for PRSR.

***Corresponding Author:** Tel. 055-350-1234, E-mail: heeya91@korea.kr

PE-0021

이삭포엽 생산성이 높은 옥수수 신품종 ‘색소5호’

최재근[1*], 박종열[2], 류시환[1], 김희연[1], 남궁민[1], 김문종[1], 한정헌[1], 왕승현[1], 용우식[1], 이승훈[1], 홍대기[1]

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

최근 건강에 대한 인식이 높아지면서 인공적인 식재료보다는 천연물질을 이용한 건강기능성 식품에 대한 소비와 연구가 활발히 이루어지고 있다. 특히 기능성을 갖는 여러 가지 물질 중에 안토시아닌 색소는 250여종으로 식물에서 광범위하게 존재하는 색소로 다양한 식물체에서 추출되어 이용되고 있다. 옥수수에서 추출한 붉은 계열 식용색소인 ‘Corn red’에는 10여종의 안토시아닌 계열의 색소가 있다고 하였다. 안토시아닌 색소는 천연 착색료, 항산화, 항비만, 항당뇨 및 합병증 예방 등 여러 가지 효능이 알려져 있다. 옥수수연구소에서 이런 고기능성 안토시아닌이 함유되어있는 옥수수를 개발하여 부가가치를 높이고자 품종 육성을 하였다. 옥수수에는 안토시아닌 색소가 식물체 전체에서 발현될 수 있으며, 특히 이삭의 포엽에서 함량이 높게 나타난다. 따라서 본 연구는 옥수수 안토시아닌 색소가 많이 발현되는 이삭 포엽의 생산성이 높은 품종을 개발하기 위해 수행하였다. “색소5호”는 색소용 모집단에서 분리된 HA9를 모본, HA10을 부본으로 하여 2014년에 인공교배 하였으며, 이삭 포엽 수량성은 “색소1호” 대비 36% 증수한 68kg/10a로 이삭 포엽 수량이 높으며, 도복지수는 1로 낮아 내재해성도 강하며, 100립중은 24.1g으로 “색소1호” 26.4g보다 소립인 특성을 갖고 있다. 출사일수는 “색소1호”와 같은 80일이며, 착수고율은 60% 이다. “색소5호”는 이삭 포엽의 생산성이 높아 천연색소 추출용으로 적합한 특성을 가지고 있다. 앞으로 농가에 보급하여 식의약품 소재로 활용되면 부가가치를 높여 색소옥수수를 이용한 산업화에 기여할 것으로 기대된다.

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

PE-0022

Interaction of OsRopGEF3 protein with OsRac3 to regulate root hair elongation and reactive oxygen species formation in rice (Oryza sativa)

Eui-Jung Kim[1], Woo-Jong Hong[1], Win Tun[1], Gynheung An[1], Sun-Tae Kim[2], Yu-Jin Kim[3*], Ki-Hong Jung[1*]

[1]Graduate School of Biotechnology & Crop Biotech Institute, Kyung Hee University, Yongin 17104, Republic of Korea

[2]Department of Plant Bioscience, Pusan National University, Miryang, 50463, Republic of Korea

[3]Department of Life Science and Environmental Biochemistry, Pusan National University, Miryang, 50463, Republic of Korea

Root hairs are tip-growing cells that emerge from the root epidermis and play a role in water and nutrient uptake. One of the key signaling steps for polar cell elongation is the formation of Rho-GTP by accelerating the intrinsic exchange activity of the Rho-of-plant (ROP) or the Rac GTPase protein; this step is activated through the interaction with the plant Rho guanine nucleotide exchange factor (RopGEFs). The molecular players involved in root hair growth in rice are largely unknown. Here we performed the functional analysis of *OsRopGEF3*, which is highly expressed in the root hair tissues among the *OsRopGEF* family genes in rice. To reveal the role of *OsRopGEF3*, we analyzed the phenotype of loss-of-function mutants of *OsRopGEF3*, which were generated using the CRISPR-Cas9 system. The mutants had reduced root hair length and increased root hair width. In addition, we confirmed that reactive oxygen species (ROS) were highly reduced in the root hairs of the *osropgef3* mutant. The pairwise yeast two-hybrid experiments between OsRopGEF3 and OsROP/Rac proteins in rice revealed that the OsRopGEF3 protein interacts with OsRac3. This interaction and co-localization at the same subcellular organelles were again verified in tobacco leaf cells and rice root protoplasts via bimolecular functional complementation (BiFC) assay. Furthermore, among the three respiratory burst oxidase homolog (*OsRBOH*) genes that are highly expressed in rice root hair cells, we found that OsRBOH5 can interact with OsRac3. Our results demonstrate an interaction network model wherein OsRopGEF3 converts the GDP of OsRac3 into GTP, and OsRac3-GTP then interacts with the N-terminal of OsRBOH5 to produce ROS, thereby suggesting OsRopGEF3 as a key regulating factor in rice root hair growth.

***Corresponding Author:** Tel. 031-201-3474, E-mail: alice804@khu.ac.kr

PE-0023

Single Cross Corn Hybrid ‘Daeryuk3’ with Early Maturity, Lodging Tolerance and High Yield

Moon Jong Kim*, Min Namgung, Jaekeun Choi, Jeongheon Han, Seungchul Choi, Woosik Yong, Inseok Seo, Daeki Hong, Sihwan Ryu

Maize Research Institute, Gangwondo Agricultural Research & Extension Services, 26 Jangnam-gil, doochon-myeon, Hongcheon-gun, Gangwon-do, Korea

We are importing corn grains about ten million tons annually, and self-sufficiency rate of corn is less than one percent. It is not easy to increase total field corn production in Korea because of limited arable land. For this reason, it is necessary to develop new corn variety with higher yield and better performance against current climate. A new single cross corn hybrid ‘Daeryuk3’ was developed by Maize Research Institute, Gangwon ARES in 2020. The hybrid ‘Daeryuk3’ was acquired by crossing two inbred lines, ‘HF12’ and ‘HF20’. Silking date of ‘Daeryuk3’ was five days earlier than control cultivar ‘Jangdaok’. It is resistant to lodging due to the low ratio of upper ear height to plant height of 43%. ‘Daeryuk3’ is a yellow-orange and dent-like corn, and one hundred seed weight is 27.4g. Resistance to disease and harmful insect of ‘Daeryuk3’ were similar to those of ‘Jangdaok’. The grain yield of ‘Daeryuk3’ was 776kg/10a which was increased 10% compared with a check hybrid, ‘Jangdaok’ at the regional yield trials from 2018 to 2020. ‘Daeryuk3’ can be planted anywhere in the country. Daeryuk3 has shown a good adaptability performance in Jilin Province, China. Therefore, a new single cross hybrid, Daeryuk3, may be efficiently used in northern area such as China and North Korea. We are also expected to expand farmers choice of field corn varieties.

***Corresponding Author:** Tel. 033-248-6926, E-mail: mjkim7049@korea.kr

PE-0024

칼슘함량이 높고 기능성이 우수한 손가락조 ‘핑거1호’

추지호[1*], 이병원[1], 김지영[1], 최명은[1], 송석보[1], 고지연[2], 한상익[1], 정찬식[1]

[1]경남 밀양시 점필재로20 국립식량과학원 남부작물부
[2]전북 전주시 덕진구 농생명로 300, 농촌진흥청

‘핑거1호’는 국외에서 널리 재배되고 있는 손가락조 품종을 육성하고자 2012년에 네팔에서 분양 받은 손가락조 유전자원 중 농업형질이 우수한 ‘IT136282’을 순계분리하여 선발한 품종으로 국내에 출원된 손가락조의 첫 번째 품종이다.

2015~2016년에 수행한 생산력검정시험에서 수량성이 우수하고 생육일수가 우리나라 기후에서의 작부체계에 적합해서 ‘밀양16호’로 계통명을 부여하여 지역적응시험을 수행하였다. 2016~2018년 지역적응시험을 경남 밀양 등 6개 지역에서 수행한 결과, 수량성이 높고 기능성이 우수하여 2018년 농작물 직무육성 신품종 선정위원회에서 신규 등록 품종으로 신규 등록 품종으로 결정되었다.

‘핑거1호’의 생육일수는 99일로 대조 계통인 밀양15호와 비슷했다. 6월 상순 파종할 경우 서리가 내리기 전인 9월 중하순에 수확이 가능해 우리나라 기후 및 작부체계에 적합한 품종이다. 간장은 105cm이며 이삭의 길이는 7.4cm이다. 이삭은 한 개체 당 평균 8.7개 맺히고 낟알 천개의 무게는 1.8g인 소립 품종이다. 낟알은 적갈색을 띠는 메성 종실이다. 6개 지역에서 3년 동안 실시한 지역적응시험에서 평균 3.19MT/ha의 높은 수량을 보였다. ‘핑거1호’는 100g당 칼슘 함량이 322mg으로 조(22), 기장(19)에 비해 높은 함량을 보였다. 폴리페놀 함량도 조, 기장에 비해 높았기 때문에 건강한 잡곡을 찾은 소비자들에게 수요가 높은 잡곡이 될 것으로 기대된다.

***주저자:** Tel. 055-350-1245, E-mail: chugho@korea.kr

PE-0025

취반 후 갈변현상이 적은 쌀보리(*Hordeum vulgare* L.) ‘백수정찰’

김양길[1*], 윤영미[1], 박종호[2], 이미자[1], 김경호[1], 강천식[1], 오세관[1], 이점호[1], 김태헌[1]

1전라북도 완주군 이서면 혁신로 181 농촌진흥청 국립식량과학원
[2]전라북도 전주시 덕진구 농생명로 420 농촌진흥청 농촌인적자원개발센터

최근 식생활 변화에 따른 건강식품소재로 보리에 대한 소비자들의 관심이 높아지고 가공적성이 우수한 품종 요구에 따른 생산자 및 수요자 충족을 위해 2006년에 한해에 강하고 백도가 좋은 특성을 가진 ‘진미찹쌀(IT268947)’을 모본으로, 프로안토시아니딘-프리 2조 대립인 ‘Radiant’ 품종을 부본으로 하여 인공교배 하였다. 2007년에 F_1을 양성한 후 2008~2009년에 집단으로 F_2~F_3를 전개하였고, 2010~2013년에는 F_4-F_7 계통에서 찰성이면서 취반 후 갈변현상이 적은 저 프로안토시아니딘 계통을 선발하여 2014년에는 생산력검정예비시험 후 우량시 되는 HB16960-B-B-19-1-3-1 계통을 선발하였다. 선발된 이 계통을 2년간 생산력검정시험(2015~2016)후 우수성이 인정되어“전주135호”로 계통명을 부여 받아, 2017~2019년까지 3년간 답리작(논)재배 전주, 나주, 진주, 대구 4개 지역에서 지역적응시험을 수행하였다. 그 결과, 경기도 연천지역에서 시험한 내한성 정도는 고휴 재배시 고사주율이 66.7%, 저휴 23.3%로 새찰쌀보리(66.3, 12.3)보다 고사주율이 높아 한해는 새찰쌀보리보다 약하였으나 토양전염 바이러스병인 보리호위축병은 2정도로 새찰쌀보리와 비슷한 저항성을 보였다. 출수기는 4월 20일로 새찰쌀보리보다 1일 늦은 출수를 보였으며, 성숙기는 5월 26일로 2일 늦게 성숙하였다. 간장은 75㎝로 새찰쌀보리 대비 7㎝ 정도 짧아 도복에 안정적인 것으로 나타났다. 수장은 4.3㎝, 1수 립수는 48개, 천립중은 29.5g정도로 조곡 수량성은 4개소(전주, 나주, 진주, 대구) 평균 5.05톤/ha의 수량을 나타냈다. 시험지역 중 가장 수량성이 높게 나타낸 경남 진주지역에서 5.54톤/ha으로 새찰쌀보리 대비 22% 높은 수량성을 보였다. 품질 중 ‘백수정찰’은 프로안토시아니딘(0.15%→0.01%) 함량이 낮아, 보리밥 저장(24시간) 후 백도 변화는 ‘백수정찰’ 35.1→32.1로 새찰쌀보리(30.0→19.9)에 비해 변하지 않아 소비자들로부터 좋은 평가를 받았으며, 가공용(즉석밥 등)으로 수요가 많을 것으로 기대되며, 1월 최저평균기온이 -6℃ 이상인 보리 재배지역에 보급될 예정이다.

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***교신저자:** Tel. 063-238-5224, E-mail: kim5yk@korea.kr

PE-0026

Measurement of genetic mobility using transposon display marker system in gammaray irradiated soybean mutants

Nguyen Ngoc Hung[1,2], Soon-Jae Kwon[1*], Dong-Gun Kim[1,3], Jae-Il Lyu[1], Jung Min Kim[1,2], Ji Su Seo[1,2], Jin-Baek Kim[1], Bo-Keun Ha[2]

[1]Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongeup 56212, Korea

[2]Division of Plant Biotechnology, College of Agriculture and Life Science, Chonnam National University, Gwangju 61186, Korea

[3]Department of Life-resources, Graduate School, Sunchon National University, Sunchon 59722, Korea

Transposon or transposable elements (TEs) are ubiquitous repetitive components of eukaryotic. Under certain circumstance include gamma ray radiation, TEs are able to change location within genome and play an important role for genome diversification and evolution. PONG and Miniature Inverted-repeat Transposable Element (MITEs) are two of the major class II DNA transposon in the soybean genome. In this study, we employed information of consensus terminal inverted repeat sequence (TIRs) of Pong, MITE-Toursit, MITE-Stowaway combined with transposon display marker, a powerful technique to identify the integration of transposon in genome, to investigate genetic mobility of transposon in irradiated-gamma soybean mutant population. In M_1 generation, genetic diversity were investigated by transposon display in combination with radio-sentivity analysis. The optimal dose of gamma irradiation for inducing soybean mutation appears to be in range 400-500 Gy for four cultivars. For TD marker, total of 58 bands were amplified using 12 most efficient primer combinations, of which 30 (58%) were polymorphic. 209 M_1 soybean individuals that include polymorphic fragments were selected and used to evaluate genetic mobility of transposon in M_2 soybean mutants by TD marker. Three M_2 soybean mutant had highest polymorphic fragment percentage (ranging from 29% to 43%) and exhibited variation of genotype in comparison between M_1 and M_2 generation, were selected to accomplish further investigation of translocation of transposon in mutant population by further Pacbio whole genome sequencing. The TD marker provided useful information for assessing the genetic integration of transposon and help to improve our knowledge of soybean radiation breeding.

***Corresponding Author:** Tel. 063-570-3312, Email: soonjaekwon@kaeri.re.kr

PE-0027

Evaluation of adaptability to winter potato production under plastic film house of potato cultivars

Jin Hee Seo*, Young Eun Park, Jang Gyu Choi, Hyun Jin Park, Gyu Bin Lee

Highland Agriculture Research Institute, National Institute of Crop Science, Rural Development Administration, Pyeongchang 25342, Republic of Korea

Recently, according to comsumers' preference for fresh potatoes, winter potato production is being differentiated in various ways. However, the proper sowing day has not been identified, which is causing a problem in the potato production of farms. Therefore, this study was carried out to evaluate the proper sowing day of a cultivar suitable for winter production cultivation. Six cultivars of summer-cultivated seed potatoes harvested in September in high-land were sown in Miryang, Gyeongsangnam-do, which is the main production region for winter production cultivation, from late October to late December in a double-plastic greenhouse to examine the quantity and quality characteristics. As a result, the yields of 'Daeji' were high (48-58 ton/ha) at all sowing day, and the yield of 'Chubaek' was the highest at the time of sowing in October and decreased in subsequent sowing. The yields of 'Jopung', 'Sumi', 'Haryeong', and 'Seohong' increased as the sowing day was delayed from October to December. 'Seohong' had excellent adaptability to winter production cultivation because of the high yield in November sowing. Among the test cultivars, the adaptability to winter production cultivation was low in the 'Sumi' cultivar because of its low yield regardless of the sowing day. The 'Haryeong' cultivar showed a lot of crack in winter production cultivation.

***Corresponding Author:** Tel. 033-330-1690, E-mail: sjh329@korea.kr

PE-0028

OsABAR7 유전자를 활용한 옥수수 가뭄내성 조절 연구

홍준기, 장희정, 이연희, 김범기, 박상렬*

농촌진흥청 국립농업과학원 농업생명자원부

옥수수는 밀, 벼와 함께 세계 3대 작물 중의 하나로 식용, 사료, 에너지, 산업소재, 제약 원료 등 분야에 광범위하게 활용되고 있다. 최근까지 생명공학 기술을 적용하여 해충저항성 및 제초제 저항성의 형질을 가진 GM 옥수수 개발과 유전자 편집기술을 활용하여 스트레스에 내성을 갖거나 웅성불임을 갖는 옥수수 등을 개발하고 있다. 본 연구는 농과원에서 확립된 옥수수 형질전환 기술을 이용하여 벼 가뭄내성 *OsABAR7* (ABA receptor *OsPYL/RCAR7*) 유전자를 옥수수에 도입하여 농업적 형질을 개선하고자 하였다. *OsABAR7* 유전자를 *Ubiquitin* 프로모터에 조합하였고 선발마커로 제초제 저항성 유전자 *bar*를 CaMV35S프로모터에 융합하여 제작된 벡터를 *Agrobacterium*균주 AGL1에 도입 한 후 분리된 Hi IIA미성숙배에 *Agrobacterium* 공동배양법을 이용하여 형질전환체를 생산하였다. Bialaphos가 첨가된 배지에서 저항성 캘러스를 형성하는 형질전환 효율은 최대 20.8%를 나타냈다. PAT 단백질 발현 검사와 제초제 Basta 저항성 분석을 통해 형질전환체에 도입된 *bar* 유전자가 안정적으로 발현되는 것을 확인하였다. 또한 *bar* 및 *Adh* 유전자 특이 프라이머를 이용하여 Genomic DNA PCR 및 TaqMan 분석법을 통해 유전자 도입 유무 및 copy 수를 확인하여 단일 T-DNA가 도입된 계통들을 확인하여 종자를 확보하였다, Flanking DNA sequencing 분석으로 single copy계통에서 T-DNA가 직접적으로 유전자 결실과 변이를 유도하지 않은 계통을 선발하였다. 현재 선발된 *OsABAR7* 형질전환 옥수수 계통들은 가뭄내성 특성을 분석 진행중이며 안정적으로 가뭄내성 특성이 증가한 계통을 선발하여 후대를 육성할 예정이다.

***교신저자:** Tel. 063-238-4582, E-mail: srpark@korea.kr

PE-0029

Towards the Development of Good Potato breeding lines for French fries

Jang Gyu Choi*, Ji Hong Cho, Hyun Jin Park, Jin Hee Seo, Gyu Bin Lee, Chung Ki Choen, Yeong Eun Park

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

Potato varieties have been breeding for processing such as potato chip, according to development of the processed potato industry since 1980s. These varieties for processing potato chip have a round or oval shape, but they are not suitable for french fries to long shape. ‘Sepung(Shepody)’ was introduced for french fries processing in the past. But this cultivar has the susceptibility of disease such as late blight and was not rarely cultivated. The purpose of this study was to make good potato breeding lines for french fries through crossbreeding. So, we get 7,500 TPS of 17 combinations thorough cross between potato resources in 2019. We proceed first clonal generation in greenhouse in Daegwallyeong in 2020. And then potato breeding lines were divided to single cropping and double cropping by dormancy at second generation in 2020. We are conducting third generation of potato lines in mesh house and will select excellent potato lines through evaluation of shape, yield, tuber quality.

***Corresponding Author:** Tel. 033-330-1610, E-mail: dndn012@korea.kr

PE-0030

Expression profiling of wheat Nuclear Factor Y transcription factors under drought conditions

Ji Woo Kim, Jeong Hwan Lee*

Division of Life Sciences, Jeonbuk National University, 567 Baekje-daero, Deokjin-gu, Jeonju, Jeollabuk-do 54896, Republic of Korea

Nuclear Factor Y transcription factors (NF-Y) that directly bind to the CCAAT box regulate diverse genes in all eukaryotes. They forms a heterotrimeric complex consisting of three unique subunits called NF-YA, NF-YB, and NF-YC. In plants, multiple genes encode each subunit type, thereby leading to form many possible NF-Y complexes that play key roles under various abiotic stress conditions such as drought. However, our current knowledge about the role of wheat (*Triticum aestivum*) NF-Y transcription factors (TaNF-Y) in the response to drought remains limited. Here, we performed phylogenetic analysis of TaNF-Y with *Arabidopsis* and rice NF-Y, and investigated the expression patterns of TaNF-YA, TaNF-YB, and TaNF-YC in drought-treated wheat leaves and roots. Phylogenetic trees showed that various TaNF-Y transcription factors may function in flowering, chloroplast biogenesis, and drought stress. Furthermore, expression analyses revealed that a variety of *TaNF-Y* genes (*TaNF-YA2/4/5/6/9*, *TaNF-YB10/11*, and *TaNF-YC7/8/14*) were up-regulated in leaves, but not in roots under drought conditions, suggesting that they may possible targets for transgenic approaches. Taken together, our results provided that TaNF-Y transcription factors may play an important role in response to drought stress.

***Corresponding Author:** Tel. 063-270-3375, E-mail: jhwanlee90@jbnu.ac.kr

PE-0031

GW2 and its interacting proteins regulate seed development in rice (*Oryza sativa* L.)

Dae Hwan Kwon[1], Jong Tae Song[2], Hak Soo Seo[1*]

[1]Department of Plant Science, Research Institute of Agriculture and Life Sciences, Seoul National University, Seoul 151-921, Korea
[2]Department of Applied Biosciences, Kyungpook National University, Daegu 41566, Korea

Seed size has been extensively studied in crop plants, as it determines crop yield. However, the mechanism of seed development remains elusive. In this study, we explored the mechanism of seed development in rice (*Oryza sativa* L.), and identified proteins affecting seed size. Proteomic analysis showed that glyceraldehyde 3-phosphate dehydrogenase (GAPDH), chitinase 14 (CHT14), and phosphoglycerate kinase (PGK) accumulated to high levels in the seeds of the natural *japonica* rice mutant Oochikara, which carries a loss-of-function mutation in the *Grain Width 2* (*GW2*) gene; *GW2* encodes a RING-type E3 ubiquitin ligase. In vitro pull-down and ubiquitination assays showed that CHT14 and PGK directly interacted with GW2 but were not ubiquitinated by GW2. Immunoblot analysis revealed that protein disulfide isomerase-like 1-1 (PDIL1-1) accumulated to high levels in young developing seeds of the *gw2* mutant compared with the wild type. Histochemical *β-glucuronidase* (*GUS*) staining showed strong expression of *GW2* in leaf and root tissues but weak expression in leaf sheaths and internodes. In addition, transformation of the *green fluorescent protein* (*GFP*) gene under the control of the *GW2* promoter in rice revealed *GFP* expression in the aleurone layer of seeds. Collectively, these results suggest that GW2 regulates seed size through direct interactions with proteins involved in carbohydrate metabolism by modulating their activity or stability and controlling disulfide bond formation in various proteins during seed development. Additionally, GW2 participates in vegetative as well as reproductive growth, and protects the seed from pathogen attack.

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

PE-0032

국내 밀 품종의 *Gli-1*과 *Gli-2* 유전자 검정

홍수민[1], 최리[1], 유진희[1], 이윤아[1], 김선숙[1], 정한용[2], 모영준[1], 박철수[1*]

[1]전북대학교 농업생명과학대학 작물생명과학과

[2]국립식량과학원 밀연구팀

글리아딘(gliadin)이 밀가루 반죽의 인장성(extensibility)을 결정하는 중요한 저장 단백질임에도 불구하고 국내 연구는 매우 부족한 실정이다. 본 연구에서는 글리아딘의 유전적 조성에 대한 기초 정보 수집을 위해 국내 49개 밀 품종의 *Gli-1*과 *Gli-2* 유전자에 대한 마커 검정을 실시하였다. *Gli-1*과 *Gli-2* 유전자는 각각 1번 염색체와 6번 염색체의 단완에 위치하며, γ-/ω-글리아딘(*Gli-1*)과 α-/β-글리아딘(*Gli-2*)의 발현을 조절한다. *Gli-1* 분석 결과, Gli1.1과 Gli1.2의 밴드 발현 여부에 따라 타입 1과 2로 분류되었으며, *Gli-A1*은 타입 1이 67.3%(33 품종)였고, 타입 2는 32.7%(16 품종)이었으며, *Gli-B1*은 타입 1이 16.7%(8 품종), 타입 2는 83.3%(40 품종)였고, 조광은 Gli-B1.1과 Gli-B1.2에서 밴드가 나타나지 않는 타입 3으로 분류되었다. *Gli-D1*는 타입 1이 89.8%(44 품종)로 타입 2보다 (10.2%, 5품종) 높은 빈도를 나타내었다. *Gli-2* 마커 분석 결과, *Gli-A2*는 국내 49품종에서 모두 a-1 타입을 나타냈지만, *Gli-B2*는 b-1 타입이 87.8%(43 품종)로 가장 빈도가 높았으며, b-2 타입이 8.2%(4개 품종)였고, 한백과 안백은 b-7과 b-8 타입이었다. *Gli-D2*는 d-1과 d-2 타입이 각각 49.0%(24 품종)과 46.9%(23 품종)로 빈도가 높았고, 백찰과 고소는 d-3 타입을 나타냈다. *Gli-B1*에서 타입 1과 2를 나타내는 품종의 *Gli-B2* 조성은 b-1 타입이 각각 75.0%와 90.0%로 다른 타입에 비해서 높게 나타났으며, 타입 3인 조광의 *Gli-B2* 조성도 b-1 타입이었다. *Gli-D1*에서 타입 1을 나타내는 품종의 52.3%는 *Gli-D2*에서 타입 d-1을 나타냈지만 *Gli-D1*에서 타입 2를 지닌 품종의 *Gli-D2* 조성은 d-2 타입이 80.0%로 d-1 타입(20%)보다 높은 빈도를 나타내었다.

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***교신저자:** Tel. 063-270-2533, E-mail: pcs89@jbnu.ac.kr

PE-0033

Multiplex STS 마커를 활용한 국내 밀 품종 판별

최리[1], 홍수민[1], 유진희[1], 이윤아[1], 김선숙[1], 정한용[2], 모영준[1], 박철수[1*]

[1]전북대학교 농업생명과학대학 작물생명과학과
[2]국립식량과학원 밀연구팀

본 연구는 국내 밀과 수입 밀 및 혼합밀의 판별을 위하여 NaOH와 Multiplex STS 마커를 이용한 품종 판별 체계를 확립하기 위해 수행되었다. 국내 49개 밀 품종은 1M NaOH 시약 처리를 통해 13개의 백립계와 36개의 적립계로 구분하였고 이들에 대한 STS 마커는 기존에 보고된 12개의 Primer를 사용하여 Multiplex화 실험을 통해 Multiplex STS 마커 세트를 구성하였다. 백립계는 *TaCwi-A1b*/*PPO-A1*/*Vrn-D1a*로 구성된 Set1과 *PinA-D1*/*Glu-B3d*/*Glu-B3h*로 구성된 Set2를 선발하였고 적립계는 백립계의 Set 1과 동일한 마커를 Set1, *Glu-A1c*/*Rht-B1b*/*Glu-B3i*로 구성된 Set 2, *Glu-A3d*/*Glu-B3d*/*Glu-B3g*/*Glu-B1b*로 구성된 Set 3를 선발하였다. 백립계 Set 1에서 연백, 다분 2개의 품종이 구분되며, Set 2에서 남은 한백, 백중, 조경 등 11개의 품종이 구분가능하다. 적립계 Set 1에서 안백, Set 2에서 그루, 조은, 새금강, 조중, 수강 등 12개의 품종이 구분되며 Set 3에서는 수안, 다중, 조농, 조한, 경광 등 18개의 품종이 구분된다. 두 개의 백립계 세트를 수행한 결과 백립계 품종이 모두 구분되었고 세 개의 적립계 세트를 수행한 결과 청계, 서둔, 우리밀과 장광, 영광밀을 제외한 44개의 품종이 구분되었다.

사사: 본 발표는 농촌진흥청 연구사업(과제명: 고품질 밀 안정생산을 위한 수분・양분 관리 재배기술 개발 및 생리연구, 과제번호: PJ0159652021)에 의해 이루어진 것임

***교신저자:** Tel. 063-270-2533, E-mail: pcs89@jbnu.ac.kr

PE-0034

The role of *OsMYB1* for anthocyanin biosynthesis in rice pericarp

Da-Hye Kim[1,2], Jea-A Jung[3], Jong-Yeol Lee[2*], Sun-Hyung Lim[1*]

[1]Division of Horticultural Biotechnology, School of Biotechnology, Hankyong National University, Anseong, 17579, Korea

[2]National Academy of Agricultural Science, Rural Development Administration, Jeonju, 54874, Republic of Korea

[3]Floriculture Research Division, National Institute of Horticultural & Herbal Science, Rural Development Administration, Wanju 55365, Korea

Rice (*Oryza sativa*) pericarp exhibits various colors due to the accumulation of anthocyanins and/or proanthocyanidins. Previous work revealed that the two basic helix-loop-helix (bHLH) transcription factors OsbHLH1 and OsRc are key regulators for the black and red pericarp traits, respectively, and their inactivation results in rice with white pericarp. However, their pericarp-specific R2R3 MYB partner remained unknown. Here, we characterized the role of the R2R3 MYB gene *OsMYB1* in rice pericarp pigmentation through genetic and molecular approaches. A rice protoplast transfection assay showed that OsMYB1 is a nuclear-localized protein. Furthermore, OsMYB1 physically interacted with OsbHLH1 in a yeast two-hybrid analysis. Co-transfection assays in rice protoplasts revealed that OsMYB1 and OsbHLH1 mediate the activation of anthocyanin biosynthetic genes. Notably, the *OsMYB1* promoter region exhibited an insertion polymorphism specifically in rice cultivars with black pericarp, creating two tandem repeats where red and white varieties harbor only one. The number of repeats within the *OsMYB1* promoter correlated with increased transactivation by OsMYB1, thus providing a rationale for the black pericarp characteristic of cultivars with two repeats. These results thus provide evidence for the molecular basis of anthocyanin biosynthesis in rice pericarp and may facilitate the introduction of this beneficial trait to other rice cultivars through marker-assisted breeding.

***Corresponding Author:** Tel. 031-670-5105, E-mail: limsh2@hknu.ac.kr

PE-0035

Screening for flooding tolerance in two soybean populations (EMS-induced ‘Pungsannamul’ population and Korean *Glycine soja* core population)

Hai Anh Tran[1], Cuc Thi Nguyen[1], Jeong-Dong Lee[1], Hak Soo Seo[2], Jong Tae Song[1*]

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

Flooding is one of the most serious abiotic stresses that reduce productivity of crops in many important agricultural regions of the world. Soybean (*Glycine max* (L.) Merr.) is the important legume crop, which is generally sensitive to flooding stress. The present study is aimed to screen and isolate the flood-tolerant soybean lines/ accessions in EMS-induced ‘Pungsannamul’ mutant and Korean wild soybean core populations. In this study soybean plants at V2 stage were subjected in conditions of submergence for 5-7 days, or waterlogging for 21 days. Foliar damage after the removal of water was used to evaluate the level of flooding tolerance. Evaluation data showed that 2 wild soybean accessions were very tolerant to submergence, and 2 other wild soybean accessions and 3 EMS soybean lines were tolerant. Besides, in a waterlogged soil condition, 2 accessions and 10 others in the wild core population were very tolerant and tolerant, respectively. A genome-wide association analysis (GWAS) was conducted using the phenotypic data of the wild soybean population. Eighteen and fourteen single nucleotide polymorphisms (SNPs) were identified to be associated with submergence and waterlogging tolerance, respectively, at a significance level of $-\mathrm{Log}(P) \geq 5.0$. Four SNPs strongly associated with foliar damage reduction were found in the regions spanning approximately 630 kb of chromosome 10 under both flooding conditions. In a later experiment, two wild soybean accessions out of them were determined to be tolerant to submergence stress at germination stage, with normal seedling rate higher than 90% compared to control condition. In further studies, the tolerant lines isolated will be utilized for the breeding program to identify the genetic resources involved in the flooding tolerance.

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

PE-0036

QTL mapping for grain weight with early maturing Korean *japonica* rice varieties

Yunji Shin[1], Yong Jae Won[2], Kyeong-Seong Cheon[3], Chaewon Lee[1], Hyo Ja Oh[1], Jeongho Baek[1], Song Lim Kim[1], Kyung-Hwan Kim[1], In Sun Yoon[1], Young-Soon Cha[1], Hyeonso Ji[1*]

[1]Gene Engineering Division, Department of Agricultural Biotechnology, National Institute of Agricultural Sciences, Jeonju 54874, Republic of Korea

[2]Cheorwon Branch, National Institute of Crop Science, Rural Development Administration (RDA), Cheorwon 24010, Republic of Korea

[3]Division of Forest Tree Improvement and Biotechnology, Department of Forest Bioresources, National Institute of Forest Science, Suwon 16631, Republic of Korea

Rice yield, a complex agronomic trait is evaluated by panicles per unit area of land, number of spikelets per panicle, percentage of filled grains, and grain weight. Therefore, grain weight is a primary breeding target trait to improve yield. To this end, we performed QTL mapping for grain weight with F8 and F9 recombinant inbred populations derived from a cross between Joun (small grain) and Odae (large grain) which are early maturing Korean *japonica* rice varieties. A genetic map comprising 248 KASP markers which are polymorphic between the parents was constructed with 162 F8 recombinant inbred lines (RILs). The total distance of the genetic map was 1,302.8 cM, and the average distance between markers was 5.5 cM. We measured thousand grain weight using unhulled rice and brown rice harvested in 2019 (F8) and in 2020 (F9), and calculated the coefficients of phenotypic correlations. Moreover, by the combining the QTL mapping results from the F8 and F9, a total of seven QTLs for grain weight were detected on chromosome 2, 3, 7 and 11. Among these, three QTLs were commonly detected on chromosome 2, 7 and 11 in both F8 and F9, which might have stable effects over different environments. These QTLs presented here will be utilized in breeding rice varieties with desirable grain weight.

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

PE-0037

‘미백2호’와 닮은 붉은색 색소찰옥수수 신품종 ‘미홍찰’

남궁민[1*], 박기진[2], 한정헌[1], 류시환[1], 최재근[1], 김문종[1], 최승출[1], 용우식[1], 서인석[1], 홍대기[1]

[1]강원도농업기술원 옥수수연구소, 강원도 홍천군 두촌면 장남길 26
[2]강원도농업기술원 산채연구소, 강원도 평창군 봉평면 흥정계곡길 114-5

찰옥수수는 우리나라 여름철 대표 간식으로 사랑받고 있으며 전국적으로 15,000~16,000ha 수준으로 재배되고 있다. 하지만, 판매되는 품종들이 흰색 또는 검정색으로 한정되어 다양성이 부족하고 여름철 한시적으로만 판매되어 시장 규모가 작다. 따라서, 본 연구에서는 찰옥수수의 품종 다양화에 기여하고 신 부가가치 창출을 통한 시장 규모를 확대하기 위해 기능성 성분을 함유한 색소찰옥수수 품종을 육성하고자 하였다. 2016년 미백2호의 교배친 HW9를 모본으로 하고 기능성 자색옥수수를 1회친으로 교잡 후 3~4회 여교배 육성한 색소HW3 계통을 부본으로 하여 교배한 뒤 ‘색찰교52호’라고 교잡종명을 부여하였다. 2017~2019년 강원지역 3개소에서 지역적응시험 결과 ‘색찰교52호’는 중만생종(출사일수 72일)에 착수고가 낮고 도복에 강한 생육 특성을 보였으며, 이삭 모양, 길이, 착립율 등 이삭 특성도 ‘미백2호’와 비슷하게 평가되었다. 하지만, 과피에 안토시아닌 색소가 있어 풋옥수수가 진한 붉은색이며 함량분석 결과 116.2mg/100g으로 ‘미흑찰’ 대비 약 13배 이상 높은 것으로 확인되었다. ‘색찰교52호’는 2019년 도내 직무육성 신품종 선정위원회에서 우수성이 인정되어 2020년 ‘미홍찰’로 명명하여 품종출원(출원 2020-263)하였다. 신품종 ‘미홍찰’은 시장 평가와 칼라패키지 시범사업 농가 실증을 거쳐 건강 기능성 찰옥수수로 소비자에게 선보일 예정이다.

***교신저자:** Tel. 033-248-6923, E-mail: ngm0623@korea.kr

PE-0038

A Medium-Maturing, Lodging Tolerance and Good Eating-Quality Rice Variety ‘Gyeonggi12ho’

Eun Kyu Jang*, Young Rok Kim, Jong Hyeong Lee, Byoung Rourl Choi, Jung Hee Jang,
Hyeun Yong Do, Tae Jin Won, Ji Hye Lee, Jung Hyeun Ji, Hae Chan Jung, Chnag Hui Cho

Gyeonggi Do Agricultural Research & Extension Services, Byeongjeomjungang-ro 283-33, Hwaseong-si, Republic of Korea

‘Gyeonggi12ho’ is a medium-late maturing and high quality rice variety developed by the crop breeding team of Crop Research Division, GARES, Hwaseong, Korea in 2020. ‘Gyeonggi12ho’ was derived from a cross between ‘Hopum’ and ‘Matdream’ in 2008. The heading date of this variety is August 15th in Gyeonggi Province. Its culm length is 69 cm. This variety has 14 tillers per hill and 110 spikelets per panicle. It is medium-grain variety that 1,000 grain weight of brown rice is 23.7 g. Its cold tolerance is weaker than ‘Hwaseongbyeo’ and its degree of lodging is similar with ‘Hwaseongbyeo’. It is moderately resistant to rice blast diseases and have bacterial leaf blight and stripe virus resistance, but is susceptible for other virus diseases and insect pest. Its appearance of milled rice is clear and its protein contents of milled rice is 6.3% which is similar to that of ‘Hwaseongbyeo’. Its palatability of cooked rice is better than ‘Chucheongbyeo’ which is main cultivar of Gyeonggi Province. Its milling ratio is 76.8% which is higher than ‘Hwaseongbyeo’. The yield of milled rice was 5.54 MT/ha under the ordinary cultivation of the local adaptability test in 4 areas for three years. ‘Gyeonggi12ho’ is highly adaptable to Gyeonggi Province.

***Corresponding Author:** Tel. 031-229-5772, E-mail: jek0428@gg.go.kr

PE-0039

Evaluation of drought-tolerant lines in an EMS-induced population and core populations

Cuc Thi Nguyen[1], Jeong-Dong Lee[1], Hak Soo Seo[2], Jong Tae Song[1*]

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

Drought is one of the major abiotic stresses that strongly limit crop productivity and yield. Soybean (*Glycine max* (L.) *Merr*.) is an important leguminous plant that is popularly known as a drought-sensitive crop. The purpose of the present study is to screen drought-tolerant accessions and utilize them as genetic resources for the development of high-yielding drought-tolerant varieties. A total of 769 accessions (384 accessions of *G. max* and 385 accessions of *G. soja*) of soybean core populations in Korea and 1362 lines of EMS-induced Pungsannamul population were screened for drought tolerance at the vegetative stage in greenhouse condition. Out of them, 6 very tolerant and 21 tolerant accessions were identified from the *G. soja* core population, whereas only a single tolerant line was isolated from the *G. max* EMS population. However, two wild soybean accessions showed better performance than other accessions at all growth stages as well as represented the effectiveness and reliability of multiple phenotypic and yield-related characteristics in soybean. These tolerant accessions defined in this study can be useful in breeding programs. Further, a genome-wide association study was carried out to detect the genome region that controls the quantitative trait loci (QTL) for drought tolerance in genetically diverse sets of the 377 *G. max* and 318 *G. soja* accessions. Association analysis identified 8 SNPs in *G. max* and 2 SNPs in *G. soja* that are associated with canopy wilting at the significance level of -Log10 (P) > 5. The chromosomal regions defined in this study can be used for further analysis to identify the causal gene(s) as well as to identify DNA markers that can be used in selection to drought tolerance soybean.

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

PE-0040

Quantitative trait loci (QTL) analysis of protein and oil contents in *Glycine soja* using two mapping populations

Woon Ji Kim[1], Byeong Hee Kang[1,2], Chang Yeok Moon[1,2], Sehee Kang[1], Bo-Keun Ha[1,2*]

[1]Department of Applied Plant Science, Chonnam National University, Gwangju, 61186, Korea
[2]BK21 FOUR Center for IT-Bio Convergence System Agriculture, Chonnam National University, Gwangju, 61186, Korea

Soybeans are mainly composed of 40% protein and 20% oil. However, these traits are negatively correlated with each other and regulated by quantitative trait loci (QTL) that are controlled by several genes. In this study, total of 190 F2 and 90 BC1F2 populations, which were derived from a cross of Daepung (*Glycin max*) X GWS-1887 (*Glycine soja*), were used for construction of linkage map with 6K SNP Illumina array and QTL analysis. In F3 population, average contents of protein and oil were 45.52 and 7.84, respectively. QTL associated with protein contents (LOD=10.65 and R^2=22.8%) was detected at Gm20_29512680 on chr. 20. Also, one QTL associated with oil contents (LOD=5.61 and R^2=12.7%) was detected at Gm15_3621773 on chr. 15. In BC1F3 population, average contents of protein and oil were 44.43 and 7.73, respectively. Two QTLs associated with protein contents were detected at Gm20_27578013 (LOD=3.77 and R^2=15.4%) on chr. 20 and Gm15_2072075 (LOD=3.12 and R^2=12.5%) on chr. 15. Also, QTLs associated with oil contents were detected at Gm04_43645980 (LOD=3.54 and R^2=11.0%) on chr. 4 and Gm20_32603292 (LOD=3.43 and R^2=10.6%) on chr.20. Based on these results, it will be possible to identify the protein and oil-related candidate genes within the QTL interval in both populations.

***Corresponding Author:** Tel. 062-530-2050, E-mail: bkha@jnu.ac.kr

PE-0041

Interactions between F-box protein and glycosylphosphatidylinositol-anchored protein in wheat

Min Jeong Hong[1], Dae Yeon Kim[2], Hong-Il Choi[1], Yeong Deuk Jo[1], Sungyul Chang[1], Yong Weon Seo[3], Jin-Baek Kim[1*]

[1]Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, 29 Geumgu, Jeongeup 56212, Korea
[2]Institute of Animal Molecular Biotechnology, Korea University, 145 Anam-ro, Seongbuk-Gu, Seoul 02841, Korea
[3]Division of Biotechnology, Korea University, 145 Anam-ro, Seongbuk-Gu, Seoul 02841, Korea

F-box proteins play a variety of roles in plant developmental and physiological processes including floral organ development, circadian rhythms, abiotic stress response, plant defense, and phytohormone signal transduction. In this study, we cloned and characterized F-box/LRR-repeat (FBXL) protein in wheat. The *TaFBXL* ORF was 1,062 bp in size and was predicted to encode a 379-aa protein. The TaFBXL consisted of one F-box domain (SMART accession: SM000256), five Leu-rich repeat domains (SMART accession: SM000370), and three Leu-rich repeat, cysteine (Cys)-containing domains (SMART accession: SM000367). qRT-PCR analysis revealed that *TaFBXL* expression was up-regulated during vegetative growth. We confirmed the interactions between TaFBXL and TaSKPs throughout yeast co-transformation. Using the yeast two-hybrid screen, we identified potential TaFBXL-interacting proteins in a wheat seedling library. Among the five clones that were identified as potential partners of TaFBXL, we found the strongest interaction between TaFBXL and glycosylphosphatidylinositol-anchored protein (GPI-AP). The TaFBXL protein was localized nucleus and plasma membrane, and the florescence signal of TaGPI-AP was observed in the plasma membrane and endoplasmic reticulum (ER). Yeast two-hybrid and bimolecular fluorescence complementation (BiFC) assays revealed that TaFBXL specifically interacts with TaGPI-AP in the nucleus and plasma membrane. Our results suggest that TaFBXL is involved in the 26S proteasome pathway by interacting with TaSKP and that it targets the substrate TaGPI-AP for degradation. These data will aid in function analysis of wheat F-box proteins.

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

PE-0042

Wheat germplasm adaptation analysis in Korean environment for two years

Yong Jin Lee[1], Jin Seok Yoon[1], Chon-Sik Kang[2], Chang-Hyun Choi[2], Kyung-Hoon Kim[2], Kyung-Min Kim[2], Yu-Mi Choi[3], Hyemyeong Yoon[3], Myoung-Jae Shin[3], Kyong Hee Joung[4], Jong-Tae Lee[4], Chang-Hee Son[4], Yong Weon Seo[1*]

[1]Department of Biotechnology, Korea University, Seoul 02841, Republic of Korea
[2]National Institute of Crop Science, RDA, Wanju 55365, Republic of Korea
[3]National Agrobiodiversity Center, National Institute of Agricultural Science, RDA, Jeonju 54874, Republic of Korea
[4]Agricultural Product Research Department, Gyeongsangnam-do Agricultural Research and Extension Services, Jinju 52733, Republic of Korea

Wheat has been one of the most important food crops in the world. Although the demand of hard wheat flour increased to 32.4 kg per capita per year (KOSIS 2019), self-sufficiency is less than 2% in Korea, mainly due to the relatively lower breadmaking quality than the imported wheat. Total 200 wheat genetic resources that were provided by National Agrobiodiversity Center, RDA, were incorporated to select lines that are adapted in Korean growing environment and posess good storage proteins. Numerous agronomic and quality parameters were measured in three different locations (mid-north part: Namyangju-si, middle part: Wanju-gun, south part: Jinju-si) for two years (2018-2019 and 2019-2020). Introduction of selected wheat germplasms in this study with high protein contents and superior agronomic performances would be an effective strategies for the improvement of Korean hard wheat breeding programs.

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***Corresponding Author:** Tel. 02-3290-3005, E-mail: seoag@korea.ac.kr

PE-0043

다수성으로 병해에 강하며 폴리코사놀 함량이 높은 새싹용 겉보리 ‘싹이랑’

윤영미[1*], 김양길[1], 김태헌[1], 박종호[2], 김경호[1], 구자환[1], 서우덕[1], 오세관[1], 이점호[1]

[1]전라북도 완주군 이서면 혁신로 181 농촌진흥청 국립식량과학원
[2]전라북도 전주시 덕진구 농생명로 420 농촌진흥청 농촌인적자원개발센터

추위에 강한 새싹용 겉보리 품종 육성을 위해, 새싹용으로 우수하고 다수성인 ‘큰알보리1호(IT213217)’를 한해에 강한 ‘Arta(IT302383)’와 2008년 인공교배 하였다. F_1 양성 후 2010~2011년 집단으로 F2~F3를 전개하였다. F4~F6세대를 진전시키면서 추위에 강하고 새싹 수량이 많은 계통을 지속적으로 선발하였다. 선발된 IC08003-B-B-8-2-2 계통을 대상으로 2년간 생산력검정시험(2016~2017)후 우수성이 인정되어 ‘전주510호’로 계통명을 부여하였다. 2018~2020년 3년간 전작(밭) 수원, 춘천, 청주 3개 지역, 답리작(논) 전주, 대구 2개 지역에서 지역적응시험을 수행하였다(농진청, 2018~2020). ‘전주510호’는 간장이 80cm로 ‘올보리’(84cm)보다 작아 쓰러짐에 잘 견디고, 천립중은 35.2g으로 ‘올보리’(34.0g)보다 무거웠다. 보리호위축병에는 강했으며 흰가루병은 올보리와 비슷하게 이병성이었다. 내한성은 고사주율이 고휴 55%(‘올보리’ 57%) 저휴 3.3%(올보리 7.7%)로 ‘올보리’와 같은 추위에 강한 특성을 보였다. 쓰러짐 저항성은 도복지수 4로 ‘올보리’ 6보다 강하게 나타났다. 수량성은 전체 평균 557kg/10a, 전작 589kg/10a, 답리작 508kg/10a로 ‘올보리’보다 각각 21%, 15%, 31% 증수한 다수성을 보였다. ‘전주510호’의 품질 실험 결과 단백질과 베타글루칸은 각각 10.2%, 4.3%로 올보리와 비슷하였으며 폴리페놀은 178mg/100g으로 ‘올보리’(164mg/100g)보다 8.5% 많았다. 새싹 재배시 건조 중량은 157g/m^2(‘올보리’ 133g/m^2), 폴리코사놀 448mg/100g(‘올보리’ 245mg/100g)으로 많았으며, 사포나린은 494mg/100g(‘올보리’ 525mg/100g)으로 ‘올보리’보다 적었다. ‘전주510호’는 2020년 농촌진흥청 농작물 직무육성 신품종 선정위원회에서 우수성이 인정되어 신품종으로 선정되었고 ‘싹이랑’으로 명명되었다.

겉보리 ‘싹이랑’은 기존 품종보다 재배안정성이 높고 새싹품질이 좋아 생산자 및 가공업체의 수요가 많을 것으로 기대되며, 1월 최저평균기온이 -8℃ 이상인 보리 재배지역에 보급될 예정이다.

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***교신저자:** Tel. 063-238-5227, E-mail: mi3710@korea.kr

PE-0044

감자칩 가공용 2기작감자 신품종 '수지'

조지홍[1*], 최장규[1], 천충기[1], 한선경[2], 조만현[3], 문애경[4], 박영은[1], 이영규[1], 진용익[1], 박현진[1], 서진희[1], 이규빈[1]

[1]강원도 평창군 대관령면 경강로 5481 국립식량과학원 고령지농업연구소
[2]전라북도 완주군 이서면 혁신로 181 국립식량과학원
[3]충청남도 예산군 오가면 오가중앙로 101-12 충청남도농업기술원 종자관리소
[4]제주특별자치도 제주시 애월읍 월각로 563-20 제주특별자치도농업기술원 농산물원종장

우리나라에서는 2013년부터 골든시드프로젝트 사업을 통하여 수출용 감자 품종을 육성하여 왔다. 특히 동남아시아 지역은 감자를 겨울동안 재배하는 지역으로, 우리나라 봄재배를 통해 생산된 씨감자를 수출할 경우 감자의 휴면이 적절하게 타파되어 파종시 최적의 생리적 서령 상태를 유지할 수 있다. 또한 현지에 진출한 국내 가공업체를 지원하기 위하여 전분함량이 높고 환원당 함량이 낮은 칩가공용 품종을 육성하고자 하였다. '수지' 품종은 2010년 국내에서 육성한 칩가공용으로 바이러스에 강한 '새봉'과 괴경의 크기는 작으나 튀김 특성이 우수한 '방울'을 인공교배하여 육성하였다. 2011년과 2012년에 강릉에서 봄, 가을 2기작으로 실생1~4세대를 거쳤고, 생산력검정시험은 2013년부터 2015년까지 강릉에서 실시하였다. 이후 2016년부터 2018년까지 강릉, 제주, 무안 등에서 지역적응시험을 실시하였고, 가공업체와 공동으로 농가 현장재배를 통해 수량성과 가공특성을 분석하였다. 이에 따라 전분함량이 높고 봄재배시 칩 품질이 우수하며 역병과 더뎅이병에 중도저항성인 2기작 칩가공용 감자로 선발되어 '수지'로 명명되었다. '수지'는 반직립형으로 자라며 꽃은 흰색이다. 모자이크 바이러스에 다소 약하지만 기형서와 열개서 발생이 적다. 괴경의 휴면기간은 상온에서 저장하였을 때 수확후 60~70일 정도이다. '수지'는 국내에서는 2기작 식용 및 칩가공용으로 유망한 품종이며, 봄재배는 전국, 가을재배시에는 금강 이남 해안지역 재배에 적합하다. 또 휴면기간이 다소 길어 가을에 씨감자를 생산한 후 봄에 가공원료용으로 생산하는 것이 유리하다. '수지' 품종은 골든시드프로젝트사업(세부과제: 중국 남부/동남아시아 적응 수출용 품종 육성, 213009-05-3-SB410)의 지원으로 수행된 결과의 일부이다.

***교신저자:** Tel. 033-330-1650, E-mail: jhcho0108@korea.kr

PE-0045

Characterization of EMS-induced salt-tolerance silage maize mutant

Dool-Yi Kim, Kyung Hwa Kim, Chuloh Cho, Mi-Suk Seo, Mina Jin, Dool-Yi Kim*

Crop Foundation Research Division, National Institute of Crop Science, RDA, Wanju 55365, Korea

Maize (*Zea mays* L.) is one of the most valuable agricultural crops and grown under a wide spectrum of environmental conditions. However, maize is due to moderately sensitive to salt stress, soil salinity is a serious threat to its production worldwide. In this study, we used ethyl methanesulfonate (EMS) for generate the salt-tolerant silage maize mutants. We screened salt-tolerant lines from 203 M_3 mutant populations by evaluating the morphological phenotype after salt stress treatment and selected 141ES172 line. The 141ES mutant shows improved plant growth, higher proline contents and leaf photosynthetic capacity compared with wild-type under salt stress conditions. Furthermore, the expression pattern of three genes involved in salt stress response was increased in the 141ES172 mutant by salt stress. In whole-genome re-sequencing analysis, 28 single nucleotide polymorphisms (SNPs) in CDS regions identified as common variants between KS141 and 141ES172 against reference genome. The salt tolerant mutant line selected in our study could be used as an improved breeding materials for maize variety.

***Corresponding Author:** Tel. 063-238-5323, E-mail: dykim22@korea. kr

PE-0046

Profiling volatile compounds related to the eating quality of *japonica* rice (*Oryza sativa* L.)

Yoon Kyung Lee, Hee-Jong Koh*

Department of Agriculture, Forestry and Bioresources, Plant Genomics and Breeding Institute, Research Institute for Agriculture and Life Sciences, Seoul National University, Seoul, South Korea

The quality of rice is an important trait in the market. Of the several criteria used to determine the eating quality of rice, aroma of cooked rice is critical yet studied the least due to its complex nature and technical limitations. Here, the composition of volatile organic compounds in cooked rice was profiled using headspace SPME GC/MS. The cultivars were grouped into high, intermediate, and low eating quality based on the results of sensory panel test. Total of 63 compounds were identified from 24 *japonica* rice cultivars. The correlation analysis on eating quality and log scaled peak area of identified volatile compounds of each variety revealed that 11 compounds were positively correlated, and 16 compounds were negatively correlated to the eating quality. The significant compounds could further be used in breeding high eating quality *japonica* rice by controlling the levels or presence and absence of the compounds.

***Corresponding Author:** Tel. 02-880-4541, E-mail: heejkoh@snu.ac.kr

PE-0047

Screening Index for Line Selection of Good Eating Quality in Indica Breeding Program

Hyeon-Su Park, Man-Kee Baek, Chang-Min Lee, Jong-Min Jeong, Jong-Hee Lee, O-Young Jeong, Ji-Ung Jeung, Jong-Cheol Ko, Jeom-Ho Lee, Young-Chan Cho*

National Institute of Crop Science, RDA, Wanju 55365, Republic of Korea

High eating quality is the most important objective in breeding program of indica as well as japonica rice. The population of breeding lines of generations advanced was evaluated to the characteristics, RVA properties, texture analysis using My Boy II System (Taketomo Co., Japan) and sensory evaluation for cooked rice, physicochemical traits of protein and amylose content, and Wx-allele by DNA marker. The final goal is decided to objective characteristic for line selection of good eating quality of glossiness and soft texture in indica rice breeding program. In correlation relationship analysis among 15 characteristics and two gene-allele types, all characteristics except hot-paste viscosity and protein contents showed high positive and negative correlation in each other. The low setback and high breakdown have been known to relate good quality in cooked rice. The characteristics of texture analyzer showed high correlation relationship with traits of sensory evaluation. We thought that these results were related with amylose contents. The Wx^b allele types were lower amylose contents of 18.7±1.44 and Wx^a types were higher amylose contents of 25.7±1.14. The correlation relationship between amylose content and Wx-allele type was 0.91. There are very difficult to apply in line selection because the texture analysis and sensory evaluation must be tested using cooked rice. We suggest that the objective characteristics for line selection of good eating quality of glossy and soft texture are low setback and high breakdown of RVA properties and Wx^b-allele type of Wx gene in indica rice breeding program. These results could be apply to indica rice because indica cooked rice has the characteristic to become quickly hard.

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***Corresponding Author:** Tel. +82-63-238-5211, E-mail: yccho62@hanmail.net

PE-0048

Prominent expression of *BrF3'H* leads to a specific metabolic profile of flavonoids in purple variety of *Brassica rapa*

Sangkyu Park[1], Hyo Lee[1], Chan Ju Lim[2], Jinpyo Oh[2], Myung Ki Min[1], Jihee Ha[1], Jaeeun Song[1], Jong-Yeol Lee[1], Saet Buyl Lee[1], Jin A kim[1], Beom-Gi Kim[1*]

[1]Metabolic Engineering Division, National Institute of Agricultural Science, Rural Development Administration, JeonJu, 54874, Republic of Korea
[2]Research Institute of Biotechnology Breeding, Asia Seed Co., Icheon, 17414, Republic of Korea

Flavonols and anthocyanins are the two major classes of flavonoids in *Brassica rapa*. To understand the flavonoid biosynthesis pathway in *B. rapa*, we analyzed and compared the contents of different classes of flavonoids between two varieties of *B. rapa* with normal green (Hyb-G) and purple (Hyb-P) traits. The Hyb-P accumulates predominant levels of quercetin, isorhamnetin, and cyanidin compared to the Hyb-G, indicating that the 3′ 4′ -dihydroxylated flavonoids are prevalent in the Hyb-P. Gene expression analysis showed that most of the early- and late-biosynthetic genes of flavonoid pathway are highly expressed in the Hyb-P. In particular, *BrF3'H* is expressed almost exclusively in the Hyb-P. We isolated *BrF3'H* cDNAs from the two varieties, both encode identical amino acid sequence and are highly conserved with other *F3'H* genes from different species. The *BrF3'H* from Hyb-G (*BrF3'H-Hyb-G*) was transiently expressed in *Nicotiana benthamiana* and flavonoid substrates were co-infiltrated later, which showed productions of 3'4'-dihydroxylated products from the 4'-hydroxylated substrates of different classes of flavonoid, demonstrating that *BrF3'H-Hyb-G* encode functional enzyme with broad substrate specificity. Our study suggests that the high level of *BrF3'H* expression can be a critical factor in determining the external and metabolic trait of the Hyb-P variety.

***Corresponding Author:** Tel. 063-238-4614, E-mail: bgkimpeace@korea.kr

PE-0049

Participatory varietal development: A premium rice variety, ‘Haemalgeun’, for premium rice brand in Chungnam province, Korea

Woong Jo Hyun[1*], Yong Jae Won[1], Eok Keun Ahn[1], Kuk Hyun Jung[1], Hyang Mi Park[1], Eung Gi Jeong[1], Jeong Heui Lee[2], Ji Eun Kwak[1], Yoon Sung Lee[1], Jeong Ju Kim[1], Kyung Ho Kang[1], Ki Yeong Kim[1]

[1]National Institute of Crop Science, RDA, Korea
[2]Rural Development Administration, Korea

The National Institute of Crop Science invented a new type of rice variety development program called ‘Stakeholder Participatory Program(SPP)’. The participants of SPP program are breeders, local government, farmers, local residents, RPC(Rice Processing Complex) and distributors. This participatory breeding required series of activities including elite line selections, participatory testing, demonstrations, seed productions, sensitization of farmers by education and training, and propaganda etc. Stakeholders directly participate in each major stage of breeding program and evaluate and select varietal candidates tested by using local agricultural environment (climate, soil, water, pests) and local cultivation technology. The final variety will be determined by the taste of consumers for candidate varieties that have received good evaluation in the field. Through this program, a premium quality late-maturing rice, ‘Haemalgeun’ was developed and released in 2018 by collaboration among various stakeholders; rice breeders of NICS, Asan City, rice processing center and farmers in Asan. ‘Haemalgeun’ was mated in 2008 with ‘Hiami’ and ‘Jinbaek’ as the parent. To shorten the generation, it was advanced in the winter green house by bulk method until F_5 generation and a SR34462-B-B-B-2-2 which showed excellent rice quality and resistance to blast, bacterial blight(race K1, K2, K3, K3a) and rice strip virus was selected in fixed generation and given the name of Suwon 602. At the new variety council, this variety was chosen as the new rice variety in recognition of its excellent performance in the two-year yield trial and the four-year local adaptability test. ‘Haemalgeun’ is late maturing variety with excellent taste and multiple disease resistance, so it can satisfy from farmers to consumers and be expected to play a role as a variety of premium rice brand in Chungnam province.

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***Corresponding Author:** Tel. 031-695-4028, E-mail: onlybio@korea.kr

PE-0050

Comprehensive wheat (*Triticum aestivum*) transformation efficiency via *Agrobacterium*-mediated using ‘Speed Breeding’

Geon Hee Lee[1], Tae Kyeum Kim[1], Ji Yoo Jung[1], Chang Hyun Choi[2], Song Yi Jeong[3], Jae Yoon Kim[1*]

[1]Department of Plant Resources, College of Industrial Science, Kongju National University, Yesan 32439, Republic of Korea
[2]National Institute of Crop Science, Rural Development Administration, Wanju 55365, Republic of Korea
[3]Chungnam Agricultural Research & Extension Service, Yesan, Chungnam 32418, Korea

Agrobacterium-mediated transformation is a good way to integrate transgenes into the host genome of plant as a single copy event. However, because the genome of wheat is extremely large and complex, the frequency of transformation occurred with a very low probability. Sequentially embryogenesis is one of most important factors in wheat transformation. In the previous study, we reported the successful possibility of immature embryogenesis culture method applied ‘Speed Breeding’. In order to generate transgenic wheat, calli were induced after co-cultivation with *Agrobacterium* and embryos in a medium supplemented with 100 μM or 200 μM of acetosyringone, respectively, and the survival rates of calli against G418 antibiotic were investigated. In addition, the ability to generate fertile plants was confirmed by culturing the inoculated embryos with *Agrobacterium* in a medium without antibiotics. Then, the transgene integration was confirmed by PCR screening for calli and one regenerated callus that had been selected for 5 weeks by G418 antibiotics. Therefore, several putative transgenic calli against G418 were observed in 200 μM acetosyringone, and the calli inoculated with *Agrobacterium* were regenerated into fertile plants in the medium without antibiotics. Finally, PCR screenings were confirmed that the transgene was integrated with a 1.52% probability, and the backbone was not detected in the regenerated in callus. This study can be useful information in the development of the wheat transformation system.

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***Corresponding Author:** Tel. 041-330-1203, E-mail: jaeyoonkim@kongju.ac.kr

PE-0051

Expression Regulation of Voltage-Dependent Anion Channels (*VDACs*) under Phytohormone Treatment during Germination in Monocot Plants

Tae Kyeom Kim[1], Geon Hee Lee[1], Chae Sun Na[2], Jae Yoon Kim[1*]

[1]Department of Plant Resources, Kongju National University, Yesan, Chungnam, Republic of Korea
[2]Division of wild plant seeds research, Department of Wild Plants and Seeds Conservation, Baekdudaegan National Arboretum, Bonghwa, Gyeongbuk, Republic of Korea

Voltage-Dependent Anion Channels are membrane transporter proteins that exist in the outer mitochondrial membrane. In a previous study, we identified the *TaVDAC* that is down-regulated during pre-harvest germination (PHS) in wheat spikes and generated Cas9-mediated *vdac* mutant lines with monocot model plant *Brachypodium distachyon*, which were inhibited germination and were changed gibberellic acid (GA) biosynthesis gene expression. In this study, function analyses were performed to figure out the expression regulation between *VDAC* and GA using *vdac* mutant lines of model plant and barley. It was confirmed that the *vdac* mutant lines identified as the *BdVDAC* mutant showed resistance to PHS and longer growth period than WT. The expression of genes that regulate the biosynthesis and signaling of representative plant growth hormones was significantly different compared to WT. As a result of measuring the endogenous GA content in dry seeds of mutant lines, the active GA decreased and the inactive GA increased in the dry seeds of mutant lines compared to WT. Additionally, *HvVDAC* expressions were observed gradually increase during imbibition and germination in barley seeds under hormone treatment, and then rapidly decreased after germination, and mainly expressed in root and shoot. The expression of the transcription factor gene *GAMYB*, which activates α-amylase expression in the seed imbibition mechanism, increased rapidly during imbibition treatment and gradually decreased during germination. Moreover, the *SLN1* gene, which inhibits GA signaling, was similar to the expression pattern of *HvVDAC*. These results suggest that *VDAC* affects endogenous GA content and plays an important role in seed germination.

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***Corresponding Author:** Tel. 041-330-1203, E-mail: jaeyoonkim@kongju.ac.kr

PE-0052

Phenotypic and Comparative Transcriptome Analysis of Weedy and Cultivar Soybean Related to Growth Trait Obtained from Crossing of *G. max* and *G. soja*

Prakash Basnet, Neha Samir Roy, Tae Young Um, Ik Young Choi*

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

The cultivated soybean (*Glycine max* L. mer) is domesticated from a wild soybean (*Glycine soja*), nevertheless, these plants exhibit morphological differences. Molecular advancement and genomic tools has enabled scientist to pinpoint specific genes that are responsible for morphological differences that distinguish crop relatives. Although comprehensive study of morphology in soybean plants is still limited. To understand the molecular mechanism of the genes concern to morphological differences and expression levels we applied the transcripomes between weedy and cultivar soybean obtained from crossing of wild and domesticated soybean. A total of 12513, 14255 and 11850 differentially expressed genes (DEGs) were identified in leaf, stem and node from weedy and cultivar soybean. Especially, stem was found the most distinct feature which makes plant morphologically different. In the results, we found plant phytohormones plays a significant role for phenotype differentiation. Gene expression pattern showed that 22 genes response to major phytohormones gibberellin, auxin and cytokinin were identified and validated through RT-qPCR. The results obtained provides preliminary evidence of the genes concern to plant hormones which makes morphological difference in weedy and cultivar.

Keywords: Weedy, cultivar, growth type, transcriptome, differentially expressed genes

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

PE-0053

육질이 부드럽고 식미가 우수한 고구마 ‘소담미’

이형운[1*], 정미남[1], 고산[1], 남상식[2], 김재명[1], 유경단[1], 한선경[2], 양정욱[2], 노재환[1], 이임빈[1], 문진영[3], 강영식[4], 조수현[5], 이재웅[6], 최규환[7]

[1]전남 무안군 무안로 199 국립식량과학원 바이오에너지작물연구소
[2]전북 완주군 이서면 혁신로 181 농촌진흥청 국립식량과학원
[3]경상남도 진주시 대신로 570 경상남도농업기술원
[4]충청남도 예산군 신암면 추사로 167 충청남도농업기술원
[5]강원도 강릉시 사천면 중앙서로 216 강원도농업기술원 감자연구소
[6]충청북도 청주시 청원구 오창읍 가곡길 46 충청북도농업기술원
[7]전북 익산시 서동로 413 전라북도농업기술원

최근 들어 고구마는 참살이 식품이라는 인식이 확대되면서 소비가 꾸준히 이루어지고 있고, 재배면적도 최근 5년간(’16~’20) 22천 ha 수준을 유지하고 있다. 2019년 기준 국내 고구마 농업생산액은 6,375억 원으로 식량작물 중에서 벼 다음 두 번째로 높고 단위면적당 농가 소득은 1,446천원으로 식량작물 중에서 가장 높다. 국내 소비자는 단맛이 강하고 육질이 부드러운 고구마를 선호하며 고구마 재배농가 및 유통업자는 시장가격이 높은 시기까지 장기간 저장하면서 출하할 수 있는 저장성이 좋은 품종을 선호한다. ‘소담미(Sodammi)’는 찐고구마 육질이 부드럽고 식미, 저장성이 우수한 ‘호감미’(IT327288)를 모본으로 하고 외관상품성이 우수한 ‘규슈121’(IT309496)을 부본으로 하여 2020년에 육성되었다. ‘소담미’는 괴근 껍질색이 자줏빛빨강색, 육색은 농황색이며 괴근 모양은 방추형이다. 고구마 주요 병해충인 덩굴쪼김병과 고구마뿌리혹선충에 중도저항성이다. 찐고구마 육질이 약점질로 부드럽고 찐고구마의 감미도가 19.1로 진홍미(15.3), 베니하루까(16.6)보다 단맛이 강하고, 찐고구마 식미는 1.7로 진홍미(0)와 베니하루까(1.3)보다 우수하다. ‘소담미’는 보통기 120일 재배시 주당상품괴근수는 2.6 개/주, 상품괴근평균중은 136 g, 상품괴근수량은 19.7 MT/ha이었으며. 150일 재배시 상품괴근수량은 24.4 MT/ha이었다. ‘소담미’는 9개월 이상 장기간 저장을 해도 괴근의 부패와 내부 공동화 발생이 거의 없어 연중 출하가 가능하여 저장하면서 가격이 높게 형성되는 시기에 출하할 수 있다. ‘소담미’는 소비자, 생산자, 유통업자가 선호하는 특성을 두루 갖추고 있어 국내 품종의 점유율이 확대되는 데 기여할 것으로 기대된다(품종출원 번호: 출원-2021-72, 2021.2.18.).

***교신저자:** Tel. 061-450-0141, E-mail: leehu79@korea.kr

PE-0054

Fine mapping of a rice fissure QTL on chromosome 11 using Saeilmi × Nampyeong backcross population

So-Myeong Lee, Dong-Soo Park, Young-Ho Kwon, Dongjin Shin, Jin-Kyung Cha, Jong-Hee Lee*, Jong-Min Ko

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

Rice is a major food crop in South Korea and the importance of quality of eating rice is growing under the climate change caused by global warming. One of the main reasons of rice fissure is high temperature stress in filling stage, and rice fissure affects head rice yield and eating quality. In this study, 899 F_2 and 640 BC_1F_2 Saeilmi×Nampyeong plants were used to analyze genotype and phenotype. DNA samples were extracted by CTAB method and genotyped by KASP SNP assay. Ratio of rice fissure of milled rice was measured by RN600 (Kett, Japan). In F_2 population, 92 plants were selected to analyze QTL sorting by the ratio of rice fissure. Among the 92 plants, 46 plants had the highest rice fissure ratio and another 46 plants had the lowest rice fissure ratio. 112 KASP SNP markers were used to genotype the selected 92 F_2 plants. QTL analysis program was ICIMapping version 4.1.0.0. In F_2 population, rice fissure QTL *qFIS9* and *qFIS11* were found on chromosome 9 and 11. Both QTLs have fissure-reducing effect when the allele is Nampyeong allele. In BC_1F_2 population which has segregation region including *qFIS11*, QTL analysis was processed same as F_2 population using genotyping data of 4 KASP SNP markers. As a result, *qFIS11* was narrowed down to 0.92Mbp region. Further genetic analysis to identify causal genes of rice fissure will be an asset to heat-tolerant rice breeding program.

***Corresponding Author:** Tel. 055-350-1168, E-mail: ccriljh@korea.kr

PE-0055

Biosynthetic Pathways of Proanthocyanidins in Major Cash Crops

Insu Lim, Jungmin Ha*

Department of Plant Science, Gangneung-Wonju National University, Gangneung, Korea

Proanthocyanidins (PAs) are a group of oligo- or polymers that are composed of monomeric flavanols. They are widely found in the plant kingdom and have many benefits for human fitness such as anticancer, anti-inflammatory, and antioxidant activities. To date, three types of PAs have been observed in nature: procyanidin, propelargonidin, and prodelphinidin. They are synthesized as one of the end products in the flavonoids pathway by different consecutive enzymic activities from same precursor, naringenin. Although the general biosynthetic pathways of PAs have been reported in a few model plant species, little is known for the species-specific pathways in major crops containing different types of PAs. Here, we identified the species-specific pathways in ten major crops based on the presence/absence of the flavanol-based intermediates in the metabolic pathway, and found 202 orthologous genes in the reference genomic database of each species, which may encode key enzymes involved in the biosynthetic pathways of PAs. Among 202 genes, 22 (Flavonoids 3'hydroxylase) and 53 (flavonoids 3',5'hydroxylase) orthologs are responsible to synthesize procyanidin and prodelphinidin from naringenin, respectively. The enzymatic competitions among leucoanthocyanidin reductase (31 orthologs), anthocyanidin synthesizes (26 orthologs) and anthocyanidin reductase (14 orthologs) determine whether leucoanthocyanidins are synthesized into PAs or anthocyanins. These enzymatic parallel pathways are responsible for the ratio not only between PAs and anthocyanins, but also among three types of PAs. Our study suggests a promising strategy in molecular breeding to regulate the contents of PAs and anthocyanins and to improve the nutritional quality of food sources globally.

***Corresponding Author:** Tel. 033-640-2352, E-mail: limis1014@gmail.com

PE-0056

Identification of QTLs for rice grain size in populations derived from the Large Grain Line

Jeonghwan Seo[1,2], Ja-Hong Lee[1,3], San Mar Lar[1], Junhee Hong[1,2], Soon-Wook Kwon[1,2*]

[1]Department of Plant Bioscience, College of Natural Resources and Life Science, Pusan National University, Miryang 50463, Korea
[2]Life and Industry Convergence Research Institute, Pusan National University, Miryang 50463, Korea
[3]SEEDPIA INC., Suwon 16395, Korea

Grain size affects rice yield and quality. The Large Grain Line (LGL), showing large grain size and a *japonica*-like genome, was selected in the breeding field. A total of 94 F_2 plants derived from a cross between LGL and Hanareum (a high-yielding Tongil-type variety) were used for the quantitative trait loci (QTL) analysis of grain length (GL), grain width (GW), and grain thickness (GT). A linkage map of the F_2 population covering 1,312 cM for all 12 chromosomes was constructed using 123 Fluidigm *indica-japonica* SNP markers. A total of nine QTLs for three traits were detected on chromosomes 2, 3, 4, 6, and 7. Two QTLs for GL on chromosomes 2 and 6 explained 17.3% and 16.2% of the phenotypic variation, respectively. Two QTLs were identified for GW on chromosomes 2 and 3 and explained 24.3% and 23.5% of the phenotypic variation, respectively. Five QTLs for GT detected on chromosomes 2, 3, 5, 6 and 7, explained 13.2%, 14.5%, 16.6%, 10.9%, and 10.2% of the phenotypic variation, respectively. A novel QTL for GT, *qGT2*, was validated on the same region of chromosome 2 in the selected F_3 population. The LGL and QTLs related to grain size identified in this study could be applied in a breeding program developing large grain rice. A novel genetic locus for GT detected and validated in this study lays the foundation for further fine mapping and positional cloning to discover the mechanism of grain size regulation.

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***Corresponding Author:** Tel. +82-55-350-5506, E-mail: swkwon@pusan.ac.kr

PE-0057

Effects of chilling acclimation on wheat (*Triticum aestivum* L.) with different seed coat colors

Paulina Calderon Flores[1], Jin Seok Yoon[1], Dae Yeon Kim[2], Yong Weon Seo[1]*

[1]Department of Plant Biotechnology, Korea University, Seoul 02841, Korea
[2]Department of Biotechnology, Korea University, Seoul 02841, Korea

Flavonoids can protect plants against extreme temperatures and ROS due to their antioxidant activities. $F_{2:3}$ seeds were grouped in 3 by seed coat color and germinated under chilling (4°C) and non-acclimated conditions (18°C) for a week, followed by normal conditions (18°C) for three weeks and a subsequent chilling stress (4°C) induction. We analyzed mean daily germination in each group. Additionally, to study the acclimation in relationship to the different seed coat colors on the germination ability and seedling performances under the cold temperatures, chlorophyll content, ROS scavenging enzymes, and gene expression response was measured. Genetic analysis suggests a two-gene model for color segregation between yellow and purple seeds. In the germination study, unstressed environmental conditions induced the germination of light-colored seeds, while under chilling conditions darker seed coat colors had higher germination rate. Moreover, darker seed coat colors were highly responsive to chilling acclimation based on the ROS scavenging enzymes activity and gene expression of ROS scavenging enzymes, flavonoid biosynthetic pathway and cold responsive genes. Low temperature has a large impact on the yield of crops. Thus, understanding the benefit of seed coat color response to chilling stress and the identification of limiting factors are useful for developing breeding strategies in order to improve the yield of wheat under chilling stress.

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***Corresponding Author:** Tel. 02-3290-3005, E-mail: seoag@korea.ac.kr

PE-0058

Identification of U-box containing E3 Ubiquitin Ligases in related to abiotic stress response in wheat

Moon Seok Kim[1†], Jae Ho Kim[1†], Dae Yeon Kim[2], Yong Weon Seo[1,2*]

[1]Department of Plant Biotechnology, Korea University, Seoul 02841, Korea
[2]Department of Biotechnology, Korea University, Seoul 02841, Korea

U-box E3 ligase play various roles in proteasomal degradation by post-translational modification in variety of abiotic and biotic stress responses. However, the cellular mechanism of wheat U-box protein against abiotic stress has not been well studied. In this study, we isolated two genes *TaPUB2 (TraesCS5A02G198800) and TaPUB3 (TraesCS2B02G499300)* that are highly involved in metabolism of drought stress responses. These two genes were highly induced not only in drought stress but also in other abiotic stresses in wheat. Furthermore, both TaPUB2 and TaPUB3 exhibited ubiquitination activities and physically interact making hetero-dimeric complex. Our results implicated that the hetero dimeric form of TaPUB2/TaPUB3 could provide valuable information to elucidate the function for molecular mechanism in wheat.

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Corresponding Author: Tel. 02-3290-3005, E-mail: seoag@korea.ac.kr

PE-0059

염색체 변이 유발을 통한 보리 돌연변이 계통 육성 연구

한지윤[1], 강성욱[1], 전재범[2], 김양길[3], 윤영미[3], 조성우[1]*

[1]경남 진주시 동진로 33 경상국립대학교 스마트농산업학과
[2]전북 전주시 덕진구 농생명로 300 농촌진흥청 디지털농업추진단
[3]전북 완주군 이서면 혁신로 181 국립식량과학원 작물육종과

보리 돌연변이 계통 육성을 위하여 국내 보리 품종인 흰찰쌀보리에 제부라린을 침종 처리하였다. DNA메틸화 억제제인 제부라린은 염색체 절단에 의한 염색체 변이를 유발하여 돌연변이 유발원으로 사용하였다. 제부라린 농도는 1, 2.5, 5.0, 그리고 10.0 μM로 희석하여 이용하였으며, 충분한 흡수를 위하여 4℃, 암조건에서 침종 처리하였다. 침종 처리 결과, 10.0 μM에서 급격한 뿌리 신장의 억제가 확인되었으며, 염색체 절단에 의한 비정상적인 염색체도 뿌리분열세포에서 관찰되었다. 비정상적인 염색체는 다른 염색체에 비하여 짧은 염색체 길이를 보였으며, 염색체 절단이 유발되었음에도 동원체를 기준으로 단완(short arm)과 장완(long arm)으로 구분되는 것을 관찰하였다. 염색체 절단에 의한 염색체 길이의 변이는 장완과 단완에서 특정 비율의 형태를 가지고 있지 않았으며, 상대적으로 장완보다 단완의 형태적 변이가 다양하게 관찰되었다. 이러한 결과를 바탕으로 변이 유발 빈도를 높이기 위하여 200 μM의 제부라린을 침종한 종자의 배유 부분만을 이용하여 종실 저장 단백질 발현양상을 비교하였다. 단백질 발현양상을 비교하기 위하여 전기영동실험(sodium dodecyl sulfate-poly acrylamide gel electrophoresis)을 수행하였으며, 단백질 분리에는 12%의 분리겔을 사용하였다. 단백질 발현 양상을 비교한 결과, 41 kDa 부근의 단백질 발현양상이 대조구와 차이를 보였으며 18, 22, 그리고 70 kDa 부근의 단백질 발현 정도가 대조구에 비하여 과발현되는 것을 확인하였다. 표현형 비교 결과, 처리구는 주경이 고숙기임에도 불구하고 신아가 출현하는 특이한 형질을 보였으며, 이외에도 야생형(wild type)보다 수장이 짧고 간장이 단간인 표현형을 가진 처리구도 확인되었다. 이러한 특징을 정밀히 분석하기 위하여 이차원전기영동 및 질량분석을 통한 변이 단백질에 대한 동정 및 해석을 바탕으로 세대진전을 통한 고정 돌연변이 계통에 대한 표현형 관찰 및 유전형 분석이 필요할 것으로 생각한다.

***교신저자:** Tel. 055-772-3225, E-mail: chsw78@gnu.ac.kr

PE-0060

Proteomic analysis of seed proteins differentially expressed in high and low eating-quality rice

Jun Soo Kwak[1], Jong Tae Song[2], Hak Soo Seo[1,2*]

[1]Department of Agriculture, Forestry and Bioresources, Research Institute of Agriculture and Life Sciences, Seoul National University, Seoul 08826, Korea
[2]Department of Applied Biosciences, Kyungpook National University, Daegu 41566, Korea

Good eating quality of rice is important to attract consumers and it affects market value. Although the factors that determine this trait have been studied, the molecular mechanisms underlying eating quality remain largely unknown. Here, the high eating-quality rice cultivar Gopum and the low eating-quality cultivar Dobong were analyzed by comparative proteomics to identify the proteins related to eating quality. The results showed that protein disulfide isomerase like 1-1 (PDIL1-1) and cytochrome P450 accumulated in immature and mature seeds of Gopum, and five proteins including OsPrMC3, a rice homologue of *Pinus radiate* Male Cone 3, accumulated in immature and mature seeds of Dobong, indicating that PDIL1-1 and cytochrome P450 may function as positive regulators of eating quality. The transcript levels and expression patterns of *PDIL1-1* were the same in Gopum and Dobong cultivars during seed development, indicating that PDIL1-1 is more stable in Gopum. The highest *PDIL1-1* transcript levels were detected at 20 days after flowering (DAF) in both Gopum and Dobong, whereas protein levels were comparable between DAF 5 and 50. The expression patterns of the other four genes encoding cytochrome P450, 60S acidic ribosomal protein P0 (OsRPL0), rice pathogenesis-related 10 (OsPR10) and *chromatin assembly factor-1* (CAF1) family ribonuclease during seed development were also different from protein accumulation patterns. The present data indicate that the levels and stability of eating quality-related proteins can be modulated after translation, and that PDIL1-1 and cytochrome P450 may be involved in determining high eating quality in rice.

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

PE-0061

속잎이 잘 자라고, 잎 생산성이 뛰어난 잎들깨 품종 '새봄' 육성

김정인*, 이명희, 김상우, 김성업, 오은영, 김민영, 이정은, 조광수, 정찬식

경상남도 밀양시 점필재로 20 국립식량과학원 남부작물부 밭작물개발과

잎들깨는 신선잎채소로 이용하는 양이 증가하고 있으며, 경남 밀양과 충남 금산을 중심으로 하우스와 노지에서 약 1,000ha 재배되고 있다. 잎들깨는 채엽에 따른 노동력이 발생되는데 이를 완화하기 위하여 속잎이 잘 자라고, 상품잎의 크기가 16cm 이상 크지 않는 품종을 목표로 한다. 또한 잎모양이 둥근심장형으로 둥글고 잎뒷면 보라색의 발현이 좋으며, 잎 생산성이 우수한 품종개발이 필요하다. 이에 2011년 잎모양이 둥근심장형으로 유망한 YPL54-2B-36-1-1-1-2-2계통을 모본으로, 잎크기가 작고 두꺼운 YPL83-2B-5-2-5를 부본으로 교배한 후 계통육종법을 통해 세대를 진전시켰고, 육종목표에 부합하는 '밀양83호'를 선발하여 3년간(2018~2020년) 생산력 검정시험을 거쳐 잎들깨 품종 '새봄'을 육성하였다. '새봄'은 잎모양이 둥근심장형이고 최대엽장이 13.1cm로 작고 잎뒷면 자주색이 진하여 상품성이 높다. 속잎이 잘자라서(속잎비율 55.8%) 잎 수확 후 재생에 유리하다. 엽수량성에서 '남천들깨' 대비 엽무게(5,634kg/10a)와 엽수(4,536천매/10a)가 각각 10%, 8% 증수하였다. 또한 채엽 후 10일간 냉장(4℃) 저장 후 저장성을 측정한 결과 '새봄'의 신선도가 높게 나타나 저장성이 우수하였다. 이렇게 채엽 효율이 높은 품종 개발을 통하여 노동력 절감에 기여하고 농가 생산성이 향상될 것으로 기대된다.

***교신저자:** Tel. 055-350-1228, E-mail: kji1204@korea.kr

PE-0062

Mapping of QTLs for rice mineral element content in introgression line population from an interspecific cross

Cheryl Adeva[1], Yeo-Tae Yun[2], Hyun-Sook Lee[3], Kyu-Chan Shim[1], Ngoc Ha Luong[1], Sang-Nag Ahn[1*]

[1]Department of Agronomy, Chungnam National University, Daejeon 34134, Republic of Korea
[2]Chungcheongnamdo Agricultural Research and Extension Services, Yesan, 340-861, Republic of Korea
[3]Crop Breeding Division, National Institute of Crop Science, Rural Development Administration, Wanju, 55365, Republic of Korea

Wild rice germplasm is an essential gene pool for rice cultivar improvement. Mineral elements in brown rice play a significant role in human health. In this study, 96 introgression lines (ILs) derived from a cross between the Korean elite *O. sativa japonica* cultivar 'Hwaseong' and *O. rufipogon* (IRGC 105491) was used to identify quantitative trait loci (QTLs) associated with rice mineral elements. The population was grown in two years in two locations with the contents of iron (Fe), zinc (Zn), manganese (Mn), and calcium (Ca) in brown rice measured in both trials. Significant phenotypic correlations were observed between Fe and Zn and between Mn and Ca across years and locations. A total of seven QTLs were identified for the four mineral elements on chromosomes 6, 7, 8, and 10 by single marker analysis using one-way analysis of variance including two for Fe content, two for Zn content, two for Mn content, and one for Ca content. Most of the QTLs had the enhancing allele derived from *O. rufipogon.* The QTLs identified on chromosome 10 largely influenced the mineral elements in ILs. Possibly, the QTLs of different mineral elements located on the same chromosome explained the significant phenotypic correlations across years and locations. High value alleles from *O. rufipogon* showed advantageous effects for mineral elements signifying that wild rice germplasm is a valuable donor to enhance the nutritional quality in rice.

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

PE-0063

열대적응성이 도입되고 '오대' 쌀 입형을 키운 '철원105호' 특성

원용재[1*], 안억근[2], 정국현[2], 현웅조[2], 이윤승[2], 김정주[3], 이진범[1], 박향미[2]

[1]강원도 철원군 동송읍 태봉로 2346, 국립식량과학원 철원출장소
[2]경기도 수원시 권선구 수인로 125, 국립식량과학원 중부작물과
[3]강원도 춘천시 충열로 251, 국립식량과학원 춘천출장소

최근 지구온난화와 기후변화가 작물 생산성 및 품질에 영향을 끼쳐 재배안정성이 더욱 중요한 특성으로 부각되고 있다. 중북부 및 중산간지에서 재배되는 조생 벼 품종인 '오대'는 쌀알이 굵어 재배안정성이 양호한 품종이지만 최근 등숙기 고온장애와 장기간 장마에 도열병 발병 및 등숙 불량으로 쌀에 심복백 발생이 심하여 수량 및 품질 저하가 문제가 되었다. 본 연구는 '오대'에 열대적응성을 도입하고 쌀 입형을 키운 '철원105호'를 육성하여 그 특성을 밝히고자 하였다. '철원105호'는 '오대'를 모본, 조생이면서 열대지역 적응성 중립 'MS11'을 부본으로 교배하고 '오대'로 여교배하여 중대립이면서 잎내병성, 내수발아성 등 재배안전성이 높고 심복백이 감소된 고품질 계통이다. '철원105호'의 출수기는 7월 28일로 '오대'와 같다. 간장은 77㎝로 '오대'보다 약 5㎝ 크고, 현미천립중은 28.5g으로 약 3g 무겁다. 쌀 수량성은 568kg/10a 로 '오대'보다 9% 증수되었다. 키가 크지만 쓰러짐에 강하고 도열병, 흰잎마름병에 강하며, 수발아는 10.3%로 중강 정도의 반응을 보였다. 쌀알 외관이 깨끗하고 단백질함량이 낮으며 윤기치는 '오대'와 비슷하다. '철원105호'는 밥 냄새와 밥맛이 '오대'와 비슷하여 향후 쌀 입형이 더 크고 재배안정성이 개선되어 '오대' 대체 품종으로 활용이 가능할 것으로 기대된다.

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***교신저자:** Tel. 033-455-2031, E-mail: yjwon@korea.kr

PE-0064

준조생 복합내병성 고품질 벼 '철원106호' 특성

원용재[1*], 안억근[2], 정국현[2], 현웅조[2], 이윤승[2], 김정주[3], 이진범[1], 박향미[2]

[1]강원도 철원군 동송읍 태봉로 2346, 국립식량과학원 철원출장소
[2]경기도 수원시 권선구 수인로 125, 국립식량과학원 중부작물과
[3]강원도 춘천시 충열로 251, 국립식량과학원 춘천출장소

최근 기온 상승으로 인하여 조생종 벼 재배지역에서는 조기재배를 시도하는데 등숙기 고온에 의하여 등숙이 불량하고 품질이 저하되어 상품성 하락의 위험이 있다. 이를 해결하기 위하여 벼 출수기를 다양화하여 지역별 수확시기를 다변화한 맞춤형 품종 개발이 필요하다. 또한 조기재배를 하여도 출수기를 늦춘 준조생 품종은 등숙기 고온에 노출되는 기간을 줄여 생산성 및 품질에 영향을 적게 받을 수 있을 것이다. 본 연구는 중북부 중간지 및 중산간지 재배에 적응하고 복합내병성을 갖추었으며 출수기를 늦춘 준조생 고품질 '철원106호'를 육성하여 그 특성을 밝히고자 수행하였다. '철원106호'는 중생종 '수원527호'를 모본, 중생이면서 흰잎마름병, 줄무늬잎마름병에 저항성이면서 밥맛이 양호한 '해오르미'를 부본으로 교배하여 준조생이면서 복합내병성, 내수발아성 등 재배안전성을 갖추고 밥맛이 우수한 고품질 계통이다. '철원106호'의 출수기는 8월 4일로 '오대'보다 7일 늦다. 간장은 75㎝로 '오대'보다 약 3㎝ 크고, 현미천립중은 22.1g으로 약 3g 가볍다. 쌀 수량성은 562㎏/10a로 '오대'보다 8% 증수되었다. 키가 크지만 쓰러짐에 강하고 도열병, 흰잎마름병, 줄무늬잎마름병에 강하며, 수발아는 8.4%로 중강 정도의 반응을 보였다. 쌀알 외관이 깨끗하고 단백질함량이 낮으며 윤기치는 '오대'보다 높 다. '철원106호'는 밥맛이 '오대'보다 우수하여 향후 조생종 재배 지역에서 출수기를 다변화하여 조기재배에서 고품질 쌀 생산이 가능한 품종으로 활용이 가능할 것으로 기대된다.

사사: 본 연구는 농촌진흥청 연구사업(세부과제명: 중북부지역 중간지 적응 수요자 참여형 조숙 고품질 벼 품종개발, 세부과제번호: PJ01315007)의 지원에 의해 이루어진 결과임.

***교신저자:** Tel. 033-455-2031, E-mail: yjwon@korea.kr

PE-0065

국내 육종 밀 품종별 항산화 활성 및 세포 보호효과

성은정[1], 이민아[1], 임진영[1], 허희진[1], 김경훈[2], 이준수[1]*

[1]충청북도 청주시 서원구 충대로 1 충북대학교 식품생명공학과
[2]전라북도 완주군 이서면 혁신로 181 국립식량과학원 밀연구팀

밀(*Triticum aestivum* L.)은 전세계적으로 많이 소비되고 있는 곡물이며 phenolic compounds, carotenoids, tocopherols과 같은 pytochemical들이 많이 함유되어 있어 항산화 활성 및 생리활성을 가지고 있다고 알려져 있다. 그러나 다양한 밀 품종별 항산화 활성과 세포보호활성에 대한 연구는 미비한 실정이다. 본 연구에서는 국내에서 육종된 41개의 밀 품종별 항산화 활성 및 세포 보호효과를 비교해보고자 하였다. 항산화 활성은 총 폴리페놀 함량, DPPH, ABTS 라디칼 소거능을 통해 측정하였으며 세포 보호효과는 간세포(HepG2), 근육세포(C2C12), 혈관내피세포(EA.hy926)를 사용하여 측정하였다. 상대적 항산화능 지수(Relative antioxidant capacity index, RACI)에서는 '다중' 품종이 5.12로 가장 높았으며 '탑동' 품종이 -5.89로 가장 낮은 지수를 나타냈다. 간세포에서의 세포 보호효과는 DPPH, ABTS 라디칼 소거능과 유의적인 상관관계를 보였다. 주성분 분석에서는 principal component(PC)1과 PC2가 성분이 전체 변동성의 53.48%를 나타냈다. 측정변수에 기반한 계층적 군집 분석을 통해 41가지 밀 추출물은 3개의 그룹으로 분류할 수 있었다. A그룹은 혈관내피세포에서의 보호효과가 다른 그룹에 비해 우수하였다. C그룹에는 RACI값이 높았던 '다중' 품종이 속해있으며, C그룹은 항산화활성 및 간세포 보호효과가 우수하였다. 본 연구는 국내에서 육종된 밀 품종간의 항산화 활성 및 세포 보호효과에 대한 정보를 제공한다. 이러한 결과는 41가지 국내 밀 품종의 항산화 활성과 세포 보호효과 비교를 통해 기능성 식량작물과 새로운 식재료로서 가치가 있는 밀 품종 개발에 대한 기초자료로 사용될 것으로 기대된다.

***교신저자:** Tel. 043-261-2566, E-mail: junsoo@chungbuk.ac.kr

PE-0066

Analysis of population structure and genetic diversity of traditional rice (*Oryza sativa* L.) varieties in North of Vietnam

Ngoc Ha Luong[1], Hung Linh Le[2], Kyu-Chan Shim[1], Cheryl Adeva[1], Sang-Nag Ahn[1*]

[1]Department of Agronomy, College of Agriculture and Life Sciences, Chungnam National University, Daejeon 34134, Korea
[2]Agricultural Genetics Institute, Tu Liem, Hanoi, Vietnam

In this study, the genetic diversity and population structure of 98 rice accessions were evaluated by using 45 DNA markers including 25 simple sequence repeat (SSR), 10 INDEL, and 10 Kompetitive Allele-Specific PCR (KASP) markers. A total of 150 alleles with mean values of 0.681 (major allele frequency) and 0.432 (gene diversity) were detected. With SSR markers, the number of alleles ranged from 2 to 13, with an average of 4.4. Average polymorphism information content for all markers was 0.382, with the lowest being 0.108 and the highest 0.868. Population structure analysis classified 98 rice accessions into two main subgroups having consistent results with clustering method of neighbor joining tree and principal component analysis. Analysis of the molecular variance (AMOVA) results revealed 14% variance among populations, and 86% variance within populations. The combined phenotype and genotype data of this population revealed the association of an InDel marker (DEL-LABA1) with LABA1 gene located on chromosome 4 which is responsible for awn length development. In addition, one InDel marker (Pi9) where found to be linked with Hd1 on chromosome 6, which is involved in heading date. Another InDel marker (Glu-23) on chromosome 6 was identified to be associated with Waxy gene, which controls amylose synthesis in rice. These results suggest that genetic diversity of the Vietnamese accessions can be utilized to exploit the natural genetic variation existing in this population which can be applied in future breeding programs and molecular approaches.

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

PE-0067

Optimization of plant growth enhance fruit harvest and yield traits in Micro-Tom

Hong Kwan Beak[1*], Seung Han Son[1], Sujeevan Rajendran[1], Jung Heo[1], Jong Hyang Bae[2], Soon Ju Park[1]

[1]Division of Biological Sciences and Institute for Basic Science, Wonkwang University, Iksan 54538, Republic of Korea

[2]Department of horticulture industry, Wonkwang University, Iksan 54538, Korea

Plant size is an important factor which determines the biomass and yield performance. Micro-Tom had been bred as a compact tomato cultivar to growing in a limted space at the building or greenhouse due to its compact nature and short flowering span. To optimize the plant size of the micro-Tom, identifying mutants that can modify plant size and improving yield is an advanced process for modern breeding practices. In this study, a mutant from TOMATOMA under Micro-Tom background, TOMJPG2385-1 which has an increased plant size and yield will be characterized and explored for potentials in modern plant breeding techniques. Phenotypic examination revealed that is mutant comprises of higher vegetative and reproductive organs such as inflorescence number, fruit size, fruit number, thus total yield and some architectural traits such as plant height, Plant weight, axillary branch number and length and leaf size. RNA seq was performed for genotyping of mutants. Luckily, RNA seq data provided evidence of a large deletion in chromosome 2. The interval contained genes such as XTH8, GA2OX7 and HSPs. GA2OX7 was choosen as a candidate and CR-GA2OX7 plants were able to reproduce the mutant. However, CR-GA2OX7 plants shoed similar BRIX values where the mutant did not. WGS approach was used to identify the deletions precisely and a sum of 120.6Kb deletion was found in chromosome 2. Introgression lines of the mutant under M82 also showed increased vegetative parameters. Further studies are in progress for the identification of potential field and green house applications of this newfound mutant.

Keywords: TOMATOMA, GA2OX7, Yield, Inflorescence number, Plant architecture

***Corresponding Author:** Tel. 063-850-6096, E-mail: sjpark75@wku.ac.kr

PE-0068

Identification of albino mutant triggered by transplanting derived from an interspecific cross in rice

Kyu-Chan Shim[1], Luong Ngoc Ha[1], Adeva Cheryl[1], Hyun-Sook Lee[2], Yun-A Jeon[1], SunHa Kim[1], Sang-Nag Ahn[1*]

[1]Department of Agronomy, College of Agriculture and Life Sciences, Chungnam National University, Daejeon 34134, Republic of Korea
[2]Crop Breeding Division, National Institute of Crop Science, Rural Development Administration, Wanju 55365, Republic of Korea

Albino mutants are valuable resource for genetic study of chlorophyll biosynthesis and chloroplast development. In this study, we found albino plants which showed the albino after transplanting in the F_2 population derived from an interspecific cross between Hwaseong and CR5028 (introgression line which harbor *O. grandiglumis* chromosome segments in the Hwaseong genetic background). A total of 10 albino F_2 plants were detected from 440 F_2 plants at two weeks after transplanting and additional four albino F_2 plants were found from remained plants for transplanting. This phenotype was not observed in the Hwaseong and CR5028, and observed albino frequency indicated that more than two loci might be responsible for albinism. To know the loci which are controlling albino phenotype, 14 albino plants were genotyped using polymorphic KASP and InDel markers. At locus on chromosome 11, 14 albino plants showed *O. grandiglumis* allele genotype and we named this locus as *qALB11*. For fine-mapping of *qALB11*, we screened F_3 population. Three lines which showed albino phenotype after transplanting were detected and albino phenotype was co-segregated with *qALB11* genotype. Using these three lines, *qALB11* locus was narrowed down to 1-Mb. Previously, transplanting shock mutant which showed albino phenotype after transplanting was reported on chromosome 11. The gene (LOC_Os11g29850) controlling this phenotype was encoded a chloroplast-located noncanonical ABC protein and this gene was located in *qALB11*. To know the transplanting shock gene (LOC_Os11g29850) is responsible for our mutant, further studies are underway. Identifying other loci causing albino phenotype are being examined using QTL-seq method.

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

PE-0069

Natural variation of *APX9* gene controls yield-related QTL cluster in rice

Yun-A Jeon[1], Hyun-Sook Lee[2], SunHa Kim[1], Kyu-Chan Shim[1], Sang-Nag Ahn[1*]

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

[2]Crop Breeding Division, National Institute of Crop Science, Rural Development Administration, Wanju 55365, Republic of Korea

Previously, quantitative trait loci (QTL) for grain weight was identified using a near-isogenic line (NIL) derived from an interspecific cross between *Oryza sativa* (*cv.*Hwaseong) and *O. rufipogon*. Map-based cloning and transgenic approaches indicated that *L-ascorbate peroxidase 4* (*APX9*) gene is responsible for this QTL. In addition, this gene controls drought stress and antioxidant activity, and *O. rufipogon* allele increased drought tolerance and antioxidant activity in Hwaseong genetic background. Sequence analysis of *APX9* gene revealed that 3-bp Insertion and deletion (InDel) detected in the 4th exon clearly differentiates *japonica* (Hwaseong) and *O. rufipogon* alleles. *Indica* rice accessions have both alleles, indicating that *APX9* of *japonica* allele might introgress into *indica* group followed by crossing. These results indicated that the 3-bp insertion in *japonica* group was specifically selected during the domestication of rice and *APX9* act as a major regulator of plant development controlling important agronomic traits in rice.

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

PE-0070

Expression pattern of flowering regulators in Hwaseong and near-isogenic line derived from an interspecific cross between Hwaseong and *O. rufipogon*

Yun-A Jeon[1], Hyun-Sook Lee[2], SunHa Kim[1], Kyu-Chan Shim[1], Sang-Nag Ahn[1*]

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

[2]Crop Breeding Division, National Institute of Crop Science, Rural Development Administration, Wanju 55365, Republic of Korea

Flowering time (called as heading date in rice) is one of the important agronomic traits that largely affect the rice yield. In our study, we developed near-isogenic line (NIL) which harbors 25.5-kb region of *O. rufipogon* chromosome segment in Hwaseong (*japonica*) genetic background. This NIL showed 6 days of delayed flowering time than Hwaseong in the natural long-day field condition. In addition, we examined the flowering time under short-day (12/12h, light/dark) and long-day (14/10h, light/dark) conditions. No difference was observed between Hwaseong and NIL under short-day condition, while NIL plants showed delayed flowering under long-day condition. To understand the mechanism of delayed flowering time in NIL, we examined the expression levels for flowering time regulators under short-day, long-day, and natural long-day conditions. Gene expression analysis indicated that variation of flowering time might be associated with *Ehd1* pathway. To know the gene responsible for controlling flowering time in 25.5-kb region, further study is underway.

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

PE-0071

재배시기에 따른 저아밀로스 벼 ‘미호’ 품질 특성 평가

강주원*, 이지윤, 조수민, 이종희, 박동수, 송유천, 고종민, 조준현

경상남도 밀양시 점필재로20, 국립식량과학원 남부작물부 논이용작물과

최근 밥쌀에 대한 소비자 기호의 다양화 및 가경간편식 가공밥 소비 증가로 저아밀로스 쌀에 대한 수요가 증가하면서 ‘미호’ 재배면적이 크게 늘어나고 있다. ‘미호’는 아밀로스 함량 11.2%의 저아밀로스 품종으로, 밥을 지은 후 시간이 지나도 찰기와 밥알 물성, 윤기 등 밥알 고유의 특성이 잘 유지되는 특성이 있다. 그러나 ‘미호’의 늦은 출수특성으로 농가에서 조기재배가 늘어나면서 재배시기에 따른 품질특성 구명이 필요하였다. 이에 ‘미호’의 이앙시기별 품질 차이를 규명하기 위해 조기(5월10일) 보통기(6월 5일) 이모작(6월20일) 등 3시기별로 이앙을 하고 농업형질과 품질특성을 조사하였다. 간장과 수장은 조기 및 보통기에 비해 이모작에서 약간 큰 경향이었으며 정현비율 역시 같은 경향을 보였다. 쌀수량은 조기재배시 보통기와 이모작에 비해 5~13% 증가하는 경향을 보였으나 등숙률은 낮았다. 천립중은 조기재배에 비해 보통기 및 이모작에서 더 무거운 경향을 보였다.

특히 ‘미호’의 재배시기에 따른 품질분석 결과 조기재배에 비해 보통기 및 이모작 재배에서 윤기와 밥맛이 양호 하였다. 백미 색도는 재배시기별 유의한 차이를 보이지 않았다. 취사 특성에서 보통기 및 이모작 재배에 비해 조기재배의 경우 밥의 윤기치가 크게 낮아지고 밥알이 황화 되면서 색깔이 불량하였다. 밥맛 관능평가에서 색깔, 밥맛 등 대부분의 항목에서 조기재배가 보통기 및 이모작에 비해 낮은 점수를 얻었다.

따라서 중만생 품종인 ‘미호’의 출수기를 앞당기고자 조기재배를 하게 되면 쌀수량은 높아지지만 품질이 낮은 쌀이 생산되므로 ‘미호’는 보통기 및 이모작기 재배가 적합하였다.

***교신저자:** Tel. 055-350-1156, E-mail: kangjw81@korea.kr

PE-0072

수발아 저항성 기능성 적미 ‘적진주2호(밀양310호)’

강주원*, 이지윤, 조수민, 이종희, 송유천, 박동수, 고종민, 조준현

경상남도 밀양시 점필재로20, 국립식량과학원 남부작물부 논이용작물과

적미는 흑미가 가지고 있는 기능성 물질인 안토시아닌과 달리 폴리페놀 등의 다양한 기능성물질을 함유하고 있으나, 일반적으로 등숙기 강우에 의한 수발아가 잘 되는 약점이 있다. 따라서 수발아에 저항성인 기능성 적미를 개발하고자, 2005년 하계에 고기능성 적미 ‘홍진주(수원501)’를 모본으로 하고 수발아저항성 및 단간, 다얼인 도입 유전자원 ‘620209’를 부본으로 하여 인공교배를 실시하였다. 이후 ’06/‘07 동계에 F_1 양성, 2007년 F_2, 2008년 F_3 계통을 전개하였다. 이후 2010년 까지 계통육종법에 따라 세대를 진전시켜 2010년 YR26815-1-3-3계통을 최종 선발하고, 2013~2015년 3개년간 지역적응성시험을 거쳐 ‘적진주2호’ 품종명이 부여되었다.

‘적진주2호’의 주요 농업적 특성에서 출수기는 8월13일인 중만생종이며, 간장은 68㎝로 대비품종인 ‘적진주’보다 작아 내도복성이며, 저온발아성은 65.3%로 적진주보다 높고, 내냉성 검정 결과 냉수고 출수지연일수는 ‘적진주’에 비해 11일 짧았고, 임실률과 등숙기 내냉성은 ‘적진주’보다 강했으며, 불시출수는 발생되지 않았다.

‘적진주2호’는 항산화 성분인 폴리페놀 함량이 163.7㎍/㎎으로 기존 ‘적진주’의 89.6㎍/㎎ 보다 약 1.8배 높으며, 현미수량성은 560kg/10a로 ‘적진주’보다 21% 높았다. 또한 흰잎마름병(K1~k3)과 줄무늬잎마름병에 강하며, 수발아율이 5.9%로 기존 적미에 비해 재배안정성이 크게 강화된 적미품종으로, ‘적진주2호’는 쌀의 부가가치를 높이고 건강기능성 식품 시장 활성화에도 이바지할 것으로 기대된다.

***교신저자:** Tel. 055-350-1156, E-mail: kangjw81@korea.kr

PE-0073

Single nucleotide amplified polymorphism (SNAP) marker for selection of resistance to *Phytophthora sojae* in soybean (*Glycine max* L.)

Jeong Sun Lee, Young Eun Jang, Sungwoo Lee*

Department of Crop Science, College of Agriculture and Life Sciences, Chungnam National University, Daejeon 34134, Republic of Korea

Occurrence of Phytophthora root and stem rot (PRR) of soybean becomes an emerging threat for soybean production in South Korea as soybean cultivation in paddy fields increases. *Phytophthora sojae* is a soil-borne oomycete that causes pre- and post-emergence damping-off of soybean in poorly drained soils. A 573 kb region of chromosome 3 was previously identified in the cultivar Daewon for resistance to *P. sojae* isolate 2457 using Daepung (DP) x Daewon (DW) recombinant inbred line (RIL) population. This study aimed to develop a single nucleotide amplified polymorphism (SNAP) marker that can be utilized in selection for resistance allele to *P. sojae* at the 573 kb locus. Three sets of were initially designed based on genic SNPs on the identified genomic region. Of them, SNAP-Set2 successfully showed allele-specific amplifications for each of DP and DW alleles in the parental genotypes and 20 RILs of the DP x DW RIL population. For validation of this marker, 11 soybean germplasms were randomly selected and genotyped. Allele-specific amplification was also successful and the marker genotype of each agreed with 180K Axiom® SoyaSNP array data. Phenotypic evaluation for resistance to *P. soaje* isolate 2457, subsequently, demonstrated that DP-type amplification and DW-type amplification of the marker SNAP-Set2 are associated with susceptibility and resistance to *P. sojae* isolate 2457. Development of a SNAP marker linked to this resistance locus would expedite the use of the valuable resistance allele in soybean breeding programs for resistance to *P. sojae*.

***Corresponding Author:** Tel. 042-821-5727, E-mail: sungwoolee@cnu.ac.kr

PE-0074

Exploration for salinity and drought tolerant resources in Korean wheat core collection accession

Kyeong Do Min[1], Da Won Seo[1], Ji Yu Jung[1], Deok Ryong Koo[1], Ha Neul Lee[1], Chang-Hyun Choi[2], Jae Yoon Kim[1*]

[1]Department of Plant Resources, College of Industrial Science, Kongju National University, Yesan 32439, Republic of Korea
[2]National Institute of Crop Science, RDA, Wanju 55365, Korea

Environmental effect is one of very important factors for the growth of all crops. Soil condition and moisture content are expected to have a huge impact on the overall growth period plants. Recently, due to global warming and climate changes, the domestic weather has been altering to subtropical climate and is getting non-clear season. Therefore, the viability of crops is threatened by floods and droughts caused by extreme climates. In order to cope with these circumstance, we would like to explore resources with resistant drought and salt stress. In previous study, we constructed Korean wheat core collection and investigating agricultural trait of each resources. It provide possibility to explore novel genes and useful SNP markers in loading and heading date.

In this study, we are evaluating salt or drought tolerant index in seedling, vegetative, and ripening stage under stress treatment with Korean wheat core collection for phenotyping. For genotyping, extracted genomic DNA from selected Korean wheat core collection were analyzed using Axiom wheat breeder's genotyping 35K 384 array plate. Therefore, a total of 566 accessions of the 614 core collection selected after consideration of DNA QC and local adaptability. Salt treatment and drought treatment carried out for seedling, vegetative and ripening stage. During seeding stage, the length and thickness of the roots and the area above the soil were measured with WinRhizor pro (3D root scanner) to compare the treated alleles and the control alleles. In addition changes in soil moisture, pH, and chlorophyll content were compared in the seedling and maturation period using a spad-502(chlorophyll meter). In wheat at the drought treated in vegetative stage, 8 accessions (Samcheok9, P59, Chapingo, Suwon246, Norkan, GRSS93SH18-0M-12SH-2M-1Y-4M-0Y, trego, S-22, Mindszentpusztai, Kirmizi Tir, Bahri) were selected for excellent candidate resources by chlorophyll measurement. Additionally, genotyping by SNP chip analysis revealed that 21,708 identified SNPs. A total of 19,947 SNPs were selected by more 1% of minor allele frequency and higher 90% calling rate. The statistical linkage disequilibrium (LD) was predicted that the core collection has genetic diversity with a distance of 8.95CM threshold value. Then, discovery salt and drought tolerance gene or SNP for performing Genome Wide Associated Study (GWAS) based on the collected phenotype data and SNP chip genotype data.

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***Corresponding Author:** Tel. +82-041-330-1203, E-mail: jaeyoonkim@kongju.ac.kr

PE-0075

밀 수발아 특성차이가 큰 품종 간 등숙기 ABA와 ROS 함량 변화 차이

양진우*, 최창현, 이명희, 김경민, 박진희, 김유림, 정한용, 김경훈, 강천식, 손지영, 박태일

전라북도 완주군 이서면 혁신로 181 국립식량과학원 밀연구팀

본 연구 수발아 민감성 품종인 ‘조경(백립계)’과 수발아 내성품종인 ‘다홍(적립계)’에 대해 등숙기간 동안 ROS와 ABA 함량 변화를 분석하고 종피색과 발아하였다. 개화 후 20일부터 7일 간격으로 4주 종자를 수확하여 ABA 및 ROS의 변화를 조사하였다. 조경은 개화 후 34일(DAF 34)까지 ABA 함량이 증가하다가 이후 감소하으며, ROS(H_2O_2) 함량 양상을 보였다.반면, 다홍은 등숙기간이 경과할수록 ABA 함량이 지속적으로 증가한 반면 ROS(H_2O_2)의 함량은 낮은 수준을 유지하였다. 항산화효소로서 H_2O_2를 소거하는 CAT활성은 조경 등숙기간 동안 지속적으로 감소하였고, 다홍은 초기에는 감소하다가 등숙후기(DAF 34)부터 증가다. SOD함량 변화는 두 품종 모두 큰 차이가 없었다.CAT(Catalase)는 조경은 성숙 과정 중 지속적으로 감소하였고, 다홍은 초반에 감소한 후 다시 증가하는 경향을 나타내었다. Ascorbic acid(AsA)함량 변화는 두 품종 모두 감소하였으나, 다홍은 마지막 성숙 단계에서 오히려 증가하는 경향을 보였다.

***교신저자:** Tel. 063-238-5464, E-mail: jinwoo1127@korea.kr

PE-0076

밀 조기 육종을 위한 파성별 저온처리 기간에 따른 출수 소요일수 변이 분석

김경민[1*], 최창현[1], 김경훈[1], 강천식[1], 차진경[2], 양진우[1], 이명희[1], 손지영[1], 박태일[1]

[1]전라북도 완주군 이서면 혁신로 181 국립식량과학원 밀연구팀
[2]경상남도 밀양시 점필재로 20 국립식량과학원 남부작물부 논이용작물과

밀 신품종개발을 위한 계통육성방법은 교배에서 품종출원까지 10년 이상 기간이 소요되므로 대내외 트렌드 변화를 신속하게 반영하기는 힘들다. 기존품종을 개선하기 위해서는 우량 인자를 도입하고 여러세대를 거쳐 유전형질을 고정시켜야 하는데, 이와 같은 밀의 육종 기간을 단축시키는 방법으로 최근 온도와 광 조절을 통한 Speed breeding 방법이 개발되었다. 하지만 우리나라는 주로 겨울밀을 재배하므로 파성을 제거하기 위한 저온(춘화)처리 기간이 필요하다. 본 연구는 국내 겨울밀 세대단축에 필요한 최소 저온기간을 구명하기 위해 파성 특성이 뚜렷한 품종을 대상으로 저온기간에 따른 주간엽수와 출수 소요일수의 변이를 분석하였다. 밀 파성별 대표 시험품종으로는 오월소맥(파성Ⅰ), 조경(Ⅱ), 금강(Ⅲ), 호중(Ⅳ), 자선1호(Ⅴ) 5 품종을 사용하였다. 시험방법은 종자 발아 3일 후 4℃ 저온 냉장실에 처리기간(무처리, 1, 2, 3주)을 달리 한 식물체를 온도(23±2℃)와 광(22시간 명, 2시간 암)조건이 일정한 growth room에서 생육한 후 주간엽수와 출수 소요일수를 조사하였다. 주간엽수는 출수 전 발생한 엽수를 조사하였고, 출수 소요일수는 종자 발아일부터 출수일까지의 저온처리기간을 포함한 누적일수로 나타냈다. 밀 품종별 저온처리기간에 따른 주간엽수는 오월소맥(Ⅰ) 5~6매, 조경(Ⅱ) 5~7매, 금강(Ⅲ) 7~8매, 호중(Ⅳ) 7~11매, 자선1호(Ⅴ) 9~11매로 나타났으며, 파성이 높은 품종일수록 주간엽수가 많았고 저온처리기간이 길수록 주간엽수가 적은 경향을 보였다. 밀 품종별 저온처리 기간에 따른 출수소요일수는 오월소맥(Ⅰ) 36~52일, 조경(Ⅱ) 33~49일, 금강(Ⅲ) 57~64일, 호중(Ⅳ) 56일~82일, 자선1호(Ⅴ) 64~91일로 나타났으며, 파성이 높은 품종일수록 출수까지 소요되는 일수가 길었다. 결론적으로 저온처리기간에 따른 출수 소요일수는 파성 Ⅱ 이하의 품종은 저온요구도가 낮아 1주 처리시 가장 짧았고, 파성 Ⅲ 이상의 품종은 저온요구도가 높아 3주 처리에서 가장 짧았다. 따라서 Speed breeding 방법을 이용한 국내 밀 계통의 안정적인 세대촉진을 위해서는 최소한 3주의 저온처리가 필요하며, 이 결과는 목적형질이 분명한 밀 계통의 조기육성을 위한 Speed breeding 육종시 핵심기술로서 활용할 수 있다.

***교신저자:** Tel. 063-238-5458, E-mail: raiders87@korea.kr

PE-0077

Fine mapping of a *restorer-of-fertility* (*Rf*) gene for the novel cytoplasmic male sterility in rice (*Oryza sativa* L.)

Seung Young Lee[1], Zhuo Jin[1], Su Jang[1], Backki Kim[1], Jeonghwan Seo[2], Hee-Jong Koh[1*]

[1]Department of Agriculture, Forestry and Bioresources, Plant Genomics and Breeding Institute, Research Institute for Agriculture and Life Sciences, Seoul National University, Seoul 08826, Korea
[2]Department of Plant Bioscience, College of Natural Resources and Life Science, Pusan National University, Miryang 50463, Korea

The cytoplasmic male sterility (CMS) and *restorer-of-fertility* (*Rf*) system provides genetic explanation of interaction between the mitochondria and nucleus in hybrid seed production. *Rf* gene rescues the sterile phenotype by suppressing the expression of chimeric CMS gene via various mechanism such as gene editing, splicing and cleavage. In this study, BC_3F_2 population was used for bulked segregant analysis (BSA) and QTL-seq analysis. Whole genome sequencing (WGS) of DNAs from fertile bulk and sterile bulk as basis for the QTL-seq pipeline, a peak was identified between 17 Mb and 24 Mb of chromosome 10. Using F_2 population derived from the cross between CMS line Hopum A and BC_3F_2, InDel and sequence-tagged site (STS) markers were designed for fine mapping, which narrowed the flanking region to 330 Kb between M-5 and M-6 markers. In this region, several restorer genes such as *Rf4*, *Rf1a, Rf1b* and restorer-like (RFL) genes have been previously reported. We have identified seven candidate genes that are pentatricopeptide repeat (PPR) proteins that may be responsible for fertility restoration. Further studies will help to delimit to a candidate gene to be applied for breeding restorer line in three-line system in hybrid rice.

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

PE-0078

Development of abiotic stress-tolerant rice plants using CRISPR/Cas9 genome editing

Kiyoon Kang*

Division of Life Sciences, Incheon National University, Incheon 22012, Republic of Korea

Rice (*Oryza sativa*) genome encodes approximately 2,500 transcription factors (TFs). Among them, over 55% TFs are closely involved in abiotic stress tolerance pathways. Here, we investigated the expression profiles of rice TFs under salt and drought stress using GENEVESTIGATOR database. We selected 120 candidate genes whose expression are altered in drought stress for subsequent genome editing mutagenesis. The TF families encoded by candidate genes included EREBP, MYB, NAC, WRKY, and bHLH. The binary vectors containing guide RNA (gRNA) and codon-optimized Cas9 were introduced into calli derived from *O. sativa japonica* cultivar ‘Dongjin’ seeds using the *Agrobacterium tumefaciens* (strain LBA4404)-mediated transformation method. These approaches will be good strategies for understanding underlying mechanisms of abiotic stress tolerance and generating abiotic stress-tolerant rice plants.

***Corresponding Author:** Tel. 032-835-8894, E-mail: kykang@inu.ac.kr

PE-0079

콩 용도별 육성계통의 주요 병해 실내접종 반응

김남걸[1*], 이인혜[1], 서민정[2], 윤홍태[1]

[1]경기도 수원시 권선구 수인로 126, 국립식량과학원 중부작물과
[2]전라북도 완주군 이서면 혁신로 181, 국립식량과학원 기획조정과

콩(*Glycine max* (L.) Merr.)에서 가장 문제가 되는 병은 Soybean Mosaic Virus(콩모자이크바이러스병, SMV)와 잎이 조기에 떨어지는 세균병인 들불병 및 불마름병이 있다. 해당 병에 저항성을 가진 품종을 육성하기 위해, 수원에서 육성한 21개의 고세대 계통에 균주를 실내접종해 저항성을 평가하였다. 접종시기는 SMV는 G6H strain을 VC~V1시기에 접종하였고, 들불병과 불마름병은 각각 GGS13-8, 8ra 균주를 V3시기에 접종하였다. 표준품종으로는 장류콩인 대원콩, 나물콩인 풍산나물콩, 특수콩인 청자3호를 사용하였고, SMV 대비품종으로는 해당 바이러스에 감수성을 가진 것으로 알려진 소원콩을 사용하였다. SMV 접종 결과, 접종엽과 상위엽 모두 반응을 보이지 않은 SS15231-3S-5-2 등 4개의 계통과 접종엽에서는 병반이 보였으나 상위엽에서 병증을 보이지 않은 SS15108-8-1-3 등 8개의 계통을 확인하였다. 들불병 접종 결과, SS15101-10-1-4 등 10개의 계통에서 표준품종보다 들불병이 강해 유망할 것으로 판단되었다. 반면에 SS15114-14-1-2(대풍2호/우람), SS15120-3S-2-1(진풍/중황35호) 등은 불마름병에 약한 것으로 나타났다. 불마름병 접종 결과, 나물콩 계통(SS15230, SS15231)에서 강한 저항성을 보인 반면, SS15120-3S(진풍/중황35호) 등 3계통이 감수성인 것으로 나타났다. 따라서 3개의 주요 병해에 강한 SS15119-3S-40-4(태선/청아) 등 3계통과 2개의 주요 병해에 강한 SS15101-10-1-4(연풍/새금) 등 7개의 계통은 앞으로 복합내병성 품종육성에 주요 재료로 활용할 계획이다. 또한, 특정 병해에 감수성인 조합들은 저항성 기작 연구에 활용할 수 있을 것으로 판단된다.

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***교신저자:** Tel. 031-695-4047, E-mail: qoo2010@korea.kr

PE-0080

볶음밥용 가공용 복합내병성 초다수 벼 ‘보끄미’

이지윤*, 조준현, 이종희, 박동수, 송유천, 조수민, 강주원, 권영호, 이소명, 고종민

경상남도 밀양시 점필재로 20 국립식량과학원 남부작물부

“보끄미”는 2010/2011년 동계 1차에 수량성이 높은 한아름과 등숙률이 높고 재배안정성이 우수한 삼강을 교배하여 양성한 F_1(YR29192)에 한아름을 반복친으로 여교배하여 2010/2011년 동계 2차에 F_1을 양성하였다. 이 후 계통육종법에 따라 계통을 전개하여 2015년부터 2년간의 생산력검정시험을 거쳐 2016년 밀양329호의 계통명이 부여되었다. 2017년부터 2020년까지 4년간의 지역적응시험 결과, 수량성이 높고 벼 주요 병해에 강하며, 볶음밥 가공적성 등의 우수성이 인정되어 2020년 농작물 직무육성 신품종선정위원회에서 “보끄미”로 명명되었다. “보끄미”는 출수기가 8월 12일인 중생종이며, 간장은 88㎝로 “다산”보다 크고, 수장, 주당수수, 수당립수는 “다산”과 비슷하다. “보끄미”는 등숙률이 81.8%로 “다산”보다 5.4% 높고, 쌀수량은 773kg/10a으로 “다산”보다 18% 많다. 종자의 형태는 다산과 비슷하며, “다산”보다 도정률이 높다. “보끄미”는 볶음밥 조리 시 밥알의 응집성과 점착성이 다산이나 신동진보다 낮았다. 볶음밥 조리 직후 및 냉동·해동 후 다른 품종보다 쌀알 모양을 유지하면서 낮은 점착성을 보였으며, 전반적인 기호도에서 가장 우수하였다.

***교신저자:** Tel. 055-350-1164, E-mail: minitia@korea.kr

PE-0081

QTL mapping for bakanae disease resistance with Korean *japonica* rice varieties using image analysis

Chaewon Lee[1], Yunji Shin[1], Kyeong-Seong Cheon[2], Hyo Ja Oh[1], Jeongho Baek[1], Kyung-Hwan Kim[1], Young-Soon Cha[1], Hyeonso Ji[1*]

[1]Gene Engineering Division, Department of Agricultural Biotechnology, National Institute of Agricultural Sciences, Jeonju 54874, Republic of Korea

[2]Division of Forest Tree Improvement and Biotechnology, Department of Forest Bioresources, National Institute of Forest Science, Suwon 16631, Republic of Korea

Bakanae disease is caused by a fungal pathogen, *Fusarium fujikuroi*. The optimum temperature for disease development is as high as 35℃, and the incidence of this disease is increasing with temperature rise due to global warming. In addition, the advent of fungicide-resistant strains has rendered disease control difficult. Thus, this disease has become a serious threat in almost all rice cultivation regions worldwide. We performed QTL mapping for bakanae disease resistance with an F2:F3 population derived from a cross between Junam (susceptible) and Hwayeong (moderately resistant). A genetic map comprising 141 KASP markers which are polymorphic between the parents was constructed with 188 F2 plants. The total distance of the genetic map was 1,444.2 cM, and the average distance between markers was 11.1 cM. Bioassay of 188 F3 families derived from the F2 plants was performed by in vitro seedling screening. We measured mortality rate of the F3 families by both manual method and newly developed image analysis method. A major QTL was found on chromosome 4 by both manual measurement and image analysis measurement of mortality rate. This QTL will be utilized in breeding rice varieties resistant to bakanae disease. Moreover, the image analysis method developed in this study will be helpful for more accurate and efficient assessment of bakanae disease response.

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

PE-0082

MABC를 이용한 오대벼 줄무늬잎마름병 근동질 계통 육성

이종희*, 권영호, 이소명, 신동진, 강주원, 조준현, 누클루롤리카방지

농촌진흥청 국립식량과학원 논이용작물과

오대벼는 밥맛이 우수하며 내도복 내냉성이 우수하여 강원도 지역의 브랜드쌀로 정착한 품종이다. 그러나 줄무늬잎마름병을 비롯한 바이러스 병에 이병성이여서 지구온난화에 따른 바이러스병의 북상에 대응한 저항성 육종이 필요한 실정이다. 본 실험은 분자육종 기술 접목 수요자 맞춤형 벼 품종을 신속히 육성하고자 MABC(Marker assisted backcrossing)를 이용하여 오대벼 배경의 줄무늬잎마름병 저항성 근동질 계통을 육성하고자 수행하였다. 해담쌀과 오대벼를 교배하여 2017년 하계에 F1 식물체를 양성 후 오대벼를 반복친으로 하여 BC1F1 종자를 얻었으며, 저항성 분자마커로 알려진 Indel7 마커를 이용하여 헤테로를 선발하였고, 약배양을 통해 BC2F1 생성 후, 2차 MAS를 실시하여 18개의 이형접합체를 나타내는 식물체를 얻었다. 추후 315개의 KASP 마커를 이용하여 다형성을 보이는 마커를 선발 후, 유전자 지도 작성에 이용하였으며, BC2F2로 진전되어 얻어진 계통들에 Indel7 마커를 이용하여 MAS를 실시하여 71개체를 선발하였다. 오대벼는 천립중이 큰 것이 브랜드 차별화의 장점으로 마케팅에 활용하고 있다. 따라서 선발된 개쳉의 천립중을 분석한 결과 천립중은 22-26까지 양적으로 정규분포하는 양상을 나타내었다. 오대벼의 천립중은 평균 25.0g 이상으로 오대벼 수준의 천립중을 가진 31계통이 선발되었다. BC2F2개체의 립장, 립폭 및 장폭비 특성을 분석하였으며, 천립중과 이들 형질간의 상관분석을 수행하였다. 천립중은 립폭과 0.65로 고도의 유의한 상관을 나타내었으며, 립장과도 0.34의 유의한 상관을 나타내었다. 또한, 저항성 유전자형을 보이는 71개체를 얻어 Background selection을 실시한 결과 해담쌀 염색체 단편과 헤테로의 평균 이입률은 각각 9.0%, 11.2%로 나타났다. 오대벼로의 평균 반복친 회복률이 88.5%이며 공여친 염색체 단편이입률 1.58%, 헤테로 이입률 11.2%인 개체를 선발하였다.

***교신저자:** Tel. +82-53-350-1168, E-mail: ccriljh@korea.kr

PE-0083

‘Heukchan’: A New Purple-Skin Peanut Variety with Small Grain and High Uniformity

Eunyoung Oh*, Sungup Kim, Jung In Kim, Min Young Kim, Sang Woo Kim, Jeongeun Lee, Kwang-Soo Cho, Myoung-Hee Lee

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

A new peanut (*Arachis hypogaea L.*) variety ‘Heukchan’ was developed at the Department of Southern Area Crop Science, National Institute of Crop Science (NICS), Miryang, and approved for release in 2019. ‘Heukchan’ selected from the single cross between black-testa peanut accession, ‘Heukhuaseng(IT217332)’ and short-stem Virginia-type elite line ‘HP825(IT310160)’. ‘Heukchan’ has 19 branches per plant and a flowering habit on both main stem and branch. The length of main stem and branch was 39 cm and 44 cm, respectively, showing shorter height than reference cultivar, ‘Daekwang’. ‘Heukchan’ has a dark-purple testa and comparably small-sized grain, which weight of 100 grains is 64g and short-ellipse-shaped kernel. During the selection of advanced line, it was considered to improve the seed quality by reducing the pre-harvest sprouting traits of ‘Heuksaeng’, the first purple-skin variety that was released on 2013. ‘Heukchan’ has demonstrated remarkable yield performance through the regional yield trial (2017-2019), showing 4.56MT per ha, and comparably stronger at early leaf blight and lodging than ‘Daekwang’. ‘Heukchan’ had 61 pods per plant and 78% of mature pod ratio on average, which is 45% and 7% higher than ‘Daekwang’. The dried kernel consists of 30.1% of protein, 50.7% of crude fat, and the seed coat contain two major pigments, cyanidin-3-O-sophoroside and cyanidin-3-O-sambubioside, which give unique characteristics of purple-skin peanut.

***Corresponding Author:** Tel. 055-350-1232, E-mail: lavondy10@korea.kr

PE-0084

벼 저산소 발아 유전자 이전계통의 담수직파 적성 검토

정종민*, 정지웅, 이현숙, 하수경, 김진희

전라북도 완주군 이서면 혁신로 181 농촌진흥청 국립식량과학원

벼 직파재배는 파종 및 육묘과정 없이 볍씨를 바로 논에 파종하기 때문에 이앙재배에 비해 절차가 간단하여 노력 및 비용절감 효과가 크다. 하지만 파종초기 불량환경으로 인해 종자의 발아와 입모가 불량해지는 단점이 있다. 본 연구에서는 담수 직파재배 초기입모가 안정적인 품종개발을 위해 잡초벼에서 유래한 저산소 발아 유전자를 국내 벼 품종에 이전하여 육성된 혐기발아 계통(전주643호, 전주656호, 전주657호)을 이용하여 담수직파 재배 적응성을 검토하였다. 담수직파 재배시 담수에 따른 입모특성 비교결과, 재배 조건에서 혐기발아 계통의 담수직파 10㎡ 당 입모수는 각각 457, 401, 166개로 전주657호를 제외한 2계통은 비교 품종 (동안: 162개, 신동진: 188개, KHO: 239개) 보다 매우 높은 입모율을 나타내었다. 상시 담수조건으로 인해 간장, 수장, 수수는 및 수량은 이앙 조건에 비해 현저히 감소하는 경향이었으나 혐기발아 계통은 비교품종 보다 높은 수량성을 나타내었으며 전주643호와 전주656호는 담수 비교품종인 동안벼 및 일반벼 품종인 신동진에 비해 매우 높은 입모율과 수량을 나타내어 담수직파 시 적절한 재배관리와 시비 관리가 된다면 담수직파 전용 품종으로 우수한 성능을 나타낼 것으로 판단되었다.

사사: 본 연구는 농촌진흥청 아젠다 사업 (과제번호: PJ013807012021)의 지원에 의해 수행되었음

***교신저자:** Tel. 063-238-5236, E-mail: jjm0820@korea.kr

PE-0085

비선택 제초제 Tiafenacil 내성계통, Samkwnag(SA)-Tfnl2

정종민*, 정지웅, 이현숙, 하수경, 김진희

전라북도 완주군 이서면 혁신로 181 농촌진흥청 국립식량과학원

잡초벼(앵미)는 재배 벼와 생리적 · 형태적으로 유사하여 기존 수도용 제초제로는 방제가 어렵고 쌀의 수량성 및 품질을 저하시켜 직파 재배에서 큰 문제가 되고 있다. 미국 등 주요 벼 직파재배 국가에서는 제초제에 내성을 가지는 벼 품종을 이용하여 효과적으로 잡초벼를 방제하고 있다. 본 연구는 제초제 내성벼 소재 개발을 위해 돌연변이 집단을 이용하여 비선택 제초제 Tiafenacil에 내성을 발현하는 Samkwang(SA)-Tfnl2 선발하고 그 특성을 보고하는 바이다. 유묘기 내성을 반응을 검정한 결과, 원품종(삼광벼)은 30μM 농도에서 고사반응을 나타내었으나 Samkwang(SA)-Tfnl2는 60μM까지 안정적인 내성을 나타내었으며 분얼기에 실시한 0.6배로 희석된 Tiafenacil을 살포한 후 원품종은 대부분 고사하였으나 Samkwang(SA)-Tfnl2는 강한 내성 반응을 나타내었다. Samkwang(SA)-Tfnl2 계통은 비선택 제초제 내성을 나타내며 종래의 벼 형질전환 방법이 아닌 돌연변이 육종방법으로 육성된 계통으로 제초제 내성 벼 품종 개발의 목적으로 사용할 수 있을 것이다.

사사: 본 연구는 농촌진흥청 아젠다 사업(과제번호: PJ013807022021)의 지원에 의해 수행되었음

***교신저자:** Tel. 063-238-5236, E-mail: jjm0820@korea.kr

PE-0086

국내 밀 품종의 잎녹병 저항성 유전자 검정

김선숙[1], 유진희[1], 이윤아[1], 홍수민[1], 최리[1], 김경민[2], 박철수[1], 모영준[1*]

[1]전라북도 전주시 덕진구 백제대로 567 전북대학교 농업생명과학대학 작물생명과학과
[2]전라북도 완주군 이서면 혁신로 181 농촌진흥청 국립식량과학원 밀연구팀

밀의 잎녹병을 일으키는 *Puccinia triticina* Eriks (Pt)는 공기전염력이 빠르고 생존력이 강해 다양한 밀 재배지대에서 최대 50%에 이르는 수량 감소를 일으키고 있다. 최근 들어 밀 잎녹병의 국내 발생 증가가 보고되고 있고 이상기후와 밀 재배면적 확대에 따라 국내 밀 재배환경에서 잎녹병 저항성 증진이 절실한 시점이다. 본 연구는 국내 밀 49 품종에 대한 잎녹병 저항성 유전자 보유 여부 검정을 위하여 현재까지 보고된 80여종의 잎녹병 저항성 유전자 중 주요 유전자 10개에 대해 분자표지 검정을 실시하였다. 보통밀 유래 *Lr46*, *Lr49, Lr75* 유전자를 분석한 결과 모든 국내 품종은 *Lr75* 저항성으로 나타났고, *Lr46, Lr49* 저항성을 지닌 품종은 각각 밀성 등 9 품종과 다홍 등 13 품종이었다. 야생밀 유래 *Lr29, Lr32, Lr47, Lr50* 유전자 분석 결과, 국내 품종은 모두 *Lr47* 저항성 대립유전자를 보유한 반면 *Lr32*에 대해서는 감수성 대립유전자를 보유한 것으로 나타났다. *Lr29*과 *Lr50* 저항성을 지닌 품종은 각각 38 품종과 44 품종이었다. 복합저항성 유전자 보유 품종 분석 결과, 국내 밀 품종은 모두 *Lr52/Yr47*에서 감수성 대립유전자를 지녔으며 *Lr56/Yr38, Lr34/Sr57/Yr18* 저항성 대립 유전자를 지닌 품종은 각각 장광 등 8품종, 진풍 등 15품종이었다. 국내 밀 49개 품종 중 그루, 진풍, 다홍, 신미찰, 은파, 호중, 올그루, 우리 8개 품종은 다양한 조합으로 구성된 6개의 잎녹병 저항성 유전자를 가진 것으로 나타났다. 따라서 국내 밀 잎녹병 저항성 육종 프로그램에서 유용하게 활용 가능할 것이라 판단된다. 앞으로 국내 밀 품종의 잎녹병 저항성 증진을 위해서 보다 다양한 저항성 유전자를 지닌 유용 자원의 평가와 도입이 시급한 상황이며 녹병 복합 저항성 증진을 위한 체계화된 육종 프로그램 구축도 필요하다.

***교신저자:** Tel. 063-270-2530, E-mail: yjmo@jbnu.ac.kr

PE-0087

국내 밀 품종의 줄녹병 저항성 유전자 검정

이윤아[1], 유진희[1], 김선숙[1], 홍수민[1], 최리[1], 김경민[2], 박철수[1], 모영준[1*]

[1]전라북도 전주시 덕진구 백제대로 567 전북대학교 농업생명과학대학 작물생명과학과
[2]전라북도 완주군 이서면 혁신로 181 농촌진흥청 국립식량과학원 밀연구팀

밀 줄녹병은 *Puccinia striiformis* Westend. f. sp. tritici (*Pst*)균에 의해 발생되는 곰팡이병으로 전세계 밀 품종의 88%는 줄녹병에 대한 저항성이 없어 매년 약 10억 달러의 경제적 손실이 발생하고 있는 상황이다. 현재 줄녹병 저항성 유전자는 80여개 정도가 보고되어있으며, 최근 *Pst*균계의 빠른 변이 발생으로 인해 국내 밀 품종에 대한 줄녹병 저항성 증진이 매우 중요한 시점이다. 본 연구에서는 주요 줄녹병 9개 유전자에 대한 국내 밀 49 품종의 저항성 유전자 보유여부를 알아보기 위한 분자표지 검정을 실시하였다. *Yr5*과 *Yr15*는 야생밀 유래 유전자이며, 한백 등 34개 품종은 *Yr5* 저항성 유전자를 지녔고, *Yr15*에 대해서는 백중을 제외한 나머지 품종에서 모두 저항성 유전자를 가진 것으로 나타났다. 보통밀 유래 유전자인 *Yr48, Yr51*, *Yr59* 분석 결과, *Yr48* 저항성 유전자를 지닌 품종은 한백이 유일했으며, 13개 품종과 15개 품종은 각각 *Yr51*과 *Yr59* 저항성 유전자를 지닌 것으로 나타났다. 복합저항성 유전자 보유 품종 분석 결과, 국내 밀 품종은 모두 *Yr47/Lr52* 감수성이었으며, *Yr38/Lr56, Yr18/Lr34/Sr57, Yr46/Sr55/Lr67* 저항성 대립 유전자를 지닌 품종은 각각 장광 등 8 품종과 진풍 등 15 품종, 경광 등 27 품종이었다. 줄녹병 저항성 유전자를 다수 보유하고 있는 품종은 알찬, 장광, 우리, 조광, 탑동, 청계, 금강, 서둔으로 총 8개의 품종이 다양한 조합의 5개 *Yr* 유전자에 대해서 저항성 대립유전자를 지녀 국내 밀 육종 프로그램에서 줄녹병 저항성 증진을 위하여 유용하게 활용이 가능할 것이다. 국내 밀 품종의 줄녹병 저항성 증진을 위해서는 다양한 저항성 유전자를 지닌 유용 자원의 평가와 도입이 시급하고, 국산 밀의 생산 안정성 증진과 녹병 복합 저항성 증진을 위한 체계화된 육종 프로그램 구축과 관련 기초 연구가 필요하다.

***교신저자:** Tel. 063-270-2530, E-mail: yjmo@jbnu.ac.kr

PE-0088

국내 밀 품종의 줄기녹병 저항성 유전자 검정

유진희[1], 김선숙[1], 이윤아[1], 홍수민[1], 최리[1], 김경민[2], 박철수[1], 모영준[1*]

[1]전라북도 전주시 덕진구 백제대로 567 전북대학교 농업생명과학대학 작물생명과학과
[2]전라북도 완주군 이서면 혁신로 181 농촌진흥청 국립식량과학원 밀연구팀

밀 줄기녹병(*Sr*)은 *P. graminis f. sp. tritici* (*Pgt*)을 매개로 발생하는 곰팡이병으로 수량 감소와 도복 등 피해가 다른 녹병에 비해서 상당히 심각하며, 남아시아와 아프리카에 큰 피해를 입힌 *Ug99*이 대표적 균계이다. 전세계적으로 밀 줄기녹병 저항성 증진을 위한 연구가 활발하게 이루어지고 있지만, 국내에서는 관련 연구가 미흡한 실정이다. 본 연구에서는 국내 밀 49 품종에 대한 줄기녹병 저항성 주요 유전자 보유 여부의 검정을 실시하였다. 현재까지 60여개 줄기녹병 저항성 유전자가 보고되었으며, 본 연구에서는 저항성 증진에 효과적일 것이라 예상되는 주요 유전자 12개를 분자표지로 검정하였다. 보통밀에서 유래된 *Sr28*, *Sr49*와 *Sr56*를 분석한 결과, 조중을 제외한 48품종이 *Sr49* 저항성 유전자를 지녔고 장광 등 7품종이 *Sr56* 저항성 유전자를 지녔다. 야생밀로부터 유래된 *Sr22*, *Sr26*, *Sr36*, *Sr43*, *Sr45*와 *Sr47*을 분석한 결과 *Sr43*에서 경광, 알찬을 포함한 8품종이 저항성 대립유전자를 보유하였으며, *Sr45*에서는 국내 품종 모두 저항성 유전자를 보유한 것으로 확인되었다. 복합 저항성 유전자 *Sr24/Lr24, Sr25/Lr19* 그리고 *Sr55/Lr67/Yr46*의 저항성 유전자 보유여부 분석결과 장광, 경광을 포함한 27품종이 *Sr55/Lr67/Yr46* 저항성 유전자를 보유한 것으로 나타났다. 종합적으로는 *Sr43, Sr45, Sr49, Sr55/Lr67/Yr46*을 보유한 경광, 알찬, 적중, 조경, 중모 2003과 *Sr45, Sr49, Sr56, Sr55/Lr67/Yr46*을 지닌 신미찰1, 장광, 중모 2012, 호중 품종이 줄기녹병 저항성 증진을 위한 유용한 육종 소재로 활용도가 우수할 것으로 판단되며, 국산 밀의 생산 안정성 증진과 녹병 복합 저항성 증진을 위하여 보다 다양한 국내외 유용자원 평가와 저항성원의 확보가 필요하다.

***교신저자:** Tel. 063-270-2530, E-mail: yjmo@jbnu.ac.kr

PE-0089

OsPUB14, OsMTD2 interacting protein, is involved in late pollen development in rice

Jung-Hyun Lee[1], Myung-Hee Kim[1], Yu-Jin Kim[2], Sang Dae Yun[1], Sung Aeong Oh[1], Ki-Hong Jung[3], Soon Ki Park[1*]

[1]School of Applied Biosciences, Kyungpook National University, Daegu 41566, Republic of Korea
[2]Department of Life Science and Environmental Biochemistry, Pusan National University, Miryang 50463, Republic of Korea
[3]Graduate School of Biotechnology and Crop Biotech Institute, Kyung Hee University, Yongin 17104, Republic of Korea

In flowering plants, successful pollen tube growth leads to deliver male gametes to embryo sacs during pollination. The pollen germination and tube growth is essential for plant reproduction and seed formation, although the molecular mechanisms in pollen tube growth remain largely unknown, in crop plants. Previous research has been established that OsMTD2 has important roles in promoting pollen- tube elongation through cell-wall by conferring ROS homeostasis during pollen-tube growth. In screening of late pollen-preferred genes in rice, we found a male-gamete defective mutant by T-DNA insertion, *male-gene transfer defective 2* in rice (*osmtd2*), which encodes the CrRLK1L gene family. We identified that *OsMTD2* interacts with *OsPUB14* (*Plant U-box protein 14*) by yeast two-hybrid and Co-IP analysis. In 77 of OsPUB proteins, *OsPUB14* contains one U-box and four ARM domains. Phylogenetic analysis of rice and *Arabidopsis* revealed that *OsPUB14* is closely linked with *OsPUB13* and *AtPUB15*. Integrated anatomical expression analysis of *OsPUB14* and *OsPUB13* showed that the pollen is highly expressed at the late stage. In Arabidopsis transgenic plants, the OsPUB14 promoter-GUS was highly expressed in early pollen stage, filament, and stigma. Our study suggests that *OsPUB14* may be the essential male factors participating in pollen-tube growth.

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

PE-0090

끝달림률이 높고 식미가 우수한 단옥수수 신품종 ‘고당옥2호’

배환희[1*], 김정태[2], 이진석[2], 하준영[1], 고영삼[1], 손범영[1], 최유찬[1], 손재한[1], 신성휴[1], 정태욱[1]

[1]경기도 수원시 권선구 수인로 126 농촌진흥청 국립식량과학원 중부작물부 중부작물과
[2]전북 전주시 덕진구 농생명로 300 농촌진흥청 연구정책국 연구운영과

‘고당옥2호’는 KSE14를 모본으로 하고 KSE23을 부본으로 하여 교잡된 단교잡종 단옥수수로, se인자를 가지고 있으며 끝달림률(97%)이 높고 식미가 우수하다. ‘고당옥2호’는 2016년 생산력검정 본시험을 거쳐, ’18~’20년 전국 6개 지역에서 지역적응시험을 실시한 결과 그 우수성이 인정되어 2020년 직무육성 신품종으로 결정되었다. ‘고당옥2호’는 엽초의 안토시아닌 색소가 강하게 발현되고, 과피색은 황색이며 이삭모양은 중간형이다. ‘고당옥2호’의 출사일수는 65일로 대조품종인 ‘단옥3호’(62일)에 비해 3일 늦으며, 이삭의 길이와 직경은 각각 18.9cm, 4.1cm로 ‘단옥3호’와 이삭길이는 비슷하였지만 직경은 작았다. 깨씨무늬병, 그을음무늬병, 조명나방에 대한 저항성은 ‘단옥3호’와 비슷하였지만 도복 저항성은 더 강하였다. 3년간 지역적응시험 결과 10a당 평균 이삭수는 6,177개로 ‘단옥3호’(5,947개)보다 많았고, 이삭중은 1,075kg으로 ‘단옥3호’(1,121kg)보다 적었다. 당도는 23.4 °Bx로 ‘단옥3호’(17.1 °Bx)보다 높았다. 과피두께는 21,4㎛로 ‘단옥3호’(24.5㎛) 보다 얇았으며 관능검사 결과 전체기호도가 5.6으로 ‘단옥3호’(4.6)보다 우수하였다. 2020년 강원도 영월에서 실시한 채종시험결과 ‘고당옥2호’ 모본의 출사기와 부본의 화분비산기간이 잘 일치하였으며 채종량은 모, 부본 4:1파종이 10a당 270kg으로 3:1파종 201kg, 2:1파종 120kg보다 많았다.

***주저자:** Tel. 031-695-4042, E-mail: miami9@kprea.kr

PE-0091

열대적응형 다수성 옥수수 신품종 ‘케이엠5’

배환희[1*], 신성휴[1], 김정태[2], 이진석[2], 하준영[1], 고영삼[1], 손범영[1], 최유찬[1], 손재한[1], 정태욱[1]

[1]경기도 수원시 권선구 수인로 126 농촌진흥청 국립식량과학원 중부작물부 중부작물과
[2]전북 전주시 덕진구 농생명로 300 농촌진흥청 연구정책국 연구운영과

‘케이엠5’는 14K23을 모본으로 하고 CL59를 부본으로 하여 교잡된 열대적응형 다수성 옥수수 신품종이다. ‘케이엠5’는 2017년 생산력검정 본시험을 거쳐, '17~'18년 베트남, 캄보디아, 인도네시아 등 3개 국가에서 지역적응 시험을 실시한 결과 그 우수성이 인정되어 2018년 직무육성 신품종으로 결정되었다. ‘케이엠5’의 수염색은 자색, 립색은 적오렌지색, 립형은 반경립종이다. 출사일수는 베트남에서는 74일로 대조품종 ‘LCH9’과 같았고, 캄보디아서는 55일로 대조품종 ‘CP88’보다 2일 빨랐으며, 인도네시아에서는 59일로 대조품종인 ‘P21’보다 3일 늦었다. 이삭길이는 베트남, 캄보디아, 인도네시아에서 각각 18.7cm, 20.6cm, 21.0cm로 대조품종보다 0.3cm, 4.1cm, 3.1cm 길었다. ‘케이엠5’는 깨씨무늬병과 녹병에 강하며, 동남아 등 열대지방에서 피해가 심한 노균병에도 강하다. 베트남, 캄보디아, 인도네시아 등 3개국에서 도복에 강하다. 2년간 베트남에서 실시한 수량성 검정 결과 10당 종실수량은 695kg으로 대비품종 ‘LCH9’(680kg)보다 2%, 캄보디아에서는 764kg으로 대비품종 ‘CP88’(599kg)보다 27%, 인도네시아에서는 678kg으로 대비품종 ‘P21’(634kg)보다 8% 증수되었다. 조단백질 함량은 베트남 7.2%, 캄보디아 9.7%, 인도네시아 7.8%로 베트남과 인도네시아에서는 조단백질 함량이 대조품종과 비슷하였고 캄보디아에서는 ‘CP888’보다 높았다.

***주저자:** Tel. 031-695-4042, E-mail: miami9@kprea.kr

PE-0092

Evaluation of Rice Breeding Lines using Genetic Markers related to Hybrid Rice and Genes Resistant to Diseases and Insects using Marker-Assisted Selection

Sothea Ouk[1], Me-Sun Kim[1], Kuk-Hyun Jung[2], Yoohan Song[1], Le Van Trang[1], Seo-Rin Ko[1], Yong-Gu Cho[1*]

[1]Department of Crop Science, Chungbuk National University, Cheongju 28644, Korea
[2]Department of Central Area Crop Science, National Institute of Crop Science, RDA, Suwon 16429, Korea

Molecular markers are useful tools for evaluation genes and determining cultivars or breeding lines identity. In this case study, we have some of rice varieties and rice breeding lines that are using alleles frequencies and genetic diversities analysis with SSRs markers (Simple Sequence Repeats). The analysis of the genetic diversity and genetic relationships of 161 of rice varieties and breeding lines were varied out using 20 SSRs markers, gene related to F1 hybrid, blast, bacterial blight, brow plant hopper and tungro virus. In this case, 161 of varieties and breeding lines were analyzed with twenty-one markers by using Agarose gel 1%, 2%, High Resolution Melting analysis (HRM analysis) and a fragment analyzer-based on those markers. Finally, we found the combined group of varieties and F1 hybrid lines that have related to disease/insect resistance genes after analyzing with PCR-base markers and the markers for the restorer of fertility genes. This result might be very useful for plant breeders using the genetic information for development of new elite breeding lines that can adapt to climate change.

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***Corresponding Author:** Tel. +82-43-261-2514, E-mail: ygcho@cbnu.ac.kr

PE-0093

국내 잡초벼 유래 재조합자식집단의 수발아 관련 QTL 탐색

이창민*, 김석만, 박현수, 백만기, 정오영, 고종철, 조영찬

전라북도 완주군 이서면 혁신로 181국립식량과학원

국내 잡초벼 완도앵미6에서 유래된 157계통의 재조합자식집단(RILs)을 이용하여 수발아 특성을 분석하였다. 모본인 화영과 부본인 완도앵미6의 평균 수발아율은 각각 36.6-44.6%, 0.7-4.8%로 큰 차이를 보였는데, 화영과 완도앵미6 종자 모두 30℃ 조건에서96% 이상의 높은 발아율을 보여 종자 발아에는 이상이 없는 것을 확인할 수 있었다. RIL 집단의 수발아율은 2019-2020년에 평균10.1%(범위0-76.2%)과 20.8%(범위 0-92.2%)로 각각 조사되었다. 표현형 데이터와 유전자형데이터를 이용하여 QTL을 분석한 결과, 2번 염색체와 7번 염색체에서 수발아 관련 QTL(*qPH2*와 *qPH7*)이 반복적으로 탐지되었다. *qPH7*는 완도앵미6에서 유래된 QTL로 LOD값이 4.26-4.43였고, 표현형변이는 17.5-19.1%였다. *qPH2*는 화영에서 유래된 QTL로 LOD는 3.57-3.27였고, 표현형변이는 14.5-13.8%였다. 탐지된 QTL을 이용하여 조합간 수발아율을 분석한 결과 QTL이 없는 계통의 수발아율은 36.2-39.5%, *qPH2*를 보유한 계통은 21.3-23.8%, *qPH7*을 보유한 계통은 2.2-4.9%, *qPH2*과 *qPH7*을 모두 보유한 계통은 1.3-4.5%로, *qPH7*을 보유한 계통들이 유의미하게 낮은 수발아율을 보였다. 특히 *qPH7*의 경우 fine mapping을 통해 target region을 정밀화했으며, 그 결과 23.55-23.79Mb사이에서 수발아와 관련하여 총 31개의 ORF를 특정하였다. 추후 qPCR 분석 등을 통해 수발아 관련 유전자를 분석하고, MAS용 분자표지를 제작하여 국내 내수발아 계통 육성을 위한 육종효율 증진에 기여하고자 한다.

***교신저자:** Tel. 063-238-5215, E-mail: cropas@korea.kr

PE-0094

QTL analysis was performed on the data of material composition analysis of rice leaves after BLB inoculation by HPLC (*Oryza sativa* L.)

Xiao-Xuan Du[1,2], Kyung-Min Kim[2], Gang-Seob Lee[1*]

[1]National Institute of Agricultural Science, Rural Development Administration, 370 Nongsaengmyeong-ro, Jeonju-si, 54874, Republic of Korea

[2]Coastal Agriculture Research Institute, Kyungpook National University, Daegu 41566, Republic of Korea

The quantitative trait data used in general QTL analysis are all traditional phenotypic traits in the phenotype (traits that can be observed and measured with the naked eye). However, in this method, we use the peak area data of each substance component in the HPLC analysis results of each leaf in the CNDH population after BLB inoculation as quantitative trait data and perform QTL analysis. At the same time, through the HPLC analysis results of each leaf sample, the peak area of each substance component corresponds to the infection length of each leaf for correlation analysis. We can not only obtain the gene interval of BLB resistance in each chromosome, but also confirm which of these substances are related to the length and resistance of each leaf surface lesion after BLB inoculation. This method can provide a wider range of applications for future QTL technology, and it also means that the significance of phenotypes and main analysis methods in various research fields has been further deepened.

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

PE-0095

QTL analysis of the leaf surface infection length data of rice inoculated with BLB to screen the major resistance genes (*Oryza sativa* L.)

Xiao-Xuan Du[1,2], Kyung-Min Kim[2], Gang-Seob Lee[1*]

[1]National Institute of Agricultural Science, Rural Development Administration, 370 Nongsaengmyeong-ro, Jeonju-si, 54874, Republic of Korea
[2]Coastal Agriculture Research Institute, Kyungpook National University, Daegu 41566, Republic of Korea

Bacterial leaf blight (BLB) is an important and devastating rice disease caused by the pathogen Xanthomonas oryzae pv. oryzae (Xoo). The Cheongcheong/Nagdong double haploid (CNDH) line used in this research shows a distinct phenotype due to the fixation of genes through many generations. QTL analysis is to obtain the target region in each chromosome where the target gene that affects the trait is located by combining the data of the associated trait and the molecular markers of the genetic map. This makes the sorting of candidate genes and the screening of target genes more targeted. In this research, we found OsWRKYq6 gene, detected through QTL mapping from Chromosome 6 of CNDH population, it showed a significant difference when selecting the BLB resistance line and the susceptible line from the CNDH population and confirming the relative gene expression levels, was expressed at a high level in the BLB resistance line. It will help to development a new breed by releasing the OsWRKYq6, which has identified traits and genetic characteristics using an CNDH population among the QTL results. These lines not only can create cultivars right away, but also serve as intermediate models that can be transgenic into excellent cultivars.

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

PE-0096

QTL analysis of microscopic traits of rice BLB (Bacterial Leaf Blight) using OCT (Optical Coherence Tomography) technology (*Oryza sativa* L.)

Xiao-Xuan Du[1,2], Kyung-Min Kim[2], Gang-Seob Lee[1*]

[1]National Institute of Agricultural Science, Rural Development Administration, 370 Nongsaengmyeong-ro, Jeonju-si, 54874, Republic of Korea
[2]Coastal Agriculture Research Institute, Kyungpook National University, Daegu 41566, Republic of Korea

Humans have consciously domesticated animals and plants according to their needs long ago, and the history of the investigation of the phenotypes of animals and plants is much earlier than that of the genotypes. In recent years, with the rapid development of high-throughput sequencing technology, the study of genotypes has become simpler and faster. However, due to the complexity of the plant phenotype itself and the characteristics of dynamic changes, phenotypic research lags behind genotype research seriously.

Accompanied by the continuous deterioration of the world's environmental resources and the increasingly severe food crisis. In the future, agriculture will gradually deepen the research in various fields of resistance breeding. We found that the research on macroscopic visualization traits has gradually entered a bottleneck period. In this research, we have introduced high-throughput oct technology to observe the microscopic traits of plants. Using these micro traits data for QTL analysis, we successfully screened out the candidate genes for related BLB resistance in different intervals were screened out.

At the same time, the QTL results also showed that the target interval shown by the QTL results before and after the inoculation obtained through the microscopic trait data has perfect coincidence. It shows that the application of microscopic traits in the field of QTL and molecular breeding is effective and accurate.

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

PE-0097

Identification of a Novel Chimeric Gene for Cytoplasmic Male Sterility from the cytoplasm of the *indica* Rice (*Oryza sativa* L.) cultivar Tetep

Zhuo Jin[1], Jeonghwan Seo[1,2], Backki Kim[1], Seung Young Lee[1], Hee-Jong Koh[1*]

[1]Department of Agriculture, Forestry and Bioresources, Plant Genomics and Breeding Institute, Research Institute for Agriculture and Life Sciences, Seoul National University, Seoul 08826, Korea
[2]Department of Plant Bioscience, Life and Industry Convergence Research Institute, College of Natural Resources and Life Science, Pusan National University, Miryang 50463, Korea

Tetep cytoplasmic male sterility (Tetep-CMS) was developed through successive backcrosses between subspecies *indica* and *japonica* in rice (*Oryza sativa* L.), which showed abnormal anther dehiscence phenotypes. The mitochondrial genome of Tetep-CMS was completed through whole genome sequencing and de novo assembly. A novel chimeric gene *orf312* was identified from the Tetep-CMS mitochondrial genome which possesses a transmembrane domain and overlaps with two mitotype-specific sequences (MSSs) that are unique to the Tetep-CMS line. The encoded peptide of *orf312* was toxic to *Escherichia coli* and inhibited cell growth compared to the control under isopropyl-β-D-1-thiogalactopyranoside (IPTG) induction. The peptide of *orf312* contains COX11-interaction domains, which are thought to be a main functional domain for *WA352c* in the wild abortive (WA) CMS line of rice. Further studies on *orf312* and isolation will help to identify the underlying molecular mechanism of mitochondrial ORFs with the COX11-interaction domains.

***Corresponding Author:** Tel. 02-880-4541, E-mail: heejkoh@snu.ac.kr

PE-0098

Mapping of QTLs for starch-related traits in *japonica* rice

Cheryl Adeva[1], Hyun-Sook Lee[2], Sun-Ha Kim[1], Yun-A Jeon[1], Kyu-Chan Shim[1], Ngoc Ha Luong[1], Ju-Won Kang[3], Chang-Soo Kim[1], Jun-Hyeon Cho[3], Sang-Nag Ahn[1]*

[1]Department of Agronomy, Chungnam National University, Daejeon 34134, Republic of Korea
[2]Crop Breeding Division, National Institute of Crop Science, Rural Development Administration, Wanju, 55365, Republic of Korea
[3]Department of Southern Area Crop Science, National Institute of Crop Science, Rural Development Administration, Miryang 50424, Republic of Korea

Cereals high in both amylose content (AC) and resistant starch (RS) content provide potential health benefits to human. In this study, a recombinant inbred line (RIL) population consisting of 92 lines derived from two *japonica* cultivars ‘Dodamssal’ and ‘Hwayeong’ with large differences in their AC and RS content was used to identify quantitative trait loci (QTLs) associated with starch-related traits in a two-year field experiment. Three QTLs for AC on chromosomes 2, 6, and 11 and one QTL on chromosome 2 for RS content were identified in RILs. Among three QTLs for AC, two QTLs on chromosomes 2 and 6 allelic to starch branching enzyme 3 (*SBE3*) and granule-bound starch synthase 1 (*GBSS1*) were accountable for the high phenotypic variation in both years and the Dodamssal alleles increased the AC value. As *SBE3* and *GBSS1* had large effects on AC value, the combined effect of both genes in F_2 population suggested that they acted in an additive manner in increasing AC. Based on two SNPs in *GBSS1*, haplotype analysis classified 117 rice accessions into three groups. The Wx^a allele at the 5′ splice site of intron 1 was mainly occurred in all *indica*, Korean landrace, and weedy rice accessions whereas *japonica* accessions had the mutated Wx^b. Our results suggest that starch-related properties of rice could be regulated through the combined action of *SBE3* and *GBSS1*. In addition, the Wx^a allele in landrace or weedy rice accessions could be utilized in rice breeding programs to alter AC in cultivated *japonica* rice.

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***Corresponding Author:** Tel. 042-821-5728, E-mail: ahnsn@cnu.ac.kr

PE-0099

Differential roles of three transmembrane domains of rice phytoene synthase 2 for sub-organellar localization in chloroplasts

Ji Su Yu†, Min Kyoung You†, Yeo Jin Lee, Sun-Hwa Ha*

Department of Genetics and Biotechnology, Graduate School of Biotechnology, College of Life Sciences, Kyung Hee University, Yongin-si 17104, Korea

Chloroplasts are complexes of membranous sub-organelles including plastoglobules (PGs), which are known as a main factory for terpenoids-derived metabolites such as carotenoids. Phytoene synthase (PSY) is the first committed enzyme in the carotenoid biosynthesis. Three PSY genes have been annotated in rice and their PG-localization have been presented. Previously, we reported the function of transit peptide of OsPSY2 (PTp) including two transmembrane domains (PTM1 and PTM2) showing dual potentials as stroma and PG-targeting signals. Interestingly, OsPSY2 has another TM domain (PTM3) in the mature protein region. To elucidate their sophisticated roles as targeting signals, we examined the effects of PTM1, 2 and 3 on localization among plastidic sub-organelles by production of diverse GFP fusion proteins. As results, a PTM1 was a stroma-localized signal. No PTM2 alone acts as a transit peptide showing cytosol localization. However, PTM2 was a partial PG-localized signal when fused with a transit peptide of RuBisCO small subunit (RTp) in N-terminus (RTp-PTM2-GFP) displaying blurred stromal signal and spot-like PG signal together. In case of PTM3, a RTp-GFP-PTM3 showed the precise PG-targeting but a RTp-PTM3-GFP was barely targeted to PGs, suggesting positional effect. In summary, a PTM1 can act alone as a transit peptide, PTM2 has a dual targeting ability of stroma and PGs, and a PTM3 is a surefire PG-targeting signal. Eventually, each TM is differently functional and very crucial to PG-targeting of OsPSY2 and the position of TMs is also critical to it. Using this, it is possible to control the elaborate sub-organellar localization in chloroplasts.

† Co-first authors who contributed equally.

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

PE-0100

Overexpression of chorismate mutase mitigate UV and drought combined stress via alteration of proline and aspartic acid accumulation in rice

Nari Kim, Kyung-Min Kim*

Division of Plant Biosciences, School of Applied Biosciences, College of Agriculture and Life Science, Kyungpook National University, Daegu 41566, Republic of Korea

Salinity, drought, UV-light and high temperature are common abiotic stresses which causes several physiological and molecular changes in plant and leading to yield losses. To deal with these stresses, either to adopt to the stress condition or to develop transgenic plants. In this study, we assessed the effect of UV and drought combined stresses on Cheongcheong and Chorismate mutase transgenic rice plant. Combined stresses cause oxidative stress due to imbalance osmoregulation. In the current experiment, we used Cheongcheong-control, Cheongcheong-treated and OxCM-treated plants and applied UV and drought stresses. Samples were collected after 0, 3, 6, 12, and 24hr exposer to stress condition. We used trypan blue and DAB histochemical analysis to detect the oxidative stress, confocal microscope for detection of accumulation of kaempferol and quercetin in leaf and roots and also checked the phenotypic variation. Many staining spots were detected at Cheongcheong-treated compared to OxCM-treated in DAB and Trypan blue staining. It signifies that OxCM-treated were reduced oxidative stress. OxCM-treated plants appeared a high level of kaempferol and quercetin accumulation. Root and shoot length and leaf width of OxCM-treated were observed higher than the other plants. As a result, OxCM-treated plants were tolerant to combined stress.

***Corresponding Author:** Tel. 053-950-5711, E-mail: kkm@knu.ac.kr

PE-0101

Identification of quantitative trait loci and screening major secondary metabolite-related gene, *OsF3H*, which is resistance to whitebacked planthopper

Eun-Gyeong Kim, Kyung-Min Kim*

Division of Plant Biosciences, School of Applied Biosciences, College of Agriculture and Life Science, Kyungpook National University, Daegu 41566, Republic of Korea

Whitebacked planthopper (WBPH) is a destructive pest that causes serious damage that yields losses to rice in Asian countries. Finding, characterizing WBPH resistance genes have become increasingly recognized as an efficient approach to cope with the frequent infestations by WBPH. In this research, quantitative trait locus (QTL) were mapped that are related to WBPH using a Cheongcheong/Nagdong double haploid 120 population. The *qWBPH4-1* which is resistant to WBPH were mapped on the same region chromosome 4, with a LOD of 3.5. The SSR Marker interval of *qWBPH4-1* was derived from Cheongcheong. This region includes candidate genes such as kinases, transcript factor regulators, related phytohormone signaling, and secondary metabolite synthase that defend plants from environmental stress. Finally screening *OsF3H* that are similar to the flavanone 3-hydroxylase (*F3H*) of rice in this region. The sequence has been found not only in *Oryza sativa* but also in *Zea mays*, *Prunus avium*, *Vitis vinifera*. The *OsF3H* are homologous genes, which play an important role in biosynthesis defending against biotic stress in plants. After WBPH inoculation, the relative expression level of *OsF3H* was higher in resistant population than in susceptible population. The result has significant implications in researching the interactions between insects and plants. The newly detected by QTL mapping can be used for the breeding program of rice cultivars that are resistant to WBPH.

***Corresponding Author:** Tel. 053-950-5711, E-mail: kkm@knu.ac.kr

PE-0102

QTL analysis of chlorophyll content-related traits in rice leaf

Yoon-Hee Jang, Jae-Ryoung Park, Eun-Gyeong Kim, Kyung-Min Kim*

Division of Plant Biosciences, School of Applied Biosciences, College of Agriculture and Life Science, Kyungpook National University, Daegu 41566, Republic of Korea

Photosynthesis occurs in chloroplasts, and chlorophyll (chl) plays the most important role in photosynthesis by absorbing light energy in the chloroplasts of plant leaves. The yield of crops depends on the scale and efficiency of the photosynthetic system, so the chlorophyll content of leaves affects the yield of rice. In this study, we measured color space, chlorophyll content, and chlorophyll fluorescence of rice leaves after the heading date using a 120 Cheongcheong/Nagdong double haploid (CNDH) population, and performed quantitative trait loci (QTL) mapping. Chlorophyll content showed a highly significant correlation with yield. Also, the Hue angle, which indicates the leaf color, and the maximum quantum yield (Fv/Fm) of Photosystem II, which indicates the potential for photosynthesis, showed a significant correlation with the chlorophyll content. 26 QTLs for 6 traits were identified in 8 chromosomes. 16 QTLs (*qCa*, *qCb*, *qHa*, *qCab*) related to leaf color were detected on chromosome 1, 2, 3, 6, 7, 8, 12, and 8 QTLs (*qCc*) related to chlorophyll content were detected on chromosome 1, 6, 7, 11, 12 and 1 QTL (*qPe*) related with photosynthetic efficiency was detected on chromosome 3. These results provide a basis for the search for and functional studies of genes involved in chlorophyll content, which is important for the photosynthetic performance of rice in heading stage.

***Corresponding Author:** Tel. 053-950-5711, E-mail: kkm@knu.ac.kr

PE-0103

Screening and identification of major QTLs which reduce the deleterious effects of high temperature on rice starch content and structures

Jae-Ryoung Park[1,2], Eun-Gyeong Kim[1], Yoon-Hee Jang[1], Kyung-Min Kim[1,2*]

[1]Division of Plant Biosciences, School of Applied Biosciences, College of Agriculture and Life Science, Kyungpook National University, Daegu 41566, Republic of Korea

[2]Coastal Agriculture Research Institute, Kyungpook National University, Daegu 41566, Republic of Korea

Most crops, including rice, are severely negatively affected by unpredictable climate change. Rice is affected differently by high temperatures depending on the growth stage. When subjected to high-temperature stress from the heading date to the grain filling stage, the yield decreases and a chalkiness grain is formed. Chalkiness grains are formed due to problems in the sugar/energy signaling system, and the amylose content decreases. In this research, the effect of high temperature on rice phenotype, content of major nutrients, and major agricultural traits was analyzed, and candidate genes that may be involved in high-temperature resistance were searched through QTL mapping. When QTL mapping was analyzed after high temperature treatment, QTLs were detected with LOD score of 3.0 or higher in RM15749-RM15689 on chromosome 3 and RM149-RM23191 on chromosome 8. There were numerous ORFs related to high-temperature in these areas, and they were classified according to their respective functions. Finally, *OsSFq3* was screened, and the relative expression level of *OsSFq3* was higher in the tolerance line than in the susceptible line under high temperature conditions. *OsSFq3* has high homology with sugar signaling proteins, and can be effectively used for cultivating high-temperature resistant rice varieties in the future.

***Corresponding Author:** Tel. 053-950-5711, E-mail: kkm@knu.ac.kr

PE-0104

벼 친환경재배 복합내병충성 유전자원 ‘제이제이621엠알’

백만기[1*], 김우재[2], 박현수[1], 조영찬[1], 서정필[1], 이창민[1], 정오영[1], 이점호[1]

[1]전라북도 완주군 이서면 혁신로 181 농촌진흥청 국립식량과학원
[2]전라북도 전주시 완산구 농생명로 300 농촌진흥청

‘제이제이621엠알’은 벼 친환경재배를 위한 육종소재를 개발하기 위하여 기존의 품종보다 내병충성이 강화된 품종 육성을 목적으로 국립식량과학원에서 2011/2012년 동계에 밥맛이 좋고 쌀 외관이 좋으며 단간인 중생 복합내병성 익산537호(해품)을 모본으로 하고 벼멸구저항성 Bph18 유전자를 가고 있는 HR28354-AC34-4을 부본으로 교배하여 생육이 우수하고 균일하며 복합내병충성인 계통을 육성하였다. 인공교배로 교배립 25립을 수확하였고 이 교배립은 세대진전을 위하여 2012년 하계에 국립식량과학원 벼육종포장에서 F1 20개체를 재배하였다. 우량품종을 조기 육성하기 위하여 F2 1,100개체를 양성하였고 이후 계통육종법으로 육성하였다. 2014년 F3이후부터는 초형과 수량성, 미질, 잎도열병검정, 흰잎마름병검정을 실시하여 F3에서 120계통, F4에서 50계통, F5에서 40계통을 선발하였고, 2016년과 2017년에 우수계통인 HR30110-22-3에 대하여 계통육성과 동시에 생산력검정을 실시하였고 생육특성, 수량성, 내병성(도열병, 흰잎마름병, 줄무늬잎마름병), 벼멸구저항성, 밥맛, 쌀 외관 품위가 우수한 HR30110-22-3-3-1 계통을 선발 ‘전주621호’로 계통명을 부여하였다. ‘전주621호’는 2018~2020년 전국 8개소에 보통기 재배에서 지역적응시험을 실시한 결과 중생종으로 초형이 우수하고, 도복과 수발아에 강하며 복합내병성(도열병, 흰잎마름병(K1-K3a), 줄무늬잎마름병), 벼멸구 저항성 계통으로 2020년 12월 농촌진흥청 농작물직무육성 신품종선정심의회에서 그 우수성이 인정되어 품종명을 ‘제이제이621엠알(JJ621MR)’으로 명명하였고 친환경재배를 위한 복합내병충성 중간모본으로 활용계획이다.

***교신저자:** Tel. 063-238-5213, E-mail: baekmg@korea.kr

PE-0105

Breeding and growth characteristics of a newly bred *Lentinula edodes* strain, Chungheung 1

Gu-Min Jeong[1], Eui-Young Joung[1], Hea-Young Jung[1], Myoung-Jun Jang[2*]

[1]Cheongheung Mushroom Farming Association Corporation, Cheongyang, Chungnam, Republic of Korea
[2]Department of Plant Resources, Kongju National University, Yesan, Chungnam, Republic of Korea

This study was conducted to foster medium and low temperature varieties suitable for Korean conditions with the aim of responding to the influx of foreign varieties and diversifying them for year-round production, along with securing domestic *Lentinual edodes* genetic resources in the seed war. For the cultivation of *Lentinual edodes*, new varieties were cultivated through the hybrid breeding method, and the cultivated strains were subjected to DNA polymorphism assay using 11 URP-primers. It was confirmed the formation of PCR polymorphic bands in six primers. As a result of examination of fruiting body characteristics, 'Chungheung 1ho' showed a smaller diameter of cap and longer stipe, and a thicker stipe compared to the control variety. In addition, the number of germination and growth days for each strain showed a tendency of 'Chungheung 1ho' to be delayed by about 20 days compared to the control variety. The empirical test for 'Chungheung 1ho' was conducted for two years from 2018 to 2019, and as a result of the empirical test, it was confirmed that the experimental strain takes 170 to 180 days, including culture and ripening period, from strain inoculation to mushroom generation. Mushroom-generating temperature type was suitable for cultivation from late autumn to spring of the following year as it is medium-low temperature.

***Corresponding Author:** Tel. 041-330-1204, E-mail: plant119@kongju.ac.kr

PF-0001

Identification of a Novel Haplotype of the *Ms* Locus Controlling Restoration of Male-Fertility and Its Implication in Origination of Cytoplasmic Male-Sterility in Onion (*Allium cepa* L.)

Taeheon Kim, Sunggil Kim*

Department of Horticulture, Biotechnology Research Institute, Chonnam National University, Gwangju 61186, Republic of Korea

Seeds of F_1 hybrid cultivars of onions have been exclusively produced by utilizing cytoplasmic male-sterility (CMS). A single locus, *Ms*, controls restoration of male-fertility of CMS onions. When a molecular marker tagging the *AcPMS1* gene, a candidate gene for the *Ms* locus, was used to genotype diverse breeding lines, an unusual marker genotype showing an intermediate size of PCR product was identified in one breeding line (ORI854). The male-fertility phenotype of ORI854 was all male-sterile. Full-length genomic DNA sequence (16,464 bp) of this novel *AcPMS1* allele from ORI854 was more closely related to a recessive *AcPMS1* allele than to a dominant allele. However, there were more than 200 polymorphic sequences between this novel allele and the recessive allele, indicating that this novel *AcPMS1* allele might not have recently diverged from the recessive allele. Phylogenetic analysis implied that onion male-sterility might have first appeared in a common ancestor before divergence of this novel allele and recessive allele of *AcPMS1*. Analysis of full-length cDNA sequences of additional 12 genes showing almost perfect linkage disequilibrium with the *Ms* locus indicated that no recombination might have happened among 13 genes including *AcPMS1* in the novel *Ms* haplotype after divergence from the recessive *Ms* haplotype.

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

PF-0002

Construction of a High-density Integrated Genetic Linkage Map Using Genotyping-by-Sequencing Analysis in an Interspecific Pear hybrid (*Pyrus* spp.)

Keumsun Kim*, Haewon Jung, Arang Kang, Janghoon Song, Sam-Seog Kang

Pear Research Institute, National Institute of Horticultural & Herbal Science, Rural Development Administration, Naju 58216, Republic of Korea

Pear (*Pyrus* spp.) is an economically important fruit tree grown extensively worldwide. To facilitate the identification of agronomically important traits and provide new information for genetic and genomic research on this fruit tree, a high-density integrated genetic linkage map of pear was constructed using 187 F_1 population derived from a cross between ‘Manpungbae’ (*P. pyrifolia*) and ‘Ooharabeni’ (*P. pyrifolia* × *P. communis*). Single nucleotide polymorphisms (SNPs) detected by genotyping-by-sequencing (GBS) and simple sequence repeats (SSRs) developed from ‘Wonhwang’ (*P. pyrifolia*) were analyzed for construction of genetic linkage map. The SSR marker was used for locating the corresponding chromosome number for each linkage group (LG). A total of 1,807 GBS-SNPs and 41 SSRs were anchored to integrated genetic linkage map. Seventeen LGs were identified, which covered a genetic distance of 1,519.4 cM with an average marker density of 0.87 cM. The length of the LGs ranged from 70.9 cM (LG 14) to 160.4 cM (LG 15). Each LG has SSR markers from 1 to 5 except for LG 7, 8, and 9. Our integrated genetic map of pear could be used as a basic frame map for comparative analysis of genomic structure between different research groups in pear.

***Corresponding Author:** Tel. 061-330-1543, E-mail: keumsunk@korea.kr

PF-0003

수박 대목용 박과채소 유묘의 온도별 생육특성

김태복*, 이옥진, 김상규

농촌진흥청 국립원예특작과학원 채소과

수박 재배 시 대목으로 주로 이용하고 있는 박, 호박, 야생수박 유묘의 생육온도별 지상부와 지하부 발달정도를 비교하기 위한 시험을 수행하였다. 작물별로 각 10계통의 종자를 32공 육묘트레이에 파종 후 유리온실에 7일간 두었다가 12℃와 36℃ 생장상으로 옮겼다. 대조구는 유리온실에서 재배하였고 재배기간 중 온도는 평균 23.4℃, 최저 17.6℃, 최고 37.9℃였다. 온도처리를 시작하고 25일 후에 지상부(초장)과 지하부(뿌리무게) 생육을 조사하였다. 대조구, 36℃, 12℃ 순으로 지상부, 지하부 모두 생육량 많았다. 대조구와 비교했을 때 박, 호박, 수박 모두 12℃와 36℃처리구에서 지상부보다 지하부의 발달이 상대적으로 더 부진했고, 특히 12℃에서는 지하부 발달이 극히 제한적이었다. 수박은 박과 호박에 비해 모든 처리구에서 뿌리 발달이 부진했다. 12℃에서는 호박, 대조구와 36℃에서는 박의 뿌리발달이 가장 우수했다. 처리구/대조구 값을 비교했을 때 12℃, 36℃에서 지상부는 수박이 각각 50.9와 91.4, 지하부는 호박이 각각 10.1과 38.9로 대조구 대비 생육이 가장 양호하였다.

***교신저자:** Tel. 063-238-6641, Fax. 063-238-6605, E-mail: biok@korea.kr

PF-0004

Construction of an Onion (*Allium cepa* L.) Genetic Linkage Map using Genotyping-by-Sequencing and Identification of QTLs Controlling Sugar Contents

Hye-Eun Lee*, Ye-Rin Lee, Eun Su Lee, Koeun Han, JiWon Han

Vegetable Research Division, National Institute of Horticultural and Herbal Science, RDA, 100, Nongsaengmyeong-ro, Iseo-myeon, Wanju-gun, 55365, Jeollabuk-do, Republic of Korea

Onion (*Allium cepa* L.) (2n=2x=16) is a widely cultivated vegetable crop since ancient times due to its nutritional value. Genetic linkage maps facilitate the identification of quantitative trait loci (QTLs) associated with vital traits and thus aids in the molecular breeding of crops. However, genetic linkage map of onion remains relatively basic because onion has a large genome (about 16.3 Gbp), biennial life cycle, cross-pollinated, and high inbreeding depression. Therefore, high-resolution genetic map is certainly required for the accurate assembly of highly quality reference genome. In this study, we constructed a single nucleotide polymorphism (SNP)-based high-resolution genetic linkage map of onion using an F_2 segregating population derived from a cross between the F_1 hybrid doubled haploid line '16P118' and 'Sweet Green' through genotyping-by-sequencing (GBS). The genetic map was utilized for the identification of QTLs associated with traits controlling sucrose, glucose, fructose, and total sugar contents. A total of 207.3 Gbp of raw sequences were generated using Illumina HiSeq X system and a total of 815 SNPs were identified with the criteria of three minimum depths lower than 60% missing rate, and more than 5% minor allele frequency (MAF). As a result, an onion genetic linkage map consisting of 216 GBS-based SNPs were constructed with eight linkage groups with the entire genetic distance of 827.0 cM. In addition, the linkage groups were compared to the previously reported onion genetic linkage map, SP3B x H6. We identified four QTLs associated with *qSC4.1* (sucrose), *qGC5.1* (glucose), *qFC5.1* (fructose), and *qTSC5.1* (total sugar content) detected on linkage groups 4 and 5, respectively. The phenotypic variation (R^2 values) were distributed in the range of 6.07 - 11.47 %. The present high-density genetic linkage map and QTL information will contribute to the development of markers and breeding Onions with high sugar contents.

***Corresponding Author:** Tel. 031-238-6674, E-mail: helee72@korea.kr

PF-0005

Genomic selection using SNPs derived from genome-wide association study for capsaicinoid content in pepper (*Capsicum* spp.)

Geno Woo Kim[1], Ju-Pyo Hong[1], Hea-Young Lee[1], Jinkwan Jo[1], Jin-Kyung Kwon[1], Dong-Am Kim[2], Byoung-Cheorl Kang[1*]

[1]Department of Agriculture, Forestry and Bioresources, Research Institute, College of Agriculture and Life Sciences, Seoul National University, 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Republic of Korea
[2]HANA Seed. Co., Ltd., R&D Center, Anseong 17601, Republic of Korea

Pepper (*Capsicum* spp.) is an economically important vegetable crop because of its unique characteristics of pungency. There are many genes controlling the capsaicinoid content, which makes it difficult to develop pepper cultivars with various capsaicinoid content. Genomic selection (GS) is a method of predicting the plant phenotypes in a breeding population using genome-wide markers and statistical models to achieve more reliable selection. In this study, SNPs obtained from the genome-wide association study (GWAS) were used in the modeling process of GS to improve the power of GS. For GS, a core collection consisted of 351 accessions and 96 elite lines from a seed company were used as a training set and a testing set, respectively. The genome-wide SNPs or SNPs selected from GWAS were used in the modeling process. The precidtion was the highest when 3,294 SNPs were used, and the lowest when 896 SNPs were used. The highly significant 98 SNPs were obtained from GWAS for capsaicinoid content. The average prediction accuracy of the model using the 98 SNPs was 0.583. Furthermore, the prediction accuracy using SNPs derived from GWAS were much higher than that of 896 SNPs despite smaller number of markers. These results demonstrated that a high prediction accuracy can be obtained for capsaicinoid content in pepper with a small number of markers derived from GWAS.

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

PF-0006

GIGANTEA reduced Chinese cabbage sprouts (*Brassica rapa* L.) improved of health-related total phenol, total flavonoid and spontaneously reduced of glucosinolates

Nan-Sun Kim, Hyo Seon Choi, Soo In Lee, Jin A Kim*

Department of Agricultural Biotechnology, National Academy of Agricultural Science, Rural Development Administration, 370, Nongsaengmyeong-ro, Deokjin-gu, Jeonju-si, Jeollabuk-do, Korea, 54874

In the previous study, we developed that *GIGANTEA* (*GI*) gene reduced Chinese cabbage (GK1) enhanced salt tolerance in *Brassica rapa* L. We tested whether *GI* gene mutated Chinese cabbage will be changed the secondary metabolites accumulation including total phenol, total flavonoid and glucosinolates (GSLs) under white, red and blue light quality. We found that the fresh weights, hypocotyl length and cotyledon area of GK1 sprouts were higher than those of DH03 (negative control) exposed to three kinds of light quality. Hypocotyl lengths of blue light-irradiated sprouts of both DH03 and GK1 were higher than those of sprouts exposed to white and red light. Cotyledon areas of red light-irradiated sprouts both DH03 and GK1 were higher than those of sprouts exposed to white and blue light, whereas root length was not notably different among white, red and blue light treatments. The accumulation of total phenol, total flavonoid and antioxidant ability of GK1 sprouts were improved more than DH03 in three kinds of light quality. Especially, the sprouts exposed to blue light both DH03 and GK1 showed 1.3 times higher than other light quality. The accumulations of total GSLs both DH03 and GK1 sprouts irradiated with white, red, and blue lights were not significantly different. However, we found that GSL levels in GK1 sprouts reduced to 57-66 % compare to that of DH03 under three kinds of light quality. These results demonstrate that red light-emitting diode (LED) light is suitable for sprout growth and that blue LED light is effective the accumulation of secondary metabolites in *B.rapa.*

***Corresponding Author:** Tel. 063-238-4619, E-mail: jakim72@korea.kr

PF-0007

Development of Primer Sets for the Real-Time PCR Analysis of Carotenoid Pathway Gene Expression in Citrus

Chang Jae Oh[1], Eun-Sil Kim[1], Hye-Young Lee[1], Minju Kim[2], Cheol Woo Choi[2], Su-Hyun Yun[2], Ju Won Lee[3], Yi Lee[4], Kwan Jeong Song[5], Ho Bang Kim[1*]

[1]Life Sciences Research Institute, Biomedic Co., Ltd., Bucheon 14548, Korea
[2]Citrus Research Institute, National Institute of Horticultural & Herbal Science, Seogwipo 63607, Korea
[3]Seed Business Department, Jenong Co., Ltd., Jeju 63309, Korea
[4]Department of Industrial Plant Science and Technology, Chungbuk National University, Cheongju 28644, Korea
[5]Major of Horticultural Science, Faculty of Bioscience and Industry, Jeju National University, Jeju 63243, Korea

Carotenoids, a family of isoprenoid molecules, are natural pigments essential for the coloration of various organs in many plant species. Carotenoids are not only pigments, but also act as membrane stabilizers and play key roles in photosynthesis. Moreover, they are beneficial to human health by acting as health-promoting phytonutrients that have been linked to the prevention of degenerative processes, certain cancers and cardiovascular illness. Citrus fruit is an important reservoir of carotenoids. Because of their important functional roles, many efforts have been made to identify genes involved in carotenogenesis and factors that regulate carotenoid formation and deposition in plants. In this study, in order to better understand the molecular biological aspects of carotenoid biosynthesis and its regulation in citrus cultivars and F_1 individuals, we mined carotenoid pathway genes from two citrus reference genomes and resulted in the identification of 34 isoforms of 16 gene groups involved in biosynthetic steps and a transcription factor (TF) encoding MADS protein. We established real-time PCR primer sets for the mined 17 genes (16 biosynthetic genes and one TF gene) and their PCR conditions including PCR efficiency and primer specificity, and applied them to analyze gene expression patterns in fruit peel/flesh of two representative citrus cultivars, *Citrus clementina* and *C. sinensis*.

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***Corresponding Author:** Tel. 032-218-1515, E-mail: hobang@ibiomedic.co.kr

PF-0008

철쭉 유전자원의 형태적 특성과 RAPD 방법에 의한 분류

정효진*, 최재진, 윤영범

전라남도 순천시 순천만관리센터 정원산업과

순천시는 철쭉류 14,765,765본, 전국의 54%(2019 임산물생산조사, 산림청)를 생산하는 주산지이다. 주산지로서 정원식물산업 육성 및 순천지역에서 생산되는 철쭉 차별화를 위해 2019년부터 철쭉 신품종 개발을 시작하였으며 겹산철쭉 등 45종의 철쭉류 유전자원을 수집하였다. 이 중 35종의 화형, 꽃잎 수 등 수집 품종의 형태적 특성을 조사하였고 유전적 관계 분석을 위해 24종의 프라이머(Zhou et al., 2009)를 이용하여 RAPD 방법에 의해 PCR 증폭 중이다. 지금까지 24종 프라이머 중 M5, K12, R10, AB2 등 17종의 프라이머에 대한 PCR 증폭을 완료하였다.

***교신저자:** Tel. 061-749-2946, E-mail: jhj81@korea.kr

PF-0009

Fine mapping and candidate gene identification for the *CapUp* locus controlling fruit orientation in pepper (*Capsicum* spp.)

Tae-Gun Kim[1*], Abate Mekonnen Solomon[2*], Koeun Han[2], Hea-Young Lee[2], Abhinandan Patil[2], Muhammad Irfan Siddique[2], Jeonghwan Ahn[3], Byoung-Cheorl Kang[1,2*]

[1]Interdisciplinary Program in Agricultural Genomics, Department of Agriculture, Forestry and Bioresources, Research Institute of Agriculture and Life Sciences, Plant Genomics Breeding Institute, College of Agriculture and Life Sciences, Seoul National University, Seoul, Republic of Korea
[2]Department of Agriculture, Forestry and Bioresources, Research Institute of Agriculture and Life Sciences, Plant Genomics Breeding Institute, College of Agriculture and Life Sciences, Seoul National University, Seoul, Republic of Korea
[3]ECOSEED, Hajeong-ro, Baeksan-myeon, Gimje-si 54324, Jeonbuk, Republic of Korea

The orientation of fruits is a distinguishing morphological feature of pepper (*Capsicum* spp.) varieties. The pendent (downward curved) growth of the fruit stalks, known as pedicels, is highly correlated with fruit weight and pedicel length. A previous genetic analysis revealed that the pendent fruit orientation is governed by a dominant gene, and incomplete inheritance is also observed in some *Capsicum* accessions. To identify and localize this gene, a single quantitative trait locus (QTL) analysis was performed on one F_2 and two recombinant inbred line (RIL) populations, and a genome-wide association study (GWAS) was performed using a core collection. Common QTL regions associated with fruit orientation were detected on chromosome 12. A total of 187,966 SNPs were identified in a genotyping-by-sequencing (GBS) for GWAS analysis of 196 *C. annuum*, 25 *C. baccatum*, 21 *C. chinense*, and 14 *C. frutescens* accessions, representing the germplasm collection of Korea. The results of these analyses enabled us to narrow down the *CapUp* region of interest to 200-250 Mbp on chromosome 12. Seven candidate genes were found to be located between two markers that were completely cosegregated with the fruit orientation phenotype. The findings and markers developed in this study will be helpful for additional understanding of pepper fruit development and breeding for fruit orientation.

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

PF-0010

씨가 적고 당도가 높은 중생종 단감 ‘썬스위트’ 육성

김은경*, 박여옥, 손지영, 안광환, 윤혜숙

경상남도농업기술원 단감연구소

우리나라 단감 생산규모(’19년)는 재배면적 8,639 ha, 생산량 96천톤인데, 만생종의 비율이 88%로 편중되어 있다. 이로써 노동력의 일시집중, 홍수출하에 의한 가격하락 등의 문제점이 있다. 본 연구는 숙기가 빠른 단감 품종을 육성하여 만생종 편중 문제를 해소하고자 수행되었다. 2010년도에 중생종 단감 ‘단연104’를 모본으로 ‘태추’를 부본으로 교배하였다. 교배실생 98계통 중에서 씨가 적고 당도가 높은 ‘단연10-1-80’을 2015년에 1차 선발하였다. 이후 공대에 접목 증식하여 12주의 묘목을 양성하였다. 2018년부터 2020년까지 3년간 수체 생육과 과실 특성을 조사한 결과, 연차간 변이가 적고 과실품질이 우수하여 최종 선발하였다. ‘썬스위트’로 품종명칭을 정하고, 2021년 1월 품종보호출원 하였다. ‘썬스위트’의 숙기는 김해에서 10월 3일로 중생종이며, 만생종 ‘부유’(11월 10일)보다 38일 빠르다. 과중은 260 g으로 대과이고, 종자수는 평균 1.8개로 ‘부유’(4.0개)보다 적고, 당도는 16.7 °Bx로 ‘부유’(15.0 °Bx)보다 높은 고당도 품종이다. 과형이 균일하고, 수량산출 결과 5년생을 기준으로 나무당 약10 kg을 수확할 수 있었다.

***교신저자:** Tel. 055-254-1562, E-mail: kim2471@korea.kr

PF-0011

Optimization of the leaf-to-whole plant spread bioassay of pepper to determine the inheritance of bacterial wilt resistance against *Ralstonia solanacearum*

Ji-Su Kwon[1†], Yu-Jim Sim[1†], Jae-Young Nam[2], Seon-In Yeom[1,2], Won-Hee Kang[2*]

[1]Department of Horticulture, Division of Applied Life Science (BK21 four), Gyeongsang National University, Jinju 52828, Korea
[2]Institute of Agriculture & Life Science, Gyeongsang National University, Jinju 52828, Korea

The soilborne pathogen *Ralstonia solanacearum* (Rsol) is a causal agent of bacterial wilt (BW) and occur severe yield losses in chili peppers worldwide. The most effective method to control BW is breeding resistant cultivars. For this, a reliable and straightforward evaluation method is required to determine disease response for further breeding programs. Here, we developed a reliable leaf-to-whole plant spread bioassay for evaluating BW disease and then, using this, determined the inheritance of resistance to Rsol in peppers. *Capsicum annuum* 'MC4' following Rsol-infected leaves showed a clear resistant phenotype with less disease symptom, a restricted bacterial cell growth, and substantially up-regulation of defense-related genes compared to those in susceptible 'Subicho'. We also observed the spreading of wilt symptoms from the leaves to the whole plant in susceptible plants, which denotes the typical BW wilt symptoms similar to the root-drenching method. The method of evaluating resistance to BW was optimized, and we determined the genetic analysis for resistance inheritance. Consequently, the two major complementary genes related to the BW resistance trait were confirmed through evaluated parents, F_1 and 90 F_2 progenies. These could present an accurate evaluation to improve resistant pepper breeding efficiency against BW.

[†] These authors contributed equally to this work

***Corresponding Author:** Tel. 055-772-1917, E-mail: wh81kang@gmail.com

PF-0012

Toward to comparative analysis of plant stress-responsive transcriptomes through co-expression network in *Capsicum annuum L.*

Junesung Lee[1], Hakgi Jang[1], Nayoung Kim[1], Won-Hee Kang[2], Seon-In Yeom[1,2*]

[1]Department of Horticulture, Division of Applied Life Science, Gyeongsang National University, Korea
[2]Institute of Agriculture & Life Science, Gyeongsang National University, Korea

Environmental stress conditions such as drought, heat, salinity, cold, or pathogen infection can have a devastating impact on plant growth and yield under field conditions. In order to correspond with various environmental stresses, the transcriptional changes of defense-related and resistance genes are regulated to reduce the damage caused by stress. Next generation sequencing (NGS) technology is becoming widely useful to reveal and identify the expression profiling of all the genes in plants, which can construct the gene co-expression network to confirm interactions between genes. In this study, we present a roadmap for understanding plant stresses-responsive mechanisms by identifying expression patterns for complex environmental stresses using establishing a whole gene interaction network. Analysis was performed using 282 datasets of RNA-seq for abiotic stress, biotic stress, and signal molecules. The entire data removed the adapter and low-quality sequences based on Q20, and most of them had more than 80% of high-quality sequences. The expression of the genes was confirmed by mapping to the Pepper reference genome. An individual stress network was built through the DEG following each treatment. By re-integrating each network, a stress integration network was constructed, and the expression pattern of the network for each stress was confirmed. Further analyses to determine conserved and/or specific modules with candidate genes resistant to complex environmental stresses are in progress.

***Corresponding Author:** Tel. 055-772-1917, E-mail: sunin78@gnu.ac.kr

PF-0013

Genetic Mapping of *CaAN3* that Regulates Fruit-specific Anthocyanin Accumulation in Pepper (*Capsicum annuum*) via Bulked Segregant RNA-Seq

Jinyoung Byun, Joung-Ho Lee, Soyoung Jung, Byoung-Cheorl Kang*

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

The key regulatory gene *CaAN2* encoding R2R3 MYB transcription factor has been known to regulate anthocyanin biosynthesis in diverse tissues in pepper. *CaAN2* is not expressed in certain pepper accessions showing fruit-specific anthocyanin biosynthesis. In this study, a novel locus named *CaAN3* that regulates fruit-specific anthocyanin accumulation was investigated. An F_2 segregating population derived from *C. annuum* 'Japanese Purple Hybrid' was developed. Total RNA was extracted from F_2 plants and pooled according to purple and green phenotypes. Three RNA pools containing 6 individuals were prepared for each phenotype. Bulked Segregant RNA Sequencing (BSR-Seq) was conducted for two different RNA pools via Illumina platform. Average 121,311,633 reads were produced in each of the RNA pools, and total read bases per a pooled RNA were 12.3 Gbp. Raw Illumina sequences were aligned to a pepper reference genome and used to call SNPs between two BSR-Seq. A total of 12,836 significant SNPs were identified by calculating △ (SNP-index)i between two BSR-Seq data. The candidate gene was expected to locate at 0 ~ 100 Mb and 121.8 ~ 239.8 Mb regions on chromosome 10 according to SNP index analysis. Transcriptome analysis showed that 121 genes were differentially expressed between two phenotypes. Among them, 25 genes that showed significant differences in expression levels were selected as candidate genes of *CaAN3*.

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

PF-0014

Genetic mapping of a locus for restorer gene of Ogura cytoplasmic male sterility in radish (*Raphanus sativus* L.)

Koeun Han[1], Jieun Lee[1], Eun Su Lee[1], Muhammad Irfan Siddique[1], Hye-Eun Lee[1], Han Yong Park[2], Do-Sun Kim[1*]

[1]Vegetable Research Division, National Institute of Horticultural and Herbal Science, Rural Development Administration, Wanju 55365, Republic of Korea
[2]Sejong University, 209 Neungdong-ro, Gwangjin-gu, Seoul 05006, Republic of Korea

Ogura cytoplasmic male sterility (CMS) is widely used in Brassicaceae crops including radish for F_1 hybrid seed production. The first cloned restorer gene was *Rfo*, which was identified from European radishes. Another restorer gene named *Rft* was identified from Japanese wild radishes. In this study, we mapped a locus for restorer gene in a F_2 population derived from inbred lines widely used for Korean radish breeding. Presence/absence of pollens were observed and a total of 90 F_2 individuals were genotyped by 384 Fluidigm assays. The locus was mapped on chromosome 5, and one marker was tightly linked to the restorer phenotype. To identify the candidate genes and understand the fertility-restoring mechanism, additional studies like fine-mapping and complementation tests with the *Rfo* and *Rft* genes are required. The marker developed in this study will be useful for breeding new CGMS lines in radish.

***Corresponding Author:** Tel. 063-238-6670, E-mail: greenever@korea.kr

PF-0015

QTL mapping for the leaf chlorophyll content in strawberry (*Fragaria x ananassa*)

Muhammad Irfan Siddique, Koeun Han, Jieun Lee, Hye-Eun Lee, Ye-Rin Lee, Sun Yi Lee, Eun Su Lee, Do-Sun Kim*

Vegetable Research Division, National Institute of Horticultural and Herbal Science, Rural Development Administration, Wanju 55365, South Korea

Chlorophyll is an important factor enabling plants to absorb, transfer and transform light energy and plays an important role in yield formation. Strawberry is one of the most important horticultural crops. Breeding Strawberry for high light efficiency by improving photosynthetic efficiency is obtaining considerable social and economic value. Genetic mapping of the QTLs controlling chlorophyll contents in other horticultural crops such as lettuce and Chinese cabbage has been carried out. However, in strawberry, there have been no studies on the mapping of chlorophyll contents related QTLs. We used an F_2 mapping population and GBS-SNP based linkage map to identify the QTLs controlling leaves chlorophyll contents. Parental lines and F_2 segregating population was evaluated for leaf greenness, a surrogate measure of leaf chlorophyll content using a Minolta Chlorophyll Meter SPAD 502. A total of two QTLs including one major qChl_chr1-3 and one minor qChl_chr5-2 were detected on chromosome 1-3 and 5-2, respectively. The qChl_chr1_3 explained 17.4 % phenotypic variation (PEV) with 4.5 LOD score while qChl_chr5-2 explained 7.2 % phenotypic variation (PEV) with 3.4 LOD score. The physical positions of the QTLs will be compared and candidate genes related to the photosynthesis and chlorophyll biosynthesis pathway will be sorted and analyzed. Moreover, the molecular markers flanking with the QTLs can be utilized in strawberry breeding to select the plants for required chlorophyll content.

Keywords: Fragaria x ananassa, chlorophyll content, QTL analysis, leaf color, greenness, SPAD

***Corresponding Author:** Tel. 063-238-6670, E-mail: greenever@korea.kr

PF-0016

Analysis of the effect of drought on the occurrence of TYLCV in tomatoes

Hong-Il Ahn, Jinjeong Lee, HwangWeon Jeong, Su Jung Ra, Sung Mi Kim, Eunhee Kim, Il Pyung Ahn, Hye-Jin Yoon, Young-Joo Seol*

Gene Engineering Div., National Institute of Agricultural Science, RDA, Jeonju-si, Jeollabuk-do, 54874, Korea

Tomato (*Solanum lycopersicum*) is a member of the *Solanaceae* family and has the world's largest production and consumption among horticultural crops. These plants are mainly cultivated in a facility house, which causes various diseases. *Tomato yellow leaf curl virus* (TYLCV), which is causing the biggest problem in tomato production, is a plant virus with a circular single-stranded DNA genome (ssDNA) belonging to the genus *Geminiviridae* and *Begomovirus*. It is a disease mediated by whitefly. Drought, abiotic stress, is a near-extinction catastrophe for tomatoes. Therefore, the physiological change of the individual will appear very dramatic, and the response to the viral disease will also be different. In this experiment, 4 varieties for cultivation Seokwang, Tenten, Tory, and Lucky were used. Seokwang and Tenten were sensitive and Tory and Lucky were resistant. In these two groups, drought treatment showed a growth difference of about 10-30% compared with controls, which must have influenced the TYLCV outbreak in some way.

***Corresponding Author:** Tel. 063-238-4665, E-mail: yjseol@korea.kr

PF-0017

Alternative Splicing of the Basic Helix-Loop-Helix Transcription Factor Gene *CmbHLH2* Affects Anthocyanin Biosynthesis in Ray Florets of Chrysanthemum (*Chrysanthemum morifolium*)

Sun-Hyung Lim[1*], Da-Hye Kim[1,2], Jea-A Jung[3], Jong-Yeol Lee[2*]

[1]Division of Horticultural Biotechnology, School of Biotechnology, Hankyong National University, Anseong, 17579, Korea

[2]National Academy of Agricultural Science, Rural Development Administration, Jeonju, 54874, Republic of Korea

[3]Floriculture Research Division, National Institute of Horticultural & Herbal Science, Rural Development Administration, Wanju 55365, Korea

Chrysanthemum is an important ornamental crop worldwide. Some white-flowered chrysanthemum cultivars produce red ray florets under natural cultivation conditions, but little is known about how this occurs. To comprehend comprehend explore the underlying mechanism, we compared the expression of anthocyanin biosynthetic and transcription factor genes between white ray florets and those that turned red based on cultivation conditions. Significant differences in the expression of *CmbHLH2* were detected between the florets of different colors. *CmbHLH2* generated two alternatively spliced transcripts, designated *CmbHLH2*^{Full} and *CmbHLH2*^{Short}. Compared to *CmbHLH2*^{Full}, *CmbHLH2*^{Short} encoded a truncated protein with only a partial MYB-interaction region and no other domains normally present in the full-length protein. Unlike the full-length form, the splicing variant protein *CmbHLH2*^{Short} localized to the cytoplasm as well as the nucleus and lacked the ability to interact with CmMYB6. Additionally, *CmbHLH2*^{Short} failed to activate anthocyanin biosynthetic genes and induce pigment accumulation in transiently transfected tobacco leaves, whereas *CmbHLH2*^{Full} promoted both processes when simultaneously expressed with CmMYB6. Co-expressing *CmbHLH2*^{Full} and CmMYB6 also enhanced the promoter activities of *CmCHS* and *CmDFR*. Notably, the Arabidopsis *tt8-1* mutant, which lacks red pigmentation in the leaves and seeds, could be complemented by heterologous expression of *CmbHLH2*^{Full}, which restored red pigmentation and resulted in high anthocyanin and proanthocyanidin contents in the leaves and seeds, respectively, whereas expression of *CmbHLH2*^{Short} did not. Together, these results indicate that *CmbHLH2* and *CmMYB6* interaction plays a key role in the anthocyanin pigmentation changes of ray florets in chrysanthemum. Our findings highlight alternative splicing as a potential approach to modulate anthocyanin biosynthesis in specific tissues.

***Corresponding Author:** Tel. 031-670-5105, E-mail: limsh2@hknu.ac.kr

PF-0018

Sensory qualities and physicochemical properties of different Korean apple cultivars

Keono Kim[1], Yejin Kim[1], Soon-il Kwon[2], Young Soon Kwon[2], Chuleui Jung[3], Sunghoon Baek[4], Jeehye Sung[1*]

[1]Department of Food Science and Biotechnology, Andong National University 1375 Gyeongdong-ro, Andong 36729, Republic of Korea
[2]Apple Research Institute, National Institute of Horticultural and Herbal Science, RDA 107 Soboangye-ro, Sobo-myeon, Gunwi 39000, Republic of Korea
[3]Department of Plant Medicals, Andong National University 1375 Gyeongdong-ro, Andong 36729, Republic of Korea
[4]Department of Industrial Entomology, Korea National College of Agriculture and Fisheries 1515 Kongjwipatjwi-ro, Deokjin-gu, Jeonju 54874, Republic of Korea

The present study investigated sensory qualities and physicochemical properties of different Korean apple cultivars (‘Arihaw’, ‘Arisoo’, ‘Easypple’, ‘Picnic’, and ‘Hongro’). The sensory characteristics were based on quantitative descriptive analysis (QDA) and consumer hedonic assessment. QDA was performed by trained panels (n = 10) to investigate the intensities of different tastes (sweetness and sourness) and flavors (pineapple, pear, vanilla, apple, cucumber, floral, fruity, green and honey). The physicochemical profiles were determined by ^{o}Brix, titratable acidity, ^{o}Brix/acid ratio, color and the sugar contents (fructose, glucose, sorbitol and sucrose). The results showed that ‘Arisoo’ had the highest hedonic rating with high intensities of sweetness, sourness, and apple, pineapple and green flavors compared to the other apples with significant differences ($p<0.05$). On the other hand, the sensory characteristics of ‘Hongro’ were shown to have the opposite sensory attributes compared with ‘Arisoo’. Although ^{o}Brix/acid ratio has been known as a predictor of consumer acceptability of apples, ‘Arisoo’ had the lowest ^{o}Brix and ^{o}Brix/acid ratio. The lowest total sugar content was also found in ‘Arisoo’, which did not influence the sweetness intensity and the overall liking of the apples. These observations suggested that ^{o}Brix and ^{o}Brix/acid ratio were not completely informative when measuring apple sensory quality. Collectively, a balanced combination of sweetness/sourness and pleasant flavors could contribute to positive hedonic perception of apples.

***Corresponding Author:** Tel. 054-820-5752, E-mail: jeehye@anu.ac.kr

PF-0019

Antioxidant properties of different apple cultivars grown in Korea

Myeongbin Park[1], Geubrae Kim[1], Chuleui Jung[2], Soon-il Kwon[3], Young Soon Kwon[3], Jeehye Sung[1*]

[1]Department of Food Science and Biotechnology, Andong National University 1375 Gyeongdong-ro, Andong 36729, Republic of Korea

[2]Department of Plant Medicals, Andong National University 1375 Gyeongdong-ro, Andong 36729, Republic of Korea

[3]Apple Research Institute, National Institute of Horticultural and Herbal Science, RDA, Gunwi 39000, Republic of Korea

The total phenolic and flavonoid contents and antioxidant capacities of peel, flesh, and whole ethanolic extracts were examined in eight apple cultivars ('RubiS', 'Fuji', 'Hongro', 'Arihwa', 'Easypple', 'Hwangok', 'Picnic' and 'Arisoo') grown in Korea. The peel extracts significantly exhibited stronger antioxidant activities and higher total phenolic/flavonoid contents than the flesh and whole extracts. Total phenolic content was ranged from 234.77 ± 6.51 mg gallic acid equivalents (GAE)/100 g freeze-dried sample (FDS) (Arisoo) to 531.00 ± 6.26 mg GAE/100 g FDS (Hwangok) in the fleshes and from 398.91 ± 9.63mg GAE/100 g FDS (RubiS) to 773.37 ± 28.51 mg GAE/100 g (Hwangok) in the peels. Total flavonoid content was varied from 23.08 ± 0.80 mg catechin equivalents (CAE)/100 g FDS (Arisoo) to 156.41 ± 1.70 mg CAE/100 g FDS (Hongro) and from 78.25 ± 0.45 mg CAE/100 g FDS (RubiS) to 293.73 ± 1.21 mg CAE/100 g FDS (Hongro) in the fleshes and the peels, respectively. The peel extract of 'Hongro' had the highest ABTS and DPPH radical scavenging activities while the highest reducing power was determined in the peel extract of 'Picnic'. The total phenolic content was significantly correlated with ABTS and DPPH radical scavenging activities in both fleshes ($R^2 > 0.84$) and peels ($R^2 > 0.85$). Based on these findings, this study suggests that apple peels could be promising sources of potential natural antioxidants.

***Corresponding Author:** Tel. 054-820-5752, E-mail: jeehye@anu.ac.kr

PF-0020

완숙토마토의 대목사용에 따른 풋마름병 증상 및 생육변화 분석

안율균[1*], 이혜원[1], 이준구[2], 홍규현[1], 권덕호[1], 조명철[3], 황인덕[4]

[1]전라북도 전주시 완산구 콩쥐팥쥐로 1515 한국농수산대학
[2]전라북도 전주시 덕진구 백제대로 전북대학교 원예학과
[3]전라북도 완주군 이서면 농생명로 100 국립원예특작과학원 채소과
[4]전라북도 김제시 백산면 하정로 236 부농종묘(주)

토경재배 시설 토마토는 연작하는 작부체계가 일반화되면서 토양 전염성병인 풋마름병에 심각한 피해를 입고 있다. 풋마름병의 원인균은 *Ralstonia solanacearum*으로 토양에 수 년간 서식할 수 있기 때문에 화학적 또는 생물학적 방제가 어려워 대책으로 대목을 사용하고 있다. 또한 토마토는 장기재배에 대한 요구도가 커 재배 후기까지 초세를 유지할 수 있는 대목의 사용이 필요하다. 국내에서 사용하는 토마토 대목품종은 주로 외국품종으로 국산 대목품종의 보급을 위해 토마토 대목품종의 평가 및 선발이 필요하다. 본 연구는 완숙토마토 대목별 병 저항성 평가와 생육변화 분석을 통하여 대목 성능 검정을 하고자 수행하였다. 실험재료는 국내 개발 대목 품종 및 계통을 사용하였다. 접종 14일 후 생물검정한 결과 접목한 처리 구는 풋마름병에 저항성을 보였으며 접목하지 않은 처리 구는 감수성을 보였다. 접종 후 줄기직경은 접종 7일 후부터 대목을 사용한 처리 구와 사용하지 않은 처리 구 간의 생육차이가 벌어지기 시작했으며 Sap flow를 사용하여 접종 후 처리별 양수분 이동 속도를 측정한 결과 대목을 사용하지 않은 처리 구의 양수분 이동 속도가 가장 낮았다. 대목을 사용한 처리 구 중에는 국내에서 개발된 대목계통이 가장 높은 양수분 이동 속도를 보여 국내 개발 대목계통이 선발될 것으로 예상된다.

***교신저자:** Tel. 063-238-9153, E-mail: aykyun@korea.kr

PF-0021

Identification of Candidate Genes Regulating Capsaiciniod Biosynthesis Using an EMS-induced Mutant (*Capsicum annuum* L.)

Seungki Back, Joohyun Lee, Doyeon Hwang, Joung-Ho Lee, Byoung-Cheorl Kang*

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

The pungency of pepper fruit is caused by capsaicinoids, the unique alkaloid mixture of *Capsicum*. The capsaicinoids are synthesized through condensing byproducts from the phenylpropanoid and the branched-chain fatty acid pathways and sequestered in the glandular cells on the epidermal tissues of fruit placenta. Among the structural and regulatory genes in the capsaicinoid biosynthetic pathway, functions of only a few genes including *Pun1*, *pAMT*, *Pun3*, and *CaKR1* have been identified using natural loss-of-function mutants. However, many genes in the capsaicinoid biosynthetic pathway are still unknown due to the lack of natural variations. In this study, an EMS-induced non-pungent mutant line ‘221-2-1a’ derived from pungent Korean landrace ‘Yuwolcho’ was used to reveal novel genetic factors controlling capsaicinoid biosynthesis in pepper. The segregation ratio of an F_2 population derived from the cross between ‘221-2-1a’ and pungent Indian landrace ‘Lam32’ fitted to a 13:3 ratio. The segregation ratio indicated the non-pungency of ‘221-2-1a’ may be controlled by two genes. To identify genetic loci controlling the non-pungency, genetic mapping was performed using genome-wide markers and BSA-seq analysis, and one locus on chromosome 6 was identified and named *Pun4*. Using SNP markers, the *Pun4* region was delimited to 655.1 kb region and 12 candidate genes were predicted.

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

PF-0022

Development of SNP markers for *capsanthin-capsorubin synthase* and *zeaxanthin epoxidase* genes to distinguish between red, orange, and yellow fruit colors in paprika (*Capsicum annuum* L.)

Kang Min Lee[1], Jongbin Park[1], Jong-Suk Park[2], Ju Kim[2], Jundae Lee[1*]

[1]Department of Horticulture, Institute of Agricultural Science and Technology, Jeonbuk National University, Jeonju 54896, Republic of Korea

[2]Fruit & Vegetable Research Institute, Jeonbuk Agricultural Research and Extension Services, Gunsan 54062, Republic of Korea

Paprika (*Capsicum annuum* L.) is one of the vegetable crops that are the major sources of income for farmers in Korea. The quality of paprika fruits is determined by size, freshness, shape, and color. Among these, paprika fruit color plays a major role in demand. In this study, we aimed to develop SNP markers to distinguish between red, orange, and yellow fruit colors in paprika. *Phytoene synthase* (*PSY*), *β-carotene hydroxylase* (*BCH*), *zeaxanthin epoxidase* (*ZEP*), and *capsanthin-capsorubin synthase* (*CCS*) genes were sequenced and compared using four red (KNMR, 19BR201, Sirocco, GINA), three yellow (KNMY, Volante, Romance Gold), and three orange (KNMOR, DSP7054, ARO-50R) cultivars. We found sequence variations cosegregating with the fruit color in *CCS* and *ZEP* genes and developed two codominant SNP markers (CCS-InDel-HRM and ZEP1.2-HRM) based on the sequence variations. The markers were tested in 44 F_1 varieties, 31 inbred lines, two F_2 populations consisting of 29 and 79 individuals, and 82 germplasms. In results, these two markers were able to predict paprika fruit colors. In CCS-InDel-HRM marker, at least one normal *CCS* allele (*ccs*+/_) made red paprika fruit color, whereas homozygous deleted *CCS* alleles (*ccs*-/*ccs*-) made orange or yellow. In ZEP1.2-HRM marker, homozygous A/A or heterozygous A/G showed yellow paprika fruit color, whereas homozygous G/G showed orange paprika fruit color. The developed markers will be useful for paprika breeding crossing between different fruit colors.

***Corresponding Author:** Tel. 063-270-2560, E-mail: ajfall@jbnu.ac.kr

PF-0023

Pun1 and *Pun3* Alleles from *C. chinense* 'Habanero' Significantly Increased Capsaicinoids Contents in an RIL population

Shieun Yi, Koeun Han, Seungki Back, Geon Woo Kim, Siyoung Jang, Byoung-Cheorl Kang*

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

Capsaicinoids are unique compounds that contribute a hot taste to pepper (*Capsicum spp.*). There are several genes identified to be involved in the biosynthesis of capsaicinoids, such as *Pun1*, *Pun2*, *Pun3*, *CaKR1*, *pAMT*. *Pun1* encodes acyltransferase, also known as capsaicin synthase (CS) which are located at the end of the biosynthesis pathway. *Pun3* is a transcription factor that plays a role as a master regulator of the capsaicinoids biosynthesis pathway. In this study, we investigated the correlation between capsaicinoids contents and *Pun1* and *Pun3* alleles. A RIL population consisting of plants derived from a cross between *Capsicum annuum* 'TF68' and *Capsicum chinense* 'Habanero' was used and genotyped by High-Resolution Melt (HRM) analysis for *Pun1* and *Pun3* alleles. Capsaicinoids contents of RILs were measured by High-performance Liquid Chromatography (HPLC) for two years. The result indicated that the capsaicinoids contents were significantly correlated with the allele types of both *Pun1* and *Pun3* in the TH RIL population. The individuals carrying Habanero alleles of *Pun1* and *Pun3* showed significantly higher capsaicinoids contents than the plants carrying alleles of TF68 in both years. This result suggested the possibility that introducing alleles from 'Habanero' can be used for breeding extremely pungent peppers.

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

PF-0024

Comparison of chemical profiles in stems of *Dendrobium* in two different species and their hybrid and their cytotoxicities against FaDu cell line

Ah-Reum Han[1*], Bomi Nam[2], Jisu Park[1], Ye-Ram Kim[1], Hyun Mi Kim[1], Hyeon Hwa Park[1], Chan Hyun Jin[1], Sang Hoon Kim[1], Min Jeong Hong[1], Jin-Baek Kim[1]

[1]Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongeup-si, Jeollabuk-do 56212, Republic of Korea
[2]Institute of Natural Cosmetic Industry for Namwon, Namwon-si, Jeollabuk-do 55801, Republic of Korea

Dendrobium is a genus of orchids in the family Orchidaceae, containing more than 1,800 species that are found in diverse habitats throughout south, east and southeast Asia and the islands of the Pacific. Many species are cultivated as ornamentals and important in the horticultural industry. The genera with medicinal importance include *D. nobile*, *D. chrysanthum, D. officinale*, *D. loddigessi*, *D. fimbriatum* var. *oculatum*, *D. moniliforme*, and *D. candidum*. It has been used as traditional folk remedies for the treatment of various disease, such as chronic atrophic gastritis, diabetes, and cardiovascular disease. In this study, the chemical profiles of Dendrobii Herba and *Dendrobium* in two different species and their hybrid were investigated by ultra-performance liquid chromatography coupled with quadrupole time-of-flight mass spectrometry (UPLC-QTOF MS). Among the numerous peaks detected, 17 peaks were unambiguously identified by comparing their retention time and the accurate masses with those of compounds isolated from Dendrobii Herba in our previous study and the standards. All compounds were detected in Dendrobii Herba, while compounds 1, 2, and 16 in *D. candidum*; compounds 1, 11, and 16 were detected in *D. nobile*; compounds 1, 2, and 16 in the hybrid, *D. nobile* × *candidum*. Their methanol extracts were examined for their cytotoxicity against FaDu human hypopharynx squamous carcinoma cells and Dendrobii Herba showed the greatest cytotoxicity compared to other samples.

***Corresponding Author:** Tel. 063-570-3167, E-mail: arhan@kaeri.re.kr

PF-0025

Comparison of chemical profiles and bioactivities of mutant cultivars of *Coreopsis rosea* and *C. verticillata*

Ah-Reum Han[1*], Bo-Ram Kim[2], Jisu Park[1], Ye-Ram Kim[1], Hyun Mi Kim[1], Hyeon Hwa Park[1], Chan Hyun Jin[1], Jin-Baek Kim[1], Yeo Gyeong Jeon[3], Kong Young Park[3], Si-Yong Kang[4]

[1]Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongeup-si, Jeollabuk-do 56212, Republic of Korea
[2]Natural Products Research Institute, Korea Institute of Science and Technology (KIST), Gangneung-si, Gangwon-do 25451, Republic of Korea
[3]Uriseed Group, Icheon-si, Gyeonggi-do 17408, Republic of Korea
[4]Department of Horticulture, College of Industrial Sciences, Kongju National University, Yesan-gun, Chungcheongnam-do 32439, Republic of Korea

Coreopsis species is an annual or perennial plant belonging to the Asteraceae (Compositae) family and is natively about 80 species in North America and currently wide spread to America, Asia and Oceania regions. It is usually cultivated for ornamental purpose in the garden or on the roadsides. The color and size of Coreopsis flowers has commercially important value and is the purpose of Coreopsis breeding, however Coreopsis flowers have been also ethnopharmacologically used for the treatment of diarrhea, vomiting, and hemorrhage in North America and as a drink to control diabetes in China and Portugal. In this study, to identify and evaluation of the mutant cultivars of *C. rosea* and *C. verticillata* by comparing them with their original cultivars, their phytochemical profiles were systematically characterized using ultra-performance liquid chromatography time-of-flight mass spectrometry (UPLC-QTof MS), as well as their anti-diabetes effect was tested using dipeptidyl peptidase (DPP)-IV inhibitor screening assay. In the UPLC-QTof MS analysis, a total of 41 compounds, including 36 flavonoids, four phenolic acids, and a polyacetylene were tentatively identified based on the comparison of the high-resolution mass information, MS/MS fragmentations, and retention times with reported values and database. The 70% methanol extract of 32 cultivars of *C. rosea* and *C. verticillata* were evaluated for their DPP-IV inhibitory activity and all of them inhibited DPP-IV activity with IC_{50} values from 34.01 to 158.83 μg/mL.

***Corresponding Author:** Tel. 063-570-3167, E-mail: arhan@kaeri.re.kr

PF-0026

Identification of SNPs associated with bulb size in onion (*Allium cepa* L.) using genome-wide association study

Geonyong Jin[1], Hye-Eun Lee[2], JiWon Han[2], Jundae Lee[1*]

[1]Department of Horticulture, Institute of Agricultural Science & Technology, Jeonbuk National University, Jeonju 54896, Republic of Korea

[2]Vegetable Research Division, National Institute of Horticultural & Herbal Science, Wanju 55365, Republic of Korea

Bulb onion (*Allium cepa* L.) is one of the most important economical vegetable crops in the world, and the height and width of onion bulb are the valuable agronomic trait related to the yield. However, molecular understanding of the height and width of the bulb is very poor. In this study, we focused to identify SNPs associated with bulb size (height and width) in onion accessions using genome-wide association study (GWAS). A total of 120 red onion plants derived from 40 accessions were used for bulb size and genotyping-by-sequencing (GBS) analyses. The height and width of onion bulbs ranges from 65.47 to 118.39 mm and from 56.01 to 116.56 mm, showing the average of 93.81 mm and 83.22 mm, respectively. A total of 3,280 SNPs was generated by GBS analysis. GWAS analysis revealed 98 significant SNPs with LOD values of 4.0 or higher associated with bulb height and 68 significant SNPs with LOD values of 7.0 or higher associated with bulb width. This study provides basic information to develop SNP markers linked to the gene controlling onion bulb height and width.

***Corresponding Author:** Tel. 063-270-2560, E-mail: ajfall@jbnu.ac.kr

PF-0027

Genetic Mapping of BBWV2 (Broad bean wilt virus 2) Resistance in Hot pepper

Jung-Min Kim[1], Joung-Ho Lee[2], Myoung-Suk Han[2], Jin-Kyoung Kwon[2], Byoung-Cheorl Kang[2*]

[1]Interdisciplinary Program in Agricultural Biotechnology, College of Agriculture and Life Sciences, Seoul National University 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Republic of Korea

[2]Department of Plant Science and Plant Genomics and Breeding Institute, College of Agriculture and Life Sciences, Seoul National University 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Republic of Korea

Broad bean wilt virus (BBWV) which belongs to Fabavirus genus containing two single strand RNAs, is a threatening virus with wide host range including bean, spinach, grape, and pepper. Previous studies reported two BBWV1 isolates and six BBWV2 isolates, which have been steadily expanding their host range. In contrast to the discoveries of BBWV in other crops, resistance genes that render resistance to BBWV have not been reported in peppers. In this study, we obtained a novel BBWV2 resistant hot pepper accession 'SNU-0' by screening germplasm. 183 RILs derived from a cross between resistant accession 'SNU-0' and susceptible accession 'ECW30R' were genotyped by GBS method. As a result, we obtained 2,995 bin markers out of 13,019 SNP markers. Ten plants from each RIL were inoculated with BBWV2 for resistance screening. We found that resistant and susceptible phenotypes segregate in a 1:1 ratio. Using these GBS markers and BBWV2 screening data, we were able to find the approximate location of the BBWV2 resistance gene on chromosome 1. These findings will serve as a foundation for breeding BBWV resistant cultivars in pepper.

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

PF-0028

Development of a Speed Breeding System in Pepper (*Capsicum* spp.)

Hayoung Choi, Seungki Back, Geon Woo Kim, Byoung-Cheorl Kang*

College of Agriculture and Life Sciences, Seoul National University 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Republic of Korea

The bottleneck of conventional breeding is the generation time of crop plants. Recently, speed breeding has been introduced for long-day field crops, but there have been only a few researches on speed breeding in vegetable crops. In this study, a new protocol for speed breeding was developed in pepper. The protocol is based on controlling the photoperiod, temperature, and light quality. As a result, extending the photoperiod up to 20 hours and supplementing far-red light shortened the flowering time in half compared to normal growth conditions (16/8 hours of light/dark cycle and white light). To confirm whether the far-red light accelerated flowering by inducing flowering promoting genes, genome-wide association study (GWAS) was conducted. In the GWAS analysis, several flowering genes showed significantly associated with the flowering time and the *GI* gene was selected as a candidate gene. *GI* was highly expressed in the supplemented far-red light treatment, which indicated that far-red light could be a signal for expression of flowering genes and shorten the flowering time. Because the lower R: FR ratio promoted stem overgrowth, the anti-GA chemical diniconazole was sprayed. However, the application of diniconazole inhibited not only overgrowth but also flowering. The speed breeding protocol developed in this study will accelerate the breeding cycle in pepper.

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

PF-0029

Multiplex-PCR Using Insertion and Deletion Markers Associated with Restorer-fertility Genes in Pear (*Pyrus* spp.)

Sewon Oh[1], Hyeondae Han[1,2], Yumi Kim[1], Hae Won Jeong[3], Daeil Kim[1*]

[1]Department of Horticulture, Chungbuk National University, 1 Chungdae-ro, Seowon-gu, Cheongju 28644, Republic of Korea

[2]Department of Horticultural Science, Culf Coast Research and Education Center, Institute of Food and Agricultural Science, University of Florida, Wimuama, FL 33598, USA

[3]Pear Research Institute, National Institute of Horticultural and Herbal Science, RDA, Naju 58216, Republic of Korea

Multiplex PCR can save time and labor by using more than one primer pair in one reaction. The previously developed two InDel markers linked to restorer-fertility genes of pear were used in multiplex-PCR. One of the InDel markers located in linkage group (LG) 4 of ‘Whangkeumbae’ × ‘Minibae’ generates 157 bp or 133/157 bp of PCR amplicons. The other InDel marker located in LG 5 and generates 126/140 bp of PCR amplicons in ‘Whangkeumbae’ and ‘Minibae’. In agarose gel electrophoresis, it is difficult to discriminate PCR product size differences of less than 10 bp. Thus, a primer pair targeting the InDel in LG5 was newly designed. As a result, 98/112 bp of PCR amplicons were produced in both parents. Multiplex PCR was performed using the previously developed InDel marker located in LG4 and the newly designed InDel marker located in LG5. As a result, 98/133/157 bp of PCR amplicons were generated in male sterile ‘Whangkeumbae’ and 98/112/133/157 bp of PCR amplicons were produced in the male fertile ‘Minibae’. Based on the segregation genotypes of F_1, we can select 72% of F_1 that accorded with phenotype. Multiplex PCR using the two InDel markers will fulfill marker-assisted selection related to male sterile in pear more efficient.

***Corresponding Author:** Tel. 043-261-2527, E-mail: oseng1234@cbnu.ac.kr

PF-0030

Leaf Margin Related QTLs in 'Whangkeumbae' × 'Bartlett' (*Pyrus pyrifolia* × *P. communis*)

Yumi Kim[1], Sewon Oh[1], Do-yeon Cho[1], Hae Won Jeong[2], Daeil Kim[1*]

[1]Department of Horticulture, Chungbuk National University 1 Chungdae-ro, Seowon-gu, Cheongju 28644, Republic of Korea

[2]Pear Research Institute, National Institute of Horticultural & Herbal Science, RDA, Naju 58220, Republic of Korea

Leaf size and shape are important traits in the plant because its affect photosynthetic efficiency. The serrated leaf margin is closely associated with transpiration and photosynthesis. The yield of horticultural crops could be increased depending on photosynthetic efficiency. The present study was performed to detect the quantitative trait loci (QTL) related to the margin development of pear leaf. The 'Whangkeumbae' (*Pyrus pyrifolia*, dentate margin), 'Bartlett' (*P. communis*, crenate margin), and their 119 F_1 individuals were used in this study. The five mature leaves per individual were collected at 60 days after full bloom. Three types of leaf margin that are crenate, dentate, and serrate were investigated. The integrated map anchoring GBS-SNPs, array-SNPs, and SSR markers were used for QTL analysis. QTL controlling related to margin development was identified in linkage groups (LGs) 2, 10, 13, and 17. The QTLs related to margin development covered 1.5, 11.3, 12.1, and 4.5 cM of LG 2, 10, 13, and 17, respectively. These results could help in the development of molecular markers that could select cultivar with high photosynthetic efficiency.

***Corresponding Author:** Tel. 043-261-2527, E-mail: yumi@cbnu.ac.kr

PF-0031

A Missense Mutation in *ZEP* Results in Scarlet Mature Fruit Color and Increased Carotenoid Contents in Pepper (*Capsicum annuum*)

Se-Young Lee, Joung-Ho Lee, So-Jeong Jang, Seo-Young Lee, Hyo-Bong Jeong, Byoung-Cheorl Kang*

Department of Agriculture, Forestry and Bioresources, Research Institute of Agriculture and Life Sciences, Plant Genomics and Breeding Institute, College of Agriculture and Life Sciences Seoul National University, Seoul, 08826, South Korea

Pepper mature fruit colors are known to be determined by the three independent loci (*C1, C2*, and *Y*): *C1* and *C2* encode *Pseudo response regulator2-like* (*PRR2*) and *Phytoene synthase* (*PSY1*) and *Y* locus encode *Capsanthin capsorubin synthase* (*CCS*). However, the diversity of fruit color in pepper cannot be explained by only these three genes. In this study, we used an EMS induced scarlet color mutant *C. annuum* 'EMS 204' (204) derived from dark red Korean landrace *C. annuum* 'Yuwolcho' (Yuw) both harboring functional *PRR2, PSY1,* and *CCS*. To identify the genetic locus controlling the scarlet color, we performed MutMap analysis and mapped the genetic locus controlling scarlet color to a 2.5-Mb region on chromosome 2, where *Zeaxanthin epoxidase* (*ZEP*) is located. We detected a missense mutation located in the monooxygenase domain of *ZEP*. HPLC analysis showed that EMS204 contained higher amount of zeaxanthin and total carotenoid in mature fruit color than Yuw. A color complementation assay using *E.coli* harboring carotenoid biosynthetic genes showed that the mutant *ZEP* protein had reduced enzymatic activity. To validate the role of *ZEP* in fruit color formation, we performed virus-induced gene silencing (VIGS) of *ZEP* in the red-fruit cultivar *C.annuum* 'Micropep Red' (MR). The silencing of *ZEP* caused significant change in the ratios of zeaxanthin to its downstream products and increased total carotenoid contents. Thus, we conclude that the mutation in *ZEP* resulted in scarlet color of 'EMS 204'.

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

PF-0032

Reproducibility Analysis of Sex-linked Marker in Kiwifruits (*Actinidia* spp.)

Jung Kim[1], Sewon Oh[1], Yumi Kim[1], Haemi Cho[1], Mockhee Lee[2], Daeil Kim[1*]

[1]Department of Horticulture, Chungbuk National University 1 Chungdae-ro, Seowon-gu, Cheongju 28644, Republic of Korea

[2]Namhae Branch, National Institute of Horticultural and Herbal Science, RDA, Namhae 52430, Republic of Korea

Kiwifruits (*Actinidia* spp.) are dioecious species that are not able to distinguish the sex in the juvenile phase. Development and application of sex-linked markers could increase the breeding efficiency in dioecious species. Several sex-linked markers have been developed in kiwifruits. However, developed markers have not been applicated in kiwifruit breeding. Therefore, this study was performed to confirm applicability of pre-existing sex-linked markers in 6 kiwifruit species, including *A. arguta* (tetraploid), *A. chinensis* (diploid and tetraploid), *A. deliciosa* (hexaploid), *A. eriantha* (diploid), *A. macrosperma* (diploid), *A. polygama* (diploid). A total of 7 pre-existing sex-linked markers, including 2 sequence-characterized amplified regions markers SmX and SmY, 3 simple sequence repeat (SSR) markers A001, A002, and A003, and 2 PCR markers aC36306 and kC72369, were used in this study. PCR and 2% agarose gel electrophoresis were performed according to the protocol of each marker. As a result, A001, A002, A003, and kC72369 could not distinguish the male and female cultivars in all kiwifruit species. The amplicon must be shown in all female and male species by SmX, but amplicons were only shown in diploid *A. chinensis* and hexaploid *A. deliciosa*. SmY could distinguish the male in *A. arguta*, *A. deliciosa*, and *A. chienesis*, whereas aC36306 could only distinguish the male in *A. arguta*. The pre-existing sex-linked markers have shown low reproducibility depending on the species and ploidy level. These results suggested that development of species-specific sex-linked marker is demanded in kiwifruits.

***Corresponding Author:** Tel. 043-261-2527, E-mail: rlawjdtkswjd@cbnu.ac.kr

PF-0033

Identification of *RsTTG1* for Flavonoid Biosynthesis in Radish

Da-Hye Kim[1], Ji-Yeon Kim[1], Jong-Yeol Lee[2], Sun-Hyung Lim[1*]

[1]Division of Horticultural Biotechnology, School of Biotechnology, Hankyong National University, Anseong, 17579, Republic of Korea

[2]National Institute of Agricultural Science, Rural Development Administration, JeonJu, 54874, Republic of Korea

Flavonoids are reported exhibiting various functionalities such as antioxidant activity, anti-cancer, anti-inflammatory, and other pharmacological effects for health promotion. Flavonoid biosynthesis is known to be regulated by MBW polymer consisting of R2R3 MYB, basic helix-loop-helix (bHLH), and WD40 transcription factors. Studies on structural genes and transcription factors related to flavonoid biosynthesis have been actively conducted in model crops, but molecular biological studies related to the production of anthocyanins in the radish have not been much studied. The R2R2-MYB and the bHLH transcription factors (TFs) on the anthocyanin biosynthesis has been reported, but the WD40 TF in the radish is not still unknown. In this study, we identify the WD40 protein, *RsTTG1*, in the radish. The *RsTTG1* amino acid sequences showed that it has four conserved WD repeat domains that involved in the flavonoid biosynthesis. In the phylogenetic tree, *RsTTG1* groups into TTG1 proteins of Brassicaceae family, which have function on flavonoid biosynthesis. Notably, the Arabidopsis ttg1 mutant, which lacks red pigmentation in the leaves and seeds, could be complemented by heterologous expression of *RsTTG1*, which restored red pigmentation and resulted in high anthocyanin and proanthocyanidin contents in the leaves and seeds, respectively. Together, these results indicate that *RsTTG1* plays a key role in the anthocyanin and proanthocyanidin pigmentation changes in radish.

***Corresponding Author:** Tel. 031-670-5105, E-mail: limsh2@hknu.ac.kr

PF-0034

Characterization of *RsMYB1* Function for Anthocyanin Biosynthesis

Da-Hye Kim[1], Ji-Yeon Kim[1], JuHee Rhee[2], Jong-Yeol Lee[2*], Sun-Hyung Lim[1*]

[1]Division of Horticultural Biotechnology, School of Biotechnology, Hankyong National University, Anseong, 17579, Republic of Korea

[2]National Institute of Agricultural Science, Rural Development Administration, JeonJu, 54874, Republic of Korea

Radishes (*Raphanus sativus* L.) are one of the economically important vegetable crops cultivated for producing seed oil and sprouts, as well as edible taproots. In the radish taproot, the various colors including white, red, purple, and green are accumulated. In the case of red and purple taproots, the anthocyanin derivatives were detected. To investigate the transcript levels of anthocyanin biosynthetic genes and regulatory genes, we performed the qRT-PCR with different tissues including skins and fleshes of root and leaves. root skins, root fleshes, and leaves. We detected that the both of *RsMYB1* and *RsTT8* genes were highly expressed in skins and fleshes of red radish. To decipher the anthocyanin biosynthetic mechanism in radish, the *RsMYB1* sequence was analyzed in red and white radish. The *RsMYB1 (RsMYB1*^{N}*)* derived from red radishes are containing conserved R2 and R3 domain, whereas *RsMYB1 (RsMYB1*^{M}*)* derived from white radishes are containing partial R2 and conserved R3 domain. Based on these difference between *RsMYB1*^{N} and *RsMYB1*^{M}, we developed the CAPS marker for discriminating taproot skin color. Through yeast two hybrid, it was confirmed that *RsMYB1*^{N} and *RsMYB1*^{M} physically interacted with *RsTT8*. *RsMYB1*^{N} and *RsTT8* has the function to activate the *RsCHS* and *RsDFR* promoter, but *RsMYB1*^{M} does not activate *RsCHS* and *RsDFR* promoters. Transient expression analysis with agroinfilteration showed the difference roles of *RsMYB1*^{N} and *RsMYB1*^{M} on anthocyanin biosynthesis. *RsMYB1*^{N} induced the anthocyanin production with cooperatively work with *RsTT8,* whereas, *RsMYB1*^{M} did not accumulate the anthocyanin biosynthesis. Interestingly, it was confirmed that *RsMYB1*^{M} not only interferes with the anthocyanin production function of *RsMYB1*^{N}, but also acts as a competitor to *RsTT8* to inhibit anthocyanin production. Taken together these results, *RsMYB1*^{N} is crucial regulator on anthocyanin biosynthesis on taproot color development.

***Corresponding Author:** Sun-Hyung Lim (Tel. 031-670-5105, E-mail: limsh2@hknu.ac.kr))
Jong-Yeol Lee (Tel. 063-238-4616, E-mail: jy0820@korea.kr)

PF-0035

향기 물질 고함유 배 '진향' 육성

정해원[1*], 김윤경[2], 강아랑[1], 김금선[1], 송장훈[1], 강삼석[1]

[1]전라남도 나주시 금천면 벽류길 121, 국립원예특작과학원 배연구소
[2]전라북도 전주시 덕진구 농생명로 300, 농촌진흥청

좋은 향기를 가지는 맛은 풍미, 향미, 방향이라 불린다. 향미는 맛뿐만 아니라 향의 중대한 인자이며, 음식의 맛은 혀로 느끼는 맛과 코로 느끼는 향이 함께 감지된다. 소비자들은 식품을 섭취할 때 맛뿐만 아니라 식감, 향 등 복합적인 자극을 원하지만, 국내에서 재배되는 남방형 동양배(*Pyrus pyrifolia*)는 북방형 동양배(*P.ussuriensis, P.bretschneideri*)나 서양배(*P.communis*)에 비해 향기를 내는 휘발성 성분이 적어 다양한 자극을 주지는 못하였다. 이에 향기성분이 비교적 많은 북방형 동양배 '봉리'를 부본으로 활용하여 향기형질을 도입한 '진향'을 육성하였다. 1984년 '만삼길'에 '봉리'를 교배하여 2007년 과육에서 파인애플 향이 나는 84-16-5계통을 1차 선발하고, 2010년 과실 및 수체 특성에 대한 정밀평가 결과 2차 선발하였다. 2011년부터 2019년까지 5개 지역에서 지역적응성을 평가한 결과 품질의 우수성이 인정되어 향기 나는 배 품종으로 최종 선발하였으며, 2021년 국립종자원에 품종보호를 출원 중에 있다. 황갈색 배 '진향'은 과중은 503 g, 당도는 13.4 °Bx로 당산의 조화가 좋고 과즙이 풍부하다. 향기 성분을 분석한 결과 파인애플, 망고 등이 함유하고 있는 Ethyl hexanoate, Ethyl butanoate 성분을 다량 함유하여 독특한 향이 나는데 과육보다 과피, 과심 쪽에 가까울수록 향이 진하다. 저온에서는 3개월, 상온에서 15일 보관이 가능하며 시간이 흐를수록 향이 진해지는 것을 확인하였다. 직립성이 강하므로 꽃눈 유지를 위해 가지 유인 등 재배관리가 필요하며, 검은무늬병에는 저항성이며 검은별무늬병에는 비교적 약하다.

***교신저자:** Tel. 061-330-1541, E-mail: jjhhhwwww@korea.kr

PF-0036

고색도 비가림재배용 고추 ‘고홍빛’ 육성

이마리나*, 김찬용, 권오훈, 박나윤, 신지혜, 고진용

경상북도농업기술원 영양고추연구소

고추(*Capsicum annuum* L.)는 주요 경제작물이지만 최근 이상기상의 영향으로 고추의 수급 및 가격 불안정이 심화되고 있다. 이러한 이상기상에 대비하고 안정적인 생산을 위한 고추의 비가림재배 면적은 증가하는 추세이나 비가림재배에 적합한 전용 품종은 국내 5품종 정도로 매우 적은 상태이다. 또한, 현재 재배되고 있는 대부분의 시판품종은 수량성 및 내병성은 향상되었지만 색도, 매운맛 등 품질적인 측면은 다소 약화되어 다양한 특성의 고품질 품종이 요구되고 있다. 따라서 영양고추연구소에서는 비가림재배에 적합하고 고색도의 특성을 가진 고추 ‘고홍빛’을 육성하였다. ‘고홍빛’은 2011년 수집한 대과형 계통의 자원 SPBGR2를 5세대까지 고정・선발 과정을 거쳐 육성한 SPBGR2-2-2-1-1계통을 모본으로 하였으며, 2014년 육성한 고색도의 수비초 특성을 보유한 고정 계통 HG09004을 부본으로 하여 제웅 교배를 통해 육성하였다. 2016년~2017년 특성평가 및 안정성 여부를 확인하였으며, 2018년~2019년 영양군 3개소(해발 100 m씩 차이)에서 농가실증시험을 수행하였다. ‘고홍빛’의 개화소요일수는 88일로 대비품종 ‘비가림스피드’와 비교하여 10일 빨랐다. ‘고홍빛’의 초장은 128 cm, 주경장은 19 cm로 초형이 크지 않고 절간이 짧아 비가림 재배에 적합하며, 과장은 13.3 cm, 과경은 1.8 cm, 생과중은 12.0 g이었다. ‘고홍빛’의 고춧가루의 색소함량은 ASTA value 166으로 대비품종 ‘비가림스피드’의 119보다 1.4배로 색도가 상당히 높아 고춧가루로 가공했을 때 빛깔이 매우 우수하며, capsaicinoids 함량은 36.3 mg/100 g이었다.

***교신저자:** Tel. 054-683-1691, Fax. 054-683-1690, E-mail: mrn613@korea.kr

PF-0037

SSR Markers를 이용한 수국 종 분류

박성화[1,2], 한태호[1,2*]

[1]광주광역시 용봉로 77 전남대학교 원예학과
[2]광주광역시 용봉로 77 전남대학교 IT-Bio 융합시스템전공

수국은 다양한 화색과 풍성한 화형으로 절화 및 정원용으로써 많은 인기가 있는 화훼류이다. 수국속은 수국과에 속하고 23개의 종으로 이루어져있다(McClintock 1957; Mortreau 2003). 그 중 대표적인 종으로는 *Hydrangea macrophylla* (수국), *H. serrata* (산수국), *H. arborescense* (아나벨류), *H. quercifolia* (떡갈잎수국), *H. paniculata* (나무수국), *H. anomala* (등수국), *H. involucrata* 그리고 *H. aspera*가 있다. 특히, *H. macrphylla*는 가장 인기가 많은 종이나 내한성이 낮아 식재 지역의 한계가 있어 그것을 극복하기 위한 육종적 노력이 지속되고 있으나 쉽지 않다. 종간 교잡은 종내의 유전적 다양성 한계를 극복 할 수 있는 좋은 수단이 되나, pre- 또는 post-fertilization barriers로 인해 종자 형성 및 발달 저해가 발생 되어 정상 종자를 얻기 대단히 어렵고 이는 배주배양을 통한 극복이 일부 가능하다. 따라서 다양한 방법으로 수분 장벽을 극복하기 위한 연구들이 시도되어지고 있다. 본연구는 수국 품종의 종을 명확히 구별하고 수국 품종 육종에서 수국의 종간 거리를 파악하여 종간 교배의 기초가 되고자 하였다. 더 나아가 수국 종간 교배를 통한 자손의 혼종성 확인의 기초가 되고자 함에 목적이 있다. 본 실험의 식물 재료로는 *H.macrophylla, H. serrata, H. arborescsense, H. quercifolia, H. paniculat, H. aspera, H. anomala*로 총 7종으로 구성된 37개의 품종을 이용하였다. primer는 선행 연구에서 테스트되어진 SSR Markers primer 68개를 선정하였다. 37개 품종의 PCR 결과는 군집분석을 시행하였다. 그 결과 *H. paniculata*와 나머지 종들로 총 2개의 그룹으로 나뉘었다. 나머지 그룹에서는 *H. macrophylla*와 *H. serrata*는 같은 그룹에 속하였고, *H. quercifolia*, *H. arborescense*, *H. anomala*, *H.aspera*가 나머지 그룹으로 나뉘었다.

***교신저자:** Tel. 062-530-0624, E-mail: wageningen@hanmail.net

PF-0038

Delimitation of QTL regions conferring bacterial wilt resistance in pepper through SNP marker development

Sunjeong Joung[1], Je Min Lee[2], Jundae Lee[1]*

[1]Department of Horticulture, Institute of Agricultural Science & Technology, Jeonbuk National University, Jeonju 54896, Korea

[2]Department of Horticultural Science, College of Agriculture and Life Sciences, Kyungpook National University, Daegu 41566, Korea

Bacterial wilt, caused by *Ralstonia solanacearum*, is one of the most serious pepper diseases in Korea. In previous studies, the resistance was reported to be quantitatively controlled and the QTLs were different depending on isolates of *R. solanacearum*. In this study, we aimed to identify candidate genes for the previously reported QTLs conferring the resistance to the highly pathogenic isolate 'HWA' of *R. solanacearum* by adding the newly developed HRM markers. An F_2 population, derived from a highly resistant pepper hybrid cultivar 'Konesian Hot', was used for genetic mapping and QTL analysis. A total of 136 HRM markers were developed to delimit the previously detected QTL regions. In result, we detected three consistent QTLs (*qBwr6w-5.1*, *qBwr6w-7.1*, and *qBwr6w-9.2*) on chromosomes 5, 7, and 9, respectively. The three QTLs ranged from 223,954,447 to 224,958,688 bp, from 70,700,631 to 115,482,180, and from 3,453,876 to 3,693,026, respectively. In the regions, we found 19, 131, and 15 genes as possible candidate genes. However, there is no *R* gene within the regions. Further studies are required to identify the resistance gene to pepper bacterial wilt. These results provide candidate genes for further studies on resistance gene cloning.

***Corresponding Author:** Tel. 063-270-2560, E-mail: ajfall@jbnu.ac.kr

PF-0039

Development and Application of Gene-Specific Markers for Tomato Yellow Leaf Curl Virus Resistance in both Field and Artificial Infections

Jang Hee Lee[1,2], Dae Jun Chung[1], Je Min Lee[1*], Inhwa Yeam[2*]

[1]Department of Horticultural Science, Kyungpook National University, Daegu 41566, Korea
[2]Department of Horticultural and Breeding, Andong National University, Andong, Gyeonbuk 36729, Korea

Tomato yellow leaf curl virus (TYLCV) is a disease that is damaging to tomato production worldwide. Resistance to TYLCV has been intensively investigated, and single resistance genes such as *Ty-1* have been widely deployed in breeding programs. However, resistance-breaking incidences are frequently reported, and achieving durable resistance against TYLCV in the field is important. In this study, gene-specific markers for *Ty-2* and *ty-5*, and closely-linked markers for *Ty-4* were developed and applied to distinguish TYLCV resistance in various tomato genotypes. Quantitative infectivity assays using both natural infection in the field and artificial inoculation utilizing infectious TYLCV clones in a growth chamber were optimized and performed to investigate the individual and cumulative levels of resistance. We confirmed that *Ty-2* could also be an effective source of resistance for TYLCV control, together with *Ty-1*. Improvement of resistance as a result of gene-pyramiding was speculated, and breeding lines including both *Ty-1* and *Ty-2* showed the strongest resistance in both field and artificial infections.

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

PF-0040

Development of high-throughput marker set for marker-assisted breeding in *Cucurbita moschata*

Eun Su Lee*, Ye-Rin Lee, Do-Sun Kim, Hye-Eun Lee, Koeun Han, Oakjin Lee

Vegetable Research Division, National Institute of Horticultural and Herbal Science, RDA, Wanju 55365, Republic of Korea

Pumpkin (2n=2x=40) are the economically important *Cucurbitaceae* crops all over the world. Among them, *Cucurbita moschata* is used for food (young squash) as well as the rootstock for cucumber and watermelon cultivation. Genotyping-by-sequencing (GBS) is a reduced representation sequencing method which can identify SNPs cost-effectively. In this study, GBS analysis was carried out using 167 *C. moschata* accessions. The GBS library was prepared by digesting genomic DNA with *Apek* Ⅰ, and sequenced by using Illumina Nextseq 500. A Read mapping rate of 83.68% was obtained for the GSB data. Further, SNPs were collected and filtered based on filtering parameter (depth≥5, missing rate≤0.05). A total of 10,549 SNPs were obtained and among them, 396 SNPs were selected based on the stringent filtering parameters such as bi-allelic genotype, single copy number, polymorphism information content (PIC~0.5) value, adjacent SNPs (60 bp). Further, 380 SNPs were converted to Fluidigm® SNP Type™ assays that can be used for SNP genotyping of 88 accessions using Fluidigm® genotyping platform. The results suggested that the designed high-throughput marker set can be used to distinguish the accessions and aid in the background selection for MAB (Marker-assisted Backcross) breeding in *C. moschata*.

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

PF-0041

Quantification and Heritability Analysis of Stone Cell Content in Pear Flesh

Haemi Cho, Sewon Oh, Yumi Kim, Do Yeong Kim, Jung Kim, Daeil Kim*

Department of Horticulture, Chungbuk National University 1 Chungdae-ro, Seowon-gu, Cheongju 28644, Republic of Korea

Stone cells existing in pear flesh are cause of gritty and rough texture. Quantification of stone cells is a demanding task and takes a long time. However, image processing could be an effective method for stone cell quantification. Therefore, the present study investigated availability of image processing for stone cell quantification using ‘Whangkeumbae’ (*Pyrus pyrifolia*) × ‘Minibae’ (*P.* hybrid). Stone cell content was quantified by extracting stone cell from fruit flesh and investigating the number of pixels of stained stone cell using MATLAB. In addition, heritability analysis was performed. Weight of stone cells in ‘Whangkeumbae’ and ‘Minibae’ were 0.04 ± 0.005 and 0.23 ± 0.026, respectively and F_1 individuals showed stone cell content ranging from 0.03 ± 0.004 to 0.32 ± 0.012 g. The percentage of stone cell investigated by image processing was average 0.74 ± 0.07 and 2.52 ± 0.32% in ‘Whangkeumbae’ and ‘Minibae’, respectively and F_1 individuals showed percentage of stone cell ranging from 0.37 ± 0.05 to 2.94 ± 0.69%. The weight and percentage of stone cells content in ‘Whangkeumbae’ × ‘Minibae’ displayed normal distribution. Heritability values calculated as weight and percentage of stone cells content were 0.92 ± 0.01 and 0.88 ± 0.06, respectively. These results suggest that image processing method is a reliable method for stone cell quantification in pear flesh. The high heritability value implies that stone cell content is influenced by genetic factor than environmental factor.

***Corresponding Author:** Tel. 043-261-2527, E-mail: haemimaemi@cbnu.ac.kr

PF-0042

세계 최초 무측지 수박 ‘순제로’ 육성

노솔지[1*], 김태일[1], 윤건식[1], 박성원[1], 김은정[1], 전유민[1], 김영호[2]

[1]충청북도 음성군 대소면 대금로 326-8 수박딸기연구소
[2]충청북도 청주시 청원구 오창읍 가곡길 46 충청북도농업기술원

수박은 우리나라 과채류 산업에서 중요한 비중을 차지하는 작목으로, 2010년에 노지재배와 시설재배를 포함하여 재배면적이 16,396 ha, 생산량은 678,810 ton이였고, 최근 고령화시대에 노동력 감소로 인해 2019년에는 재배면적이 11,972 ha, 생산량은 475,815 ton으로 감소하였다. 2019년 수박 작업단계별 노동시간을 조사한 결과, 10 a 면적당 총 118.4시간이 소요되며, 그 중 순지르기 작업은 43.3시간이 소요되었다. 따라서 노동력 부족 농업현실에 수박 재배의 어려움을 해결하기 위해, 계통선발 및 육성 6년, 조합작성 및 특성검정 3년을 수행하여 세계 최초 무측지 수박 ‘순제로’를 육성하였다. ‘순제로’는 측지제거가 필요 없는 생력형 대과종 수박으로, 일반품종과는 다르게 어미가지 적심 후, 아들가지에서 측지 발생이 없다. 과형은 단타원형, 줄무늬 너비는 중간, 줄무늬색 녹색강도는 짙고, 과피색은 녹색 중간이고, 과육색은 분홍빛 적색이며, 과육경도는 중간이다. 과중은 8.2 kg, 당도는 11.8 °bx, 과피 두께는 1.0 cm로 대조품종인 ‘삼복꿀’과 유사하였다. ‘순제로’는 노동력이 감소하는 최근 농업 현실에 맞는 생력형 수박으로 재배할 수 있을 것으로 기대되며, 인건비 절감으로 농가 소득 증대에 기여할 수 있을 것으로 예상된다.

***교신저자:** Tel. 043-220-5862, E-mail: nosol2615@korea.kr

PF-0043

무측지 타원형계 수박 '순리스' 육성

윤건식[1*], 노솔지[1], 박성원[1], 김은정[1], 전유민[1], 김태일[1], 김영호[2]

[1]충청북도 음성군 대소면 대금로 326-8 수박딸기연구소
[2]충청북도 청주시 청원구 오창읍 가곡길 46 충북농업기술원

농가에서 수박 생산성과 수정률을 향상시키기 위해 하는 측지 제거 작업은 보통 수박의 생육기 중 5~6회를 실시한다. 그러나 이 작업은 노동력이 집중적으로 들어가 생산비를 가중시키고 있으며, 근골계 질환의 원인이 되는 등 농업인의 삶의 질을 저하시키고 있다. 이런 문제점을 해결하고자 어미가지 적심 후 아들가지에서 측지발생이 없는 생력형 수박인 순리스 품종을 육성하였다. 순리스는 CBWN01 × CBW1619를 모본으로, 2011~2016년 선발 및 계통육성, 2015 ~2017년 교배조합 작성 및 교배, 2017~2019년 조합능력 검정을 하여 종자를 채종하고, 신규성, 구별성, 균일성, 안정성이 확보되어 2019년에 품종보호 출원하였다. 순리스의 고유특성으로 배수성은 2배체이며, 줄무늬의 너비는 넓고, 줄무늬 녹색의 강도는 진하다. 과피색은 녹색이며, 과육색은 분홍빛 적색을 띄고, 과육은 부드러운 식감의 특성을 갖는다. 가변특성으로 과당 종자 수는 480립으로 삼복꿀에 비해 25립 적고, 과중은 8.6 kg으로 400 g이 삼복꿀에 비하여 무겁기 때문에 수량이 5.3% 증수된 6,450 kg/10 a로 나타났다. 과경 길이 23.8 cm에 비하여 과장이 31.1 cm로 길기 때문에 과형은 타원형이며, 과피의 두께는 1.3 cm으로 삼복꿀에 비하여 두껍고, 당도는 12 brix로 삼복꿀과 비슷하였다. 농촌의 고령화에 대응하여 순리스 품종의 보급은 유측지 품종에 비하여 노동력을 70% 절감시켜 생력화를 가능케 할 것이며, 생산비도 30% 정도 줄어 농업인 소득향상에도 기여할 것으로 기대된다.

***교신저자:** Tel. 043-220-5861, E-mail: lothmv@korea.kr

PF-0044

Molecular Tagging of the Loci Controlling Fruit Rind Color and Bloom Formation in Watermelons based on a QTL-seq

Siyoung Lee[1], Girim Park[1], Seungahn Kwon[1], Jiyeon Park[1], Yunseo Choi[1], Seoyeon Park[1], Yongjae Kim[2], Younghoon Park[1*]

[1]Department of Horticultural Bioscience, Pusan National University, Miryang 50463, South Korea
[2]Partner Seed, Ansung, Republic of Korea

Fruit rind color and bloom formation are important traits that affect fruit quality and commodity value in watermelon. The genetic control for the variation in those traits are not clearly known. This study aimed to elucidate the genetic inheritance mode and loci associated with the dark green rind color and bloom formation based on QTL-seq. A bloomless inbred ‘FD061129’ with dark green rind and a bloom inbred ‘SIT55616RN’ with light green rind were crossed to produce F_1 and F_2 progeny. Phenotypic evaluation of the F_1 and 219 F_2 plant indicated the genetic control of two complementary loci and single dominant locus for dark green rind and bloom formation, respectively. The QTL-seq results identified two genomic regions showing significant delta-SNP index on Chr. 6 (DG_6) and Chr. 8 (DG_8) and one genomic region for bloom formation on Chr.1 (BL_1). A previously reported candidate gene controlling the dark green rind by single dominance mode was found from DG_8. Several SNPs in DG_6 and BL_1 were converted to the CAPS and used for genotyping F2 progeny. This high resolution genetic map based on CAPS narrowed down the genomic region of DG_6 and BL_1 to 20kb and 230kb, respectively. The information provided in this study can be useful not only for the development of DNA markers for the selection of rind color and bloom formation of watermelon fruits but for functional analysis and identification of candidate genes.

***Corresponding Author:** Tel. 055-350-5961, E-mail: ypark@pusan.ac.kr

PF-0045

수박 분자육종을 위한 컬러수박 F_2 집단 특성 분석

노솔지[1*], 윤건식[1], 박성원[1], 김은정[1], 전유민[1], 김태일[1], 김영호[2]

[1]충청북도 음성군 대소면 대금로 326-8 수박딸기연구소
[2]충청북도 청주시 청원구 오창읍 가곡길 46 충청북도농업기술원

수박은 세계적으로 재배되는 중요한 작물로, 종자시장에서도 고부가가치 산업으로 각광받고 있다. 전통육종은 장기간이 소요되는 반면, 최근에는 생명공학 육종기술이 발전하면서 육종연한을 단축하고, 육종효율을 높이고 있다. 이에, 조기 신품종 육성을 위해 컬러수박의 유전체 정보를 확보하고, 유용형질을 조사하여 분자육종을 위한 육종집단을 구축하고자 한다. 따라서 F_1을 육성하고, F_2 집단을 전개하여 다양한 특성을 분석하였다. 모본은 흑피, 타원형, 과육색이 짙은 노란색이고, 부본은 황피, 원형, 과육색이 적색인 계통으로 교배하였다. F_1을 육성한 결과, 과피색은 황색, 과육색은 주황색, 과형은 단타원형으로, 중간형태의 특성을 보였다. F_1 세대를 자가수정하여 F_2 집단을 전개한 결과, 각 형질별로 분리양상을 보였고, 과피색은 호피, 청피, 흑피, 황피 4개로 분리되었고, 황피가 우성으로 나타났다. 과형은 원형, 단타원형, 타원형으로 1:2:1로 분리되었다. 또한, 과육색에 따라 기능성 성분인 Lycopene과 β-carotene 함량도 크게 차이를 보였다. 이러한 컬러수박의 F_2 집단 정보는 유전적 특성을 이해하는데 매우 유용한 정보를 제공할 것이며, 품종개발을 위한 육종 및 유전연구에 많은 도움을 줄 것으로 기대된다.

***교신저자:** Tel. 043-220-5862, E-mail: nosol2615@korea.kr

PF-0046

QTLs Related to Fruit Shape in Pears (*Pyrus pyrifolia* × *P. communis*)

Do Yeong Kim[1], Do-Yeon Cho[1], Sewon Oh[1], Yumi Kim[1], Hae Won Jeong[2], Daeil Kim[1*]

[1]Department of Horticulture, Chungbuk National University, 1 Chungdae-ro, Seowon-gu, Cheongju 28644, Republic of Korea

[2]Pear Research Institute, National Institute of Horticultural and Herbal Science, RDA, Naju 58216, Republic of Korea

Pears have many types of fruit shape including pyriform, oblate, spindle shaped, round, and obovate. Previously, fruit shape was evaluated as L/D ratio in pears to performing QTL analysis. The accurate fruit shape index is needed to exactly differentiate fruit shape in pears. We examined A/A' ratio indicating ratio of length from fruit stalk to the middle of fruit diameter (A) to from fruit apex to the middle of fruit diameter (A') and compared with L/D ratio in QTL analysis. The F_1 population of 'Whangkeumbae' (*P. pyrifolia*) × 'Bartlett' (*P. communis*) was used as materials and genetic linkage maps of 'Whangkeumbae' and 'Bartlett' were constructed using array-SNPs, GBS-SNPs, and SSRs. In the 'Whangkeumbae' and 'Bartlett' maps, significant QTLs related to L/D ratio were commonly detected in the linkage group (LG) 1, and significant QTLs related to A/A' ratio were commonly detected in the LG9. QTLs related to two fruit shape indices were not detected in the same LG. The L/D ratio focuses both fruit diameter and length, whereas the A/A' ratio focuses only on the fruit length. Thus, L/D ratio and A/A' ratio might be controlled by the different polygenes. Further studies will be needed as to which of the two fruit shape indices are more suitable to identify phenotype and genotype interaction.

***Corresponding Author:** Tel. 043-261-2527, E-mail: dodo@cbnu.ac.kr

PF-0047

Development of pre-harvest sprouting resistant rapeseed using CRISPR-Cas9

Seung Yong Hahm[1*], Allah Jurio[1], Soo-In Sohn[3], Min Cheol Kim[2], Sang Un Park[2], Joonyup Kim[1]

[1]Department of Horticultural Science, College of Agriculture and Life sciences, Chungnam National University, Daejeon, 34134, Korea

[2]Department of Crop Science, College of Agriculture and Life sciences, Chungnam National University, Daejeon, 34134, Korea

[3]Biosafety Division, National Institute of Agricultural Science, 370, Nongsaengmyeong-ro, Deokjin-gu, Jeonju-si, Jeollabuk-do, 54874, Korea

Pre-harvest sprouting (PHS) is one of the most detrimental factors having adverse effects on yield and grain quality of rapeseed (*Brassica napus* L.). As the rain season overlaps with the harvest season of rapeseed in Korea, the quality and yield of seeds have never been more impacted by PHS. In a previous study, we identified the candidate genes linked to the oxidative pentose phosphate pathway and jasmonic acid pathway. Here we report that we have identified additional candidate genes through reciprocal cross between *Brassica rapa* var. *nipposinica* and *Brassica chinensis* var. *parachinensis* with *Brassica napus* cv. Youngsan. RNA extracted from seeds of the off-spring of each combination were subjected to RNA-seq analysis. Among the differentially expressed genes (DEGs) we identified genes associated with the aliphatic glucosinolate (GSL) biosynthesis pathway and ABA response pathway, which of both have been shown to be essential for seed germination and seedling growth. To find out functional relevance of these genes, we employed multiplex genome editing approach by clustered regularly interspaced short palindromic repeats/CRISPR-associated protein 9 (CRISPR-Cas9) augmented with Goldengate assembly system to knock out the homeologous genes in the allotetrapolyploid genome of rapeseed. Generation of transgenic lines that target candidate genes is currently under way. As a part of this project, and as a separate experiment, we examined the metabolites associated with germination in seven Korean winter cultivars (Mokpo68, Naehan, Mokpo111, Youngsan, Tamla, Tammi, and Hanla). A total of eight GSL (4-Hydroxyglucobrassicin, Progoitrin, Gluconapin, Gluconapoleiferin, Glucobrassicanapin, Neoglucobrassicin, Glucobrassicin and 4-Methoxyglucobrassicin) belonging to the different chemical classes were detected. Among seven cultivars, Mokpo68 contained the greatest level of total GLS, which was five-fold higher than Tamla that contained the lowest level. Phenolic compounds (Gallic Acid, Chlorogenic Acid, Caffeic Acid, Epicatechin, 4-hydroxybenzoic Acid, P-coumaric Acid, Ferulic Acid, Rutin, Catechin Hydrate, Trans-cinnamic Acid, Benzoic Acid, Quercetin, and Kaempferol), which have been demonstrated to contain antioxidant properties, were present in all the cultivars. The accumulation of total phenolic compounds was significantly higher in Naehan than those of the rest. From PHS testing of generated transgenic lines along with information of metabolites analyzed it will be instrumental for future study and breeding functional cultivars of Korean rapeseed resistant to PHS.

***Corresponding Author:** E-mail: seungyon96@naver.com

PF-0048

Isolation and characterization of the *FT*-like genes in pepper (*Capsicum annuum* L.)

Yu-Jeong Kwon[1,2], Min Jeong Hong[1], Gah-Hyun Lim[1], Sungyul Chang[1], Dong-Hwan Kim[3], Jin-Baek Kim[1], JunDae Lee[1], Yeong Deuk Jo[1*]

[1]Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongeup, 56212, Republic of Korea
[2]Department of Horticulture, Chonbuk National University, Jeonju, 54896, Republic of Korea
[3]Department of Integrative Plant Science, Chung-Ang University, Anseong, 17546, Republic of Korea

The *FT* (*Flowering Locus T*)-like genes which are members of phosphatidylethanolamine-binding protein family genes regulate transition between vegetative and reproductive stages of plants. These genes include *FT* that have been well-known as a gene for florigen, a flowering inducer. In tomato, an *FT*-ortholog, *SFT*, was isolated and its mutant could increase heterosis in determinate tomato. In present study, *FT*-like genes were identified and characterized in pepper. Based on similarity to *SFT*, ten pepper genes were selected as PEBP family genes. Among these, six genes were grouped with the *FT*-like genes from other crops in phylogenic analysis and showed expression pattern similar to that of Arabidopsis *FT*. In addition, BiFC analysis showed that the product of these genes interact with FD as in Arabidoposis. Therefore, they were selected as pepper *FT*-like genes. Overexpression of six genes in Arabidopsis resulted in promotion or delay of flowering; *CaFT2*, *CaFT4*, *CaFT6* promoted flowering while *CaFT1*, *CaFT3*, *CaFT5* delayed flowering. Because the flowering promotion effect of *CaFT6* was highest among that of other genes, and CaFT6 was phylogenetically close to SFT, *CaFT6* was determined as the *FT* ortholog. Comparison of function and genomic location of *FT*-like genes between pepper and tomato showed that *CaFT6* and *SFT* evolved independently since the functional gene correspond to *CaFT6* and *SFT* in genomic location is missing in tomato and pepper, respectively. The information on *FT*-like genes obtained in this study is expected to be useful for understanding of flowering control mechanism, and application to hybrid breeding or speed breeding in pepper.

***Corresponding Author:** Tel. 063-570-3315, E-mail: jyd@kaeri.re.kr

PF-0049

혈당강하 활성이 높은 잎전용 고추 '원기2호' 육성

양은영[1*], 사무엘 틸라훈[1,3], 조명철[1], 정효봉[1], 채수영[2], 남춘우[1], 윤재복[2], 홍순철[2], 이준대[3]

[1]전라북도 완주군 이서면 농생명로 100 국립원예특작과학원 원예작물부 채소과
[2]전라북도 김제시 백산면 하정로 196-15 고추와 육종
[3]전라북도 전주시 덕진구 백제대로 567 전북대학교 원예학과

고추는 비타민, 카로티노이드, 캡사이신 등 다양한 기능성 성분이 함유된 채소로서, 대표적인 대사성 질환인 당뇨병 예방에도 효과가 있는 것으로 알려져 있다. 당뇨병은 전세계적으로 연간 400만명이 사망하며, 치료비만 연 800조원 규모인 중요한 대사성 질환이다. 또한 다양한 합병증을 유발하기 때문에 당뇨병 판정을 받게 되면 완치보다는 평생 관리차원의 치료가 필요하다. 전 세계 당뇨병 관리 시장은 2016년 801억 5000만 달러에서 연평균 성장률 12.4%로 증가하여, 2022년에는 1,616억 9000만 달러에 이르는 시장으로 높은 성장률의 시장으로 예상되고 있다. 당뇨병 치료제 중의 하나로 사용되고 있는 당질 흡수 억제제(α-glucosidase inhibitor, AGI)는 이당류를 단당류로 분해하여 소장에서의 탄수화물 흡수를 촉진시키는 효소인 α-glucosidase를 억제하여 식후 고혈당을 낮춰주는 기능을 한다. 식사 후 혈당상승을 낮추기 위해 개발한 아카보즈(Acarbose), 보글리보스(Voglibose) 등 미생물 유래 혈당강하제의 경우 혈액상의 문제, 간과 신장에 무리를 주는 등의 부작용을 초래한다고 알려져 있어 천연 당질흡수 억제제 개발이 필요하다. 고추 잎에는 이러한 AGI 활성이 높은 것으로 보고된 바 있고, 국립원예특작과학원에서는 기존 고추 잎보다 AGI 활성이 4배 정도 높은 '원기1호'를 육성한 바 있다. 본 연구는 기존 연구결과를 보완하고 상업용으로 보급이 가능한 항당뇨 잎전용 고추 품종 개발을 위해 기존 육성계통 및 도입 자원을 대상으로 2018년부터 AGI 활성 및 원예적 특성을 평가하여 상업용 품종 개발에 사용이 가능한 우수계통을 육성하고자 수행하였다. AGI 활성분석은 전북대학교가 기존에 보고된 AGI 활성 분석방법에서 α-glucosidase 및 기질(pNPG) 용량, 추출방법, 희석 배수 등을 조정하여 보완한 방법을 기준으로 하였다. 3분지 수확 잎을 55℃에서 건조하여 만든 분석샘플을 이용해 기존 육성 계통, 도입자원, 시판품종 등 총 150점에 대해 분석을 수행하였다. 분석결과 기존 육성품종보다 AGI 활성이 2.9배 높고 당뇨병 치료제인 Acarbose와 비슷한 수준의 활성을 보인 AGI29를 최종 선발하여 '원기2호'로 명명하였다. '원기2호'의 개화소요일수는 95일 전후로 대비종보다 10일 정도 빠르고 착과방향은 하향이고, 식물체 초형은 직립형이며, 식물체 줄기의 솜털이 약하게 있으며, 잎의 모양은 난형이고 과실 성숙전의 색은 녹색이다. '원기2호'의 추출물을 쥐에 투여한 전임상 시험 결과 공복혈당, 식이효율, 혈장인슐린농도, 인슐린저항성지표, 혈중지질 등이 대조군에 비하여 유의적으로 개선된 것을 확인하였다.

***교신저자:** Tel. 063-238-6613, E-mail: yangyang2@korea.kr

PF-0050

Indentification of MYB Repressor on Negatively Regulation of Anthocyanin Biosynthesis in Chinese Cabbage Leaves

Ji-Yeon Kim, Da-Hye Kim, Sun-Hyung Lim*

Division of Horticultural Biotechnology, School of Biotechnology, Hankyong National University, Anseong, 17579, Republic of Korea

Chinese cabbage (*Brassica rapa* L.) is widely cultivated as an economically important crop, and has various visible appearance of leaves comprised white, green, yellow or purple. The purple color in Chinese cabbage was exhibited by accumulation of anthocyanin which is belonging to flavonoid derived secondary metabolites and have the strong antioxidant activities. Anthocyanins biosynthesis is regulated by MBW complex consisting with a MYB transcription factor (TF), a basic helix-loop-helix (bHLH) TF and WD40 repeat protein. MYB regulators can positively or negatively regulate the anthocyanin biosynthesis through the controlling the expression level of anthocyanin biosynthetic genes and modulating the stability of MBW complex. Here, to identify the novel MYB regulator on anthocyanin biosynthesis, we compared the different level of Chinese cabbage with different colors via RNA-seq analysis and selected the differential expressed R3-and R2R3-MYB TFs. We characterized *BrMYB#1* and *BrMYB#2* genes in Chinese cabbage leaves through genetic and molecular approaches. An Arabidopsis protoplast transfection assay showed that both of *BrMYB#1* and *BrMYB#2* are a nuclear-localized protein. Furthermore, both of these *BrMYB#1* and *BrMYB#2* physically interacted with *BrTT8* (bHLH) in a yeast two-hybrid analysis. Co-transfection assays in tobacco leaves revealed that increment of *BrMYB#1* and *BrMYB#2* mediate inhibition of anthocyanin accumulation. To enhance the anthocyanin content, we are conducting to transform the Chinese cabbage via these repressor genes with genome editing. Through the these approach, it will be helpful to precise breeding for improving the health beneficial metabolites.

***Corresponding Author:** Tel. 031-670-5106, E-mail: limsh2@hknu.ac.kr

PF-0051

Meta-analysis reveals expanded transcriptomic view of strawberry fruit ripening

Gibum Yi[1*], Hosub Shin[2], Kyeonglim Min[2], Eun Jin Lee[2,3*]

[1]Department of Bio-Environmental Chemistry, College of Agriculture and Life Sciences, Chungnam National University, 99 Daehak-ro, Yuseong-gu, Daejeon 34134, Republic of Korea
[2]Department of Agriculture, Forestry and Bioresources, College of Agriculture and Life Sciences, Seoul National University, 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Republic of Korea
[3]Research Institute of Agriculture and Life Sciences, Seoul National University, 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Republic of Korea

Strawberry is an economically important horticultural crop and a model crop to study non-climacteric fruit ripening. Fruit ripening is an essential stage to affect fruit quality and postharvest storability, and researches in strawberry fruit ripening have been performed with various cultivars. However, genetic and physiological differences among the cultivars make it difficult to understand common characteristics of strawberry ripening. Therefore, we performed a meta-analysis by mapping publicly available transcriptome data from six cultivars to the newly published and improved strawberry reference genome. We investigated meta-differentially expressed genes (meta-DEGs) to provide an expanded transcriptomic view of strawberry ripening. We found common transcriptomic changes in starch metabolism, chlorophyll degradation, and cell-wall degradation during ripening through gene ontology (GO) analysis. We also identified 483 meta-DEGs not detected as DEGs in the single analysis. This novel meta-DEGs were enriched in GO categories of photosynthesis, amino acid biosynthetic process, and fatty acid biosynthetic process. Anthocyanin biosynthesis regulatory genes, including *FaMYB1*, *FabHLH27*, and *FaBHLH40*, were detected as up-regulated meta-DEGs during ripening, suggesting these genes are commonly involved in coloration of strawberry fruit. Transcription factors, including *NAC83*, *WRKY40*, and *WRKY48*, were also determined as meta-DEGs, indicating the possible relevance to ripening.

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***Corresponding Author:** Tel. 02-880-4575, E-mail: gibumyi@cnu.ac.kr (GY); ejinlee3@snu.ac.kr (EJL)

PF-0052

A Splicing mutation in *Zeaxanthin epoxidase* Contributes to Orange Mature fruit color and Alter Carotenoid Contents in Pepper Fruit (*Capsicum annuum*)

Seo-Young Lee, So-Jeong Jang, Hyo-Bong Jeong, Se-Young Lee, Jelli Venkatesh, Joung-Ho Lee, Jin-Kyung Kwon, Byoung-Cheorl Kang*

Department of Agriculture, Forestry and Bioresources, Research Institute of Agriculture and Life Sciences, Plant Genomics and Breeding Institute, College of Agriculture and Life Sciences Seoul National University, Seoul, 08826, South Korea

Phytoene synthase (*PSY1*), *Capsanthin-capsorubin synthase* (*CCS*), and *Pseudo response regulator2-like* (*PRR2*) are three major genes controlling fruit color in pepper. However, the diversity of fruit color in pepper cannot be completely explained by these three genes. Here, we used an F_2 population derived from *C. annuum* 'SNU-mini Orange' (SO) and *C. annuum* 'SNU-mini Yellow' (SY), both harboring functional *PSY1* and mutated *CCS,* and observed that yellow color was dominant over orange color. We performed genotyping-by-sequencing (GBS) and mapped the genetic locus to a 6.8 Mb region on chromosome 2, which we named *CaOr*. Among the genes located within the region, we discovered that a splicing mutation in the *Zeaxanthin epoxidase* (*ZEP*) leading to premature stop codon of the gene. HPLC analysis showed that SO contained higher amounts of zeaxanthin and total carotenoids in mature fruits than SY. A color complementation assay using *E. coli* harboring carotenoid biosynthetic genes showed that the mutant ZEP protein had reduced enzymatic activity. Transmission electron microscopy of plastids revealed that the *ZEP* mutation affected plastid development with more rod-shaped inner membrane structures in chromoplasts of mature SO fruits. To validate the role of ZEP in fruit color formation, we performed virus-induced gene silencing (VIGS) of *ZEP* in the yellow-fruit cultivar *C. annuum* 'Micropep Yellow' (MY). The silencing of *ZEP* caused significant changes in the ratios of zeaxanthin to its downstream products and increased total carotenoid contents. Thus, we conclude that the *ZEP* genotype can determine orange or yellow mature fruit color in pepper.

***Corresponding Author:** Tel. 02-880-4563, E-mail: bk154@snu.ac.kr

PG-0001

Development of seedling propagation technology of new introduced hop crops

Sang Hoon Park[1], Tae Hyun Ha[2], Si-Yong Kang[2*]

[1]Hop & Hope Co. Ltd., 18 Sunjean-gil, Haengan-myeon, Buan, Jeonbuk 56319, Republic of Korea
[2]College of Industrial Sciences, Kongju National University, 54 Daehak-ro, Yesan, Chungnam 32439, Republic of Korea

Hop (*Humulus lupulus*) is a vine-like plant belonging to the cannabiaceae family, and is a perennial dioecious plant. It forms lupuline, a type of secretion gland, in the pine shaped cones of female plants, which provides a unique bitter taste and aroma of beer, and has an effect of preventing spoilage, so it is widely used as a beer raw material. In the mid-1980s, hops cultivation in Korea was settled in Gangwon-do and inland mountainous areas, achieving almost self-sufficiency, but since the 1990s, the cultivation and related researches of hops have disappeared due to foreign imports. In recent years, due to the boom of craft beer, some businessmen and local growers are promoting domestic production by introducing foreign hops, but due to the lack of suitable varieties and expertise, they are having a lot of difficulties in expanding cultivation. It is necessary to rebuild the domestic hop production and supply system through proliferation and breeding of domestic suitable varieties, and to promote related industries. Newly introduced foreign hop varieties were cultivated by seed root propagation, and the differences in growth between varieties and regions were examined. And, the proliferation by cutting and softwood and hardwood stems were also compared and examined. Since hops are dioecious plant, male plants must be planted and seed harvesting after artificial fertilization, for the seed propagation or hybridization breeding. However, since mature hop seeds do not germinate at the same time unless dormant breakage treatment is performed, a dormancy breakage method was developed by water and low temperature treatment of seeds.

***Corresponding Author:** Tel. 041-330-1226, E-mail: sykang@kongju.ac.kr

PG-0002

Root-knot resistance assessment of wild type watermelon *Citrullus amarus*

Heejung Cho[1*], Ji Yeon Park[1], Insoo Choi[2]

[1]National Institute of Agricultural Sciences, RDA, Jeonju, 54874, Korea
[2]Nematode Research Center, Life and Industry Convergence Research Institute, Pusan National University, Miryang, 50463, Korea

Watermelon (*Citrullus lanatus*) is a worldwide cultivated cucurbit horticulture crop with growing interest in its health benefits, high nutritional value, and economical importance. Root-knot nematodes (RKNs) caused by *Meloidogyne* spp. are endoparasites affecting the root systems to various crop plants. Watermelon was also very susceptible to root-knot nematodes, it has been applied of nematicides and soil fumigants for reducing nematode populations. To find out the root-knot resistance resources, we assessed the resistance of wild type watermelon *C. amarus* P1 and P2 about four species of root-knot nematodes - *Meloidogyne incognita*, *M. arenaria*, *M. hispanica*, *M. javanica*. We also infected *C. lanatus* S and *Solanum lycopersicum* Rutger (root-knot susceptible tomato) as a control. As the result, *C. amarus* P2 was resistance to *M. incognita*, *M. arenaria*, and *M. hispanica*, and *C. amarus* P1 was only resistance to *M. incognita* and *M. javanica*. So, wild type watermelon P2 will be good resource for root-knot resistance.

***Corresponding Author:** Tel. 063-238-4567, E-mail: chohj78@korea.kr

PG-0003

Identification of saponin patterns in adzuki bean including six species of genus *Vigna*

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

[1]Department of Applied Biosciences, Kyungpook National University, Daegu 41566, Republic of Korea
[2]Department of Agriculture, Forestry and Bioresources, Seoul National University, Seoul 08826, Republic of Korea

Adzuki bean [*Vigna angularis* (Wild.) Ohwi & H. Ohashi] is known as one of the important crops widely in East Asia and Southeast Asia. In the soybean, saponins are classified as group A and DDMP saponins. However, the saponin contents are not well known in genus *Vigna.* In this study, we used seven species, *Vigna vexillata* (zombi pea), *Vigna unguiculata* (cowpea), *Vigna mungo* (black gram), *Vigna radiata* (mung bean), *Vigna angularis* (adzuki bean), *Vigna umbellata* (rice bean), and *Vigna nakashimae* (adzuki bean-related species), to study the saponin patterns in the same genus *Vigna*. To identify the saponin in genus *Vigna*, we performed the TLC analysis in hypocotyl and cotyledon. *Vigna umbellata* (rice bean) and *Vigna nakashimae* (adzuki bean-related species) showed similar saponin bands like adzuki bean but other species showed like those of *Vigna radiata* (mung bean). Representatively, we selected two main species, adzuki bean and mung bean, to perform HPLC analysis in the hypocotyl. The adzuki bean showed AzII, AzIII, and AzIV with DDMP moiety but the mung bean showed only DDMP-βg which is normally distributed in soybean. We focused on DDMP moiety and found the *Sg*-9 homologous gene which is identified in soybean that attached DDMP moiety in both species.

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

PG-0004

Mutation of a novel E3 ubiquitin ligase causes early flowering in Arabidopsis

Jeongyun Ko[1], Jinwon Lee[1], Hak Soo Seo[2], Jong Tae Song[1*]

[1]Department of Applied Biosciences, Kyungpook National University, Daegu 41566, Republic of Korea
[2]Department of Agriculture, Forestry and Bioresources, Seoul National University, Seoul 08826, Republic of Korea

An E3 ubiquitin ligase is a protein that transfers the ubiquitin to the target protein and the ubiquitinated target protein is degraded by the proteasome. In this study, we isolated the novel E3 ligase mutant involved in flowering time in Arabidopsis. The knockout mutant of the E3 ubiquitin ligase, named *ef*, showed less number of rosette leaves and early flowering phenotype compared to the wild type in the long-day condition. The sequence analysis revealed that *EF* encodes a C3H4 RING-type ubiquitin ligase. We found three homologous genes in Arabidopsis genome by using the BLAST search and we did not observe the early flowering phenotype in the T-DNA insertional mutant of the homologous genes, respectively. We also obtained and examined the phenotype of the triple mutant of homologous genes. However, the triple mutant did not show the early flowering phenotype. These results indicating that the early flower phenotype is caused by the knockout of a single novel E3 ubiquitin ligase gene. To study the role of *EF* gene, we will generate CRISPR/Cas9 transgenic plants and overexpression lines for further study.

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

PG-0005

Analysis of Lignans composition and Identification of Lignans Biosynthetic Enzyme in *perilla frutescens*

Juho Lee*, Woo-Hyun Jeong, Kyeong-Ryeol Lee, Jong-Sug Park

National Institute of Agricultural Sciences, RDA, Jeonju 54874, Republic of Korea

Lignans are secondary metabolites and phytochemicals biosynthesized in diverse plant species such as flaxseed, pumpkin seed, soybean and sesame seed. The molecular structure of lignans is phenylpropanoid dimers (C6-C3 unit) and widely known plant lignans are pinoresinol, secoisolariciresinol, lariciresinol, matairesinol and sesamin. These compounds have numerous biological effects including antioxidant and antitumor activities. However, compositions of lignans and biosynthetic enzyme in *perilla frutescens* are not yet understood. This study investigated the compositions of lignans and identified the enzyme in perilla. Perilla seeds were harvested in our greenhouse and lignans were extracted with organic solvent. Based on liquid chromatography/mass spectroscopy(LC/MS) analysis, two lignans (6.4 ug/100 g pinoresinol, 1.4 ug/100 g lariciresinol) were found in seeds extracts. Also, compared *Arabidopsis thaliana* genome information, we identified lignans biosynthetic enzyme, pinoresinol-lariciresinol reductase (*pf*PLR) in *perilla frutescens* and characterized function using substrate feeding assay. The *pf*PLR converted pinoresinol to lariciresinol with LC analysis and the enzyme activity was confirmed. These result show that compositions of lignans in perilla and identified biochemical characterization of new lignan biosynthetic enzyme.

***Corresponding Author:** Tel. 063-238-4607, E-mail: jhlee0102@korea.kr

PG-0006

Morphological variation of *Perilla* landrace accessions in Korean RDA-genebank

Dong Min Kim[1,2], Kyu Jin Sa[1], Ju Kyong Lee[1*]

[1]Department of Applied Plant Sciences, College of Agriculture and Life Sciences, Kangwon National University, Chuncheon 24341, Korea
[2]Gangwon-do Agricultural Research and Extension Services, Chuncheon 24226, Korea

In our study, we detected morphological variation in 189 accessions of cultivated var. *frutescens* of *Perilla* crop obtained from Korean RDA-genebank by measuring seven qualitative characters. In 189 accessions of cultivated var. *frutescens*, most accessions showed green color for color of leaf surface (QL1), color of reverse side leaf (QL2), and stem color (QL3). The two types of leaf shape, lanceolate and cordate were distributed in similar proportions in all accessions. Moreover, 114 accessions of the 189 accessions had a late flowering time. In case of degree of pubescence, over 60% of total accessions had a pubescence. Almost accessions (153, 81.0%) had a leaf fragrance of *Perilla frutescens* var. *frutescens*. Among correlation coefficients of the 7 qualitative characters, four combinations, QL1 and QL3, QL2 and QL6, QL5 and QL6, QL5 and QL7 showed significant correlations compared to other trait combinations at $P<0.05$. In principal components analysis (PCAs), two qualitative traits, QL1 and QL3 contributed in the positive direction on the first axis. While, another two qualitative traits, QL5 and QL6 contributed in positive direction on the second axis. In this study, we have provided the information regarding the morphological variation of cultivated var. *frutescens* of *Perilla* preserved in RDA-genebank. The results of this study are expected to provide useful information for further understanding of morphological variations in the *Perilla* accessions, and to help efficiently preserve the genetic resources of *Perilla* and breed *Perilla* varieties in South Korea.

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

PG-0007

Development of a core collection for cultivated var. *frutescens* of *Perilla* crop in Korean RDA-genebank using SSR markers

Kyu Jin Sa[1], Hyeon Park[1], Do Yoon Hyun[2], Sookyeong Lee[2], Ju Kyong Lee[1*]

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

[2]National Agrobiodiversity Center, National Institute of Agricultural Sciences, RDA, Jeonju 54874, Korea

This study was conducted to analysis the genetic diversity and to construct a core collection of 400 cultivated var. *frutescens* of *Perilla* crop conserved in RDA-genebank using SSR markers. We used 22 SSR markers to analyze the genetic variability of 400 accessions of cultivated var. *frutescens* of *Perilla* crop. As a result, a total of 173 alleles were identified at all loci, with an average of 7.86 alleles per locus and a range between 4 and 15 alleles per locus. The genetic diversity (GD) ranged from 0.138 to 0.868, with an average of 0.567. The average polymorphic information content (PIC) value was 0.522, ranging from 0.134 to 0.853. In the population structure analysis using the model-based method, the 400 *Perilla* accessions were divided into two main group and an admixed group based on a membership probability threshold of 0.8. In total of accessions, 44 (11.0%) core accessions of 400 accessions were selected in the POWERCORE analysis, a core group selection program using the alleles from 22 SSR primers. Compared to the allelic numbers and two different diversity index (Shannon & Weaver and Nei calculation) between the selected core accessions and the entire accessions, core collection was maintained a same number of alleles and similar or higher level of diversity than that of the total 400 accessions. This is the first report for development of core collections in cultivated var. *frutescens* of *Perilla* crop using SSR markers. These core collections will be useful for effective conservation and utilization of genetic resources in crop improvement programs.

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

PG-0008

Breeding and Growth Characteristics of Italian Ryegrass (*Lolium multiflorum* Lam) ‘IR605’

Sang-Hoon Lee, Ki-Won Lee, Jae Hoon Woo, Bo Ram Choi, Eun A Lim, Hee Chung Ji, Ki-Yong Kim*

Grassland & Forages Division, National Institute of Animal Science, RDA, Cheonan, 31000, Republic of Korea

Italian ryegrass (*Lolium multiflorum* Lam) is the most popular winter annual grass in Korea and is cultivated for hay, haylage, or silage. The current study compared growth characteristics of Italian ryegrass (*Lolium multiflorum* Lam) ‘IR605’, and ‘Kowinearly’. The new variety of Italian ryegrass, IR605, is a diploid with green leaves, a semi-erect growth habit before wintering, and an erect growth habit in the spring. IR605 is a medium-maturing variety with a heading date of ca. May 15. IR605 had a flag leaf width of 9.9 mm, flag leaf length of 26.7 cm, and plant length on heading date of 100 cm, which is approximately 5 cm longer than Kowinearly. The stem thickness and ear length of IR605 were 0.08 mm thicker and 0.5 cm longer, respectively, than those of Kowinearly. The resistance to cold of IR605 was weaker than that of Kowinearly, but strong enough to be cultivated in Pyeongchang, Gangwon province. The dry matter yield of IR605 (9,308 kg/hectare) was 20% higher than that of Kowinearly, a difference that was augmented by 52% ($p < 0.05$) in the southern region of the reclaimed land of Haenam. The *in vitro* dry matter digestibility of IR605 was 68.4%, which was slightly higher than that of Kowinearly. The total digestible nutrient value was 58.5%, which was slightly lower than Kowinearly. Overall, the feed quality characteristics of IR605 were similar to those of Kowinearly.

***Corresponding Author:** Tel. 041-580-6767, E-mail: kimky77@korea.kr

PG-0009

Development and Characterization of New Italian Ryegrass (*Lolium multiflorum* Lam) Variety, 'IR901'

Sang-Hoon Lee, Ki-Won Lee, Jae Hoon Woo, Bo Ram Choi, Eun A Lim, Hee Chung Ji, Ki-Yong Kim*

Grassland & Forages Division, National Institute of Animal Science, RDA, Cheonan, 31000, Republic of Korea

Italian ryegrass grows in a wide range of soil types, although it prefers fertile, well-drained soils. In Italian ryegrass breeding programs, it is necessary to select a range of traits within different cultivar types varying in ploidy and flowering time. The traits selected in Italian ryegrass breeding can be broadly grouped into production traits, such as yield and quality. This study considered the development and characterization of a new Italian ryegrass (*Lolium multiflorum* Lam) variety, 'IR901'. In order to produce this new variety, five superior including '12EtHN4NN14', '12EtHN4NN23', 'ARIXJN09', 'ARIXJN14', and 'ARIXJN18' were polycrossed. The new variety, 'IR901', was compared in regional adaptability evaluation field tests in Cheonan, Pyeongchang, and Haenam against the control variety, 'Kowinearly'. Agronomic growth characteristics such as development, cold-tolerance, plant length, heading date, lodging, blight, and leafiness were assessed. Forage production and feed value were also analyzed. IR901 is a late-maturing variety with a heading date of ca. May 22. The resistance to cold of IR901 was weaker than that of Kowinearly. The dry matter yield of IR901 (7,747 kg/hectare) was 19% higher than that of Kowinearly in the southern region of the reclaimed land of Haenam. The feed quality characteristics of IR901 were similar to those of Kowinearly, but the *in vitro* dry matter digestibility of IR901 was 72.2%, which was slightly higher than that of Kowinearly.

***Corresponding Author:** Tel. 041-580-6767, E-mail: kimky77@korea.kr

PG-0010

Determination of Forage Yield and Quality Characteristics of Orchardgrass (*Dactylis glomerata* L.) Lines

Sang-Hoon Lee, Ki-Won Lee, Yowook Song, Md. Atikur Rahman, Hee Chung Ji*

Grassland & Forages Division, National Institute of Animal Science, RDA, Cheonan, 31000, Republic of Korea

Orchardgrass (*Dactylis glomerata* L.) is a cool season, introduced, perennial, bunchgrass. Orchardgrass is adapted to moderate to well-drained basic to acidic soils (pH 5.8-7.5) on textures ranging from clay to gravelly loams and shallow to deep soils. It does not grow well in saline soils and areas with high water tables within the rooting zone. The objectives of this study were to determine the forage yield and quality of new lines. We developed new candidate varieties of orchardgrass by using half-sib family selection breeding methods and then examined forage yield and quality features for new variety registrations. The study was conducted in a randomized complete block design with three replications. In this study, yield and quality characteristics of five orchardgrass lines were compared with those of two standard varieties. In the studied lines and varieties, dry matter yield was found to be 15.6-16.2 ton/ha. The results indicated that some of the lines had similar or superior yield and quality characteristics to standard varieties. Therefore, lines 'Hapsung 47ho', 'Hapsung 48ho', 'Hapsung 49ho', 'Hapsung 50ho', and 'Hapsung 51ho' were selected for further regional yield assessments due to their high dry matter yield, crude protein yield, digestible nutrient content, and digestible nutrient yield capacity. Some of these candidate lines may be registered as cultivars for use in reclaimed land regions in the near future.

***Corresponding Author:** Tel. 064-754-5710, E-mail: cornhc@korea.kr

PG-0011

Anti-melanogenic effect of Methyl Jasmonic treated DJ526 callus

Vipada Kantayos, Jin-Suk Kim, Eui-Shik Rha, So-Hyeon Baek*

Department of well-being resources, Sunchon National University, Suncheon, Republic of Korea

Skin pigmentation is caused by the overproduction of melanin under the skin layer. The most significant risk factor of skin pigmentation is UV radiation which is unavoidable in our daily life. Since the growing trend of beauty products, particularly in Asian countries, is captured attention on skin lightening and whitening products, the active ingredient that shows reduced skin pigmentation plays a role in developing beauty science. For improving a dynamic ingredient quantity, elicitors have increased active compound production in several studies. Because the amount of active compounds significantly has an impact on its biological activity. This study examined the potential of methyl jasmonate (MeJA) on resveratrol production and its relationship to the anti-melanogenic activity of DJ526 callus extracts. As a result, MeJA-5μM stimulated resveratrol production and showed a significant inhibitory effect on melanin content and tyrosinase activity in melan-a cells. In conclusion, MeJA-5μM is a powerful treatment for improving resveratrol products and its whitening effect.

Keywords: resveratrol, rice, callus, methyl jasmonate, elicitor, melanogenesis

***Corresponding Author:** Tel. +82-61-750-3217, E-mail: baeksh@scnu.ac.kr

PG-0012

Yeast extract up-regulated resveratrol synthase in DJ526 callus

Vipada Kantayos, Jin-Suk Kim, Eui-Shik Rha, So-Hyeon Baek*

Department of Agricultural Life Science, Sunchon National University, Suncheon, Republic of Korea

DJ526 callus is a resveratrol-enriched rice callus, which is developed through genetic modification. DJ526 has a high potential for biological activities, i.e., increasing lifespan and improving physical strength during degenerative changes. The quantity of resveratrol and its derivatives provide an opportunity to promote biological activity in the DJ526 callus. In this study, yeast extract (YE) treated DJ526 callus differently from elicitation time (12, 24, 48 h.) was investigated their effect on resveratrol production and the expression of resveratrol synthase. From HPLC data, an increasing resveratrol and piceid content (resveratrol derivative) is found in YE-24h, linked to up-regulation of *resveratrol synthase* expression. Based on the results, YE-24h increased 50% of resveratrol product compared with non-treatment; however, overexposure with YE can cause reduction of resveratrol product, according to a decreasing of resveratrol production in 48h. In conclusion, exposure times and concentrations of elicitors were crucial factors for *resveratrol synthase*; moreover, YE is an effective tool to increase resveratrol production in DJ526 callus, particularly 24h treatment.

Keyword: resveratrol, rice, yeast extract, callus, gene expression

***Corresponding Author:** Tel. +82-61-750-3217, E-mail: baeksh@scnu.ac.kr

PG-0013

근적외선분광법을 이용한 수수-수단그라스 종자의 품종 판별

우제훈, 이상훈, 김지혜, 박형수, 이배훈, 이기원*

초지사료과, 국립축산과학원, 농촌진흥청

사료용 수수류는 건물생산성과 잡초와의 경합이 우수하고, 병충해에 의한 피해가 낮아 하계 사료작물로 많이 재배되고 있는 주요 초종중 하나이다. 또한 여름철 가뭄과 더위에 강하고 연중 여러 번 예취가 가능한 장점을 가지고 있다. 사료용 수수류는 크게 수수, 수단그라스 그리고 수수와 수단그라스를 교잡한 수수 × 수단그라스 교잡종 3종류로 분류하고 있다. 다양한 형태의 사료용 수수류는 모두 동일한 속 (Genus. 屬)에 속하지만 종자 상태에서는 품종 간의 형태적 차이가 나타나지 않아 육안으로 품종 판별이 어려워 작물 출현 후 잎이나 출수 여부를 통해 품종을 구별하고 있는 상황이다. 최근 품종 판별의 어려움을 해결하기 위하여 해외에서는 근적외선 분광법 (NIRS)을 이용하여 종자의 초종, 품종 그리고 순도를 신속하게 판별하는 것에 대한 연구가 이루어지고 있다. 본 연구는 근적외선 분광법 (NIRS)을 통해 수수 × 수단 그라스 잡종 (Sorghum 속) 종자의 품종의 구분 가능 여부를 확인하기 위해서 수행되었다. 정확한 검량식 개발을 위해 360개의 샘플을 분석하였다. 전체 표본에는 680-2500nm 파장 내에서 다른 세 가지 스펙트럼 범위 (가시광선, 근적외선 및 전체 범위)를 적용하고 spectra star 2500 근적외선을 사용하여 스펙트럼을 측정하였다. 판별 분석을 위한 검량식은 부분 최소 제곱 (PLS) 회귀 및 판별 방정식 (DE) 분석으로 개발되었다. 이를 통해 개발된 세 가지 스펙트럼 범위에 대한 PLS 판별 분석 모델이 12개의 다른 수수 속을 구별할 수 있음을 확인했으며, 전체 판별 정확도는 NIR 전체 범위 스펙트럼에서 82~100 %로 나타났다. 결론적으로 화학 측정과 결합된 NIRS 분석을 통해 수수 × 수단 그라스 잡종 품종을 빠르고 정확하게 구별할 수 있는 가능성을 확인할 수 있었다.

Key words: Near Infrared Spectroscopy, Sorghum-Sudangrass Hybrid, Discrimination of Feed Crops

***교신저자:** Tel. 041-580-6771, E-mail: delpire@korea.kr

PG-0014

Genetic diversity of black soybean germplasms with green cotyledon based on agronomic traits and cotyledon pigments

Ji Yun Lee[1*], Hong Jib Choi[1], Chang Ki Son[1], Jeong Suk Bae[1], Hyun Jo[2], Jeong-Dong Lee[2]

[1]Gyeongsangbuk-do Agricultural Research and Extension Services, Daegu, 41404, Republic of Korea
[2]Department of Applied Biosciences, Kyungpook National University, Daegu, 41566, Republic of Korea

Understanding of plant morphological and seed characteristics is an essential step for the utilization of the genetic resources to improve targeted traits in soybean breeding programs. The purpose of this study was the evaluation of agronomic traits and seed pigments of 469 black soybean germplasms with green cotyledons to identify useful resources according to multivariate analyses. The results showed that the range of flowering days from planting were 37.7 ~ 71.5 days, harvesting days from planting were 112.3 ~ 153.0 days, plant height was 49.6 ~ 151.6 cm, and 100-seed weight was 9.1 ~ 49.3 g. Regarding the flower and hypocotyl color, 2.6% of the total black soybean accessions (12/469 accessions) showed a white flower. According to correlations analyses with agronomic traits, flowering and harvesting days were correlated with plant height, number of nodes and branches in this study. Additionally, it was found that chlorophyll *a* and total chlorophyll content had the greatest effect on the green color of the cotyledon. Based on 13 quantitative traits, the results of PCA analysis show that PC1 accounted for 39.6% and PC2 accounted for 31.6% of the total variance. In this study, black soybean germplasms with green cotyledons were divided into 4 clusters by K-means cluster analysis (the nonhierarchical procedure). Cluster analysis showed that chlorophyll *a* and plant height had the great effect on clustering of black soybean germplasms used in this study. This study will provide opportunities to easily select useful genetic resources for the development of new black soybean cultivars.

***Corresponding Author:** Tel. 054-373-5486, E-mail: dock0409@korea.kr

PG-0015

Investigation of forage yield, nutritive value and soil composition (chemical & microorganism) through maize × legume intercropping systems on paddy fields

Yowook Song, Sang-Hoon Lee, Md Atikur Rahman, Ki-Won Lee*

Grassland and Forages Division, National Institute of Animal Science, RDA, Cheonan 31000, Korea

The study was conducted to investigate the effect of maize and legume intercropping systems on forage yield, nutritive value and soil condition (chemical & microorganism). A total of nine cropping systems, five sole cropping systems (maize and different four legumes) and four intercropping systems (maize with legumes), were planted using a randomized complete block design. The results of rhizosphere microbial analysis show that proteobacteria phylum has a high proportion in the soil where legume is grown. Furthermore the proteobacteria phylum was relatively high correlation with soil total nitrogen. The climbing habit legume growth was increased by intercropping, but the total dry matter yield was not significantly increased. Interestingly, intercropping with soybean 1 resulted in better neutral detergent fiber (NDF), however acid detergent fiber (ADF) and crude protein (CP) was higher in intercropped cowpea. Total digestible nutrients (TDN) was not significantly different between whole intercropped legumes. These results suggest that the intercropping system has greatly enhanced the nutritive value of forage legumes. The above results concerning the impact of intercropping system on dry matter yield and nutritive value provide a new insight into the role of alternative cropping in forage improvement in paddy fields.

***Corresponding Author:** Tel. 041-580-6757, E-mail: kiwon@korea.kr

PG-0016

Comparison of functional contents in the leaves of breeding line and variety of small red bean

Yeon Ju An, Sang Ik Han, Ji Young Kim, Byong Won Lee, Myeong Eun Choe, Ji Ho Chu, Seok Bo Song*

Upland Crop Breeding Research Division, National Institute of Crop Science, RDA, Miryang, 50424, Korea

Small red bean leaves, as well as seeds, are rich in nutritional and functional contents. Small red bean leaves have been to prepare various foods such as soup and Kimchi. Research on small red beans is mainly focused on seeds, and there are few studies on small red bean leaves. So, a functional content analysis of small red bean leaves was conducted to select excellent varieties. The beta-carotene and isoflavone contents were analysed for 22 breeding lines such as 'YA1402' and 17 varieties such as 'Arari'. The beta-carotene content of the breeding line was in the range of 66.5 to 82.5 ㎍/g and the highest content was in 'YA1410'. In the variety, 'Gumguseul' had the highest beta-carotene content. Four isoflavones including daidzin, daidzein, malonyl-daidzin and genistein were detected in the breeding lines and the highest content was measured in 'YA1522'. On the other hand, 5 isoflavones including daidzin, daidzein, malonyl-daidzin, acetyl-glycitin and genistin were found in the varieties and the highest amount was detected in 'Geumsil'. Both breeding line and variety had abundant malonyl-daidzin content. Genistein, which is known to be excellent for anticancer activity, was also present in a substantial amount. The presence of a significant amount of isoflavones and beta-carotene, a good nutrient for eye health, shows the potential use of small red bean leaves.

***Corresponding Author:** Tel. 055-350-1243, E-mail: songsb1254@korea.kr

PG-0017

Risk assessment of insect-resistant transgenic rice (Bt-T) on above-ground non-target arthropods in Korea

Sung-Dug Oh[1], Soo-Yun Park[1], Seong-Kon Lee[1], Doh-Won Yun[1], Gang-Seob Lee[1], Sang Jae Suh[2*]

[1]Department of Agricultural Biotechnology, National Academy of Agricultural Sciences, Jeonju 54874, Republic of Korea

[2]School of Applied Biosciences, Kyungpook National University, Daegu, 41566, Republic of Korea

The insect-resistant transgenic rice (Bt-T) shows insecticidal activity against rice leaf roller (*Cnaphalocrocis medinalis*) by transforming the *mCry1Ac1* of the soil bacterium *Bacillus thuringiensis*. Environmental risk assessment of the Bt-T rice was done along with parent variety Dongjin and cultivar Ilmi in the rice cultivation seasons of 2016 and 2017 at LMO quarantine fields of Jeonju and Gunwi, Korea. For environmental risk assessment, non-target arthropods were captured using an aspirator from the three rice ecosystems of both the locations and in total 39,734 individuals of 57 families and 11 orders were collected. The numbers of individuals collected from Bt-T, Dongjin and Ilmi rice ecosystems were 12,899, 12,730 and 14,105, respectively and the results did not differ significantly. The dominance, diversity, evenness, and richness indices of the collected insects were statistically indifferent among the rice ecosystems but showed significant variations between the two locations and survey years. The principal component analysis using combined data showed that the insects and spiders among the Bt-T and Dongjin and Ilmi rice ecosystems were separated by the study locations and years irrespective of rice varieties. Results obtained in the two consecutive years from the two non-GM rice ecosystems and Bt-T rice ecosystem showed that the Bt-T rice had no significant negative impact on the above-ground insects and spiders.

***Corresponding Author:** Tel. 063-238-4735, E-mail: sjsuh@knu.ac.kr

PG-0018

Analysis of genetic diversity and relationships of *Perilla frutescens* using novel EST-SSR markers derived from transcriptome between wild-type and mutant *Perilla*

Jung Min Kim[1,2], Jae Il Ryu[1], Dong-Gun Kim[1,3], Nguyen Ngoc Hung[1,2], Ji Su Seo[1,2], Jaihyunk Ryu[1], Jin-Baek Kim[1], Joon-Woo Ahn[1], Bo-Keun Ha[2*], Soon-Jae Kwon[1*]

[1]Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongeup 56212, Korea

[2]Department of Applied Plant Science, College of Agriculture and Life Sciences, Chonnam National University, Gwangju 61186, Korea

[3]Department of Life-resources, Graduate School. Sunchon National University, Suncheon 57922, Korea

Perilla frutescens, belonging to Lamiaceae, is commonly distributed in East Asia and is classified into *var. frutescent* and *crispa*. *Perilla* leaves and seeds contain a large number of secondary metabolites, which are used as vegetable, edible oil, and herb for human health. However, owing to the lack of genetic information, development and utilization of *Perilla* genotypes is stunted. Thus, we aimed to develop EST-SSR markers from *P. frutescens* var. *crispa* (wild-type) and Antisperill (mutant-type), and used them to assess the genetic diversity and relationship of the 94 *Perilla* genotypes. A total 65 Gb comprising 632,970 unigenes were assembled by *de novo* RNA-sequencing. Of the 14,780 common SSRs, from which 102 EST-SSRs were selected based on polymorphism, and, as a result, hexa-nucleotide (65.79%) motif was frequently distributed in SSRs. Overall, we demonstrated that 58 EST-SSRs markers revealed remarkably genetic diversity and relationship in 94 *Perilla* genotypes. A total of 270 alleles were identified, with an average of 4.66 alleles per locus, ranging from 2 (RBRC_PF_ES_12, RBRC_PF_ES_25, RBRC_PF_ES_31, RBRC_PF_ES_44, RBRC_PF_ES_54, and RBRC_PF_ES_56) to 11 (RBRC_PF_ES_50). The average polymorphisms information content (PIC) value was 0.50, ranging from 0.04 (RBRC_PF_ES_1) and 0.86 (RBRC_PF_ES_50). A phylogenetic tree and structure population indicated that all genotypes were clarified into 2 major groups; Group I (wild-type) and Group II (Antisperill). In conclusion, the 58 novel EST-SSR markers may provide potential molecular marker for population genetics, thereby enhancing comprehensive understanding of the genetic diversity and relationship in *Perilla*.

***Corresponding Author:** Soon-Jae Kwon (Tel. 063-570-3312, E-mail: soonjaekwon@kaeri.re.kr)
Bo-Keun Ha (Tel. 062-530-2055, E-mail: bkha@chonnam.ac.kr)

PG-0019

Breeding of Endophyte-Free Tall Fescue Cultivars and Minimizing Fescue Toxicity in Animals

Ki-Won Lee*, Sang-Hoon Lee, Yowook Song, Md. Atikur Rahman, Hee Chung Ji

Grassland and Forages Division, National Institute of Animal Science, RDA, Cheonan 31000, Korea

Tall fescue (*Festuca arundinacea* Schreb.) is a forage of good nutrient quality, suggesting satisfactory livestock performance. The broad distribution of tall fescue across the country is a result of its early popularity for planting as both an erosion control agent and as pasture forage. Problems in livestock associated with endophyte-infected (EI) tall fescue consumption include fescue foot, fat necrosis, and fescue toxicosis. To solve global environmental problems, we have developed the breeding of endophyte-free tall fescue. Breeding tall fescue cultivars that are free of endophytic fungus is necessary to improve animal performance. New tall fescue varieties, such as ‘Greenmaster’, ‘Greenmaster2ho’, “Greenmaster3ho”, and “Greenmaster4ho”, were developed by the National Institute of Animal Science (NIAS) of the Rural Development Administration (RDA). These varieties are endophyte-free with enhanced tolerance to multiple environmental stresses and non-toxicosis in animals. This study aimed to make a contribution to the vitalization of the Korean grassland industry by developing a new tall fescue variety with excellent environmental adaptability.

***Corresponding Author:** Tel. 041-580-6757, E-mail: kiwon@korea.kr

PG-0020

딥러닝 기술을 활용한 유전자원 빅데이터 분석기술의 동향 및 발전방향

이수경*, 노형준, 유은애

국립농업과학원 농업유전자원센터

육종기술은 마커를 이용한 분자육종, NGS 기술을 이용한 유전체 육종을 거쳐 최근 빅데이터 및 AI 기술을 적용한 디지털육종으로 발전되어 오고 있다. 대량의 high-throughput genotyping 기술과 함께 대규모의 오믹스 데이터가 쏟아져나오면서 이러한 빅데이터를 분석하여 육종에 적용하는 기술은 디지털육종에 매우 중요하다. 특히, 딥러닝 기술은 농학 및 생명과학 분야에서 유전자원의 빅데이터를 분석할 때 많이 적용되고 있다. 딥러닝 기술은 기계가 자동으로 대규모 데이터에서 중요한 패턴 및 규칙을 학습하고, 이를 토대로 의사결정이나 예측 등을 수행하는 기술을 의미하며, 크게 지도 학습(supervised learning)과 비지도 학습(unsupervised learning)으로 나뉜다. 지도 학습의 경우 target value (label)가 있는 경우를 말하며 이를 활용하여 게놈에서의 regulatory 및 non-regulatory 부위 예측, 게놈 시퀀스로부터 표현형 예측 등의 연구에 사용되고 있다. 비지도 학습의 경우 지도 학습과 다르게 target value (label)가 없는 경우를 말하며 주로 군집화(clustering)을 수행할 때 이용된다. RNA Seq 분석결과 비슷한 발현패턴의 유전자를 그룹화할 때 주로 사용되고 있다. 농촌진흥청 농업유전자원센터는 약 26만 개의 농업유전자원을 보유하고 있으며 평가된 유전자원들의 유전형 및 표현형은 농업유전자원 관리시스템(GMS)을 통해 관리되고 있다. GMS에 구축된 유전자원 빅데이터에 대한 딥러닝 기술 기반의 빅데이터 분석기술 적용은 유용 유전자원 발굴 및 디지털육종으로의 패러다임 전환에 큰 도움이 될 것이다.

***교신저자:** Tel. 063-238-4873, E-mail: xsanta7@korea.kr

PG-0021

GC-Orbitrap-MS assisted comparative metabolite profiling of safflower seed based on lipophilic compounds

Seon-Kyeong Lee*, Jiseon Kim, Vimalraj Mani, Ju Ho Lee, Kyeong-Ryeol Lee, Jong-Sug Park

Metabolic Engineering Division, Department of Agricultural Biotechnology, National Institute of Agricultural Sciences, Rural Development Administration, Jeonju 54874, Korea

Safflower is one of the most seasoned human crops, traditionally cultivated for commercial use in oil and animals feed. In the present study, we developed and validated for the separation and relative quantitative analysis of lipophilic compounds from safflower seeds were characterized to determine the diversity among their different nations of cultivars and to analyze relationships between their contents. The identification of each chemical found in extracts of nine safflower seed germplasms (Australia, Iran, Afghanistan, Ethiopia, Kenya, Turkey and India) was accomplished using available information of standard compounds (retention time, accurate mass and product ions). As a result, the following 13 targeted lipophilic compounds were identified with available standard library: palmitic acid, deoxyspergualin, linoleic acid, stearic acid, doconexent, oleamide, dioctyl phthalate, alpha-tocopherol, ergosterol, campesterol, stigmasterol, β-sitosterol, desogestrel. According to principal component analysis (PCA) results showed the sum of two components amounted to 71%. In this scenario, the diversity of metabolites was found Alpha-Tocopherol, desogestrel and deoxyspergualin in the safflower seed germplasm. Moreover, the proposed GC-Orbitrap-MS methods and a successful relative quantification of lipophilic metabolites to understand metabolite diversity within safflower seed germplasm. Meanwhile, this approach should be relevant to a wide range of fields for identifying lipophilic components in biological matrixes.

***Corresponding Author:** Tel. 063-238-4623, E-mail: lsk220@korea.kr

PG-0022

Development of Mutant Population in Japanese-Danggui (*Angelica acutiloba*) by Using Gamma Irradiation

Jaihyunk Ryu, Baul Yang, Sang Hoon Kim, Duk Man Lee, Min Soo Pak, Joon-Woo Ahn, Jin-Baek Kim*

Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongup 56212, Korea

Japanese-Danggui (*Angelica acutiloba*) have been used in oriental medicine in Northeast Asia. *Angelica* species breeding progress has been limited by a lack of genetic variation in the germplasm for agronomic traits. Therefore, mutation breeding are important breeding techniques for *Angelica* species. This study conducted to determine the optimal gamma-ray dosage for mutation breeding in *A. acutiloba.* Plants at the seeding stage were exposed to gamma rays for 24 hours, with a total irradiation dose of 10, 20, 40, and 60 Gy. After 30 days of sowing, the survival rates and growth decreased rapidly at doses above 20 Gy, while all individuals died at 60 Gy. The median lethal dose (LD_{50}) was 26.0 Gy, and the median reduction doses (RD_{50}) for plant height, root length and fresh weight were 22.0, 24.8, and 29.4 Gy, respectively. A dose of 20 to 40 Gy was found to be optimal for mutation breeding in *A. acutiloba.* The M_2 population was constructed with approximately 2000 plants from M_1 plants. In M_2 generation mutants showing dwarf plant, chlorophyll deficiencies leaf, dart violet stem, non-bolting and abnormal leaf mutants were selected as potentially mutants for breeding.

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

PG-0023

Genetic Diversity of Soybean [*Glycine max* (L.) Merr.] with Black Seed Coats and Green Cotyledons in Korean Germplasm

Hyun Jo[1], Ji Yun Lee[2], Jong Tae Song[1], Jeong-Dong Lee[1*]

[1]Department of Applied Biosciences, Kyungpook National University, 80 Daehak-ro, Buk-gu, Daegu 41566, Republic of Korea
[2]Gyeongsangbuk-do Provincial Agricultural Research & Extension Service, Daegu 41404, Republic of Korea

Soybeans [*Glycine max* (L.) Merr.] with black seed coats and green cotyledons are rich in anthocyanins and chlorophylls known as functional nutrients, antioxidants and compounds with anticarcinogenic properties. Understanding the genetic diversity of germplasm is important to determine effective strategies for improving the economic traits of these soybeans. We aimed to analyze the genetic diversity of 470 soybean accessions by 6K single nucleotide polymorphic loci to determine genetic architecture of the soybeans with black seed coats and green cotyledons. We found soybeans with black seed coats and green cotyledons showed narrow genetic variability in South Korea. The genotypic frequency of the d1d2 and psbM variants for green cotyledon indicated that soybean collections from Korea were intermingled with soybean accessions from Japan and China. Regarding the chlorophyll content, the nuclear gene variant pair d1d2 produced significantly higher chlorophyll a content than that of chloroplast genome psbM variants. Among the soybean accessions in this study, flower color plays an important role in the anthocyanin composition of seed coats. We provide 36 accessions as a core collection representing 99.5% of the genetic diversity from the total accessions used in this study to show potential as useful breeding materials for cultivars with black seed coats and green cotyledons

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

PG-0024

Complete plastome and rDNA analysis of two *Rubus* species

Young Sang Park[1], Jee Young Park[1], Jung Hwa Kang[2], Wan Hee Lee[2], Hyun Seung Park[1], Tae-Jin Yang[1*]

[1]Department of Agriculture, Forestry and Bioresources, Plant Genomics & Breeding Institute, College of Agriculture & Life Sciences, Seoul National University, 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Korea

[2]Hantaek Botanical Garden, Yongin, Korea

Rubus longisepalus Nakai and *R. longisepalus* var. *tozawai* are endemic plant in Korean Peninsula which have ‘Macdo’ and ‘Geoje’ as a common name, respectively. There is debate that each variety is distinct or not. *R. hirsutus* is included in same genus which distributed widely in Eastern Asia. It also has a similar habitat in Korea Peninsula as *R. longisepalus*. Therefore, clear taxonomic identification is needed to protect and utilize this edible plant resources. In this study, we assembled complete plastid genome (plastome) and nuclear ribosomal DNA (nrDNA) of those three *Rubus* accessions. It was confirmed that *R. longisepalus* Nakai and *R. longisepalus* var. *tozawai* have completely identical plastome and nrDNA sequences. Newly assembled complete plastomes and 45S rDNA in *R. longisepalus* and *R. hirsutus* showed different size. *R. longisepalus* have 155,957 bp of plastome and 5,809 bp of 45S rDNA while *R. hirsutus* have 156,005 bp of plastome and the 5,811 bp of 45S rDNA. All the three *Rubus* accession showed identical 5S rDNA size. To discriminate *R. longisepalus* and *R. hirsutus,* we developed three molecular markers based on plastome variations. Phylogenetic analysis also conducted to reveal genetic relationships among *Rubus* species by collecting other 11 *Rubus* species plastomes.

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

PG-0025

Evaluation of the characteristics for various sweetpotato germplasms

Im Been Lee*, Hyeong Un Lee, Mi Nam Chung, San Goh, Su Jung Kim, Won Park, Tea Hwa Kim

Bioenergy Crop Research Institute, National Institute of Crop Science, Rural Development Administration, Muan 58545, Republic of Korea

Sweetpotato is one of the major crops and many cultivars have been developed based on various consumer demands such as starch content, colors, textures etc. For breeding various new sweetpotato varieties, it is essential to investigate the physicochemical characteristics of existing varieties.

In this study, the physicochemical characteristics such as structure and free sugar, moisture, starch, amylose, viscosity of starch, 2,2-diphenyl-1-picrylhydrazyl (DPPH) radical scavenging activity and polyphenol content of 286 sweetpotato germplasms collected in Korea and abroad were investigated. As a results, the following sweetpotato varieties were excellent: ‘VISCA 131 (IT232268)’ for moisture content of 83.5%, ‘Suwon No. 118 (IT232006)’ for starch of 20.67% and ‘Kanto No. 98 (IT232239)’ for amylose of 29.9%. Especially, ‘Sinjami (IT258214)’ has excellent DPPH radical scavenging activity and total. For steamed sweetpotatoes, ‘Jeju-jaelae (IT232225)’ has highest structure sugar content (33.3brix). Starch and sugar content had a positive correlation, and DPPH radical scavenging activity and polyphenol showed a significant positive correlation. Sugar content and free sugar of raw sweet potato showed a negative correlation. In conclusion, this study indicated that 286 germplasms showed different trends in each physicochemical characteristic. Therefore, these results are expected to serve as important basic data that can be referenced in the selection of crossing combination for various purposes.

***Corresponding Author:** Tel. 061-450-0145, E-mail: imbeen@korea.kr

PG-0026

Grain Sorghum(*Sorghum bicolor*) Variety ‘Noeulchal’ with High Digestibility and Dwarf Type

Myeong-Eun Choe*, Sang-Ik Han, Ji-Young Kim, Seok-Bo Song, Ji-Ho Chu, Byong Won Lee

Department of Southern Area Crop Science, National Institute of Crop Science, Rural Development Administration, Miryang 50424, Republic of Korea

For labor and cost saving, it is important to develop sorghum cultivars suitable for mechanization. There have only a few grain sorghum varieties been developed that are suitable for mechanical harvesting. Sorghum can be processed into foods in various ways depending on the texture type. The newly developed variety, ‘Noeulchal’ with waxy endosperms, is high-yielding and suitable for mechanization. New waxy sorghum ‘Noeulchal’, developed in 2019, has light-brown kernel with obovate panicle shape. The average yield potential of ‘Noeulchal’ was 3.71MT/ha, which was 16% higher than that of ‘Sodamchal’. Because of thin stem and better head exertion, it is also suitable for mechanical harvest as compared to the standard variety ‘Sodamchal’. The seed size of ‘Noeulchal’ is smaller than that of ‘Sodamchal’ and its 1000-seed weight is 22.9 gram. The number of grains per panicle in ‘Noeulchal’ is higher than that of ‘Sodamchal’. ‘Noeulchal’ (62.4%) has higher level of the rapidly digestible starch than that of ‘Sodamchal’ (42.1%). The setback viscosity of ‘Noeulchal’ showed a lower value 130 than the standard variety ‘Sodamchal’ (183) which seems to be the result of the slow retrogradation. By the development and distribution of new high-yielding sorghum varieties suitable for mechanization, it is expected to meet the various on-site needs of sorghum industries and markets.

***Corresponding Author:** Tel. 055-350-1244, E-mail: cme0807@korea.kr

PG-0027

Comparison of Yield Components in Soybean Germplasm Planted at Two Different Years

Hyemyeong Yoon[1*], Joungyun Yi[1], Myoung-Jae Shin[1], Yoonjung Lee[1], Yu-Mi Choi[1], Sukyeung Lee[1], XiaoHan Wang[1], Kebede taye Desta[1,2]

[1]National Agrobiodiversity Center, National Institute of Agricultural Sciences, Rural Development Administration, Jeonju 54874, Republic of Korea

[2]Department of Applied Chemistry, Adama Science and Technology University, Adama 1888, Ethiopia

Soybeans have been cultivated and consumed in Korea and elsewhere since ancient times. On the other hands, due to the recent global warming, extreme weather events such as heavy rain and heat wave are frequent, making it difficult to produce stable yield of soybeans. In this study, 37 Korean soybean landraces were cultivated for two consecutive years and investigated in terms of agronomic traits related to yield including the number of pod per plant, the number of seed per pod, 100-seeds weight, days to flowering, days to maturity, and days to growth. The soybean seeds were sown on June 4, 2019 and 2020 in Jeonju, Republic of Korea, and cultivated under similar conditions in the respective years. Correlation analysis revealed some important associations between the yield traits. The number of pod per plant showed a significant and positive correlation with the number of seeds per plant, but a significant and negative correlation with 100-seeds weight. Besides, days to flowering showed a significant and positive correlation with days to maturity. Variations were also observed in soybean characteristics according to the cultivation year. Among the yield components, the highest variation was detected in the number of pod per plant where accessions IT269617 and IT311261 showed the lowest(56.0±0.0) and the highest(455.7±240) variations, respectively. When all yield components are considered, accessions IT24099 and IT 178054 showed stable yield compared to the rest accessions. Overall, the results of our study could contribute to the discovery of soybean breeding materials that consistently provide high yields.

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***Corresponding Author:** Tel. 064-238-4880, E-mail: mmihm@korea.kr

PG-0028

A Program for Clustering Agricultural Genetic Resources using Evaluation Information

Dong Su Yu, Na Young No, Manjung Kang*

National Agrobiodiversity Center, National Institute of Agricultural Sciences, RDA, Jeonju 54874, Korea

Agricultural genetic resources are important breeding materials to improve crop varieties, contribute to biodiversity, and maintain and protect food resources from potential environmental risks, such as climate change, pollution, and diseases. Although the efficient management of numerous genetic resources is difficult, it is still possible to partly regulate the clustering of genetic resources using evaluation information. To group the genetic resources, we developed a clustering program using a combination of hierarchy and k-medoids methods for the categorical variables (evaluation information) of the genetic resources. Upon testing our program on 941 pepper genetic resources obtained from the GMS (Genebank Management System, https://genebank.rda.go.kr), we identified a total of 13 groups, of which 7 and 5 groups were identified using hierarchy and k-medoids methods, respectively, and finally 10 groups were determined through applying core sets of PowerCore. From the clustered genetic resources, we compared the representative resources selected from each group and core sets of PowerCore. As a result, the Entry-to-Nearest-Entry distance (E-NE) of our program was 0.185 and that of PowerCore was 0.188; however, upon combining our program with PowerCore, the E-NE changed to 0.272, which was significantly enhanced. Therefore, we recommend that our program be applied in combination with a core-select program, such as PowerCore, to analyze the evaluation information of the phenotypic genetic resources. Moreover, we expect that our program and clustered genetic resources can be used to evaluate plant inbreeding and to manage numerous genetic resources.

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***Corresponding Author:** Tel. 063-238-4870, E-mail: mjkang@korea.kr

PG-0029

Development of wheat-*Leymus mollis* hybrid lines with salt tolerance for Korean wheat breeding program

Seong-Wook Kang[1], Ji Yoon Han[1], Chul Soo Park[2], Seong-Woo Cho[1*]

[1]Dep. of Smart Agro-Industry, Gyeongsang National University, Jinju, 52725, Republic of Korea
[2]Dep. of Crop Science and Biotechnology, Jeonbuk National University, Jeonju, 54896, Republic of Korea

Leymus mollis as wild rye is important wild spices to expand genetic diversity for wheat in Korean breeding program because it shows vigorous growth under harsh environment such as desert and mountainous areas. Also, *L. mollis* grow in seashore. Hence, *L. mollis* is strong against salt stress. To introduce the natures of *L. mollis* for wheat, we produced the hybrids through wide-hybridization with Chinese Spring, Chinese wheat cultivar as maternal line. Among 10 F_1 hybrids by wide-hybridization, five hybrids showed two coleoptiles in germination and new shoots by rhizome in vegetative growth stage. The shoots by rhizome had an adventitious root from the first node on the ground. The adventitious roots played a role as a prop root for the new shoots. After generation advancement, we tested salt tolerance with F_2 hybrids. Seeds of F_2 hybrids were under 1% sodium chloride solution for germination test. F_2 populations showed germination ratio from 66% to 83%. The germinated seeds were under 2% sodium chloride solution during vegetative growth stage to evaluate wheat-*L. mollis* addition lines with salt tolerance. In reproductive growth stage, several F_2 lines significantly showed more vigorous growth than other F_2 lines. The F_2 lines with salt tolerance showed tillering capacity and longer spikes than the F_2 lines with salt sensitivity. Also, the F_2 lines with salt tolerance had adventitious roots from the first node on the ground like the F_1 hybrids. It is necessary to study more phenotypic investigation and genetic analysis to identify the perennial characterization.

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***Corresponding Author:** Tel. 055-772-3225, E-mail: chsw78@gnu.ac.kr

PG-0030

Genetic Mobility Assessment from GM to non-GM cotton

윤도원*, 오성덕, 이성곤, 이강섭

전북 전주시 덕진구 농생명로 370, 국립농업과학원 농업생명자원부 생물안전성과

아직까지 국내에서 GM작물이 상업화를 위해 승인된 예는 없지만 생명공학기술의 발전으로 GM작물의 개발은 급속한 증가 추세에 있다. 비의도적인 방출로 인해 미승인 LMO 목화가 전국적으로 재배되어 국립종자원 주관으로 양성 판정된 재배지의 목화를 폐기 처분하였으나(2017), GM작물이 유해하다는 인식과 환경에 방출되어 생태계를 교란시킨다는 인식이 팽배해 있는 현실에서 과학적으로 유전자의 이동성을 검증하는 노력이 중요하다. 자식성 작물의 화분의 이동성 조사를 위해 중앙의 코어 위치에 LM작물을 식재한 후 LM작물 주변에 재배품종을 심어 유전자이동 가능성을 조사하고 재배 환경에 의한 영향을 평가하기 위해 포장 주변 기상상황 데이터-온도, 습도, 풍속, 풍향, 기압, 강수량 등을 분석하고 기상상황이 화분의 전이에 미치는 영향 조사하였다.

***주저자:** Tel. 063-238-4713, E-mail: dwyun@korea.kr

PG-0031

Enhanced salt stress tolerance and change levels of abiotic stress response genes in gamma-ray irradiated sorghum (*Sorghum bicolor* L.) mutant

Ji Su Seo[1,2], Jae Il Lyu[1], Jung Min Kim[1,2], Nguyen Ngoc Hung[1,2], Jaihyunk Ryu[1], Jin-baek Kim[1], Joon-Woo Ahn[1], Soon-Jae Kwon[1*]

[1]Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongeup, 580-185, Korea

[2]Division of Plant Biotechnology, Colleage of Agriculture and Life Sciences, Chonnam National University, Gwangju, Korea

Sorghum (*Sorghum bicolor* L. Moench) is the fourth most important grain crop following rice, wheat and corn, the three major grains. In addition, Compared to major crop, the potential of sorghum was emphasized to adapt the high level of salinity soil. However, unlike model plants such as Arabidopsis and rice, sorghum has rarely been studied in mechanism of salt tolerance. Among the 15 sorghums used in this study, the germination rate, root length, and plant length were investigated at the *in vitro* level for 10 mutant lines that had difference in phenotypes compared with the their original cultivars based on the salt treatment. Among them, it was confirmed that the three mutant lines(B5, SY6, SY7) from IT124115 accession increased shoot length (5-9 times) and root length (3-6 times) under salt treated condition. Furthermore, we investigated the expression levels of abiotic stress responsive genes and TFs with B5 mutant, which had strongly salt tolerance among three mutants. A total of 20 genes, 5 genes each for the genes related to salt tolerance, such as heat shock protein, aquaporin, ROS scavening system, and transcription factor. As a result, the two genes, ROS scavening system (Sb03g010900) and transcription factor (Sb01g044410), were significantly increased expression levels ($p < 0.01$) of B5 mutant compared with IT124115 accession under salt treated condition. These genes may be contribute to improving the salt tolerance in gamma-ray irradiated mutant.

***Corresponding Author:** Tel. 063-570-3312, E-mail: soonjaekwon@kaeri.re.kr

PG-0032

메밀의 수량 향상을 위한 줄뿌림 재배조건 구명

손황배[1*], 김수정[1], 남정환[1], 김기덕[1], 홍수영[2], 이종남[1], 서종택[1], 김율호[3]

[1]강원도 평창군 대관령면 경강로 5481 국립식량과학원
[2]전라북도 전주시 덕진구 농생명로 370 국립농업과학원
[3]경기도 수원시 권선구 수인로 125 국립식량과학원

우리나라의 메밀 산업의 경쟁력을 높이기 위해서는 재배관리가 용이하면서 수량을 높일 수 있는 줄뿌림재배가 필요하다. 본 연구에서는 메밀의 줄뿌림 재배조건을 구명하고자 지역별 파종간격과 재식밀도에 따른 메밀의 생산성을 조사하였다. ‘양절메밀’을 평난지인 강릉과 준고랭지인 진부에서 각각 4월 17일과 5월 15일에 줄뿌림과 흩어뿌림으로 파종하였다. 줄뿌림 간격은 20, 30, 40cm, 재식밀도는 4, 6, 8, 10, 12kg/10a 로 파종량을 달리하여 파종하였다. 각각의 재배에 따른 초장, 경태, 엽수, 분지수와 수량을 조사하여 적절한 줄뿌림 간격과 재식밀도를 구명하였다. 파종방법별 10a당 수량은 강릉에서 189kg(줄뿌림), 154kg(흩어뿌림)로 유의적인 차이를 보였으며 진부의 경우 유의적인 차이는 없었다. 강릉 지역에서 메밀의 생육은 줄간격이 20cm였을 때 초장이 길고 경태가 굵었으며 엽수와 분지수가 많아 지상부 생육상황이 좋았다. 반면 진부 지역에서는 분지수(줄간격, 20cm), 초장(30cm), 경태(40cm)가 각각 줄간격에 따라 다른 양상을 보였다. 줄간격에 따른 10a당 생산량은 강릉의 경우 30cm에서 189kg로 가장 많았으며 진부 지역에서 158kg(줄간격, 40cm), 151kg(30cm), 140kg(20cm)으로 나타났다. 재식밀도에 따른 10a당 수량은 강릉에서 8kg/10a 파종구에서 220kg로 가장 많았으며 4kg/10a구가 가장 적었으며 진부 지역의 경우 8kg/10a구에서 가장 많았다. 결론적으로 메밀 줄뿌림 파종시 파종간격을 30~40cm 재배하였을 때 수량이 유의성 있게 증가하였으며 재식밀도는 8kg/10a가 적정하였다.

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***교신저자:** Tel. 033-330-1810, E-mail: misson7@korea.kr

PG-0033

Genome-scale analysis of major metabolite biosynthesis genes associated with defense response to pathogens in rice

Kieu Thi Thuy Trinh, Kieu Thi Xuan Vo, Md Mizanor Rahman, Md Mustafizur Rahman, Jong-Seong Jeon*

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

Rice is one of the most important food crops for world's food supply. However, the productivity has been declined significantly by various biotic stressors. In the battle, rice recruits different mechanisms to limit pathogen attacks in which proteins and metabolites act as the final products. To understand the mechanism under metabolomics view, in our previous study, we catalogued 33 major metabolites that were upregulated in resistant cultivars, compared with susceptible cultivars, exposed to four groups of pathogens including *Rhizoctonia solani, Magnaporthe oryzae, Xanthomonas oryzae*, and brown plant hopper. Here, we searched enzymes and their coding genes that contribute to biosynthesis of these compounds. As a result, 599 genes were selected to analyze expression profiles in response to the pathogens. From Genevestigator public data, 98 upregulated genes associated with the upregulated metabolites were selected to create the heatmap. Next, three to four key responsive genes in each group were chosen for further investigation and application. Among the 15 genes selected, five genes were functionally characterized, while the others remain to be determined. These genes will be useful for improving defense response in rice.

***Corresponding Author:** Tel. 031-201-2025, E-mail: tttkieu.biotech@khu.ac.kr

PG-0034

덩굴쪼김병 저항성 육종소재 개발을 위한 수박 유전자원 수집 및 평가

이옥진[1*], 김상규[1], 한고은[1], 이은수[1], 김정호[2], 김태복[1]

[1]국립원예특작과학원 채소과
[2]국립원예특작과학원 기획조정과

덩굴쪼김병은 수박 재배지에서 전 세계적으로 발생하는 토양전염성 병으로, 뿌리를 통해 침입한 병원균이 물관을 막아 시들음 증상을 일으켜 농가 소득에 큰 피해를 입히고 있다. 우리나라에서는 이를 회피하기 위해 약제를 사용하여 토양을 소독하거나 대목을 이용한 접목재배를 하고 있다. 그러나 박 대목을 특이적으로 감염시키는 덩굴쪼김병 균으로 인한 시들음증 발생이 증가하고 있으며 호박 대목은 과실 품질을 저하시키는 문제가 있어 궁극적으로 저항성 수박 품종개발이 필요한 실정이다. 따라서 국내외에서 수집한 유전자원을 대상으로 덩굴쪼김병 저항성 평가를 수행하여 육종소재를 발굴하고자 하였다. 국립원예특작과학원에서 보유하고 있는 108자원과 미국 USDA에서 도입한 27자원, 국립농업과학원 농업유전자원센터에서 분양받은 94자원을 확보하여 총 227자원에 대해 수박 덩굴쪼김병에 대한 저항성 평가를 실시하였다. 파종 10일 후 본엽이 1매 전개되었을 때 유묘를 뽑아 뿌리를 수세한 후 수박 덩굴쪼김병(*Fusarium oxysporum* f. sp. *niveum*) 균을 1.0×10^6 conidia/㎖ 농도로 30분간 침지 접종하였다. 접종한 유묘는 10일 간격으로 30일 동안 발병정도를 평가하였으며 저항성 및 중도 저항성으로 선발된 자원은 DNA를 추출하여 고정도를 평가하고 기존 보고된 연관 유전자와 유사성을 확인하기 위해 분자마커 검정을 수행하였다. 발아율이 낮은 12점을 제외하고 17자원에서 발병지수가 1로 나타나 저항성 자원으로 평가되었으며 이 중 11자원에서 고정도가 95% 이상을 보여 육종에 활용 가능한 자원인 것으로 판단되었다. 선발자원을 대상으로 분자마커 분석을 수행한 결과 선발된 11자원 중 2자원에서만 저항성 결과를 보여 생물검정에서 저항성 반응을 보인 자원을 활용한 새로운 분자마커 개발이 필요한 것으로 보인다. 선발된 자원은 육종에 활용할 수 있도록 우량계통과 조합을 작성하여 덩굴쪼김병 저항성을 도입할 계획이다.

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***교신저자:** Tel. 063-238-6615, E-mail: ojlee6524@korea.kr

PG-0035

Genetic structure analysis of *Agaricus bisporus* germplasm based on SSR markers

Hyejin An[1], Hwa-Yong Lee[2], Hyeran Shin[1], Jun Hyoung Bang[1], Saehee Han[1], Youn-Lee Oh[3], Kab-Yeul Jang[3], Ick-Hyun Jo[3], Jong-Wook Chung[1*]

[1]Department of Industrial Plant Science and Technology, Chungbuk National University, Cheongju, Republic of Korea
[2]Department of Forest Science, Chungbuk National University, Cheongju, Republic of Korea
[3]Department of Herbal Crop Research, National Institute of Horticultural and Herbal Science, Eumseong, Republic of Korea

Agaricus bisporus, a prototypical edible mushroom cultivated worldwide, has a secondarily homothallic life history and limited genetic diversity. The aim of this study was to investigate the genetic diversity and population structure of globally collected *A. bisporus* strains, including commercial and wild strains, using single sequence repeat (SSR) markers. *A. bisporus* strains were divided into groups based on 1) geographical distribution, 2) distance-based clusters, and 3) model-based subpopulations. The major allele frequency (MAF), number of genotypes (NG), number of alleles (NA), observed heterozygosity (HO), expected heterozygosity (HE), and polymorphic information content (PIC) were calculated, and genetic distance, population structure, genetic differentiation, and Hardy-Weinberg equilibrium (HWE) were assessed. Strains were divided into two clusters by distance-based analysis and into three subpopulations by model-based analysis, and did not group according to geographical origin. Strains in subpopulations POP A and POP B were found in Cluster I, and strains in subpopulation POP C were found in Cluster II. Genetic differentiation between strains were ≥99%. Marker AB-gSSR-1122 in strains from all regions and marker AB-gSSR-1057 in strains in Cluster II and subpopulation POP C were confirmed to be in Hardy-Weinberg equilibrium. These results will enhance *A. bisporus* breeding programs and support the protection of genetic resources.

***Corresponding Author:** Tel. 043-261-2514, E-mail: jwchung73@chungbuk.ac.kr

PG-0036

New CAPs Marker for Genetic Structure in *Agaricus bisporus*

Hyejin An[1], Hwa-Yong Lee[2], Ick-Hyun Jo[3], Jong-Wook Chung[1*]

[1]Department of Industrial Plant Science and Technology, Chungbuk National University, Cheongju 28644, Republic of Korea
[2]Department of Forest Science, Chungbuk National University, Cheongju 28644, Republic of Korea
[3]National Institute of Horticultural and Herbal Science, RDA, Eumseong 27709, Republic of Korea

Agaricus bisporus is a globally cultivated mushroom with high economic value. Despite its widespread cultivation, commercial button mushroom strains have little genetic diversity and discrimination of strains for identification and breeding purposes is challenging. Molecular markers suitable for diversity analyses of germplasms with similar genotypes and discrimination between accessions are needed to support the development of new varieties. To develop cleaved amplified polymorphic sequences (CAPs) markers, single nucleotide polymorphism (SNP) mining was performed based on the *A. bisporus* genome and resequencing data. A total of 70 sets of CAPs markers were developed and applied to 41 *A. bisporus* accessions for diversity, multivariate, and population structure analyses. Of the 70 SNPs, 62.85% (44/70) were transitions (G/A or C/T) and 37.15% (26/70) were transversions (A/C, A/T, C/G, or G/T). The number of alleles per locus was 1 or 2 (average = 1.9), and expected heterozygosity and gene diversity were 0.0-0.499 (mean = 0.265) and 0.0-0.9367 (mean = 0.3599), respectively. Multivariate and cluster analyses of accessions produced similar groups, with F-statistic values of 0.134 and 0.153 for distance-based and model-based groups, respectively. A minimum set of 10 markers optimized for accession identification were selected based on high index of genetic diversity (GD, range 0.299-0.499) and major allele frequency (MAF, range 0.524-0.817). The CAPS markers can be used to evaluate genetic diversity and population structure and will facilitate the management of emerging genetic resources.

***Corresponding Author:** Tel. 043-261-2514, E-mail: jwchung73@chungbuk.ac.kr

PG-0037

Antioxidant Activity and Phytochemical Content in Leaf Extract of Amaranth genetic resources (*Amaranthus* spp.)

Jun-Hyoung Bang[1], Kyung Jun Lee[2], Yoon-Sup So[3], Jong-Wook Chung[1*]

[1]Department of Industrial Plant Science and Technology, Chungbuk National University, Chungbuk, Cheongju 28644, Republic of Korea
[2]Honam National Institute of Biological Resources, 99, Gohadoan-gil, Mokpo-si 58762, Republic of Korea
[3]Department of Crop Science, Chungbuk National University, Cheongju 28644, Republic of Korea

Amaranthus species are potential dietary sources of antioxidants and phytochemicals and widely used as grain and leaf vegetables around the world. In this study, we examined the variation in antioxidant activities, total flavonoid content and total polyphenol content among 120 accessions of nine *Amaranthus* species. The antioxidant activity of DPPH (2,2-diphenyl-1-picrylhydrazyl) of the 120 amaranth accessions ranged from 1.1 (*A. tricolor*) to 75.2 (*A. tricolor*) mg ascorbic acid equivalents (AAE)/g in 2018, and 8.5 (*A. tricolor*) to 68.8 (*A. dubius*) mg AAE/g in 2019. Antioxidant activity of ABTS (2,2`-azinobis (3-ethylbenzothiazoline 6-sulfonate)) ranged from 16.7 (*A. tricolor*) to 78.3 (*A. hypochondriacus*) mg AAE/g in 2018, and 36.6 (*A. tricolor*) to 79.2 (*A. dubius*) mg AAE/g in 2019. Total flavonoid content (TFC) of 2018 and 2019 ranged from 21.7 (*A. caudatus*) to 52.7 (*A. hybridus*) and from 22.3 (*A. viridis*) to 54.7 (*A. tricolor*). Total polyphenol content (TPC) of 2018 and 2019 ranged from 48.9 (*A. cruentus*) to 154.4 (*A. hypochondriacus*) and from 68.8 (*A. tricolor*) to 154.6 (*A. tricolor*). Antioxidant activities were compared using two methods and all components were measured in plants grown both in 2018 and 2019. Antioxidant activities and phytochemical contents were consistently positively correlated. The nine species and 120 accessions clustered into three groups according to their antioxidant activities and phytochemical contents in each year. These results provide information about the nutritional profiles of nine *Amaranthus* species.

***Corresponding Author:** Tel. 043-261-2514, E-mail: jwchung73@chungbuk.ac.kr

PG-0038

Comparative study of phenolic compounds in different species of amaranth

Jun-Hyoung Bang[1], Ick-Hyun Jo[2], Jong-Wook Chung[1*]

[1]Department of Industrial Plant Science and Technology, Chungbuk National University, Cheongju 28644, Republic of Korea

[2]Department of Herbal Crop Research, National Institute of Horticultural and Herbal Science, RDA, Eumseong 27709, Republic of Korea

Amaranth is a crop with high nutritional food value since it contains phenolic acids and flavonoids and produces various secondary metabolites such as phytosterol, tocopherol, and carotenoid. In this study, we examined the variation in contents of 17 phenolic compounds among 120 accessions of nine *Amaranthus* species. Different species of amaranth, including nine *Amaranthus* species, *A. hypochondriacus, A. cruentus, A. caudatus, A. tricolor, A. dubius, A. blitum, A. crispus, A. hybridus*, and *A. viridis*, were analyzed for phenolics contents by UPCL-PDA. The results showed that significant differences were observed among the phenolic compound contents in different nine *Amaranthus* species. Rutin was predominant in all *Amaranthus* species and plants grown both in 2018 and 2019. The rutin contents of the nine *Amaranthus* species ranged from 95.72±199.17 (*A. dubius*) to 1485.09±679.51 (*A. viridis*) μg g^{-1} in 2018, and 821.59±709.95 (*A. tricolor*) to 3166.52±1317.38 (*A. hypochondriacus*) μg g^{-1} in 2019. In correlation analysis, the 4-hydroxybenzoic acid_2018 and vanillic acid_2019(r=0.40), sinapic acid_2018 and 4-hydroxybenzoic acid_2019 (r=0.38) showed significantly positive correlations while kaempferol-3-O-β-rutinoside_2018 and p-coumaric acid_2019 (r=-0.54), kaempferol-3-O-β-rutinoside_2018 and p-coumaric acid_2019 (r=-0.43) showed significantly negative correlations, respectively. We identified wide variation among the accessions and between plants grown in the two years. The nine species and 120 accessions clustered into six groups according to their 17 phenolic compounds in each year. These results could lead to expanding the knowledge of the phytochemicals traits of the nine *Amaranthus* species, which are valuable resources for *Amaranthus* component breeding and development of functional materials.

***Corresponding Author:** Tel. 043-261-2514, E-mail: jwchung73@chungbuk.ac.kr

PG-0039

An improved high-quality genome assembly and annotation of the button mushroom (*Agaricus bisporus*)

Ick-Hyun Jo[1], Hyejin An[2], Donghwan Shim[3], Jong-Wook Chung[2*]

[1]National Institute of Horticultural and Herbal Science, RDA, Eumseong 27709, Republic of Korea
[2]Department of Industrial Plant Science and Technology, Chungbuk National University, Cheongju 28644, Republic of Korea
[3]Dept. Biological Sciences, Chungnam National University, Daejeon 13431, Republic of Korea

The edible button mushroom *Agaricus bisporus* is a popular food worldwide, but the lack of high-quality genome sequence data makes a barrier to its molecular analysis and breeding efforts. Although two *A. bisporus* strain genome (H39 and H97) already reported they are still not used broadly because of their low quality. To obtain a high-quality *A. bisporus* (strain KMCC00540) genome sequence and gene annotation, we employed a hybrid sequence assembly method of data generated using two types of sequencing platforms—the Oxford Nanopore MinION (generating long-read data) and MiSeq (generating short-read data). We assembled and got 36 Contigs newly KMCC00540 genome with Contigs length 33.3 Mbp, Average Length 924 kbp, N50 1.7 Mbp, and Complete BUSCOs 94.0%. Also, we annotated the number of 10,047 complete genes. The percentages of long interspersed nuclear elements, long terminal repeats, DNA transposons, and simple repeats, which comprise repeat elements were 3.93%, 8.72%, 2.13%, and 0.53% respectively, indicating greater repeat element content in the *A. bisporus* KMCC00540 genome than that in the genomes of H39 and H97. The additionally acquired 3 Mb are most likely associated with the differences in repeat elements between the strains. We conclude that long-read sequencing technology and new assembler improved the quality of the *A. bisporus* genome sequence. In the future, the high-quality assembled genome sequence can provide useful information on molecular markers that can be used to improve the agricultural traits of *A. bisporus*.

***Corresponding Author:** Tel. 043-261-2514, E-mail: jwchung73@chungbuk.ac.kr

PG-0040

Complete chloroplast genome of the inverted repeat-lacking species *Vicia bungei* and development of polymorphic simple sequence repeat markers

Seahee Han[1], Ick-Hyun Jo[2], Hyejin An[1], Hyeran Shin[1], Jun-Hyoung Bang[1], Yoon-Sup So[3], Jong-Wook Chung[1*]

[1]Department of Industrial Plant Science and Technology, Chungbuk National University, Cheongju 28644, Republic of Korea

[2]Department of Herbal Crop Research, National Institute of Horticultural and Herbal Science, RDA, Eumseong 27709, Republic of Korea

[3]Department of Crop Science, Chungbuk National University, Cheongju 28644, Republic of Korea

Vicia bungei is an economically important forage crop in Korea and China. However, detailed genetic and genomic data of *Vicia* species are sparse and no such data are available for *V. bungei*. The whole-genome sequence of *V. bungei* was generated on an Illumina MiSeq platform. De novo assembly of complete chloroplast genome sequences was performed for the low-coverage sequence using CLC Genome Assembler with a 200-600 bp overlap size. The length of the chloroplast genome was 130,796 bp, which lacked an inverted repeat unit, similar to other species in the inverted repeat-lacking clade within Fabaceae. Genome annotation using Dual Organellar GenoMe Annotator (DOGMA) identified a total of 107 genes, comprising 75 protein-coding, 28 transfer RNA, and 4 ribosomal RNA genes. We detected 432 SSRs in the *V. bungei* chloroplast genome, including 64 mono-nucleotide, 14 di-nucleotide, 5 tri-nucleotide, 4 tetra-nucleotide, 233 penta-nucleotide, 90 hexa-nucleotide, and 14 complex repeated motifs. We developed 232 novel chloroplast SSR markers, 39 of which were randomly chosen to test amplification and genetic diversity in *Vicia* species (20 accessions of 7 species). Unweighted pair group method with arithmetic mean cluster analysis identified seven clusters at the interspecies level and intraspecies differences within clusters. The complete chloroplast genome sequence was obtained for *V. bungei*. This reference genome should facilitate chloroplast resequencing and searches for additional genetic markers using population samples. These newly determined chloroplast genome resources and novel SSR markers will greatly contribute to the conservation, and genetic and evolutionary studies of the genus *Vicia* and other higher plants.

***Corresponding Author:** Tel. 043-261-2514, E-mail: jwchung73@chungbuk.ac.kr

PG-0041

Genetic Analysis of Agronomic Traits in Myanmar Rice (*Oryza sativa* L.) Germplasm

Phyu Phyu Maung, Backki Kim, Su Jang, Ji-Young Nam, Dasol Kim, Hee-Jong Koh*

Department of Agriculture, Forestry and Bioresources, Plant Genomics and Breeding Institute, Research Institute for Agriculture and Life Sciences, Seoul National University, Seoul, South Korea

Myanmar, located in mountainous regions in the northern part of Southeast Asia, is one of the centers of diversity of Asian rice and possesses high genetic rice resources. For the rice improvement program, the understanding of genetic variability and genetic diversity of rice germplasm is essential. Therefore, this study was conducted to evaluate the genetic and phenotypic variation of Myanmar rice germplasms. In frequency distribution of 46 germplasms, 23 of them were observed flowering earlier than 140 days and 23 of them were flowered later than 150 days. 30 of them possessed high spikelet fertility percent of over 70%. In addition, spikelets fertility percent was significantly and positively correlated with panicle length, primary branch number, secondary branch number and spikelets per plant. Thus, selection for the improvement of grain yield can be effective, if it is based on the high performance of above characters. According to the results of cluster analysis and their genetic distance, studied germplasms were classified into 2 clusters and the highest genetic distance was occurred between M30 (Hmway shay) and M11 (Khao Hlaing) and lowest genetic distance was found between M30 (Hmway shay) and M34 (Sin Thu Kha). This finding suggested that M30 (Hmway shay) and M11 (Khao Hlaing) can be used for hybrid production to increase grain yield.

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

PG-0042

아마란스 품종 육성을 위한 EMS 유도 돌연변이체 선발 및 농업형질 분석

손황배[1*], 김수정[1], 남정환[1], 김기덕[1], 홍수영[2], 이종남[1], 서종택[1], 김율호[3]

[1]강원도 평창군 대관령면 경강로 5481 국립식량과학원
[2]전라북도 전주시 덕진구 농생명로 370 국립농업과학원
[3]경기도 수원시 권선구 수인로 125 국립식량과학원

아마란스는 비름과에 속하는 1년생 작물로 각종 영양소가 풍부한 슈퍼 곡물 중 하나로 국내 아마란스 품종에 대한 요구도가 높다. 우리나라에서 아마란스를 재배하기 위해서 조숙(150이내)이면서 단간인 아마란스 품종 육성이 필요하다. 본 연구에서는 EMS를 이용하여 돌연변이 집단을 구축하고 개체선발과 후대 검정을 통하여 농업형질이 우수한 10계통을 확보하였다. 재래종 4계통(ASA, AJB, AWJ, AJS)에 다양한 조건으로 EMS를 처리하여 발아율 및 식물의 생육 상태를 조사하였고, 발아율에는 영향을 미치지 않으면서 생육에 큰 영향을 주지 않는 0.5% EMS를 돌연변이를 유도하기에 적정한 농도로 선정하였다. 0.5% EMS로 유기된 개체 중 후대 검정을 통해 10계통을 선발하였으며 평창, 강릉 지역에서 생육특성과 수량성을 조사하였다. ASA-1 계통의 경우 수집종인 ASA의 노란 이삭과는 달리 빨간색을 띄고 있다. 수집종인 AJB는 노란 이삭을 가지고 있으나 AJB-1, AWJ-2, AJB-3은 자주색이었다. 이중 노란 종자를 가진 다른 계통과는 달리 AJB-1은 갈색을 띄고 있었다. 강릉지역에서 5월11일 정식하였을 때 출수기는 6월 3일에서 12일까지로 정식 후 23일에서 32일 소요되었다. 수확기는 7월17일에서 8월19일로 67일에서 100일이 소요되었다. 대관령에서는 정식 후 수확까지 93일에서 94일이 소요되었다. 30일 육묘 후 강릉에 이식할 경우 초장은 117cm (AJS-3)~156cm (AJB-3), 경태는 19.7mm (AJS-3)~25.2mm (AJB-3) 보였다. 대관령의 경우 초장은 88cm (ASA-1)~132cm (AJS-2), 경태는 15.7mm (ASA-1)~23.0mm (AJS-1, AJS-2)로 강릉에 비해서 유의적으로 감소하였다. 수집종에 비해서 돌연변이 10계통의 작은 초장과 굵은 줄기로 내도복 특성을 가지고 있다. 이처럼 국내 적응성이 우수한 새로운 육종소재를 창출하였기에 향후 우리나라에서 재배 적응성이 우수한 아마란스 품종을 개발하는데 활용할 수 있을 것으로 기대된다.

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***교신저자:** Tel. 033-330-1810, E-mail: misson7@korea.kr

PG-0043

Genetic Diversity Analysis of Korean Wild *Codonopsis lanceolata* and Herbal Medicine Resources

Namsu Jo[1], Jinsu Gil[1], Sungcheol Koo[2], Yi Lee[1*]

[1]Department of Industrial Plant Science & Technology, Chungbuk National University, Cheongju 28644, Korea
[2]National Institute of Horticultural and Herbal Science, Rural Development Administration, Eumseong 27709, Korea

Forty-two species are reported in the genus *Codonopsis*, among them, *Codonopsis lanceolata* is a perennial herbaceous plant distributed mainly in East Asia. It is a plant of very high value not only for medicinal use but also for edible use. *C. lanceolata* is called ‘Deodeok’ in Republic of Korea, and the name of the herbal medicine is Yangyu (羊乳) or Yangyugeun (羊乳根). However, despite its excellent efficacy and high value as a cooking ingredient, research on it is insufficient. *C. lanceolata*, which has high value in the field of breeding, in particular, lacks research and development of molecular breeding materials for building and utilizing breeding systems. In addition, Sasam, the medicinal herb name of *Adenophora triphylla*, is misused for dried root of *C. lanceolata*. Therefore, this study attempted to analyze the genetic diversity and phylogenetic relationship of *C. lanceolata* collections using molecular markers, and to survey the mixed use and misuse with incorrect product labeling. We performed a genetic diversity analysis by applying 10 chloroplast-based InDel markers to 93 *C. lanceolata* wild resources collected nationwide and 18 herbal medicinal resources collected from 4 herbal medicine markets (54 individual plants, including 2 *A. triphylla* (6 individual plants) as an outgroup). As a result of constructing the phylogenetic tree, the genetic diversity was very rich because the wild collections were not grouped by region and did not form a specific cluster. In addition, in the resources collected from the herbal medicine market, it was found that some *C. lanceolata* products were sold with incorrect label as Sasam. Research in a category similar to this study should be continuously expanded because it can prevent misuse of herbal medicines and increase the value and trust of natural medicines through precise classification of herbal medicines using molecular biological approaches. In addition, studies of phylogenetic relationship analysis through genetic approaches using molecular markers of *C. lanceolata*, which are highly valuable as genetic resources, will further increase the value of these resources in breeding of *C. lanceolata*.

***Corresponding Author:** Tel. 043-261-3373, E-mail: leeyi22@cbnu.ac.kr

PG-0044

Fluidigm system을 이용한 고추 유전자원의 병저항성 평가

금보라, 노나영*, 허온숙, 최유미, 이수경

전북 전주시 농생명로370 국립농업과학원 농업유전자원센터, 54874

고추 재배에 있어서 오이 모자이크 바이러스(*Cucumber mosaic virus*; CMV), 담배 모자이크 바이러스(*Tobacco mosaic virus*; TMV) 및 토마토반점위조바이러스(*Tomato spotted wilt virus*; TSWV)와 같은 다양한 바이러스에 의한 피해가 지속적으로 발생하고 있다. 고추, 파프리카 시설재배시 연작장애로 인한 세균점무늬병(Bacterial spot), 흰가루병(powdery mildew)에 의한 농가의 피해가 매년 지속적으로 증가하고 있다. 이러한 고추에서 발생되는 다양한 병의 피해를 경감시키기 위해서 복합저항성 고추 품종이 개발이 필요하다. 따라서 본 연구에서는 대용량 유전자형 분석방법인 Fluidigm EP1 시스템을 이용하여 고추 유전자원 1,995자원의 세균성점무늬병(*Bs2*, *Bs3*), 흰가루병(*Ltr4.1*), TMV (*L4*), TSWV (*Tsw*), CMV (*Cmr1*) 및 Potyvirus (*pvr1*, *pvr2*, *pvr4*)에 대한 저항성 유전자들의 유전자형을 평가하였다. 세균점무늬병에 대한 저항성 유전자인 *Bs2*와 *Bs3*는 각각 1자원, 692자원의 유전자원에서 확인되었으며, 흰가루병에 대한 저항성 유전자인 *Ltr4.1*는 18 유전자원에서 확인되었으며, TSWV에 대한 저항성 유전자인 *Tsw*는 10개 유전자원에서 확인되었으며, CMV에 대한 저항성 유전자인 *Cmr1*는 576유전자원에서 확인되었으며, Potyvirus에 대한 저항성 유전자인 *pvr1*, *pvr2*, *pvr4*는 각각 13, 9, 711자원이 확인되었다. TMV에 대한 저항성 유전자인 *L4*를 가진 유전자원은 확인되지 않았다. 본 연구를 통해 다양한 유전자원의 병 저항성 특성에 대한 data base를 구축하였으며, 향후 이러한 유전자원들은 저항성 고추 품종 육성에 활용될 수 있을 것으로 기대된다.

***교신저자:** Tel. 063-238-4943, E-mail: nonaona@korea.kr

PG-0045

Selection of high red color genetic resources through ASTA Color evaluation in *Capsicum baccatum*

Nayoung Ro*, Onsook Hur, Yumi Choi, Sukyeung Lee, Bora Geum

National Agrobiodiversity Center, National Institute of Agricultural Science, RDA, Jeonju-si 54874, Korea

Pepper was introduced to Korea through Europe around the 16th century and is the most important vegetable crop with a production value of about 11.1 trillion won in Korea in 2019. Pepper (*Capsicum* spp.) fruit-related traits are critical determinants of quality. ASTA Color refers to the international standard for measuring the extractable color of paprika and pepper pods and powder, which is determined by the spectrometric method. ASTA Color was evaluated *Capsicum* germplasm in National Agrobiodiversity Center. 284 *C. baccatum* species. 0.1g of freeze-dried powder passed through a 1mm sieve is placed in a 100ml flask and filled with acetone. After shaking moderately, it was left in a dark room for 16 hours, filtered, and the absorbance was measured at 460 nm. The distribution of resources according to the ASTA Color value seemed to have 42.8~325. ASTA Color value of control varieties (GT5 and Big-star, Nongwoo bio Co., Ltd., Korea) were 273 and 280. IT218958 and IT261507 were selected as high red color resources with an ASTA value over 310. This pepper germplasm might be used as breeding resources for high red color.

***Corresponding Author:** Tel. 063-238-4943, E-mail: nonaona@korea.kr

PG-0046

Comparison of tolerant ability undergoing waterlogging at the flowering period between two rapeseed (*Brassica napus* L.) lines

Ji-Eun Lee*, Da-Hee An, Kwang-Soo Kim, Young-Lok Cha, Woon-Chul Shin

Bioenergy Crop Research Institute, National Institute of Crop Science, RDA, Muan 58545, Republic of Korea

Rapeseed oil, which is consumed in Korea, is mainly imported from Canada and Australia, etc. With the recent increase in demand for domestically produced rapeseed oil, the area for cultivating rapeseed in paddy fields in Korea is increasing. However, rapeseed is a crop that is waterlogging sensitive, and it is necessary to breed waterlogging tolerance varieties. In order to evaluate the waterlogging tolerance of the two rapeseed lines ('I8634-B-30' and 'EMS26'), we compared growth responses to waterlogging and transcriptome changes in two lines that were treated water-logging stress during flowering period. The broken-flowering shoots rate of rapeseed 'EMS26' line by waterlogging treatment was 78.5%, whereas that of 'J8634-B-30' line was 7.15%. Seed yield also decreased by 92.3% in the 'EMS26' line compared to the control (untreated), and 42.4% in the 'J8634-B-30' line. Subsequently, RNA-sequencing analysis revealed 13,279 differentially expressed genes (DEGs) for 'J8634-B-30' and 8,682 DEGs for 'EMS26' under waterlogging stress condition compared to control. Among DEGs of 'J8634-B-30', 6,818 were up-regulated and 6,461 were down-regulated. On the other hand, among the DEGs of 'EMS26', the number of down-regulated genes (5,240) were higher than that of up-regulated genes (3,442). Gene ontology enrichment analysis showed that DEGs related to glucan metabolic, cell wall, and oxidoreductase activity were significantly changed in 'J8634-B-30'. It is suggested that these different transcriptome changes related to different rates of broken-flowering shoots in the two lines. Further DEGs expression analysis will be conducted, we will identify candidate genes for genetic improvement of rapeseed tolerance to waterlogging stress.

***Corresponding Author:** Tel. 061-450-0137, E-mail: leejins212@korea.kr

PG-0047

가지 유전자원의 화방 및 결과 특성 평가

노나영[1*], 허온숙[1], 최유미[1], 이승범[1], 조규택[1], 현도윤[2], 박순주[3]

[1]전북 전주시 농생명로370 국립농업과학원 농업유전자원센터, 54874
[2]전북 완주군 이서면 농생명로 166, 55365
[3]전북 익산시 익산대로 460 원광대학교 생명과학부, 54538

가지의(*Solanum melongena* L.) 원산지는 인도로 추정되고 있으며 야생종 상태의 가지는 발견되지 않고 있지만 인도 동부에 존재하고 있는 *Solanum insanus* L.이 원종이라고 추정하고 있다. 우리나라 가지 재배면적은 2016년에 720ha이고, 생산량은 약 5.3톤/10a이다. 가지는 대개 7마디 정도에서 제1번화가 분화하고, 그 후 2~3엽 이 나온 후에 꽃눈이 분화해 나간다. 꽃눈 분화가 되는 마디수가 적을수록 높은 수량을 낼 수 있다. 농업유전자원센터에서는 576가지 유전자원의 눈꽃 분화 마디수와 화방당 꽃 발생수를 조사하였다. Sympodial shoot (SYM) index는 단위 잎 갯수당 화방 발생수를 간접적으로 나타내는 지수로 SYM index가 작을수록 화방수가 늘어나고 SYM index가 클수록 화방수가 줄어들었다. 화방당 꽃 발생수가 높을 수록 열매의 수는 증가하며, 꽃 발생수가 적으면 열매수가 줄어들었다. K15036, K160305자원은 SYM index 2이고, 화방당 꽃 발생수가 7개로 결과 특성이 우수하였다. 본 연구를 통해 다양한 가지 유전자원의 결과특성에 대한 특성평가를 수행하고 DB 구축하였으며 가지 품종 육성에 활용될 수 있을 것으로 기대한다.

***교신저자:** Tel. 063-238-4943, E-mail: nonaona@korea.kr

PG-0048

Evaluation of 200 *Capsicum chinense* germplasm for resistance to Pepper mild mottle virus

On-Sook Hur[1*], Hae-Ryun Kwak[2], Na-Young Ro[1], Yumi Choi[1]

[1]National Agrobiodiversity Center, National Institute of Agricultural Science, RDA, Jeonju 54874, Republic of Korea

[2]Crop Protection Division, National Institute of Agricultural Science, RDA, Wanju 55365, Republic of Korea

Tobamoviruses (*Tobacco mosaic virus*, TMV and *Pepper mild mottle virus*, PMMoV) are serious pathogens to reduce pepper production. They are grouped in four pathotypes (P0, P1, P1,2, and P1,2,3), resistance to which is controlled by four allelic genes (*L1, L2, L3*, and *L4*) on chromosome 11, respectively. To select pepper germplasm resistant to PMMoV, we have screened 200 *C. chinense* accessions conserved at National Agrobiodiversity Center by infectious test with PMMoV-NS-RP13, pathotype P1,2. Seven accessions including IT261209 were resistant to PMMoV developing necrotic local regions at inoculated leaves as primary symptoms. We have also confirmed that these resistant accessions showed the negative RT-PCR products made from total RNA extracted from virus-infected plants. Consequently, these accessions can be useful for breeding PMMoV resistance in pepper and to develop precise molecular marker to differentiate *L* alleles.

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

PG-0049

Biochemical evaluation and neuroprotective effects of *Cynanchum wilfordii* wild accessions

Hye Jung Hwang[1], Sae Hyun Lee[1], Padmanaban Mohanan[1], Hyun Ok Yang[2], Dowan Kwon[2], Ji Soek Kim[1], Enbi Kim[1], Jee Young Park[1], Tae Jin Yang[1*]

[1]Department of Agriculture, Forestry and Bioresources, College of Agriculture & Life Sciences, Seoul National University, 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Korea

[2]Natural Products Research Institute, Korean Institute of Science and Technology, 679 Saimdang-ro, Gangneung-si, Gangwon-do- 25451, Korea

Cynanchum wilfordii (CW) one of the important medicinal plant used in Korean traditional medicine. To produces high quality CW roots with enhanced medicinal properties, we characterize wild collections from local farmers. The growth parameters were assessed and major metabolites such as acetophenone types (cynandione A, 4-Hydroxyacetophenone (4-HAP), 2,4-dihydroxyacetophenone (2,4-DHAP), 2,5-dihydroxyacetophenone (2,5-DHAP)) steroidal glycosides (wilfoside, cynanoneside B), and aglycone caudatin were analyzed by HPLC. The accessions enriched with acetophenones were in the order of CW6-1(2.95mg/gm)>CW3-9>CW5-1>CW7-9>CW16-8>CW2-9>CW13-7>CW21-4>CW4-3>CW11-10 (1.16 mg/gm). Likewise, the steroidal compound cyanonside were rich in CW6-1 (0.67 mg/gm) and wilfoside were rich in CW16-8 (0.74mg/gm). The aglycone caudation was enriched in CW16-8 (0.92 mg/gm), and the order of abundance was CW16-8>CW5-1>CW13-7>CW7-9>CW6-1>CW21-4>CW3-9>CW4-3>CW11-10>CW2-9. To evaluate the neuroprotective effects of these accessions, the suppression of amyloid-β (Aβ) secretion and autophagy induction were measured in Bv2 microglial cells. Pre-treatment with CW13-7, CW16-8 root extract didn't show any effect in preventing Aβ42 secretion, while extracts from other CW accessions reduced the Aβ42 secretion. Notably, root extracts of CW5-1 significantly reduced the Aβ42 secretion (47.1%) which is greater than the positive control justicidin A (54.5%). To assess the induction of autophagy LC3-II and LC3-I protein expression were evaluated in the *in vitro* model SH-SY5Y cells. The CWR extracts increased LC3-II expression as similar to the positive control, suggesting that they enhance autophagy *in vitro*. Based on our results, we could suggest CW root extracts may contain diverse metabolites with varying concentration as well as the pharmacological effects should be evaluated before application.

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

PG-0050

Identification and functional analysis of novel genes involved in late pollen development in rice

Sang Dae Yun, Myung-Hee Kim, Jung Hyun Lee, Sung-Aeong Oh, Soon Ki Park*

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

Pollen germination and fertilization are the important determinants for crop yield according to the climate change and global warming. Understanding molecular mechanisms of pollen germination and tube growth are still remain largely unknown. In previous screening of rice T-DNA insertion lines, we identified five pollen-defective (PM) mutants. These PM genes were specifically expressed at the late stage of pollen in integrated anatomical expression analysis. The progeny of self-pollinated PM mutants showed that homozygous mutants was nonviable or obtained low frequencies. Heterozygous PM mutant was showed decreased grain yield compared with wild type rice. In genetic transmission analysis, the mutation in PM genes led to absence of male transmission. Our studies suggest that PM mutants are useful genetic resource for studying pollen development and tube growth in crop plants.

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

PG-0051

Antioxidant activity identification and assessment of genetic diversity in broomcorn millet (*Panicum miliaceum* L.)

Xiaohan Wang, Joungyun Yi, Hyemyeong Yoon, Yoonjung Lee, Seong-Hoon Kim, Dong-Kwan Kim, Yu-Mi Choi, Kebede taye Desta, Miae Oh, Myoung-Jae Shin*

National Agrobiodiversity Center, National Institute of Agricultural Sciences, RDA, 370 Nonsaengmyeong-Ro, Wansan-Gu, Jeonju-Si, Jeollabuk-Do, Republic of Korea

Broomcorn millet (*Panicum miliaceum L.*) is one of the first important food crops to be domesticated, widely distributed in America, Europe and Asia. In this study, 578 accessions were genotyped using 37 SSR markers to study genetic diversity and population structure. In addition, the total phenol content (TPC), antioxidant activity (SOD), and free radical scavenging ability (DPPH) were investigated and the association analysis with SSR markers was carried out. The results show that genetic diversity and genetic distance are related to geographic location, the Fixation index and migration rates between origins are listed in detail. Population structure analysis divides the population into 3 subpopulations, and phylogenetic analysis can divide the population into 6 clusters. Phenotypic differences such as TPC were observed between the clusters, so an association analysis was performed to obtain molecular markers related to TPC (SSR-195, SSR-31) and SOD (SSR-430, SSR-31). The genetic diversity of millet and the total phenol content and antioxidant capacity of the extract were evaluated. The development of TPC and SOD associated markers can also provide breeders with new tools to improve the quality of millet through marker-assisted selection.

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***Corresponding Author:** Tel. 063-238-4891, E-mail: smj1204@korea.kr

PG-0052

Natural variation in policosanol profiles of Korean soybean [*Glycine max* (L.) Merr.] varieties

So RA Jin[1], Gyeong Min Lee[2], Sung-Dug Oh[1], Tae-Hun Ryu[1], Seonwoo Oh[3], Sang-Gu Lee[1], Eun-Ha Kim[1], Hyoun-Min Park[1], Min Ho Lee[1], Yun-Young Kang[1], Oh Suk Yu[1], Soo-Yun Park[1*]

[1]National Institute of Agricultural Science, RDA, Jeonju 54874, Republic of Korea
[2]Korea National Food Cluster, Iksan 54576, Republic of Korea
[3]Rural Development Administration, Jeonju 54875, Republic of Korea

Quantitative variations in the nutrients and phytochemical profiles of edible plants could contribute to differences in health-promoting properties. Therefore, we identified policosanols and determined the variability in 13 soybean seeds. Policosanols have a variety of effective physiological functions, such as reducing platelet aggregation and endothelial damage, and provide advantages for the human blood by reducing serum cholesterol and low-density lipoprotein while increasing high-density lipoprotein. Eight policosanols were identified using trimethylsilyl (TMS) etherification and gas chromatography- time of filght-mass spectrometry (GC-tof-MS) in samples grown at three different locations. Thirteen soybean cultivars were planted together under three different environment conditions (3 regions) for a comparative investigation on the impact of genotypes versus environmental influence on policosanol profiles. Quantitative data were subjected to data mining processes, including principal components analysis (PCA) for identifying the specific chemical composition of soybean seeds. The results of PCA revealed no clear separation among the 13 cultivars. However, a small indication of separation according to the cultivation regions. These results provide fruitful information regarding future breeding programs or genetic engineering for soybean.

***Corresponding Author:** Tel. 063-238-4709, E-mail: psy22@korea.kr

PG-0053

고속중성자(Fast Neutron)를 이용한 바이오매스 생산량이 많은 아이스플랜트 품종 개발

이홍주[1], 조나연[1], 박민수[1], 백재하[1], 서현웅[2], 장철성[2], John C. Cushman[3], 임성돈[1*]

[1]강원도 원주시 상지대길 83 상지대학교 응용식물과학과
[2]강원도 춘천시 강원대학길 1 강원대학교 스마트농업융합학과
[3]Department of Biochemistry and Molecular Biology, University of Nevada, Reno, NV89557-300, USA

고부가가치의 기능성 작물인 아이스플랜트(*Mesembryanthemum crystallinum* L.)는 번생초과의 다육성이 높은 염생식물로, 남부 아프리카 나미브사막이 원산지로 알려져 있으며, 일본에서 성인병 예방에 탁월한 고기능성 식물로 알려져 있다. 국내에서도 당뇨병, 고혈압 등에 효과가 좋은 작물로 소비량이 증가하고 있으나 다육성이 높은 염생식물로 장기 보관이 어렵고, 염 처리를 하지 않으면 건물중이 낮다. 따라서 이러한 점을 보완을 위한 개량이 필요하며, 이에 돌연변이 육종 방법 중 고속 중성자(Fast neutron)를 이용해 분리된 돌연변이 라인 M_3 368개를 선발하였고, 세대를 거치며 생육 특성이 우수한 개체를 선발해 현재 M_5 라인의 종자 중 8개의 라인(150A-1, 492A-4, 511B-3, 513A1, 529D2, 550, 189C-3, 268B3)과 야생형을 재배하여 식물체의 지름, 잎의 면적, 생체중, 건물중을 통한 바이오매스량을 비교한 결과, 식물체의 지름에서는 492A-4, 513A1 라인이 야생형보다 크고, 잎의 면적에서는 8개의 라인 모두 야생형보다 넓었다. 생체중은 492A-4, 511B-3 품종이 무거웠으나, 건물중에서는 생체중과 마찬가지로 492A-4가 야생형보다 무겁고, 야생형보다 생체중이 가벼웠던 513A1 품종이 건물중은 야생형보다 무거웠다. 종합적으로 보았을 때 492A-4품종이 야생형보다 더 많은 바이오매스를 생산할 수 있을 것으로 기대된다.

***교신저자:** Tel. 033-730-0513, E-mail: sdlim@sangji.ac.kr

PG-0054

Selection of Kenaf (*Hibiscus cannabinus* L.) Pedigrees Suitable for Reclaimed Land and Paddy Field

In-Sok Lee*, Chan-Ho Kang, Jin-Jae Lee, Hee-June Kim

Jeollabukdo Agricultural Research Extension Service, Iksan, 54968, Korea

Kenaf (*Hibiscus cannabinus* L.) has been paid attentions due to high biomass. The breeding of kenaf suitable for reclaimed land and paddy field is important strategy to improve production. So, the study was conducted to select the pedigrees with higher biomass and adaptability to reclaimed land and paddy field. The pedigrees were developed from back cross, Jangdae/Hongma300// Jangdae. It was possible to select the elite lines (F_5 generation) based on the agronomic performances at two fields, reclaimed land and paddy field, in comparison with the Controls (Jangdae and Hongma300). The two pedigrees (no. bc4555 and bc4557) have a stem in green similar to Jangdae. At a reclaimed land, the bc4555 and bc4557 showed a higher plant height with 9.4 and 9.1 cm in comparison with Hongma300 (6 cm) and Jangdae (4 cm) in 14 days after planting, respectively. The leaves of Hongma300 and Jangdae had a deep discoloration, but two pedigrees had the normal green leaves. At a paddy field, the bc4555 and bc4557 showed a plant height with 8.7 and 7.5 cm similar to Hongma300 (8.2 cm), which is a significant difference from Jangdae (6.4 cm). The leaves of Hongma300 and Jangdae had a deep discoloration at a paddy field, but two pedigrees had the normal green leaves same to the result of reclaimed land. Taken together, the two pedigrees would be useful resource for high production at reclaimed land and paddy field. This work is supported by a fund of project designated as No. PJ014779012020, Rural Development Administration (RDA), Republic of Korea.

***Corresponding Author:** Tel. 063-290-6038, E-mail: bioplant325@korea.kr

PG-0055

Relative characteristic distribution of breeding and non-breeding wheat genetic resources

Miae Oh, Joungyun Yi, Hyemyeong Yoon, Yoonjung Lee, Seong-Hoon Kim, Dong-Kwan Kim, Yu-Mi Choi, Sukyeung Lee, Kebede taye Desta, XiaoHan Wang, Myoung-Jae Shin*

National Agrobiodiversity Center, National Institute of Agricultural Sciences, RDA, 370 Nonsaengmyeong-Ro, Wansan-Gu, Jeonju-Si, Jeollabuk-Do, Republic of Korea

Wheat is the second major grain consumed in Korea next to rice. On the other hand, the degree of self-sufficiency of wheat is less than 1% as of 2019. To increase the self-sufficiency rate, the discovery and cultivation of new wheat varieties are essential. This study compared the distribution of main characteristics between breeding and non-breeding wheat resources. The major objective was to discover new breeding materials and provide information to breeders. A total of 21,627 wheat genetic resources were obtained from Agricultural Genetic Resources Center. Among these, 20, 162 of them have been used for research purposes including for the development of new varieties for 10 consecutive years (between 2011 and 2020), while the remaining 1,015 wheat resources were not used for research purposes before and were selected randomly. The main agronomical characteristics considered in this study include the days of heading after sowing (HD), the days of maturity after sowing (MD), culm length (CL), ear length (EL), and thousands grain weight (TW). The average HD for the wheat resources used in research (195.6 days) was significantly different from those that were not applied in research (185.3 days). These latter wheat resources had a significantly high average TW (48.7 g) than the former wheat resources (41.7 g). However, it should be noted that there were many overlaps in these characters between the two groups. The rest agronomical characters were not significantly different between the two groups. Overall, the results of this study may help in discovering new wheat resources that could be used as breeding materials. Besides, this study compared some traits and hence, it opens room for additional investigations mainly the determination of secondary characteristics such as disaster and disease resistance.

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***Corresponding Author:** Tel. 064-238-4891, E-mail: smj1204@korea.kr

PG-0056

SSR markers associated with the content of the five fatty acids in the accessions of cultivated type of *Perilla* crop

Hyeon Park[1,2], Kyu Jin Sa[1], Do Yoon Hyun[3], Sookyeong Lee[3], Ju Kyong Lee[1,2*]

[1]Department of Applied Plant Sciences, College of Agriculture and Life Sciences, Kangwon National University, Chuncheon 24341, Korea
[2]Interdisciplinary Program in Smart Agriculture, Kangwon National University, Chuncheon 24341, Korea
[3]National Agrobiodiversity Center, National Institute of Agricultural Sciences, RDA, Jeonju 54874, Korea

In order to SSR markers associated with *Perilla* seed oil traits in cultivated var. *frutescens* of *Perilla* crop, the genetic variation, population structure, and association mapping of *Perilla* accessions were studied using five fatty acid contents of 100 *Perilla* accessions and 40 *Perilla* SSR primers. Five fatty acids of 100 *Perilla* accessions were identified as follows: palmitic acid (PA) (5.10-9.13%), stearic acid (SA) (1.70-3.99%), oleic acid (OA) (11.1-21.9%), linoleic acid (LA) (10.2-23.4%), and linolenic acid (LNA) (54.3-75.4%). In a correlation analysis among these six *Perilla* seed oil traits of the 100 *Perilla* accessions, the combinations of OA and LNA (0.724**), OA and TFAC (0.829**), and LNA and TFAC (0.929**) showed a higher positive correlation coefficient than the other combinations. The 40 SSR loci were confirmed to have a total of 231 alleles in the 100 *Perilla* accessions. The number of alleles per locus ranged from 3 to 12, and the average number of alleles per locus was 5.8. By using an association analysis of 40 SSR markers and the six *Perilla* seed oil traits in the 100 *Perilla* accessions, we detected four SSR markers associated with TFAC, five SSR markers associated with LNA, one SSR marker associated with LA, two SSR markers each associated with OA and PA, and four SSR markers associated with SA. The *Perilla* SSR markers found in our study are expected to be useful markers for genetic diversity analysis of *Perilla* germplasm and the selection of *Perilla* accessions with high seed oil composition for improving the oil yield and quality in *Perilla* breeding.

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

PG-0057

Physiological Characterization of herbicide bentazone Tolerant and Susceptible in soybean

Liakat Ali[1,2], Hyun Jo[1], Syada Nizer Sultana[1], Se-Hun Kim[1], Yoonha Kim[1], Jong Tae Song[1], Jeong-Dong Lee[1*]

[1]School of Applied Biosciences, College of Agriculture and Life Sciences, Kyungpook National University, Daegu 41566, Republic of Korea
[2]Department of Genetics and Plant Breeding, Faculty of Agriculture, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur-1706, Bangladesh

Bentazone is a broadleaf post-emergent herbicide widely used for crop production, which inhibits the photosynthetic activity resulting phytotoxicity and injury of plants. Evaluating and identifying herbicide-tolerant genotypes is a critical concern for herbicide tolerance breeding programs. We determined the reaction to bentazone for 138 Korean soybean cultivars. Among them 28 cultivars showed tolerance to bentazone. A comparative study of the effects of bentazone on physiological, and agronomic responses of tolerant and susceptible soybean cultivars was studied. Bentazone treatment initially interrupts the performance of both the tolerant and susceptible genotypes. However, soon after, the tolerant genotypes overcame the stress towards the normal conditions, while for susceptible, the stress was exaggerated. We found a faster recovery of the tolerant genotypes than susceptible genotypes from bentazone stress. Tolerant cultivars showed less reduction in biomass, photosynthesis, and other physiological parameters than sensitive ones. We found significant differences between control and treated plants one day after treatment (DAT) in the tolerant and susceptible genotypes for photosynthetic-related traits. The reduction of photosynthesis and related parameters was higher at 1 DAT than 4 DAT in both tolerant and susceptible genotypes. The NDVI of tolerant genotypes were more or less identical in control and treatment groups. However, significant differences were observed throughout the study for NDVI between control and treatment of susceptible groups. Although initial difference was significant in both tolerant and susceptible for ARI, there were no differences for the tolerant at 4 DAT. The results of this study clarify our understanding of the physiological insight of tolerance and susceptibility of soybean to bentazone.

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

PG-0058

Development of molecular markers for *Liriope platyphylla* and *Ophiopogon japonicus* by comparative analysis of complete chloroplast genome and 45S rDNA

Yeonjeong Lee[1], Hyun-Seung Park[1], Jae-Hyeon Jeon[1], Jee Young Park[1], Seung Hyun Kim[2], Jungmoo Huh[3], Sunmin Woo[3], Do-Won Jeong[4], Tae-Jin Yang[1*]

[1]Department of Agriculture, Forestry and Bioresources, Plant Genomics & Breeding Institute, College of Agriculture and Life Sciences, Seoul National University 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Republic of Korea
[2]College of Pharmacy, Yonsei Institute of Pharmaceutical Sciences, Yonsei University, Incheon, Republic of Korea
[3]Research Institute of Pharmaceutical Sciences, College of Pharmacy, Seoul National University, Seoul 08826, Republic of Korea
[4]Department of Food and Nutrition, Dongduk Women's University, Seoul, 02478, Republic of Korea

Liriope platyphylla and *Ophiopogon japonicus* are perennial herbal plants involved in the Asparagaceae family, which are used as ground cover plants as well as traditional medicine. As *L. platyphylla* and *O. japonicus* are analogous to one another both in morphological form and practical usage, it is important to develop molecular markers for discrimination and construct super barcoding information of two species. In this study, the complete chloroplast genome and 45S nuclear ribosomal DNA (45S rDNA) of two *L. platyphylla* and one *O. japonicus* samples were obtained by *de novo* assembly of low coverage whole genome sequence (dnaLCW). Structurally equivalent phylogenetic trees were constructed from complete chloroplast and 45S rDNA. Also, *L. platyphylla* and *O. japonicus* were shown as allied species by comparative analysis with 28 other species belongs to the Asparagaceae family. Inter- and intra-specific variations were identified both in complete chloroplast genomes and 45S rDNA. For the purpose of species discrimination, four dominant molecular markers based on SNPs and two codominant molecular markers based on InDels were developed from polymorphic regions of complete chloroplast genome. All of the markers were applied well to the samples collected from diverse traditional medicine markets. The complete chloroplast genomes, 45S rDNA sequences, and six molecular markers will serve as an integrated super-barcoding information of two species from genome information to species-specific mini barcode.

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

PG-0059

De novo transcriptome assembly of three Apocynaceae species and comparative analysis of monoterpenoid synthesis genes of allied species

Eunbi Kim, Sae Hyun Lee, Jiseok Kim, Tae-Jin Yang*

Department of Agriculture, Forestry and Bioresources, College of Agriculture & Life Sciences, Seoul National University, Seoul, 08826, Republic of Korea

Cynanchum wilfordii (Cw), *Cynanchum auriculatum* (Ca) and *Metaplexis japonica* (Mj) belonging to the Apocynaceae family are used as medicinal plants in Korea, China and Japan. Pharmacology characters and various phytochemicals of Cw, Ca and Mj were reported and terpenoids such as wilfoside isolated from Cw are demonstrated anti-cancer effect in particular. However, genomic study on the Apocynaceae is still insufficient and valuable metabolic pathway of Cw, Ca and Mj are unknown in advance. As *Catharanthus roseus* (Cro) is the most deeply studied species in Apocynaceae, we used monoterpenoid indole alkaloid (MIA) biosynthesis pathway of Cro as a reference. We conducted *de nove* transcriptome assembly from Cw, Ca and Mj RNA-seq data to investigate the genes involved in the biosynthesis of secondary metabolites. For more accurate data, the results of GO annotation and BLAST were conducted. Of the known 33 genes regulating MIA biosynthesis pathway in Cro, we found 16 genes in Cw and Ca, and 17 genes in Mj for now. Six representative genes which are relatively in upstream of the pathway were chosen, and we conducted comparative analysis of six allied species in Apocynaceae. Cw, Ca, and Mj showed conserved pattern on these six genes over three species generally, while showed difference with other three species that are already transcriptomic-studied. This study confirmed differentiation in metabolic pathway relative genes of six species in Apocynaceae, and approach genome-guided investigation among allied species when they are little close.

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

PG-0060

High-throughput development of KASP markers for genotyping intra-specific diversity of *Cynanchum wilfordii*, an important medicinal plant of Korea

Jiseok Kim, Sae Hyun Lee, Padmanaban Mohanan, Eunbi Kim, Yeonjeong Lee, Tae-Jin Yang*

Research Institute of Agriculture and Life Sciences, College of Agriculture and Life Sciences, Seoul National University, Seoul 08826, Republic of Korea

Cynanchum wilfordii is a domestic functional plant of Korea. *C. wilfordii* synthesizes secondary metabolites including acetophenone, terpenoids and alkaloids, and is proved to have medicinal effects including alleviation of menopausal symptoms and regulation of cholesterol levels. Lately, food industry based on *C. wilfordii* is being activated and marketing of *C. wilfordii* as ingredients of functional foods has been resumed. Compared to growth of its industry scale, breeding of *C. wilfordii* remains in primitive stages. A solid foundation for molecular breeding has not been established and cultivars of *C. wilfordii* are non-existent. In our previous study, we developed intra-species nuclear genome diversity markers based on short-read WGS data. In this study, we utilized WGS data with draft genome of *C. wilfordii* to improve marker specificity and productivity. Illumina MiSeq or Illumina HiSeq data of five different individuals were mapped on draft genome and 1,464,749 variants were called. These variants were narrowed down to 2,868 SNP positions according to seven steps. 20 KASP markers were designed and each markers were validated with 44 individuals respectively. 90 percent of these markers successfully genotyped the given populations. Also, clear segregation of genotypes are observed within self-crossed progeny. Considering throughput of marker development and success rate, this methodology has a potential to build a fluidigm chip assay system and will be able to contribute to breeding of *C. wilfordii*.

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

PG-0061

Functional characterization of *dammarenediol-Ⅱ synthase* paralog genes related with ginsenoside biosynthesis in *Panax ginseng*

Soomin Kim[1], Padmanaban Mohanan[1], Hyeonah Shim[1], Vo Ngoc Linh Giang[1], Nayoung Lee[2], Young Hun Song[2], Tae-Jin Yang[1*]

[1]Department of Agriculture, Forestry and Bioresources, Plant Genomics & Breeding Institute, College of Agriculture and Life Sciences, Seoul National University 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Republic of Korea

[2]Department of Applied Life and Chemistry, College of Agriculture and Life Science, Seoul National University 1 Gwanak-ro, Gwnak-gu Seoul 08826, Republic of Korea

Panax ginseng, a tetraploid perennial plant, is a traditional medicinal herb synthesizing ginsenosides highly known for their pharmacological activities. Dammarenediol-Ⅱ synthase (DDS) is the first committed enzyme to synthesizing the dammarane backbone, for the production of most ginsenosides. Four *DDS* paralogs genes have been identified based on Ginseng Genome Database named as *DDS1*, *1a*, *1b* and *2*. In this study, full-length cDNA of four *DDS* paralogs from *P.ginseng* were isolated and functionally characterized. All the *DDS* paralogs share the same conserved domain, Camelliol C synthase. We analyzed the digital expression profile by using RNA seq data as well as expression analysis using RT-PCR in tissue dependent and diurnal gene expression patterns. Through these expression analyses, we suggests *DDS1* and *1a* are predominantly expressed in aerial parts of *P.ginseng* while *DDS2* is rarely expressed. Also, *DDS1/1a* and *1b* have different diurnal patterns. Furthermore, to investigate the regulation of *DDS* gene expression by transcription factors, we performed transient promoter activation GUS assay using *DDS1* promoter and three bHLH transcription factors. *DDS1* promoter might be directly regulated by bHLH1 and 2. Taken together, we suggest that all *DDS* paralogs have similar functions in ginsenoside biosynthesis but might be differently regulated.

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

PG-0062

Modification of seed oil biosynthesis by base editing in *DGAT1* gene of *Arabidopsis thaliana*

Won Nyeong Kim, Hyun Uk Kim*

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

In rising concern of climate change and dissipating petroleum, importance of vegetable oil (triacylglycerol:TAG) is getting highlight. Due to the structure similarity between petroleum and vegetable oil, many industrial products which traditionally processed from petroleum can be replaced with phyto-based materials. To meet escalating demands of vegetable oil, appending agricultural farm to produce more amount is simple but there are spatial huddles such as region specificity considering growth condition of each oil producing plant. To overcome these issues, increase of vegetable oil producing amount per plant is the key. At this point, *diacylglycerol acyltransferase 1 (DGAT1*) is crucial enzyme to solve the problem. DGAT1 is endoplasmic reticulum (ER) located transmembrane enzyme and take role in final transfer of acyl chain to diacylglycerol to make TAG. In this study, we used base editing technology to edit fifty-two target sites in seven functional domains of DGAT1 expecting change of enzyme properties in manner of increasing TAG produce. By far, total five type of base changed homo transgenic Arabidopsis were generated. Also, based on 3D model of human DGAT1 protein, five base edited mutant's 3D structure of DGAT1 has built. We will discuss the changes in seed fatty acid profile of these five DGAT1 variant mutants in perspective of physical differences which newly found by building 3D structure of five edited DGAT1 protein.

***Corresponding Author:** Tel. 02-6935-2491, Email: hukim64@sejong.ac.kr

PH-0001

The role of RING-type E3 ligase during spike primordia development in wheat

Jae Ho Kim[1], Irfan Ullah Khan[1], Cheol Won Lee[1], Dae Yeon Kim[1], Cheol Seong Jang[2], Sung Don Lim[2], Yong Chan Park[2], Ju Hee Kim[2], Yong Weon Seo[1*]

[1]Department of Plant Biotechnology, Korea University, Seoul, Republic of Korea
[2]Plant Genomics Laboratory, Department of Applied Plant Sciences, Kangwon National University, Republic of Korea

Ubiquitination acts as a post-translational modification, which mediates a variety of cellular function in eukarytic cellular processes. In this study, we identified candidate genes associated with primordia development in cvs. *Keumgang* and *Yeongkwang*, that are differentially expressed during wheat reproductive stages using RNA-sequencing. Among them, the RING-type E3 ligase *TaBAH1* (*TraesCS5B01G373000*) was transcriptionally upregulated between the double-ridge (WS2.5) stage and later stages of floret primordia development (WS10). Moreover, we found that TaBAH1 physically interacts with TaSAHH1 to mediate ubiquitination through 26S proteasome pathway. Phenotypic analysis of TaBAH1-overexpressing plants demonstrated early flowering phenotype and induced rosette leaf numbers compared to that of the WT. In addition, qRT data on overexpression lines suggest that TaBAH1 acted as a positive regulator of flowering by inducing the expression of genes (*AtFT*, *AtSOC*, *AtMAF4*). Our study will help to understand molecular mechanisms of primordia development and TaBAH1 in wheats.

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***Corresponding Author:** Tel. 02-3290-3005, E-mail: seoag@korea.ac.kr

PH-0002

A wheat putative proline-rich gene, *TaELF7*, plays functional roles in the negative regulation of *Arabidopsis* flowering

Jae Ho Kim, Moon Seok Kim, Depika Prasad, Woo Joo Jung, Yong Weon Seo*

Department of Plant Biotechnology, Korea University, Seoul, Republic of Korea

Transcription elongation factors (TEFs) are involved in various metabolic processes of plant growth and development. In this study, we report the molecular function of *Triticum aestivum* TaELF7, which encoded RNA polymerase II-associated factor 1 (PAF1) containing domain. The sequence alignment and phylogenetic analysis were performed compare with ELF7 sequences of other plants. Transcripts of wheat *TaELF7* were examined in negatively respond to late stage of floret development. In addition, we also found that TaELF7 interact with TaHUB2 protein and monoubiquitnated by TaHUB2 as a substrate. Furthermore, the flowering time was delayed in *TaELF7*-overexpressing plants compared to that in wild-type. Some floral related genes were significantly induced in *TaELF7*-overexpressing *Arabidopsis*.

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***Corresponding Author:** Tel. 02-3290-3005, E-mail: seoag@korea.ac.kr

PH-0003

Antagonistic effect of vernalization on histone H2B monoubiquitination enzyme

Jae Ho Kim, Irfan Ullah Khan, Moon Seok Kim, Yong Weon Seo*

Department of Plant Biotechnology, Korea University, Seoul, Republic of Korea

Modification of histone plays a dynamic role in the regulation of DNA replication, repair, and transcription such as acetylation, sumoylation, ubiquitination, methylation in plants. We here identified a homolog of *Arabidopsis* HUB2 in wheat. Vernalization is one of the most important treatment for floral transition in wheat. In this study, we firstly find 11 *TaHUB2* like genes. Among them, *TraesCS3A02G467300 (TaHUB2)* showing decreased gene expression against increased vernalization periods (0, 10, 20, 30, 50 d). The TaHUB2 exhibited ubiquitination ativities and were rapidly degraded in the cell-free extracts with apparently 3 to 6 h after vernalization conditions. Furthermore, histone H2B was monoubiquitinated by TaHUB2 and ubiquitylated histone H2B (H2Bub1) level was decreased after vernalization conditions in wheat. These results will provide to novel information for understanding the role of wheat RING-type E3 ligase and its molecular mechanisms during vernalization for further studies.

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***Corresponding Author:** Tel. 02-3290-3005, E-mail: seoag@korea.ac.kr

PH-0004

The Role of the Sucrose Transporter Genes in Stress Induced Wheat (*Triticum aestivum L.*)

Depika Prasad[1], Woo Joo Jung[1], Yong Weon Seo[1,2*]

[1]Department of Plant Biotechnology, Korea University, Seoul 02841, Korea
[2]Department of Biotechnology, Korea University, Seoul 02841, Korea

Like every other living organism, plants, also require energy to grow and develop in order to successfully complete its life cycle. Production through photosynthesis and distribution of the photosynthates are few of the core functions of a plant. These photosynthates not only allow for growth and development but also assist the plants when induced to abiotic stresses. Plants transport this photosynthates mostly in the primary form of sucrose by the Sucrose Transporter genes (*SUT*). Bread wheat (*Triticum aestivum L.*) is one of the highly demanded and consumed crops globally. There have been two already identified and published *TaSUT* genes, *TaSUT1* and *TaSUT2* while novel *TaSUT3*, *TaSUT4*, *TaSUT6* and *TaSUT7* was identified in this study. *TaSUT5* was identified to be a pseudogene. In this study, one month old Korean wheat cultivar, “Keumgang” seedling had been subjected to abiotic stresses such as cold (4 °C), heat (40 °C), drought (20% PEG 6000), and salt (200 mM) at time intervals of 0, 6, 12 and 24 hours to observe changes in the expression levels of the *TaSUT* genes were compared and analysed. It was observed that *TaSUT2* showed significant increase in expressions when the seedlings were induced to cold and water stress while *TaSUT3*, *TaSUT4*, *TaSUT6* and *TaSUT7* showed significant upregulation in the expression levels in heat and water stress. *TaSUT6* and *TaSUT7* also showed significant difference in salt stress. In contrast *TaSUT1* was mostly downregulated in almost all stress induced seedlings. Through this study, energy production, distribution and usage mechanisms can be deduced and further research on manipulating these mechanisms for development of a better wheat cultivar with quality yield.

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***Corresponding Author:** Tel. 02-3290-3005, E-mail: seoag@korea.ac.kr

PH-0005

Investigation on effective pollination method using different flowering time of inflorescence (*Peucedanum japonicum* Thunb.)

Jintae Kim, Hong-Seob Yu, Ho Jun Joh, Tae-Jin Yang*

College of Agreculture and Life Sciences, Seoul National University 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Republic of Korea

Peucedanum japonicum Thunb.(PJ) is a perennial plant belonging to the Apiaceae family. Trademark of the Apiaceae family, is the umbrella shape inflorescence known as umbel. Studies have characterized PJ as protandrous plant with compound umbel, however inflorescence characteristics especially the fertilized period between stamens and pistil is not yet studied. In this study, we established a guidance for efficient breeding by investigating the flowering characteristics of PJ and to confirm whether self-incompatibility is present. To investigate the flowering characteristics, flowering time on each inflorescence of three individual PJ plants was measured. After flowering, isolation of umbellets was carried out on a daily basis and the quantity of seeds was counted to investigate fertilizable period on the pistil. We also, investigated the difference in flowering period between umbel from the main branch and primary umbels from primary-branches. Numerous flowers of PJ bloomed sequentially within the umbellet, and it confirmed that the pistil was fertile within few days immediately after flowering. This provides the possibility of fertilization between pollen present in umbellets and nearby fertile pistils. The flowering period interval between main umbel and primary umbel indicated that PJ are capable of self-crossing. We believe that this study will contribute to the develop a better breeding of PJ.

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***Corresponding Author:** Tel. 02-880-4547, Email: tjyang@snu.ac.kr; rlawls0812@naver.com

PH-0006

Resistant mechanisms of *Grh1* against green rice leafhopper using transcriptome analysis

Youngho Kwon*, Nukulu Rolly Kabange, Ji-Yun Lee, Dongjin Shin, So-Myoeng Lee, Jin-Kyung Cha, Jun-Hyeon Cho, Sumin Jo, Joowon Kang, Dong-Soo Park, Jong-Hee Lee

Department of southern area crop science, Paddy crop research division, NICS, RDA

The green rice leafhopper (GRH) is one of the most important pest in East Asia. GRH causes enormous yield loss by damaging rice and mediating rice dwarf virus (RDV). GRH sucks rice vascular while it secretes watery saliva containing a number of bioactive proteins including laccase and beta-glucosidase. It withers rice by ingesting host. Therefore it is necessary that breeding GRH resistant rice. In this study, we performed transcriptome analysis of GRH and GRH resistant NIL rice which has *Grh1* from cultivar Shingwang. When GRHs had sucked NIL, it died in 60hrs. So GRH, NIL and recurrent parent cultivar Ilpum (without *Grh1*) were RNA sequenced after 48hrs of feeding. Conspicuously up-regulated processes were metabolic pathway and biosynthesis of secondary metabolite on comparing with NIL and Ilpum. Also plant hormone signal transduction, plant-pathogen interaction, MAPK signaling pathway were up-regulated on NIL. According to gene ontology (GO) annotation system, cofactor metabolic process and macromolecule catabolic process were significantly up-regulated. However, NIL more up regulated genes than Ilpum ware *RRJ1*, *ICL*, *CHI1*, *RIP1*, *TIP1*, *ADF3* and *HOX24*. The genes are related to degrading insect's components and defense system against pest infests. Together, when GRH ingests rice xylem sap, it died by starving that resulted in decomposing of exoskeleton components and unable to uptake nutrients form phloem sap. Moreover, GRH was unable to feed nutrient from phloem sap according to EPG. Therefore we suggest that when GRH suck *Grh1* carrying rice, it could be died by staving to be unable to uptake nutrients from rice phloem sap and defensing system including exocytoskeleton degrading enzymes and phytohormones. This study can be basis model of mechanism study to control pest by using insect resistant gene.

***Corresponding Author:** Tel. 055-350-1162, Email: kwon6344@korea.kr

PH-0007

Fine-mapping and candidate gene analysis for the foxglove aphid resistance gene *Raso2* from wild soybean PI 366121

Ji-Min Kim[1], Ki-Seung Kim[2], Jiyeong Jung[1], Ilseob Shin[1], Sumin Park[1], Ju Seok Lee[3], Soon-Chun Jeong[3], Jeong-Dong Lee[4], Jin Kyo Jung[5], Bo-Keun Ha[6], Sungtaeg Kang[1]*

[1]Department of Crop Science and Biotechnology, Dankook University, Cheonan 31116, Korea
[2]Deparment of Innovative Technology, FarmHannong, Ltd., Nonsan 33010, Korea
[3]Bio-Evaluation Center, Korea Research Institute of Bioscience and Biotechnology, Cheongju 28116, Korea
[4]School of Applied Biosciences, Kyungpook National University, Daegu 41566, Korea
[5]National Institute of Crop Science, Rural Development Administration, Suwon 16613, Korea
[6]Department of Applied Plant Science, Chonnam National University, Gwangju 61186, Korea

The foxglove aphid (FA: *Aulacorthum solani* Kaltenbach) is an important insect pest that causes serious yield losses in soybean. The FA resistance gene *Raso2* from wild soybean PI 366121 was previously mapped to a 13 cM interval on soybean chromosome 7. However, fine-mapping of *Raso2* was needed to improve the effectiveness of marker-assisted selection (MAS) and to eventually clone it. The objectives of this study were to fine-map *Raso2* from PI 366121 using Axiom® 180 K SoyaSNP array, to confirm the resistance and inheritance of *Raso2* in a different background, and to identify candidate gene(s). The 105 F4:8 recombinant inbred lines were used to fine-map the gene and to test antibiosis and antixenosis of *Raso2* to FA. These efforts resulted in the mapping of *Raso2* on 1 cM interval which corresponds to 77 Kb containing eight annotated genes based on the Williams 82 reference genome assembly (Wm82.a2.v1). Interestingly, all nonsynonymous substitutions were in *Glyma.07g077700* which encodes the disease resistance protein containing LRR domain and expression of the gene in PI 366121 was significantly higher than that in Williams 82. In addition, distinct SNPs within *Glyma.07g077700* that can distinguish PI 366121 and diverse FA-susceptible soybeans were identified. We also confirmed that *Raso2* presented the resistance to FA and the Mendelian inheritance for single dominant gene in a different background. The results of this study would provide fundamental information on MAS for development of FA-resistant cultivars as well as functional study and cloning of the candidate gene in soybean.

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

PH-0008

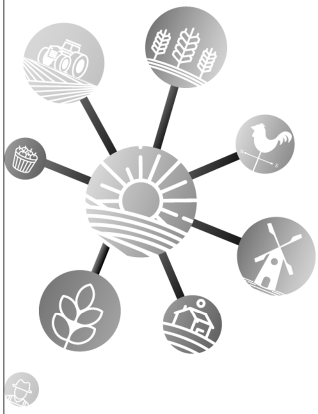
The status and function of FRIGIDA-complex are changed during vernalization in Arabidopsis winter annual

Jina Bae, Daesong Jeong and Ilha Lee*

National Research Laboratory of Plant Developmental Genetics, Department of Biological Sciences, Seoul National University, Seoul 151-742, Korea

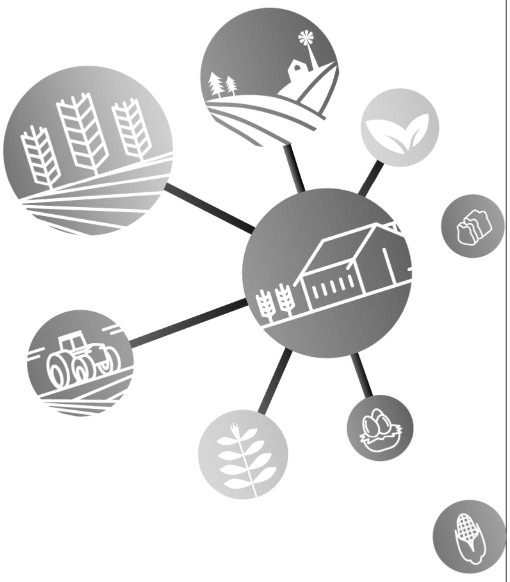
The flowering of *Arabidopsis thaliana* winter annual is strongly suppressed before winter and then occurs in the spring of the following year after prolonged exposure to winter cold. A strong floral repressor, *FLOWERING LOCUS C* (*FLC*), whose expression is epigenetically suppressed by vernalization, a long-term winter cold for flowering. FRI acts as a scaffold protein and forms FRIGIDA-complex (FRI-C), including SUPPRESSOR of FRIGIDA (SUF4), FRIGIDA LIKE1 (FRL1), FRIGIDA ESSENTIAL1 (FES1), and FRIGIDA EXPRESSOR (FLX) to activate *FLC* expression. However, it is not known the status and function of FRI-C when *FLC* is suppressed after vernalization. Here, we show that FRI-C components do not change in the transcriptional levels by vernalization. Interestingly, the protein levels of key components of FRI-C, FRI and SUF4, were increased during vernalization. In addition, the size of FRI-C was reduced to form small complexes by vernalization and these small complexes could be involved in flower organ developments. We further demonstrated that FRI was detached from *FLC* when *FLC* expression was reduced after vernalization. Therefore, taking all of these results together, we present insight of status and role of FRI-C during vernalization.

***Corresponding Author:** Tel. 02-880-8864, E-mail: ilhalee@snu.ac.kr



Special Session A.

Breeding for Woody Plants



SA-0001

Forest Reclamation integrated with Tree Breeding in the Republic of Korea

Yang-Gil Kim, Hye Jin Lee, Dayoung Lee, Sunjeong Kim, Su Vi Kim, Ei Sandi Sett, Ji-Min Park, Da Eun Gu, Ye-Ji Kim, Yeongkon Woo, Gyehong Cho, Kyu-Suk Kang*

Department of Agriculture, Forestry and Bioresources, College of Agriculture and Life Sciences, Seoul National University, Gwanak-ro, Gwanak-gu, Seoul 08826, Republic of Korea

Korean forests were started to be seriously destroyed in the early 15th century. All the mountains were barren except the areas untouched by humans due to remoted location. This situation continued until the late 20th century. During the Joseon Dynasty, all the mountains of Korean peninsula were owned and directly managed by the state. People were allowed to cut tress for wood consumption without any restriction. After the Joseon Dynasty, Korea was under Japanese occupation for 36 years. At that time, the forest cover was about 71%. The Japanese occupation (1910-1945) and the Korea War (1950-53) further devastated forests. In the 1960s, legal and institutional changes were made and an administrative basis was formed to implement the policies. In the 1970s, the Korean government formulated and implemented a comprehensive forest policy that would help increasing income and improve the quality of life so ask inducing public participation. In the 1980s, the main objectives of the reforestation policy were turn into increase forest resources and to establish commercial forests. What we learned from successful forest reclamation and tree breeding are 1) it was necessary to establish fuel-wood forests integrated by breeding programs in the Institute of Forest Genetics and managed by the Village Forestry Association, 2) job creation and forest income by 'Saemaul Tree Nursery' project was useful, 3) strong leadership, strategic approach and practical implementation tool were well cooperated, and 4) expansion of forest-related research institutes (R&D) was followed.

***Corresponding Author:** Tel. 02-880-4753, Email: kangks84@snu.ac.kr

SA-0002

Development of SNP chip for Genomic Selection of Korean Red Pine (*Pinus densiflora*) Trees

Kyeong-seong Cheon[1], Hye-In Kang[1], Yong-Woo Park[1], Jeong-Ho Song[1], In-Sik Kim[1], Donghwan Shim[2*]

[1]Dept. Forest Bio-resources, National Institute of Forest Science, Suwon 16631, Republic of Korea
[2]Dept. Biological Sciences, Chungnam National University, Daejeon 13431, Republic of Korea

Pinus densiflora (Korean red pine) is a species of evergreen conifer that is distributed in Korea, Japan, and China, and of economic, scientific, and ecological importance. The National Institute of Forest Science has made great efforts in Korean red pine breeding for the past 60 years. Nevertheless, we still have a lot of challenges to solve the limitation of tree breeding which takes a lot of time and labor. In order to overcome of these limitations, we are attempting a new paradigm tree breeding method by integrating NGS big data and ICT. Genomic Selection (GS) is one of the accelerating breeding methods. With the advent of high throughput molecular technology, numerous molecular markers distributed throughout the whole genome can be developed to characterize many genetic entries involving new perspectives in methodology of selection. In tree breeding the GS could significantly reduce the cost of genetic improvement schemes by limiting the size and number of field experiments. In this study, we used 5,228 trees of 46 half-sib F_1 families from 6 environments in Korea and we got 97,647 SNPs via GBS (Genotyping by Sequencing). And then, we designed the high-resolution DNA chip (200K chip) to validate whole SNPs. Finally, we selected and produced the 50K SNPs chip for genotyping of Korean red pine trees. Now, we are preparing to analyze 4,412 trees which are confirmed the pedigree. We expect that the red pine SNP chip will make a great contribution to shortening the tree breeding period. In addition, it may be useful for early selection and development of disease-resistant bio-markers.

***Corresponding Author:** Tel. 042-821-6279, E-mail: dshim104@cnu.ac.kr

SA-0003

Evaluation for combined tolerance of drought and heat stress of 7 species recommended for afforestation in Korea

Seong Hyeon Yong[1,2], DoHyeon Kim[1], Kwan Been Park[1], Myung Suk Choi[1,2*]

[1]Department of Forest Environment Resources, Gyeongsang National University 501 Jinjudae-ro, JInju 52828, Republic of Korea

[2]Institute of Agriculture Life Science, Gyeongsang National University 501 Jinjudae-ro, JInju 52828, Republic of Korea

Currently, 78 tree species recommended for reforestation are selected in Korea, but these are designated without considering physiological data. In this study, seven planted tree species (*Chamaecyparis obtusa*, *Fraxinus rhynchophylla*, *Juglans sinensis*, *Larix kaempferi*, *Pinus densiflora*, *Quercus acutissima*, *Ulmus davidiana* var. *japonica*) were conducted to accurately evaluate complex stress (drought+heat) resistance based on physiological indicators. The seedlings of 2 years older were used in the experiment. In order to observe biochemistry changes, electrolyte leakage method, proline, and reducing sugar content investigation experiments were conducted. In addition, the degree of cell death was measured by Evan's blue staining assay, and recovery after drying was measured by DAB staining. As a result of measuring the electrolyte leakage index was 5.0 or less in all species. The leaf proline content was the least in *U. davidiana* var. *japonica* and increased by 12 times or more in J. sinensis compared to the control. The reducing sugar showed similar results to proline. As a result of Evan's blue experiment, *F. rhynchophylla* and *J. sinensis* showed nearly 80% apoptosis. In the DAB staining experiment, the recovery of *F. rhynchophylla* and *J. sinensis* was slow. Analysis of the content of proline and reducing sugars can help clarify the drying resistance analysis. Visualizing plants under stress is very effective for measuring various inanimate stress tolerance. These results can be contributed to the selection of afforestation recommended species as scientific data on major planted species.

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***Corresponding Author:** Tel. 055-772-1856, E-mail: mschoi@gnu.ac.kr

SA-0004

Tree Improvement Research Using Information and Communication Technology

Kyungmi Lee*, Jeong Ho Song, In Sik Kim

Div. of Tree Improvement and Biotechnology, Dept. of Forest Bio-Resources, National Institute of Forest Science, 39 Onjeong-ro, Gwonseon-gu, Suwon 16631, Republic of Korea

The tree improvement research is one of the major promising field in the precision forestry affected by industry 4.0. The traditional tree improvement program in Korea has made the major accomplishments including the dissemination of the improved forest reproductive materials (FRM) of the national plantation and the development of the relevant research as well. Currently, the tree improvement research is being requested to make further advance in response to the increasing demand for the improved FRM to enhance the economic value of Korean forest. The information and communication technology (ICT) is expected to provide useful tool to overcome the challenges in the long periodic and the labor-intensive research of tree improvement. In this study, the latest research topics with applications of ICT will introduced on the phenotypic, genetic and environmental aspects. To improve the phenotyping accuracy of progeny testing with large size of trees, the extended application of LiDAR system is in progress. The genomic selection accompanying the big data analysis is ongoing in the forest tree though it is relatively in the early stage compared to the crop or animal breeding. For the precise estimation of the genetic effects, the remarkable development of the geographic information system (GIS) would ameliorate the analysis of unavoidably heterogenous environmental factors. The challenges in the future research with ICT will be discussed for the efficient tree improvement.

***Corresponding Author:** Tel. 031-290-1129, E-mail: kmile@korea.kr

SA-0005

Analysis of genetic relationships of *Pyrus pyrifolia* native to Korea using SSR markers

Sang-Hee Park[1,2], Jong-Kuk Na[2*], Eun Ju Cheong[1*]

[1]Department of Forest and Environment System, Kangwon National University, Chuncheon, ROK
[2]Department of Controlled Agriculture, Kangwon National University, Chuncheon, ROK

Pyrus pyrifolia, belonging to the genus *Pyrus*, is a deciduous broad-leaved small tree native to East Asia. Many studies have revealed that the leaves and fruits of this species contain valuable compounds beneficial to human health. It is considered a valuable species and currently on the rise in production by developing new varieties and cultivation methods. However, the genetic background of the species has not been well understood due to limited genetic studies. In this study, the genetic variations of 31 wild accessions were investigated using SSR markers. Twenty-eight accessions were obtained from the National Institute of Horticultural Science and Technology and three accessions from Gangwon Forest Science Institute. Sixty SSR primer sets were designed from genomic information available publically and tested for PCR amplification using pooled DNA from the accessions. Thirty-one primer sets exhibited polymorphism and were used for further analysis. The average number of alleles was 1.984 per primer, and the observed and the expected average heterozygosity were 0.215 and 0.172, respectively. The average polymorphism information content was 0.343. The Ochiai similarity index ranged from 0.11 to 0.64. UPGMA cluster analysis showed that 31 accessions were classified into three groups. PCoA analysis showed similar patterns with the UPGMA result. Nevertheless, a limited number of SSR markers were used for genetic relationship analysis, our results would provide valuable information to facilitate the management of selected wild pears and to develop new cultivars in the future.

***Corresponding Author:** Tel. 033-250-7769, E-mail: ejcheong@kangwon.ac.kr; jongkook@kangwon.ac.kr

SA-0006

휘발성 유기화합물(VOCs) 저감 기능성 임목 개발을 위한 식물내생 미생물의 이용

서종범[1*], 김대솔[1], 최아현[1], 이일환[2], 이위영[2], 강준원[1]

[1]대구시 북구 대학로 80, 경북대학교 농업생명과학대학, 산림과학・조경학부
[2]경기도 수원시 권선구 온정로 39, 국립산림과학원 산림생명자원연구부, 산림자원개량연구과

미세먼지로 인한 대기오염이 사회적 문제로 대두되고 있는 가운데, 대기 중의 약 72%의 미세먼지는 휘발성 유기화합물(VOCs)에 의한 화학적 반응산물이다. 전통적 임목육종 방법을 이용하여 환경정화 기능을 가진 임목을 개발하거나 선발하기 위해서는 오랜 시간이 소요되며, 생명공학 기술을 이용한 형질전환 및 유전자교정 기술은 산림생태계 내 유전적 안정성과 위해성으로 실용화에 어려움이 있다. 따라서, 전통적인 임목육종 기술로 급변하고 있는 사회의 다양한 요구를 충족시키기에는 한계가 있다. 본 연구에서는 휘발성 유기화합물 저감에 효과적인 임목의 내생미생물을 발굴하고 그 메커니즘을 이용하여 대기 중 휘발성 유기화합물을 저감할 수 있는 기능성 임목을 개발하는데 목적이 있다. 연구를 진행하기 위해 휘발성 유기화합물이 오염된 군부대와 공단지역을 포함한 여러 지역에서 식물체와 내생미생물을 수집, 선발, 평가 중에 있다. VOCs 저감 수종 개발 기술로 기능성 육종 효율성 제고 및 환경 정화능을 가진 기능성 도시숲 조성에 활용될 수 있을 것으로 기대된다.

***교신저자:** Tel. 053-950-5744, E-mail: sjba0620@knu.ac.kr

SA-0007

Parental analysis in a linkage mapping population of *Populus davidiana* genotyped by microsatellite markers

Su-Vi Kim, Yang-Gil Kim, Dayoung Lee, Sunjeong Kim, Kyu-Suk Kang*

College of Agriculture and Life Sciences, Seoul National University 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Republic of Korea

Populus davidiana is widely distributed in Korea and it is a model tree species in genomic study. In this study, we are aiming at the construction of linkage map that would be useful for QTL mapping and breeding works. Odae 19 as a mother and BongHyun4 as a father were artificially crossed and hybrid seedlings were growing at the SNU experimental forest in Suwon, Kyonggi. At age 4, a total of 290 individual trees were selected for determination of genotypes (parentage analysis), which is prerequisite for accurate linkage mapping. Based on various references, it has been reported that five DNA markers are necessary for the parental analysis. Therefore, five microsatellites makers such as ORPM26, ORPM312, PMGC2501, WPMS15, and PTR4 were employed for the parentage analysis. The ORPM26 marker could be detected in all of hybrid individuals (100%), while WPMS15 marker was founded in 91.3% of individuals. Based on the microsatellite marker analysis, on average, 90.3% of hybrid F1 individuals (262 trees) were determined as the same family. About 100 individuals are generally used to construct linkage mapping. Thus, we suggest that these F1 individuals could be appropriate for linkage and QTL mappings in the future study.

***Corresponding Author:** Tel. 02-880-4762, E-mail: flwm130@snu.ac.kr

SA-0008

Transcriptome analysis in branching seedlings of Bansong (*Pinus densiflora* f. *multicaulis*)

Hye-In Kang[1], Kyeong Seong Cheon[1], In Sik Kim[1], Kyu-Suk Kang[2], Donghwan Shim[3*]

[1]Department of Forest Bio-Resources, National Institute of Forest Science, Suwon, 13361
[2]Department of Agriculture, Forestry and Bioresources, College of Agriculture and Life Sciences, Seoul National University, Seoul, 08826
[3]Department of Biological Sciences, Chungnam National University, Daejeon, 34134

Bansong, the formae of Korean red pine, has multiple main stems and a lot of branches. Phytohormones such as auxin, cytokinin, and strigolactone are known to control the growth of axillary shoots in crop plants, but few studies have been carried on the mechanism of branching in conifers. Transcriptome of Bansong × Korean red pine hybrid was assembled and how gene expressions changed during shoots emerging were estimated in SAM and shooting node tissues through RNA-Seq. We assembled transcriptome of 33,853 unigenes with GC contents of 44.84% and N50 of 1,374bp. Differentially expressed genes (shooting seedlings vs. control) appeared throughout the overall regulation and metabolism pathways and showed different patterns in the SAM and shooting node. In SAM, jasmonic acid biosynthesis pathway was up-regulated and lipid-involved pathway was down-regulated. The results indirectly indicated that shoot branching might have been affected by strigolactone. This study is meaningful in that it suggested the possibility of identifying shoot branching regulation feature using transcriptome analysis in pine trees.

Keywords: Transcriptome, Branching, *Pinus densiflora* f. *multicaulis*

***Corresponding Author:** Tel. 042-821-6279, E-mail: shim.donghwan@gmail.com

SA-0009

Growth characteristics of 100 half-sib families of *Dalbergia cochinchinensis* in Cambodia

Ji-Min Park*, Ye-Ji Kim, Da-Eun Gu, Yeongkon Woo, Gyehong Cho, Kyu-Suk Kang

Department of Agriculture, Forestry and Bioresources, Seoul National University 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Republic of Korea

Dalbergia cochinchinensis, called Thailand rosewood or tracwood, is valuable timber species and distributed in tropical of Madagascar, Asian and African regions. A total of 100 plus trees were selected from natural stands, and seeds were collected and germinated for the establishment of open-pollinated progeny test plantation at two locations, ChanSor and KhunReam in Cambodia. We investigated height and diameter at root collar (DRC) for 4 year-old seedlings. At KhunReam site, the average of height was 287.4 cm (ranged 203.6 to 399.8), and the average of DRC was 52.3 mm (ranged 38.8 to 71.0). At ChanSor, the average of height was 295.9 cm (ranged 246.4 to 355.9) and the average of DRC was 58.2 mm (range 44.1 to 71.4). Two-way ANOVA showed significant differences among families and blocks. At KhunReam, the individual heritability(h_i^2) of height was 0.524 and the family heritability(h_f^2) of height was 0.567. The individual heritability of DRC was 0.422 and the family heritability of DRC was 0.63. At ChanSor, the individual and family heritabilities were 0.231 and 0.562 for height, and those for DRC were 0.217 and 0.573, respectively. Genetic gain would be estimated as 18.8% and 21.3% for height and DRC growth when the families with higher than average were selected at KhunReam. The genetic gain would be lower at ChanSor than KhunReam when the 46 families showing better than average growth were selected. At ChanSor, the genetic gain would be 7.48% and 7.06%, respectively for height and DRC growth if the superior families were selected.

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***Corresponding Author:** Tel. 02-880-4762, E-mail: pjm1013@snu.ac.kr

SA-0010

곰솔(*Pinus thunbergii*) 2세대 채종원에서 구과 및 종자의 유전적 특성 분석 및 유전간벌에 따른 개량효과 추정

박성민, 김예지, 박지민, 강규석*

서울대학교 농업생명과학대학 농림생물자원학부, 08826서울시 관악구 관악로1

본 연구는 2019년에 곰솔 2세대 채종원에서 채취한 풍매 종자를 대상으로 클론별 구과 및 종자의 형태적 그리고 유전적 특성을 알아보고자 실시되었다. 클론 간 유의미한 차이가 있는지 분산분석하고 광의의 유전력을 추정하며 단순상관분석을 통해 구과 및 종자 특성 간의 상관을 분석하였다. 더불어 유전간벌 시뮬레이션을 통해 적정 유전간벌 방법 및 강도를 도출하여 채종원 관리에 활용하기 위해 수행되었다. 구과의 건조 전 무게는 평균 33.31g, 길이는 평균 63.29g, 폭은 평균 34.02mm, 건중량은 평균 18.22g이었다. 구과당 종자생산 능력은 평균 156개, 고사배주는 평균 89개, 성숙종자 수는 평균 66.3개, 충실종자 수는 평균 59.81개, 충실종자율은 평균 89.4%, 종자효율은 38.36% 였다. ANOVA 분석 결과, 구과 및 종자 특성 모두 클론 간에 유의미한 차이가 관찰되었으며 유전력은 0.40-0.64로 나타났다. 단순상관분석 결과로 건조 전 구과의 무게는 길이, 폭, 건조 후 구과의 무게와 유의한 정의 상관관계를 나타냈고 건조 후 구과의 무게 역시 길이, 폭과 유의한 정의 상관관계를 나타냈다. 건조 전 구과 무게는 종자생산 능력, 성숙종자 수, 충실종자 수와 유의한 정의 상관관계가 있으며, 구과 폭과 성숙종자 수, 구과 폭과 충실종자 수, 건조 구과 무게와 충실종자 수도 유의한 정의 상관관계가 관찰되었다. 마지막으로 곰솔 2세대 채종원에서 유전간벌을 실시하기 위한 기초자료로서 가계 간벌과 가계 내 개체 간벌 방법을 비교한 결과 가계 간벌 보다 가계 내 개체 간벌 방법에서 유전다양성 감소가 적게 나타나며 적정 유효집단수 수준을 유지하였다. 따라서 본 채종원에서 적정 간벌 방법 및 강도는 가계 내 개체 간벌 방법에서 간벌율 20-30% 수준으로 고려되었다.

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***교신저자:** Tel. 02-880-4762, E-mail: kyeji1107@snu.ac.kr

SA-0011

환경 스트레스 (가뭄, 산성비) 내성 왕벚나무 품종 선발을 위한 비파괴적방법을 이용한 생리 특성 진단법 연구

정욱한, 이화, 장경주, 김소연, 정은주*

강원대학교 산림환경시스템학과

왕벚나무는 화려한 꽃과 가을 잎 색으로 가로수로서 인기가 높은 수종이다. 왕벚나무는 가로수로 많이 심기 때문에 도심지 환경에 대한 적응도 필요하다. 도시환경에서 오염 증가에 따른 산성비 강우가 늘어나고 있는 실정으로 산성비는 일시적으로는 피해를 입히지 않으나 만성적일 때 피해가 나타나게 된다. 가뭄 또한 환경 스트레스 중 가장 빈번하게 일어나고 있다. 이런 환경스트레스에 대한 피해 양상을 진단하는데 피해 요인 판별이 어려우며 이로 인한 식물생장의 영향을 예측하기 어렵다. 환경스트레스에 대한 왕벚나무의 피해 정도를 측정하여 스트레스에 대한 내성이 있는 품종을 선발하기 위해서는 생리적인 특성을 측정할 수 있어야 한다. 이에 왕벚나무에 스트레스를 처리하여 생리적 특성과 최근 육종에 이용되는 분광기술을 활용하여 스펙트럼 분석을 통하여 피해를 진단할 수 있는 방법을 개발하고자 하였다.

무처리의 대조구와 가뭄, 인공산성비를 처리한 개체의 잎의 생리적 특성을 조사한 결과 인공산성비 처리구의 식물체가 대조구에 비하여 엽록소형광반응(Fv/Fm)을 제외하고 엽록소함량 (SPAD 수치), 상대수분함량 (RWC), 기공전도도 (Gs)가 감소한 결과를 나타냈다. 스펙트럼을 전처리하여 피크점을 선별한 결과 가시광선 699nm와 근적외선 1879nm에서 피크점이 나타난 것을 확인하였다. 가뭄 처리구에서 5주간 생리 특성 값과 가시광선 699nm 간 상관관계를 분석한 결과 SPAD $R^2=-0.14$, Fv/Fm $R^2=-0.23$, RWC $R^2=-0.26$, Gs $R^2=-0.24$인 것으로 나타났으며, 근적외선 1879nm 에서는 SPAD $R^2=-0.74$, Fv/Fm $R^2=-0.52$, RWC $R^2=-0.70$, Gs $R^2=-0.64$로 나타났다. 산성비 처리구에서는 SPAD $R^2=-0.48$, Fv/Fm $R^2=-0.38$, RWC $R^2=-0.55$, Gs $R^2=-0.50$과 SPAD $R^2=-0.38$, Fv/Fm $R^2=-0.43$, RWC $R^2=-0.72$, Gs $R^2=-0.67$로 나타났다. 두 스트레스 모두 원근적외선을 이용했을 때 비교적 높은 상관관계를 나타났다. 근적외선에서 가뭄은 네 가지 모두 비교적 음의 상관관계가 나타났으나, 산성비에 대해서는 상대수분함량과 기공전도도만이 근적외선파장에서 유의한 차이를 보였다. 보다 정확한 진단을 위해 스트레스 반응과 스펙트럼 변화의 표준화 연구가 필요할 것으로 생각된다.

***교신저자:** Tel. 033-250-7769, E-mail: ejcheong@kangwon.ac.kr

SA-0012

식물-미생물 연구 동향 분석 - 마이크로바이옴 시대로의 확장

이병주, 어수형*

충청남도 예산군 예산읍 대학로 54 공주대학교 산림자원학과

식물 육종은 인위적인 형질 선택과 교배를 통해 식물 자원의 유용성을 높이고 부정적인 외부 영향에 대한 저항성을 증가시키기 위한 목적으로 실시되어 왔다. 최근에는 식물의 고유 형질 변형뿐만 아니라, 식물 생육에 영향을 미치는 미생물을 사용하여 식물의 형질을 개선하려는 시도가 이루어지고 있다. 본 연구에서는 SCI급 논문들을 대상으로 '동시출현단어' 및 '동시인용' 분석을 통해, 시간 경과에 따른 식물 관련 미생물 연구 분야의 동향과 최근의 주요 연구 주제를 파악하였다. 'Web of Science' DB를 사용하여 'plant-associated microorganism'과 관련된 키워드로 검색을 실시한 결과, 총 1,163편의 논문이 검색되었다. 동시출현단어분석 결과, 4개의 cluster로 단어들이 분류되었다. 이 중 community/microbiome/microbiota로 대표되는 'cluster 1'에 해당하는 논문의 비율과 평균 인용 횟수가 시간 경과와 함께 유의하게 증가하였다. 또한 동시인용분석에서 최신 논문을 주로 인용하는 논문 그룹의 대표 단어가 'microbial communities'와 'plant-associated bacteria'로 나타났다. 시기별 사용 급증 단어를 살펴본 결과, 'plant-microbe interactions', 'plant-associated microbiota', 'fungal communities', 'plant mcirobiome' 등과 같이 미생물 군집과 식물과의 상호작용을 나타내는 단어들 위주로 최근 사용이 급증하였다는 것을 확인하였다. 다른 생물체와 상호작용하는 미생물 군집 또는 마이크로바이옴은 최근 의학, 생태, 환경 등 다양한 연구 분야에서 다루어지고 있다. 시간이 경과함에 따라 미생물을 활용한 식물 연구 분야 또한 미생물 군집 수준의 연구로 범위가 넓어져 가는 것으로 판단된다.

사사: 본 연구는 산림청(한국임업진흥원) 산림과학기술 연구개발사업(2021332B10-2123A01)과 산림청 국립산림과학원의 '국내 유통 목재의 수종 식별을 위한 바이오지문 분석 기술 개발(FG0603-2021-02)'의 지원에 의하여 이루어진 것입니다.

***교신저자:** Tel. 041-330-1301, E-mail: eosh@kongju.ac.kr

SA-0013

Vegetation structure and soil characteristics of selected stands as base populations for the breeding program of cherry trees (*Prunus* sp.) in Korea

Jong Woo Kim*, Kyungmi Lee, Jeong Ho Song, In Sik Kim

Div. of Tree Improvement and Biotechnology, Dept. of Forest Bio-Resources, National Institute of Forest Science, 39 Onjeong-ro, Gwonseon-gu, Suwon 16631, Republic of Korea

The selection of base populations following the investigation of the species distribution, growth status and variation is the first step of the forest tree improvement. Cherry trees, *Prunus* spp., has been reviewed as the target species of the tree improvement of hardwood species in Korea. The species have high economic value of timber and ornamental value as well. The objectives of this study was to select superior forest stands of cherry trees as base populations and to understand the ecological characteristics of the species for further utilization. The field survey was conducted on 28 candidate stands of six species of genus *Prunus*. Estimation of the ecological indices and the vegetation analysis was performed on the six selected stands among the candidates. The six stands were classified into three vegetation units using hierarichical clustering analysis by dominant species in the stands: VU1 (*Quercus mongolica* - *Fraxinus rhynchophylla*), VU2 (*Pinus densiflora* - *Quercus aliena*), VU3 (*Acer pseudosieboldianum*- *Tilia amurensis*). The average crown base height of plus trees was highest in VU3, but the stem straightness did not show significant difference. The soil of the stands exhibited the higher level of pH, organic matter and total nitrogen with lower available phosphorous compared to the average value of those from the national forest soil survey. The results from this study is expected to be useful in the management of seed production area and the plantations of the species providing information about the ecological chracteristics of the cherry trees in Korea.

***Corresponding Author:** Tel. 031-290-1126, E-mail: done@korea.kr

SA-0014

Current status of willow research for short rotation coppices development in Republic of Korea

Hyunseok Lee*

Division of Horticulture & Medicinal Plant, Andong National University, 1375 Kyeongdong-ro, Andong 36729, Republic of Korea

The species and varieties of willow are reported to as 45 taxa representing 35 species and 10 varieties in Korea peninsula. There were some researches and works related on ecology, propagation, taxonomy, genetics, and breeding in South Korea. The ecology on Salix in some riverbeds and wetlands were investigated for population dynamics, standing crop biomass and primary productivity. *S. nipponica* produced 235 g/ m2/ yr and *S. glandulosa* 1.006 g/ m2/ yr. In some riverbed areas, the *S. nipponica* populations appeared firstly, mixed with *S. koreensis*, and then turned into the pure population of the latter. Texture of soil sedimentation, water content, total nitrogen amount, altitude and annual average temperature were environmental factors that influenced on Salix distribution in a river. Some clones of S. alba were introduced and investigated for adaptation ability and growth performances in landfill site. In another study, cuttings with larger diameters than longer stems were proper for early rapid revegetation and slope stabilization. In this project, the possible candidates were chosen including willows, poplars, and maples and compared with several broad- and narrow-leaved trees in caloric values and growth. Several willows were recommended by this research. They are *S. caprea* for marginal farm and/or forest land and *S. gracilistyla* for abandoned and wet farm land.

***Corresponding Author:** Tel. 054-820-6934, E-mail: hyunseoklee@anu.ac.kr

SA-0015

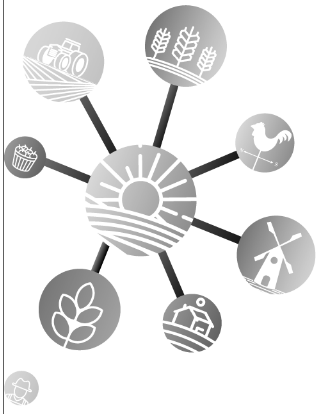
Current research status of *Xanthoceras sorbifolum* for new bioenergy plants development

Hyunseok Lee*

Division of Horticulture & Medicinal Plant, Andong National University, 1375 Kyeongdong-ro, Andong 36729, Republic of Korea

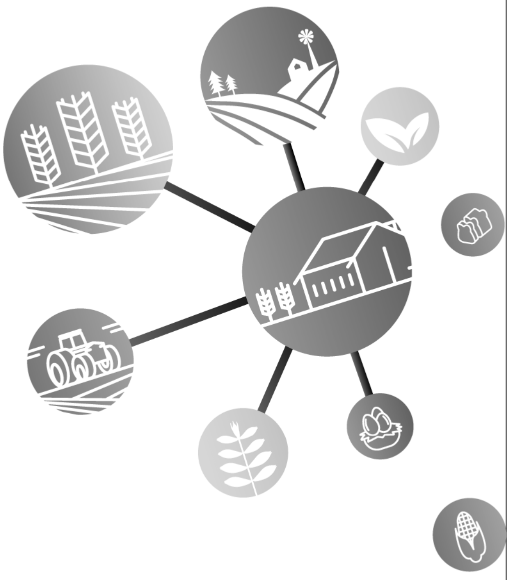
Xanthoceras sorbifolium is a woody tree in the soapberry family, Sapidaceae, native to northern China. This species has been known as a bioenergy material plant for biodiesel production because of high oil content in seeds. But this species is little known in Korea. Compared to the oil content of rapeseeds grown in Korea as 35% to 45%, it has a high level of use as a bioenergy resource plant. This species is widely distributed from Gansu, Hebei, Liaoning to Shandong, except in the southern region in China, and climate zone is similar between native habitat and Korea peninsula. It is resistant to cold enough to grow in the range of minus 30 to 41 degrees Celsius. But many flowers bloom enough to have the saying 'a thousand flowers, one fruit', but the fruiting rate is low. Although it isu bisexual flower, it is reported that the fertility rate of pollen is 30~73%, with a large deviation. Therefore, it is required to select and development individuals/populations with high fertility through breeding program. In the case of introduction woody plants, it is necessary to develop technology to facilitate the initial acquisition of individuals or to foster excellent groups or individuals. For improving bioenergy plants of *X. sorbifolium* is need to necessary performed that 1) investigating seeds characteristics, 2) analyzing genetic characteristics, 3) analyzing oil concentration and content from seeds and 4) developing efficiency propagation methods.

***Corresponding Author:** Tel. 054-820-6934, E-mail: hyunseoklee@anu.ac.kr



Special Session B.

「디지털육종 전환지원사업」을 통한 첨단육종기술 확산



SB-0001

디지털육종을 위한 생물정보분석 서비스 소개

이상춘*, 박태석, 김남훈, 이준기, 이현오, 김혜식, 김효원, 남경현, 조예진

경기도 성남시 분당구 성남대로 331번길 13 백궁프라자 1 빌딩 605호, ㈜ 파이젠 (www.phyzen.com)

염기서열 분석과 생물정보 분석 기술의 급속한 발전 덕택에 대용량 고효율의 작물 오믹스데이터 생산과 분석이 가능하게 되었으며, 또한 이를 활용한 보다 효율적인 작물 디지털육종도 역시 가능하게 되었습니다. 본 발표에서는 ㈜ 파이젠에서 제공하고 있는 디지털육종을 위한 다양한 생물정보분석 서비스 - 유전체 재분석, 전사체 분석, 변이 탐색, 분자표지 개발, 데이터베이스 구축 등 - 를 실제 사례와 함께 소개하고자 합니다.

***교신저자:** Tel. 031-716-0041, E-mail: sclee0923@phyzen.com

SB-0002

디지털육종전환지원사업에서 생물정보기업의 역할 및 제공 서비스

조성환*

씨더스, 대전광역시, 대한민국

최근 작물 육종프로그램에서 분자육종과 유전체육종을 지나 디지털육종 진입을 위한 준비가 필요성이 화두가 되고 있다. 그러나 다국적 종자기업에서의 움직임과는 다르게 국내 종자기업은 인프라나 생물정보 전문인력의 확보면에서 여러 어려움을 겪고 있는 것이 현실이다. 이러한 한계들을 최소화하고, 빠르게 개발되고 있는 R&D 결과물과 유전체 정보의 활용을 지원하기 위해 생물정보분석 지원기업과 분자마커 검정기관, 병리검정기관 등 관련기관들이 종자기업 단독적으로 해결하기 어려운 문제들을 함께 해결하고자 시도되고 있다. 생물정보기업에서 제공하는 기본임무는 방대한 유전체 데이터를 어떻게 활용할 수 있는지, 논문 등에 공개된 유전자 및 분자마커 정보를 종자기업이 가지고 있는 유전자원에 적용하는 방안 및 고려사항, 여러 사업을 통해 얻어진 유전체 정보 및 분자마커 결과의 해석을 근접해서 함께 고민하고 적용사례를 통해 향후 정보중심의 육종프로그램을 시행하기 위한 준비사항을 점검하고 있다. 종자기업과 생물정보기업은 각자의 전문성이 현격히 달라 서로의 의사소통과 필요에 대한 이해의 폭을 증가시키는 일은 반드시 넘어야 하는 가장 중요한 과정으로 종자산업의 구성원으로서 하나가 되는 중요한 계기가 되도록 노력하고 있다.

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

SB-0003

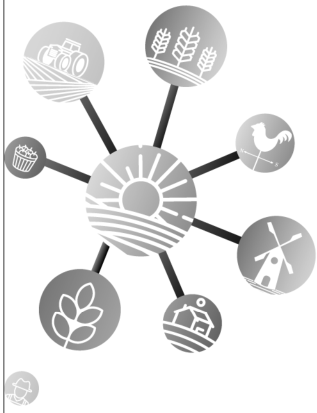
디지털육종 전환지원사업 개요 및 운영방향

정영민*

전라북도 김제시 씨앗길 232 농업기술실용화재단 종자산업진흥센터

4차산업혁명 기술은 육종에도 이미 적용이 시작되고 있으며, 향후 유전형, 표현형, 환경 등의 빅데이터와 인공지능을 활용하여 우수한 품종을 개발하는 디지털육종으로 발전할 것으로 기대된다. 이에 따라 국내 종자기업들도 디지털육종에 대한 많은 관심을 가지고 있으나 전문인력과 상당한 투자비용 등에 대한 부담으로 본격적인 활용에는 어려움을 겪는 것으로 나타났다. 농림축산식품부는 종자기업의 이러한 애로점을 해소하기 위해 「디지털육종 전환지원사업」을 2021년부터 2025년까지 추진하며, 농업기술실용화재단 종자산업진흥센터를 통해 시행하고 있다. 본 사업은 생물정보 컨설팅 및 맞춤형 분석 지원을 통해 종자기업의 신속한 디지털육종 체제 전환 촉진을 그 목표로 하고 있다. 현재 민간 컨설팅 및 분석 전문기관이 구성되어 있으며, 20개 이상의 종자기업이 사업에 참여하고 있다. 이와 함께, 디지털육종 활용을 촉진하기 위해 데이터서버 및 분석서비스 제공, 인력양성, 유관기관 연계 등을 수행하는 '디지털육종 활용플랫폼'이 종자산업진흥센터 내에 구축되고 있다. 이처럼 본 사업은 민간의 역량을 활용하는 디지털육종 컨설팅 및 분석지원과 공공의 플랫폼 구축을 통해 입체적으로 종자기업을 지원하도록 설계되어 있으며, 단기적으로는 종자기업의 기술 경쟁력을 강화하고, 장기적으로는 디지털육종 민간 생태계 구축에 기여하고자 한다.

***교신저자:** Tel. 063-219-8852, E-mail: ymjeong@efact.or.kr



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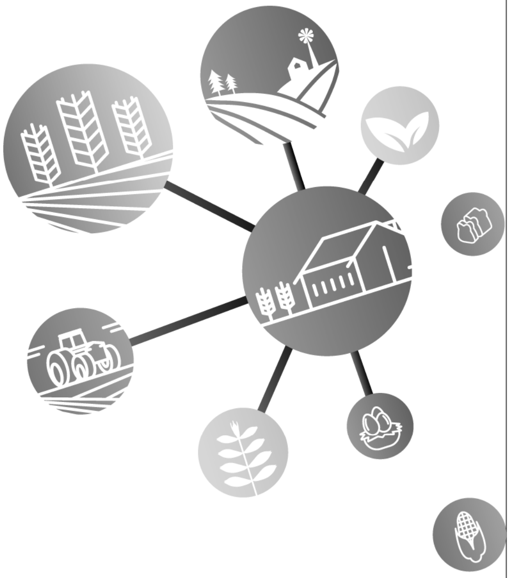

2021년 한국육종학회 학회상 시상
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○ 시상일 : 2021년 7월 1일(목)

○ 장 소 : 라마다프라자 제주호텔, 10시 30분~

○ 시상내용

1. 농우육종학회상 (11호)

수상자	최근진(국립종자원)
수상내용	국내 종자산업발전 및 한국 종자산업의 국제경쟁력 강화에 크게 기여하였으며 한국육종 분야 학문과 산업 발전을 위해 크게 공헌함
포상내용	상장 및 부상 500만원 (농우바이오)

2. 한국육종학회상 연구상 (35호)

수상자	김정선(국립농업과학원)
논문제목	배 '원황'(Pyrus pyrifolia) 유전체 해독에 기반한 SSR 마커 개발 및 유전자 지도 작성 (KJBS.2018.50.4.434)
포상내용	상장 및 부상 100만원 (한국육종학회)

3. 한국육종학회상 품종상 (31호)

수상자	장정희 (경기도농업기술원)
품종명	참드림(벼), 품종등록번호: 6065호
포상내용	상장 및 부상 100만원 (한국육종학회)

4. 코레곤품종상 (6호)

수상자	안경구 ((주)조은종묘)
품종명	월드콜(콜라비), 품종등록번호: 4527호
포상내용	상장 및 부상 200만원 (코레곤)

5. 월드그린시드피아 육종상 2020년

수상자	고희종(서울대학교)
수상내용	육종 분야의 인재양성, 우수한 품종개발, 육종기술 향상, 우수한 연구성과 등을 통해 한국육종 발전에 크게 기여하였으며 한국육종 분야 학문과 산업 발전을 위해 크게 공헌함
포상내용	상장 및 부상 1,500만원 (월드그린, 시드피아)

6. 월드그린시드피아 육종상 2021년

수상자	윤재복((주)고추와육종)
수상내용	고추 탄저병 저항성 품종 개발기술 확립을 통해 농가에 우수한 품종을 보급함으로써 종자산업 및 농업생산성 향상에 크게 기여하였으며 한국육종 분야 학문과 산업 발전을 위해 크게 공헌함
포상내용	상장 및 부상 1,500만원 (월드그린, 시드피아)

7. 월드그린시드피아 젊은육종가상 2020년

1) 수상자	현웅조(국립식량과학원)
수상내용	중부지방에 적합한 고품질의 벼 품종을 개발함으로써 농가소득증대 및 국산종자 보급에 크게 기여하였음
포상내용	상장 및 부상 500만원 (월드그린, 시드피아)

2) 수상자	박현승(서울대학교 식물유전체육종연구소)
수상내용	약용작물의 유전자분석법 확립 및 유전체 육종분야의 발전에 우수한 성과를 이루었음
포상내용	상장 및 부상 500만원 (월드그린, 시드피아)

8. 월드그린시드피아 젊은육종가상 2021년

1) 수상자	이종훈(조은종묘)
수상내용	양배추류의 유전체 연구를 기반으로 수출용 양배추류 품종 개발 등 종자 산업의 발전을 위해 우수한 성과를 이루었음
포상내용	상장 및 부상 500만원 (월드그린, 시드피아)

2) 수상자	함태호(건국대학교)
수상내용	육색미 품종육성을 통한 쌀 산업 고부가가치화에 기여하였고 벼 품종육성을 위한 다양한 연구에 우수한 성과를 이루었음
포상내용	상장 및 부상 500만원 (월드그린, 시드피아)

9. 우수논문상 다피인용부문

- 한국육종학회지 -

수상자	안억근(국립식량과학원)
논문제목	건식 쌀가루 전용 뽀얀메 ‘한가루’ (Korean J Breed Sci 2019;51(2):134-139)
포상내용	상장 및 부상 50만원 (한국육종학회)

- Plant Breeding & Biotechnology -

수상자	박수철(국립농업과학원)
논문제목	National Program for Developing Biotech Crops in Korea (Plant Breeding and Biotechnology 2018;6:171-176)
포상내용	상장 및 부상 50만원 (한국육종학회)

10. 우수논문상 다수논문게재부문

- 한국육종학회지 -

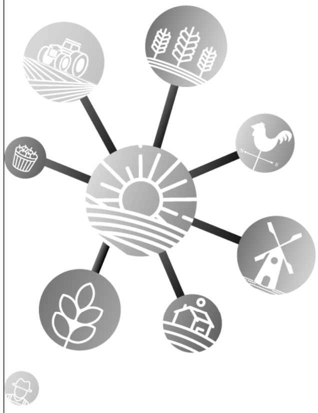
수상자	김동관(전라남도농업기술원)
포상내용	상장 및 부상 50만원 (한국육종학회)

- Plant Breeding & Biotechnology -

수상자	안상낙(충남대학교)
포상내용	상장 및 부상 50만원 (한국육종학회)

11. 한국육종학회 공로상

강시용 (공주대학교), 33대 한국육종학회장



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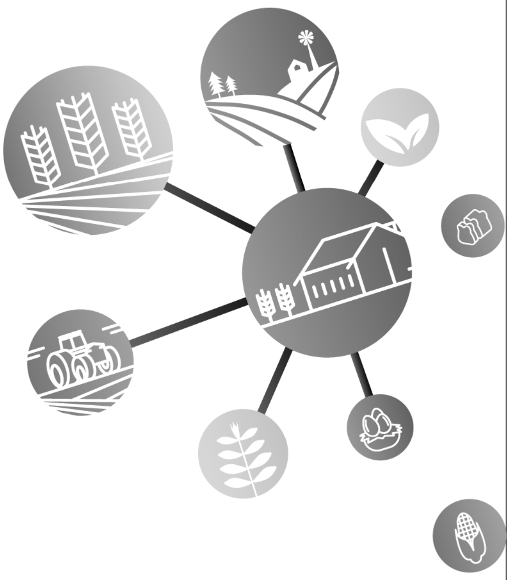

■ 영문 ■

한국육종학회
Korean Society of Breeding Science

인 쇄 2021년 6월 21일
발 행 2021년 6월 30일
발행자 **사단법인 한국육종학회**
경기도 수원시 권선구 수인로 126 국립식량과학원 중부작물부 내
인쇄처 교보문고 (02-3156-3642)