2022년 한국육종학회 공동학술발표회

지속가능 농업을 위한 5G 기반 스마트 육종 전략

Smart Breeding Strategy with 5Gs for Sustainable Agriculture

일 시 2022년 6월 29일(수) ~ 7월 1일(금) / 장 소 라마다프라자 제주 호텔

주 관 사단법인 한국육종학회
공동주관 차세대농작물신육종기술개발사업단, 서울대학교 식물유전체육종연구소 채소육종연구센터,
강원대학교 농업생명과학연구원, 국립식량과학원, 국립원예특작과학원
동아대학교 환경부 녹색 융합 기술 인재 양성 특성화 대학원
강원대학교 한방바이오연구소
후 관 한국농식품생명과학협회, 한국과학기술단체총연합회

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

사단법인 한국육종학회 The Korean Society of Breeding Science

2022년 한국육종학회 조직위원회

위 원 장	총괄	강병철(서울대학교)
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	공동	정영희(차세대농작물신육종기술개발사업단), 안병옥(국립농업과학원)
총괄총무	위원	정종욱(충북대학교)
기획분과	위원장	박향미(국립식량과학원)
	위원	권춘탁(경희대학교), 황태영(충북대학교), 이명희(국립식량과학원)
재무분과	위원장	이강섭(국립농업과학원)
	위원	조영일(농업기술실용화재단), 이종렬(국립농업과학원)
국제협력분과	위원장	김진백(한국원자력연구원)
	위원	김창수(충남대학교), 하보근(전남대학교), 권순재(한국원자력연구원)
홍보분과	위원장	강성택(단국대학교)
	위원	이성우(충남대학교), 김경도(명지대학교), 장철성(강원대학교)
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	위원	소은희(국립종자원), 정영민(농업기술실용화재단), 이제민(경북대학교)
산학협력분과	위원장	윤재복(㈜고추와 육종)
	위원	조유현(㈜시드피아), 정운화(㈜코레곤종묘), 조성환(㈜씨더스)
학술분과	위원장	심성철(세종대학교)
유전체분과	위원	김창수(충남대학교), 전태환(부산대학교)
분자육종분과	위원	조영득(한국원자력연구원), 하보근(전남대학교)
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특용, 산림육종분과	위원	심동환(충남대학교), 허윤찬(국립원예특작과학원)
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분자표지분과	위원	김혜란(강원대학교), 정기홍(경희대학교)
신진연구자	위원	김태성(한국방송통신대학), 유수철(한경대학교)

2022년 한국육종학회 임원

회장	이주경(강원대학교)		
차기회장	강병철(서울대학교)		
부회장	김기영(국립식량과학원 작물육종과), 이우문(국립원예특작과학원 원예작물부), 성순기(국립산림과학원 산림생명자원연구부), 박향미(국립식량과학원), 이강섭(국립농업과학원), 김진백(한국원자력연구원), 강성택(단국대학교), 이상직((주)농우바이오), 윤재복((주)고추와 육종), 심성철(세종대학교), 김기택(농업기술실용화재단), 김성길(전남대학교), 최익영(강원대학교), 하선화(경희대학교)		
KJBS 편집위원장	권순욱(부산대학교)	KJBS 편집위원	김재윤(공주대학교)
PBB 편집위원장	이주현(건국대학교)	PBB 편집위원	박순주(원광대학교)
감 사	이정동(경북대학교), 이준대(전북대학교)		
사무총장	정종욱(충북대학교)		

한국육종학회지 사무국

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

"이 학술지는 정부재원(과학기술진흥기금 및 복권기금)으로 한국과학기술단체총연합회의 지원을 받아 출판되었음."
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2022년 한국육종학회 공동학술발표회

지속가능 농업을 위한 5G 기반 스마트 육종 전략

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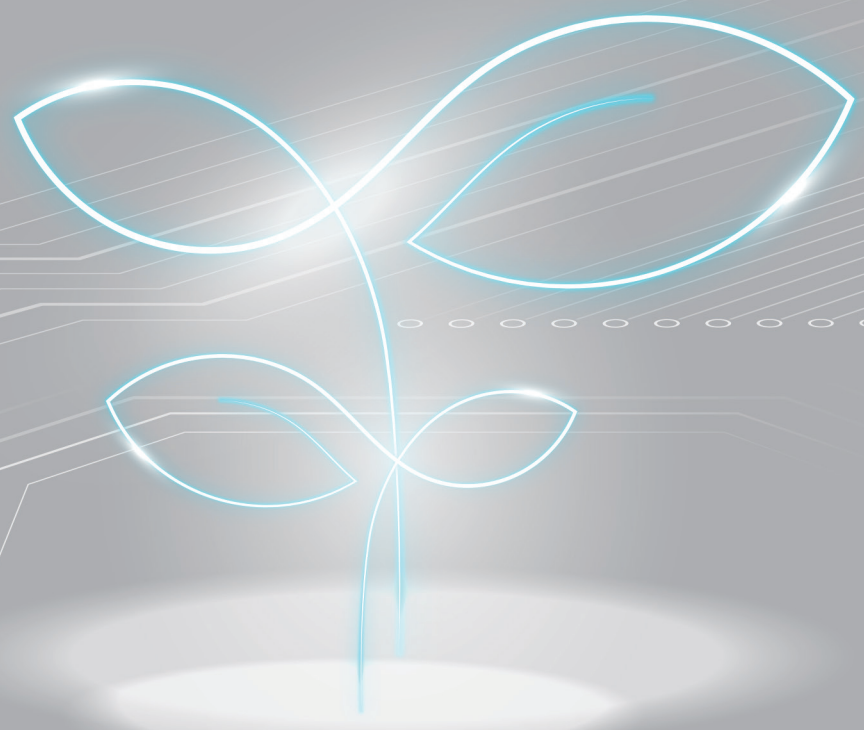

주 관 사단법인 한국육종학회
공동주관 차세대농작물신육종기술개발사업단, 서울대학교 식물유전체육종연구소 채소육종연구센터,
강원대학교 농업생명과학연구원, 국립식량과학원, 국립원예특작과학원
동아대학교 환경부 녹색 융합 기술 인재 양성 특성화 대학원
강원대학교 한방바이오연구소
후 관 한국농식품생명과학협회, 한국과학기술단체총연합회

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

[개 회 사]

(사)한국육종학회는 2022년 정기 학술대회를 6월 30일부터 7월 1일까지 제주시 라마다플라자 제주호텔에서 한국농식품생명과학협회와 한국과학기술단체총연합회 후원을 받아 차세대농작물신육종기술개발사업단, 서울대학교 식물유전체육종연구소, 강원대학교 농업과학연구원, 국립식량과학원, 국립원예특작과학원, 동아대학교 녹색융합기술인재양성 특성화대학원과 공동으로 개최하게 되었습니다.

이번 학술대회의 주제는 "지속가능 농업을 위한 5G 기반 스마트 육종 전략"입니다. 우리나라의 식량안보와 지속가능한 농업을 위해 미래육종기술의 핵심 요소인 5G(Germplasm, Genomics, Genes, Genomic Breeding, Gene Editing) 기술에 대한 우리의 현황을 진단하고, 향후 5G 기반 스마트 육종 전략에 대해 논의하는 장을 마련해 보고자 합니다. 이를 위해 Plenary Session에 6분의 국내외 연사, Concurrent Session 8개 분과에 35분의 연사를 초정하여 최신 연구결과를 듣고 논의하게 됩니다. 아울러 427건의 Poster 발표를 통해서도 학술교류가 이루어질 것입니다.

코로나로 인해 취해진 사회적 거리두기가 해제되어 학술대회를 예전처럼 대면으로 개최할 수 있게 된 것을 매우 기쁘게 생각하며, 학회회원님들의 극적인 참여와 열띤 토론을 통해 성공적인 학술대회가 되기를 기원합니다.

조직위원장 강병철 드림

[환 영 사]

안녕하세요? 한국육종학회장 이주경입니다.

금년 학술행사는 코로나19 팬데믹 종식 기대와 함께 정부의 사회적 거리두기 시책이 완화됨에 따라 예전과 같이 대면으로 개최하게 되어 매우 기쁘게 생각합니다. 2022년 한국육종학회 학술발표회는 "지속가능 농업을 위한 5G 기반 스마트 육종 전략"이라는 주제로 디지털 농업시대에 스마트 육종 전략과 식물 육종의 미래를 잘 설계하여 우리나라 육종 산업의 발전 방향을 찾아가는 계기를 마련해 보고자 합니다. 학술행사를 위해 Plenary Session과 Concurrent Session에서 발표하시는 41명의 국내 및 국외 연자 분들과 Poster Session에 발표 참석을 하시는 427명의 회원 분들께 감사드립니다.

학회 발전을 위해 물심양면 도와주신 회원님들과 공동주관 및 후원 기관에 감사드립니다. 금년도 학술대회 행사 및 프로그램 구성을 위해 많은 수고를 해주신 조직위원회 및 학술분과 위원님들, 그밖에 광고 협찬 및 기기 전시회에 참석해 주신 업체 관계자 분들께도 감사드립니다.

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

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

한국육종학회장 이주경 드림

2022년 한국육종학회 공동학술발표회 일정

6월 29일(수)		
17:00~18:00	확대이사회 및 조직위원회의	라마다볼룸 1

6월 30일(목)		
09:00~09:30	등록 및 포스터 부착	컨벤션 로비
09:30~10:30	**정기총회 & 한국육종학회 학회상 시상**	라마다볼룸
10:30~	개회식	
	기조발표 [Plenary Session] 1부	
	좌장: 강성택(단국대학교)	
10:30~11:10	PS-01 Lee Hickey (The University of Queensland, Australia) Designer Crops come of Age	
11:10~11:50	PS-02 Hitosh Ezura (University of Tsukuba, Japan) The world's first CRISPR tomato lunched to a Japanese market: The social-economic impact of its implementation on crop genome editing	
11:50~12:30	PS-03 양태진 (서울대학교 농업생명과학대학, 한국) Digital Breeding for Medicinal Plants	
12:30~13:00	PS-04 박용진 (공주대학교, 한국) Updates and Perspectives on 5Gs for Aromatic Rice Breeding in Korea	
13:00~14:00	중 식	
14:00~15:00	**포스터 발표 [Poster presentation] 1부(홀수)**	컨벤션 로비
	Company Session	라마다볼룸 1
14:00~14:20	㈜다온비에스 (김경아 본부장, 한국) Building Chromosomal Scale Haplotype-Resolved Assembly	
<온라인발표>	Illumina (Dr. Sukhjiwan Kaur, Agriculture Victoria Research, Australia) Development and Implementation of Genomic Selection in Pulse Crops	홈페이지 발표
14:50~15:00	휴식	
	분과발표 [Concurrent Session] 1부	
15:00~18:00	CS-A. Genome Sequence & Genomics	라마다볼룸 1
	CS-B. Molecular Breeding	라마다볼룸 2
	CS-C. Phenomics	라마다볼룸 3
	CS-D. New Breeding Technology	라마다볼룸 4

7월 1일(금)		
09:00~10:30	**포스터 발표 [Poster presentation] 2부(짝수)**	컨벤션로비
09:30~10:10	**기조발표 [Plenary Session] 2부**	라마다볼룸 1
	좌장: 심성철(세종대학교)	
	PS-05 윤재복(고추와 육종) Breeding and commercialization of anthracnose resistance in chili pepper	
<온라인발표>	PS-06 Amnon Levi (USDA, ARS, USA) Utilizing Genetic Resources and Genomic-Assisted Breeding for Improving Watermelon Cultivars	홈페이지 발표
	분과발표 [Concurrent Session] 2부	
10:30~13:00	CS-E. Breeding for Major Crops	라마다볼룸 1
	CS-F. Breeding for Horticultural Crops	라마다볼룸 2
	CS-G. Forest tree & Special Crops	라마다볼룸 3
	CS-H. Young Breeding Scientist	라마다볼룸 4
13:00~	**폐회식**	라마다볼룸 1

7월 4일(월)		
<온라인발표>	우수발표상 발표	홈페이지 공지

2022년 공동학술발표회 관련기관 발표

행사 진행방식에 따라 일정이 변경될 수 있습니다.

6월 30일(목)		
14:20~14:50	「디지털 육종 추진전략」 발표 (국립농업과학원)	라마다볼룸 1
13:40~14:30	저탄소 그린라이스 연구 협의회 (국립식량과학원)	오라홀(8층)

7월 1일(금)		
14:00~16:00	강원대학교 농업생명과학연구원 발표	라마다볼룸 2
13:00~17:00	한중대형산학협력과제 발표	라마다볼룸 3

2022년 한국육종학회 공동학술발표회 분과발표

행사 진행방식에 따라 일정이 변경될 수 있습니다.

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15:00~15:30	CA-01 강양제 교수(경상국립대학교) Genome of the world's smallest flowering plant, Wolffia australiana, helps explain its specialized physiology and unique morphology	
15:30~16:00	CA-02 심상래 교수(강원대학교) Web-based bioinformatic analysis application for regulatory mechanism of transcription in *Arabidopsis thaliana*	
16:00~16:30	CA-03 강유나 박사(충남대학교 농업과학연구소) Construction of genomic selection system using core collection in wheat	
16:30~17:00	CA-04 정근화 교수(메사츄세츠 주립대학교) From the field to the lab: unraveling the molecular mechanisms of field resistance to fungicides in dollar spot caused by *Sclerotinia homoeocarpa*	

	CS-B. Molecular Breeding	그랜드 볼룸 2
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15:00~15:30	CB-01 이종희 박사(국립식량과학원) Functional marker를 이용한 벼 분자육종 전략	
15:30~16:00	CB-02 이주석 박사(한국생명공학연구원) Investigation of Gene-Gene Interaction in Soybean	
16:00~16:30	CB-03 이제민 교수(경북대학교) Identifying hidden genetic determinants of carotenogenesis for improving fruit quality in tomato and pepper	
16:30~17:00	CB-04 한고은 박사(국립원예특작과학원) Assembly of chromosome-level genome to accelerate octoploid strawberry breeding	

	CS-C. Phenomics	그랜드 볼룸 3
	좌장: 김경환(국립농업과학원)	
15:00~15:30	CC-01 김도순 교수(서울대학교) 영상식물학 기반 디지털육종의 방향	
15:30~16:00	CC-02 유수철 교수(한경대학교) 이미지 기반 표현형 분석을 이용한 북한벼 집단의 출수기 및 종자형태 형질에 대한 GWAS 분석	
16:00~16:30	CC-03 백정호 박사(국립농업과학원 농업생명자원부) Exploring the various phenotypes of seeds and GWAS using images	
16:30~17:00	CC-04 이홍석 박사(국립식량과학원 남부작물부) 센서를 활용한 노지 밭작물 생육정보 진단 기술	

	CS-D. New Breeding Technology	그랜드 볼룸 4
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15:00~15:30	CD-01 정기홍 교수(경희대학교) Roles of ABC transporters for root and seed development in rice	
15:30~16:00	CD-02 김경민 교수(경북대학교) Future development of smartbreeding in response to ZERO HUNGER in rice	
16:00~16:30	CD-03 김민철 교수(경상대학교) Improvement of Soybean Nutritional Values by Using Genome Editing Technology	
16:30~17:00	CD-04 이옥란 교수(전남대학교) *In vivo* haploid induction system in dicotyledonous plant	

7월 1일(금)

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	CS-E. Breeding for Major Crops	그랜드 볼룸 1
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10:30~11:00	CE-01 조래현 교수(부산대학교) How do cytokinin and sucrose control flowering time in rice?	
11:00~11:30	CE-02 최창현 박사(국립식량과학원) Genotype study for heading date using GWAS and genomic selection in wheat core-set	
11:30~12:00	CE-03 현도윤 교수(농수산대학교) Genotyping-by-Sequencing Derived Single Nucleotide Polymorphisms Provide the First Well-Resolved Phylogeny for the Genus *Triticum* (Poaceae)	
12:00~12:30	CE-04 손재한 박사(국립식량과학원) Development of waterlogging tolerance corn variety using wild corn Teosinte	
12:30~13:00	CE-05 심규찬 박사(충남대학교) 벼 전분 합성 유전자 SBE3와 GBSS1의 상호작용에 의한 아밀로스 함량 증대 및 전분 이화학적 특성 변화	

	CS-F. Breeding for Horticultural Crops	그랜드 볼룸 2
		좌장: 채원병(단국대학교)
10:30~11:00	CF-01 이관욱 박사(국립원예특작과학원) 이상기상 대응 고추, 토마토 안정생산을 위한 고온 및 저온내성 품종개발	
11:00~11:30	CF-02 윤해근 교수(영남대학교) 포도 육종효율 증진을 위한 병저항성 관련 전사체 분석	
11:30~12:00	CF-03 김태성 교수(한국방송통신대학교) Implementation of *C. sticuspe* genome information to the cultivated K-Chrysanthemum breedings	
12:00~12:30	CF-04 강범창 교수(전북대학교) Plant Organelle DNA editing with Programmable Deaminases	
12:30~13:00	CF-05 반승현 박사(한국과학기술연구원 강릉분원 천연물 연구소) 사과 아조변이에서 발생한 retrotransposon 삽입과 deletion이 과실숙기 지연에 미친 영향	

	CS-G. Forest tree & Special Crops	그랜드 볼룸 3
	좌장: 심동환(충남대학교)	
10:30~11:00	CG-01 이이 교수(충북대학교) Applications of Molecular Breeding in Medicinal Crops and Future Prospects	
11:00~11:30	CG-02 박현승 교수(세종대학교) DNA super-barcoding for managing plant bioresource and breeding	
11:30~12:00	CG-03 강규석 교수(서울대학교) Comparative transcriptomic analysis of *Pinus densiflora* and *Pinus strobus* to find resistance candidate genes to Pine wood nematode (*Bursaphelenchus xylophilus*)	
12:00~12:30	CG-04 이경미 박사(국립산림과학원) Status and prospects of tree improvement research in industry 4.0 era	

	CS-H. Young Breeding Scientist	그랜드 볼룸 4
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10:30~11:00	CH-01 한고은 박사(국립원예특작과학원) Identification and application of genetic factors in pepper and strawberry breeding	
11:00~11:30	CH-02 김백기(서울대학교 식물유전체육종연구소) Mutation of light signal transduction machinery affects pericarp pigmentation and embryo development in rice grain	
11:30~12:00	CH-03 임유진 박사(경희대학교) Flavonoid metabolic changes regulated by UV lights in a soybean seedling model	
12:00~12:30	CH-04 함태호 박사(건국대학교) GWAS 분석을 통한 유묘기 및 출수기 내재해성 QTL 탐색	
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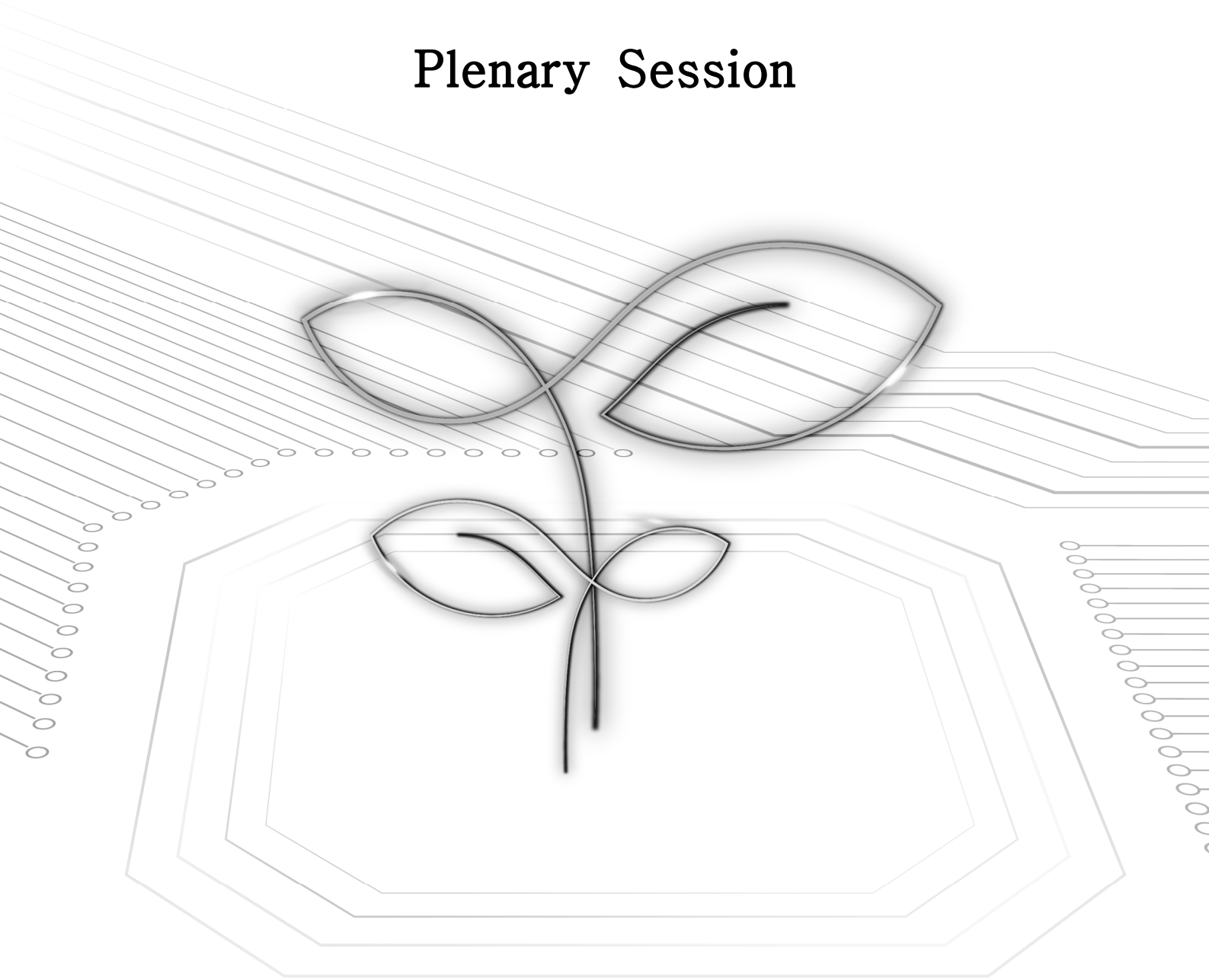

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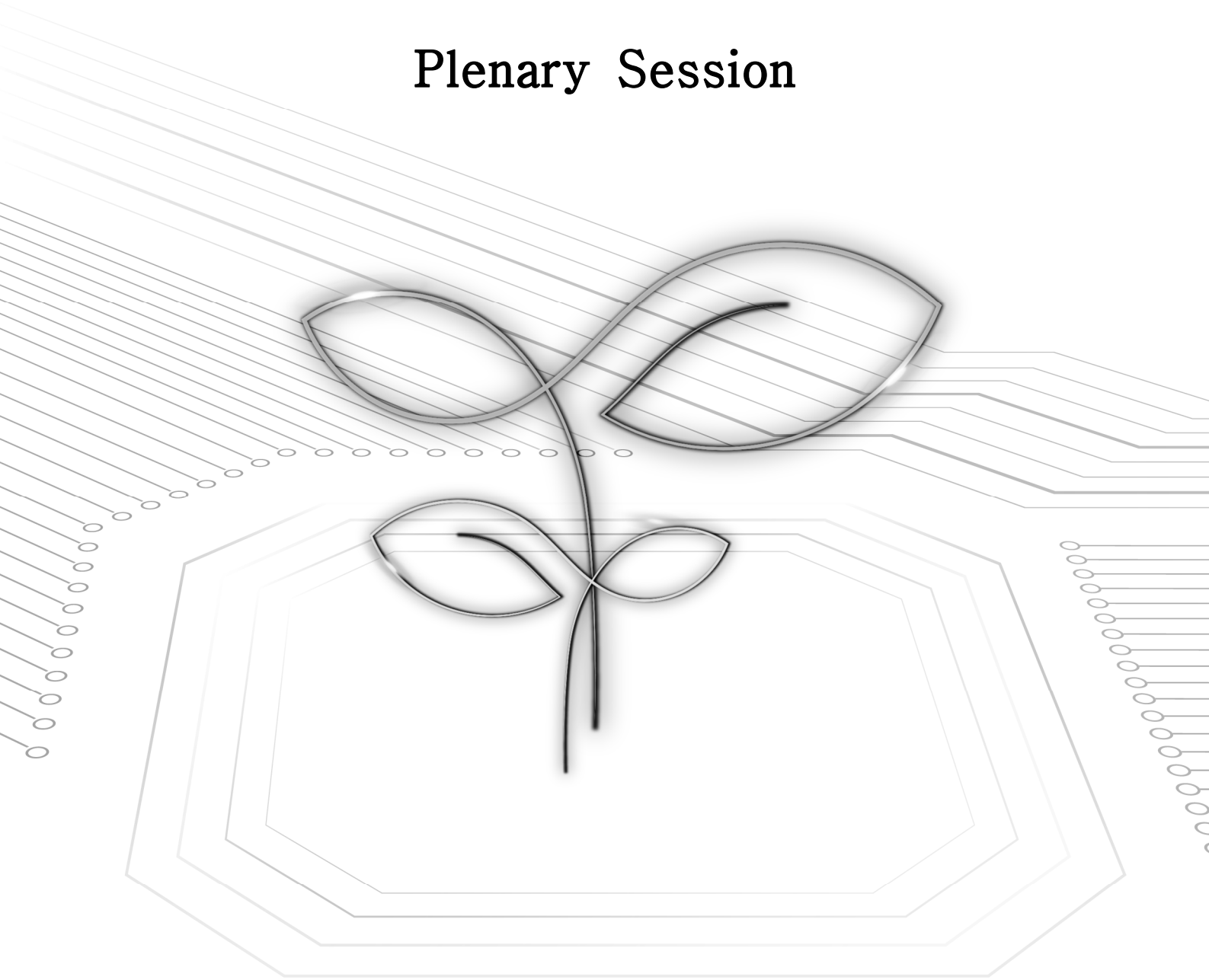

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<Selected Publications> (Up to 10)

1. PA Crisp*, P Bhatnagar-Mathur, P Hundleby, ID Godwin, PM Waterhouse, **LT Hickey***. 2021. Beyond the gene: epigenetic and cis-regulatory targets offer new breeding potential for the future. Current Opinion in Biotechnology 73, 88-94.
2. RK Varshney, A Bohra, M Roorkiwal, R Barmukh, W Cowling, A Chitikineni, H-M Lam, **LT Hickey**, J Croser, D Edwards, M Farooq, J Crossa, W Weckwerth, H Millar, A Kumar, MW Bevan, KHM Siddique. 2021. Rapid delivery systems for future food security. Nature Biotechnology, 1-3.
3. Massel K, I Godwin, **L Hickey***. 2021. Tunable crops are just a spray away. Nature Plants 7(2):102-103.
4. Massel K, Y Lam, ACS Wong, **LT Hickey**, AK Borrell, ID Godwin. 2021. Hotter, drier, CRISPR: the latest edit on climate change. Theoretical and Applied Genetics 1-19.
5. Bhatta M, Sandro P, Smith MR, Delaney O, Voss-Fels KP, Gutierrez L, **Hickey LT***. 2021. Need for speed: manipulating plant growth to accelerate breeding cycles. Current Opinion in Plant Biology 60, 101986.
6. **Hickey LT***, Hafeez A, Robinson H, Jackson SA, Leal-Bertioli SCM, Tester M, Gao C, Godwin ID, Hayes BJ, Wulff BBH*. 2019. Breeding crops to feed 10 billion. Nature Biotechnology 37:744-754.
7. Watson A, **Hickey L**, Christopher J, Rutkoski J, Poland J, Hayes B. 2019. Multivariate genomic selection and the potential of rapid indirect phenotypic selection with speed breeding to increase genetic gain in spring bread wheat. Crop Science 59:1945-1959.
8. Ghosh S, Watson A, Gonzalez-Navarro OE, Ramirez-Gonzalez RH, Yanes L, et al. Wulff BBH*, **Hickey LT***. 2018. Speed breeding in growth chambers and glasshouses for crop breeding and model plant research. Nature Protocols 13:2944-2963.
9. Li H, Rasheed A, **Hickey LT**, He Z. 2018. Fast-forwarding genetic gain. Trends in Plant Science. 23:184-186.
10. Watson A, Ghosh S, Edwards D, Batley J, Raman H, Carter J, Rogers C, et al. Wulff BBH*, **Hickey LT***. 2018. Speed breeding is a powerful tool to accelerate crop research and breeding. Nature Plants (4) 23-29.

PS-0001

Designer crops come of age

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Plant scientists are in a race against time to adapt modern crops to future environments, many of which are predicted to be hotter and drier. The concept of 'designer crops' that are equipped with optimal trait combinations for adaptation is not new. In theory, this approach could help guide the plant breeding process. Progress has been limited by our understanding of the key genes and pathways in crops with large and complex genomes, and generally a poor understanding of the value of different physiological traits in specific environments. However, knowledge is expanding and converging with technologies that create new opportunities. Here, we highlight recent breakthroughs to modulate important traits in cereal crops wheat and barley, using a range of cutting-edge technologies. Firstly, we demonstrate how diverse gene bank collections can be efficiently mined for novel allelic variation by combining high-throughput phenotyping, genotyping, epigenome profiling and artificial intelligence computing. Secondly, we demonstrate how novel alleles can be rapidly introgressed into elite crop varieties to diversify adaptive traits for a range of environments. Finally, we highlight how genome editing can be used to engineer crops with novel variation for architectural traits by exploiting learnings from basic plant research on model species, such as Arabidopsis and Medicago. Overall, the outcomes showcase the importance of fundamental plant research and how it can be translated for crop improvement in an integrated framework with a multidisciplinary team.

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2. MSc, University of Tsukuba, Microbiology (1984)
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<Selected Publications> (Up to 10)

1. Takayama M, Koike S, Kusano M, Matsukura C, Saito K, Ariizumi T, Ezura H. (2015) Tomato glutamate decarboxylase genes SlGAD2 and SlGAD3 play key roles in regulation of γ-aminobutyric acid level in tomato (*Solanum lycopersicum*). ***Plant and Cell Physiology***. 56(8): 1533-1545.
2. Takayama M, Matsukura C, Ariizumi T, Ezura H. (2017) Activating glutamate decarboxylase activity by removing the autoinhibitory domain leads to hyper γ-aminobutyric acid (GABA) accumulation in tomato fruit. ***Plant Cell Reports***. 36: 103-116.
3. Shimatani Z, Kashojiya S, Takayama M, Terada R, Arazoe T, Ishii H, Teramura H, Yamamoto T, Komatsu H, Miura K, Ezura H, Nishida K, Ariizumi T, Kondo A. (2017) Targeted base editing in rice and tomato using a CRISPR-Cas9 cytidine deaminase fusion. ***Nature Biotechnology***. 35(5):441-443.
4. Nonaka S, Arai C, Takayama M, Matsukura C, Ezura H. (2017) Efficient increase of ɣ-aminobutyric acid (GABA) content in tomato fruits by targeted mutagenesis. ***Scientific Reports***. 7(1):7057.
5. Shinozaki Y, Bertrand BP, Takahara M , Hao S , Ezura K , Andrieu MH, Nishida K, Mori K, Suzuki Y, Kuhara S, Enomoto H, Kusano M, Fukushima A, Mori T, Kojima M, Kobayshi M, Sakakibara H, Saito K, Ohtani Y , Bénard C, Prodhomme D, Gibon Y, Ezura H, Ariizumi T (2020) Fruit setting rewires central metabolism via gibberellin cascades. ***Proceedings of National Academy of Sciences, USA*** 117(38):23970-23981.
6. Hanziker J, Nishida K, Kondo A, Kishimoto S, Ariizumi T, Ezura H. (2020) Multiple gene substitution by Target-AID base-editing technology in tomato. ***Scientific Reports***. 10(1):20471.
7. Kawaguchi K, Takei-Hoshi R, Yoshikawa I, Nishida K, Kobayashi M, Kusano M, Lu Y, Ariizumi T, Ezura H, Otagaki S, Matsumoto S, Shiratake K (2021) Functional disruption of cell wall invertase inhibitor by genome editing increases sugar content of tomato fruit without decrease fruit weight. ***Scientific Reports***. 11(1):21534.
8. Nagamine A, Ezura H (2022) Genome editing for improving crop nutrition. ***Frontiers in Genome Editing***. 4:850104.

PS-0002

The world's first CRISPR tomato lunched to a Japanese market: The social-economic impact of its implementation on crop genome editing

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CRISPR/Cas9 (clustered regularly interspaced short palindromic repeats / CRISPR associated proteins 9) technology was awarded the Nobel Prize eight years after its initial publication, which represents unprecedented speed. Genome editing (GE) is featured as a technology for rapid plant breeding, and CRISPR/Cas9 technology is attracting attention due to its convenience and editing efficiency. On December 11, 2020, notification was given to the Japanese government of the first GE tomato containing a high level of GABA (γ-aminobutyric acid), which is well known for its human health-promoting benefits, developed using this technology. By May 12, 2021, a venture company launched from University of Tsukuba, Sanatech Seed Co. Ltd., had begun providing seedlings to 4,200 home gardeners free of charge to monitor cultivation. Subsequently, on September 15, 2021, online sales of GE tomato fruits began. This was the first agricultural product in the world to be launched using CRISPR/Cas9 technology. Here, I provide background into how this new development occurred, and how it prompted other governments around the world to re-evaluate GE technology for practical application.

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3. 미국 클림슨대학교, 아리조나대학교 연구원 (2000-2003)

<Selected Publications> (Up to 10)

1. Xu J, Yang TJ, Hu HY. (저서) 2021. The Ginseng Genome. Springer, Cham. 978-3-030-30346-4
2. Lee SH, Kim J, Park HS, Koo HJ, Waminal NE, Pellerin RJ, Shim H, Lee HO, Kim E, Park JY, Yu HS, Kim HH, Lee J, and Yang TJ 2022. Genome structure and diversity among *Cynanchum wilfordii* accessions. BMC Plant Biology 22:4.
3. Park HS, Jayakodi M, Lee SH, Jeon JH, Lee HO, Park JY, Moon BC, Kim CK, Wing RA, Newmaster SG, Kim JY, Yang TJ. Mitochondrial plastid DNA can cause DNA barcoding paradox in plants. *Sci Rep* 10, 6112 (2020). https://doi.org/10.1038/s41598-020-63233-y
4. Kim NH, Jayakodi M, Lee SC, Choi BS, Jang W, Lee J, Kim HH, Waminal NE, Lakshmanan M, Nguyen BV, Lee YS, Park HS, Koo HJ, Park JY, Perumal S, Joh HJ, Lee H, Kim J, Kim IS, Kim K, Koduru L, Kang KB, Sung SH. Yu Y, Park DS, Choi D, Seo E, Kim S, Kim YC, Hyun DY, Park YI, Kim C, Lee TH, Kim HU, Soh MS, Lee Y, In JG, Kim HS, Kim YM, Yang, DC, Wing RA, Lee DY, Paterson AH and Yang TJ. 2018. Genome and evolution of the shade-requiring medicinal herb Panax ginseng. Plant Biotechnol. J. 16: 1904-1917, doi: https://doi.org/10.1111/pbi.12926
5. Nguyen Van Binh, Vo Ngoc Linh Giang, Nomar Espinosa Waminal, Park HS, Kim NH, Jang WJ, Lee J, Yang TJ. 2020. Comprehensive comparative analysis of chloroplast genomes from seven Panax species and development of an authentication system based on species-unique SNP markers. Journal of Ginseng Research. 44: 135-144.

PS-0003

Digital Breeding of Medicinal Plants

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Digital breeding supported by high-throughput genome data may open a new era for precise and rapid breeding-by-design for main crops. Meanwhile, breeding for medicinal plants are in its primary phase even for conventional breeding as well as molecular breeding. Our lab tried to establish molecular digital breeding systems for ginseng (인삼), *Peucedanum japonicum* (식방풍), and *Cynanchum wilfordii* (백수오). We published one reference genome sequence for ginseng in 2018 and conducted further research for building chromosome level pseudomolecule sequences for *Panax ginseng*, *P. vietnamensis*, and *Aralia cordata* utilizing cutting-edge sequencing technologies such as Oxford Nanopore, PacBio, Illumina, and Hi-C data and validating based on chromosome level Oligo-FISH analyses. We also established digital genotyping platforms using Fluidigm SNP chips which are applied for molecular breeding of ginseng as well as mountain ginseng. Moreover, in-depth phylogenetic reconstructions and super-barcoding were conducted for diverse plant species in the family Araliaceae. We also collected wild resources and developed hundreds of breeding accessions for *Peucedanum japonicum* (식방풍) and *Cynanchum wilfordii* (백수오). For these medicinal plants, we perform convergence research combining genomics and metabolomics in collaboration with Pharmaceutical research groups. We developed complete genome sequences representing telomere-to-telomere structures for three *Cynanchum* species. Tens of plastid genomes were obtained using different collections, and high-throughput DNA markers were developed for molecular breeding of these medicinal plants. Super-barcoding is also an efficient tool for the authentication of medicinal plants that are not yet fully domesticated. We sequenced and assembled simultaneously plastid genomes and nuclear ribosomal genes from thousands of wild plant resources. Through comparative analyses, we developed high-throughput species-specific barcoding technology for authenticating at the species level in *Cynanchum*, *Ligularia*, *Allium*, *Rubus*, *Panax*, *Artemisia* species, and *Cannabis sativa*.

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2. Digital & Precise Breeding for Aromatic Rice
3. Sub-species Specific Genes for Improving Tongil-type Varieies in Rice

<Education>

1. Ph.D. in Crop Genetics & Breeding, Seoul National University (1997)
2. M.S. in Crop Genetics & Breeding, Seoul National University (1989)
3. B.S. in Crop Science, Seoul National University (1987)

<Professional Experience>

1. Professor, Department of Plant Resources, Kongju National University (2009-)
2. Professor, Department of Molecular Biotechnology, Konkuk University (2008)
3. Senior Scientist/Project Leader, Researches on Core Collection, Molecular Markers and Allele Mining, National Institute of Agricultural Biotechnology, RDA (2004-2008)
4. Visiting Scientist, Prof Buckler' Lab, Researches on Association Analysis using Rice Germplasm, Cornell University, USA (2007)
5. Visiting Scientist, Researches on Comparative Genomics of Grasses at Sequence Level, Dept. of Biological Science, Purdue University, USA (2000-2002)

<Selected Publications> (Up to 10)

1. Phitaktansakul, R., Kim, K. W., Aung, K. M., Maung, T. Z., Min, M. H., Somsri, A., ... & Park, Y. J. (2021). Multi-omics analysis reveals the genetic basis of rice fragrance mediated by betaine aldehyde dehydrogenase 2. *Journal of Advanced Research*.
2. Min, M. H., Maung, T. Z., Cao, Y., Phitaktansakul, R., Lee, G. S., Chu, S. H., ... & Park, Y. J. (2021). Haplotype analysis of BADH1 by next-generation sequencing reveals association with salt tolerance in rice during domestication. *International Journal of Molecular Sciences*, *22*(14), 7578.
3. Maung, T. Z., Yoo, J. M., Chu, S. H., Kim, K. W., Chung, I. M., & Park, Y. J. (2021). Haplotype Variations and Evolutionary Analysis of the Granule-Bound Starch Synthase 1 (GBSSI) Gene in Korean World Collection (KRICE_CORE). *Frontiers in Plant Science*, 1708.
4. Maung, T. Z., Chu, S. H., & Park, Y. J. (2021). Functional Haplotypes and Evolutionary Insight into the Granule-Bound Starch Synthase II (GBSSII) Gene in Korean Rice Accessions (KRICE_CORE). *Foods*, *10*(10), 2359.
5. Lee, S. B., Kim, G. J., Kim, K. W., Chu, S. H., Shin, J. D., Lee, Y. J., ...Park, Y. J. & Park, S. W. (2019). Functional Haplotype and eQTL Analyses of Genes Affecting Cadmium Content in Cultivated Rice. *Rice*, *12*(1), 1-17.
6. Cheng, L., Nam, J., Chu, S. H., Rungnapa, P., Min, M. H., Cao, Y., ... & Park, Y. J. (2019). Signatures of differential selection in chloroplast genome between japonica and indica. *Rice*, *12*(1), 1-13.
7. Cheng, L., Kim, K. W., & Park, Y. J. (2019). Evidence for selection events during domestication by extensive mitochondrial genome analysis between japonica and indica in cultivated rice. *Scientific Reports*, *9*(1), 1-9.
8. Yu, J., Zhao, W., Tong, W., He, Q., Yoon, M. Y., Li, F. P., ... & Park, Y. J. (2018). A Genome-wide association study reveals candidate genes related to salt tolerance in rice (Oryza sativa) at the germination stage. *International Journal of Molecular Sciences*, *19*(10), 3145.
9. Tong, W., He, Q., & Park, Y. J. (2017). Genetic variation architecture of mitochondrial genome reveals the differentiation in Korean landrace and weedy rice. *Scientific Reports*, *7*(1), 1-10.
10. He, Q., Kim, K. W., & Park, Y. J. (2017). Population genomics identifies the origin and signatures of selection of Korean weedy rice. *Plant Biotechnology Journal*, *15*(3), 357-366.

PS-0004

Updates and Perspectives on 5Gs for Aromatic Rice Breeding in Korea

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The 5Gs breeding includes Genome assembly (1G), Germplasm characterization (2G), Gene function identification (3G), Genomic breeding (4G), and Gene editing (5G). Here, we are introducing the case studies and the related activities on 5Gs for aromatic rice breeding in Korea. The fragrance is an important, economic, and quality trait in rice. Fragrance in rice is controlled by the *betaine aldehyde dehydrogenase 2* (*BADH2*) through the production of 2-acetyl-1-pyrroline (2AP). We used a core set of 475 Korean rice accessions for the whole genome resequencing together with a series of analyses, such as transcriptomics and metabolomics. We found a total of 38 haplotypes, of which four novel functional haplotypes were identified, including one detected in cultivated rice and three in the wild rice accessions. Fragrance classification by 2AP content distinguished functional haplotypes with their different fragrance intensities. 3D protein modeling of novel haplotypes revealed the mutation effect on fragrance. The homozygous progeny of CRISPR/Cas9 derived edited lines produced fragrance with the stable inheritance of various agronomic and biochemical traits. These findings have provided new breeding systems of FB (Forward Breeding), HBB (Haplotype-Based Breeding), and MABC (Marker-Assisted Back Crossing) in our aromatic rice breeding program. Based on the 5Gs breeding of aromatic rice, we are developing new Tongil-type rice varieties by improving HPPDI (*4-Hydroxy Phenyl Pyruvate Dioxygenase* Inhibitor) herbicide resistance and eating quality using the fine haplotype information of GBSSI (*Granule-Bounded Starch Synthease I*) gene now. These valuable 5Gs breeding platforms may provide many efficiencies for future aromatic rice breeding in Korea.

Keywords: Rice, 5Gs Breeding, Fragrance, Haplotype Breeding, HPPDI herbicide, GBSSI

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<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.

PS-0005

Breeding and commercialization of anthracnose resistance in chili pepper

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Pepper (*Capsicum* spp.) anthracnose caused by *Colletotrichum* spp. is one of the serious problems in many Asian countries. To reduce the damage of the disease, we have developed and released the commercial F_1 variety, resistant to anthracnose in Korea. From the genetic resources to commercial variety, we have conducted the 4 consecutive research steps as follows: 1) searching for genetic resources, 2) interspecific hybridization between *Capsicum annuum* and *C. baccatum*, 3) developing molecular markers and 4) using male sterility system for F_1 seed production. As the genetic resources resistant to anthracnose, several accessions belonging to *C. baccatum* were selected but there were double genetic barriers such as embryo abortion and hybrid sterility in interspecific cross between *C. annuum* and *C. baccatum*. To overcome the genetic barriers, partial compatible *C. annuum* line and embryo rescue techniques were used. The hybrid sterility was overcome through intensive backcrosses with their maternal line used as pollen parent. From the segregating populations including BC_1F_1 and BC_1F_2 generations, molecular markers associated with anthracnose resistance were successfully developed by using QTL mapping. The commertial F1 variety, 'AR Tanjeobaksa' was developed by crossing between the '8047', resistant to CMV and having good traits and the '42-13-3', resistant to anthracnose and Phytophthora root rot developed by using interspecific backcrosses.

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<Selected Publications> (Up to 10)

1. Bidisha Chanda, Shan Wu, Zhangjun Fei, Kai-Shu Ling & Amnon Levi. 2022. Elevated expression of ribosome-inactivating protein (RIP) genes in potyvirus-resistant watermelon in response to viral infection. Canadian Journal of Plant Pathology. https://www.tandfonline.com/doi/full/10.1080/07060661.2021.2021450
2. Sorokina, M., Mccaffrey, K.S., Ordovas, J.M., Deaton, E.E., Ma, G., Perkins-Veazie, P.M., Steinbeck, C., Levi, A., Parnell, L.D. 2021. A catalog of natural products occurring in watermelon - *Citrullus lanatus*. Frontiers in Nutrition. 8:602. https://doi.org/10.3389/fnut.2021.729822.
3. Branham, S., Wechter, W.P., Ling, K., Chanda, B., Massey, L.M., Zhao, G., Guner, N., Bello, M., Kabelka, E., Fei, Z., Levi, A. 2019. QTL mapping of resistance to Fusarium oxysporum f. sp. niveum race 2 and Papaya ringspot virus in *Citrullus amarus*. Theoretical and Applied Genetics. 133:677-687.
4. Wu, S., Wang, X., Reddy, U., Sun, H., Bao, K., Patel, T., Oritz, C., Abburi, L., Nimmakayala, P., Branham, S., Wechter, W.P., Massey, L.M., Ling, K., Kousik, C.S., Hammar, S.A., Tadmor, Y., Portnoy, V., Gur, A., Katzir, N., Guner, N., Davis, A., Hernandez, A.G., Wright, C.L., McGregor, C., Jarret, R.L., Xu, Y., Zhang, X., Wehner, T.C., Grumet, R., Levi, A*., Fei, Z* (*Corresponding authors). 2019. Genome of 'Charleston Gray', the principal American watermelon cultivar, and genetic characterization of 1,365 accessions in the U.S. National Plant Germplasm System watermelon collection. Plant Biotechnology Journal. https://doi.org/10.1111/pbi.13136
5. Guo, S., Zhao, S., Sun, H., Wang, X., Wu, S., Lin, T., Ren, Y., Deng, Y., Zhang, J., Lu, X., Zhang, H., Shang, J., Gong, G., Wen, C., He, N., Li, M., Liu, J., Wang, Y., Zhu, Y., Tian, S., Jarret, R.L., Levi, A., Huang, S., Fei, Z., Liu, W., Xu, Y. 2019. Resequencing of 414 cultivated and wild watermelon accessions identifies selection for fruit quality traits. Nature Genetics. 51:1616-1623. https://doi.org/10.1038/s41588-019-0518-4
6. Branham, S., Wechter, W.P., Lambel, S., Massey, L.M., Ma, M., Fauve, J., Farnham, M.W., Levi, A. 2018. QTL-seq and marker development for resistance to *Fusarium oxysporum* f. sp. *niveum* race 1 in cultivated watermelon. Molecular Breeding. 38:139.
7. Oren, E., Tzuri, G., Vexler, L., Dafna, A., Meir, A., Faigenboim, A., Kenigswald, M., Portnoy, V., Schaffer, A.A., Levi, A., Buckler Iv, E.S., Katzir, N., Burger, J., Tadmor, Y., Gur, A. 2019. The multi-allelic APRR2 Gene is associated with fruit pigment accumulation in melon and watermelon. Journal of Experimental Botany. https://doi.org/10.1093/jxb/erz182.
8. Branham, S.E., A. Levi, M.W. Farnham, W.P. Wechter. 2016. A GBS-SNP based linkage map and quantitative trait loci (QTL) associated with resistance to *Fusarium oxysporum* f. sp. *niveum* race 2 identified in *Citrullus lanatus* var. *citroides*. Theor. Appl. Genet. 130:319-330.
9. Levi, A., J.A. Thies, W.P. Wechter, M.W. Farnham, Y. Weng, and R. Hassel. 2013. USVL-360, a novel watermelon tetraploid germplasm line. HortScience 49:354-357.
10. Lambel, S., B. Lanini, and E. Vivoda, J. Fauve, W.P. Wechter, K.R. Harris-Shultz, L. Massey, and A. Levi. 2014. A major QTL associated with *Fusarium oxysporum* race 1 resistance identified in genetic populations derived from closely related watermelon lines using selective genotyping and genotyping-by-sequencing for SNP discovery. Theor. Appl. Genet. 127:2105-2115.

PS-0006

Utilizing Genetic Resources and Genomic-Assisted Breeding for Improving Watermelon Cultivars

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Watermelon accounts for 2% of the area devoted to vegetable production throughout the world. Many sweet watermelon cultivars share a narrow genetic base due to many years of cultivation and selection for desirable fruit quality associated with selection for fruits having high sugar levels and the bright red carotenoid lycopene. Consequently, watermelon cultivars are highly susceptible to a wide range of disease, including soilborne diseases like Fusarium wilt and Gummy stem blight, Foliage diseases like Powdery mildew, and potyviruses like Zucchini yellow mosaic virus (ZYMV), Papaya ringspot virus (PRSV), and Squash vein yellowing virus (SqVYV) that causes "Sudden Vine Decline" which resulted in tremendous losses to the watermelon industry in Florida. There is an ongoing need to improve watermelon varieties for resistance to a wide range of disease and pests. Our studies indicate that there might be limited sources of resistance to economically important diseases within the *Citrullus lanatus* which gave rise to the sweet dessert watermelon. On the other hand, the sister species *Citrullus amarus* ("citron watermelon" endemic to southern Africa) or *Citrullus colocynthis* ("desert watermelon" that exists in the deserts of Northern Africa, the Middle East and Asia) have a reservoir of resistance alleles that can be exploited to improve watermelon cultivars. Our research efforts focus on exploiting the germplasm resources collected and developed over the years at the USDA-ARS (https://www.ars-grin.gov/Pages/Collections). Our research team at the U.S. Vegetable Laboratory (Charleston, SC) has been conducting genetic and genomic studies to identify gene loci conferring resistance to major disease and pests and utilize them in breeding programs employing marker assisted selection (MAS) and/or genomic selection (GS) to improve resistance in watermelon cultivars.

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Concurrent Session

CA-0001

Genome of the world's smallest flowering plant, Wolffia australiana, helps explain its specialized physiology and unique morphology

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Watermeal, *Wolffia australiana*, is the smallest known flowering monocot that is rich in protein. Despite its great potential as a biotech crop, basic research on *Wolffia* is in its infancy and a high-quality genome assembly does not yet exist. Here, we generated the reference genome of a species of watermeal, *W. australiana*, and identified the genome-wide features that may contribute to its atypical anatomy and physiology, including the absence of roots, adaxial stomata development, and anaerobic life as a turion. In addition, we found evidence of extensive genome rearrangements that may underpin the specialized aquatic lifestyle of watermeal. Analysis of the gene inventory of this intriguing species helps explain the distinct characteristics of *W. australiana* and its unique evolutionary trajectory.

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CA-0002

Web-based bioinformatic analysis application for regulatory mechanism of transcription in *Arabidopsis thaliana*

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Understanding comprehensive regulatory mechanism of gene transcription is essential to explain biological phenomena of interest. Transcription is precisely regulated through multilayered genetic and epigenetic control. During last two decades, high-throughput sequencing (HTS) technology has been rapidly developed. One of its derivative methodologies, chromatin immunoprecipitation followed by sequencing (ChIP-seq) and DNA affinity purification followed by sequencing (DAP-seq) enabled genome-wide landscape of DNA-binding profiles of proteins and histones, which describe gene expression control. Although the massive volumes of ChIP-seq and DAP-seq data has been generated and deposited in public database, it is hard to retrieve genome-wide DNA-binding profiles without in-depth expertise in bioinformatics and computation. Here, we presented a web-based and easy-to-use bioinformatic analysis application, iRegNet, which analyzes integrative upstream regulatory network of user-submitted gene(s) of interest (GOI(s)) and/or region(s) of interest (ROI(s)) of *Arabidopsis*. iRegNet covers the largest genome-wide DNA-binding profiles of TFs and non-TF proteins, and histone modifications, which has been determined from thousands of ChIP-seq and DAP-seq libraries in *Arabidopsis*. iRegNet not only summarizes all upstream regulators and epigenetic landscapes for single query GOI or ROI, but also recommends significantly enriched upstream regulomes and chromatin states for multiple queries. Furthermore, integrations of coexpression network from ATTED-II and PPIs from BioGRID provide additional extensive evidences for the iRegNet analysis. iRegNet will help investigate upstream regulatory network for those unfamiliar with bioinformatics analysis. iRegNet service is freely available at http://chromatindynamics.snu.ac.kr:8082/iRegNet_main.

Key words: gene regulatory network, DNA-binding profile, histone modification, transcription factor, web application

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CA-0003

Construction of genomic selection system using core collection in wheat

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The continued growth of the world's population requires greater food demand. Genetic gain has increased through modern breeding techniques to meet growing food demands. Among them, genomic selection is useful for breeding by rapidly selecting superior genotypes and reducing the breeding cycles. Genome selection is a method of predicting an individual's genomic estimated breeding value by simultaneously integrating all available marker information into a model. In this study, we tried to find a suitable model by comparing genomic selection models for various agricultural traits within the wheat core collection. In addition, we constructed a set of various training populations to compare the prediction accuracy. Differences in prediction accuracy were identified depending on the size or composition of the training population. When using a genetically diverse core collection, prediction accuracy increased when using genetically similar individuals as the training population. However, since there is currently no reference group other than the core collection, more genetic composition will need to be established for continuous genomic selection, and a higher quality phenotype is required.

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CA-0004

From the field to the lab: unraveling the molecular mechanisms of field resistance to fungicides in dollar spot caused by *Sclerotinia homoeocarpa*

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Dollar spot, caused by Sclerotinia homoeocarpa, is a prevalent turfgrass disease, and the fungus exhibits widespread fungicide resistance in North America. We investigated genetic factors that govern the reduced DMI sensitivity of *S. homoeocarpa* field isolates collected during a 2-year field efficacy study on dollar spot disease of turf in five New England sites. These isolates displayed a >50-fold range of *in vitro* sensitivity to a sterol demethylation inhibitor (DMI) fungicide, propiconazole, making them ideal for investigations of genetic mechanisms of reduced DMI sensitivity. First, the *CYP51* gene homolog in *S. homoeocarpa* (*ShCYP51B*), encoding the enzyme target of DMIs, is likely a minor genetic factor for reduced propiconazole sensitivity, since there were no differences in constitutive relative expression (RE) values and only 2-fold-higher induced RE values for insensitive than for sensitive isolate groups. Following next-generation RNA sequencing (RNA-seq) analyses of *S. homoeocarpa*, a multidrug resistant (MDR) field strain was found to overexpress phase I and III genes, coding for CYP450s and ABC transporters for xenobiotic detoxification. Furthermore, there was confirmation of a gain-of-function mutation of the fungus-specific transcription factor *S. homoeocarpa* XDR1 (ShXDR1), which is responsible for constitutive and induced overexpression of the phase I and III genes, resulting in resistance to multiple classes of fungicidal chemicals. This fungal pathogen detoxifies xenobiotics through coordinated transcriptional control of CYP450s, biotransforming xenobiotics with different substrate specificities and ABC transporters, excreting a broad spectrum of xenobiotics or biotransformed metabolites. This study establishes a novel molecular mechanism of MDR through the xenobiotic detoxification pathway in filamentous fungi, which may facilitate the discovery of new antifungal drugs to control pathogenic fungi.

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CB-0001

Functional marker를 이용한 벼 분자육종 전략

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지난 20년 동안 벼의 기능유전체학(functional genomics)의 급속한 발전으로 쌀의 품질, 병해충 저항성, 생리장해 견딜성, 양분이용효율증진 및 수량성 등 농업적으로 유용한 형질을 제어하는 다양한 유전자들의 기능이 밝혀졌다. 미래의 벼 육종은 생물검정 중심의 전통육종에서 벗어나 인공지능 기반의 유전체선발(genomic selection)수준까지 발전할 것으로 예측되고 있다. 반면, 국내의 벼 육종 연구는 아직도 전통육종을 중심으로 품종이 개발되고 있으며, 1-2개의 분자마커를 이용한 MAS(marker assisted selection)을 병행하는 수준에 머물러 있다. 현재 까지 연구된 기능유전체연구 결과를 효율적으로 벼 신품종개발에 적극적으로 활용하기 위해서는 functional marker 기반의 분자육종 전략이 수립하였다. 이를 위해서는 첫째 기존에 유전자 기능이 밝혀진 유전자(수량, 품질, 병해충 저항성 등)를 이용하여 유전자와 표현형이 일치하는 SNP 또는 Indel 영역을 탐색하고, 이를 분자마커로 전환한 functional marker를 개발해야 한다. functional marker는 목적하는 유전자를 가진 품종 또는 유전자원에서 positive하게 선발할 수 있어야 하며, 다른 유전자좌에 존재하는 유전자와 gene pyramiding시 유전자간 구분이 가능한 마커가 유용하다. 둘째 국내 벼 육종은 자포니카를 유전적 배경으로 하고 있기 때문에 유전적 다양성이 부족하고, 현재까지 기능이 밝혀진 유용한 유전자가 도입된 육종소재 및 품종이 미흡한 실정이다. 유전자 특이적인 functional marker를 이용하여 유용유전자를 국내 엘리트 품종에 도입한 중간모본 또는 육종소재(prebreeding line)을 육성해야 한다. 셋째는 급변하는 소비자의 요구에 신속하게 대응하기 위해서는 분자육종 기반의 스피드브리딩 시스템의 구축이 필요하다. 이를 위해서는 교배모본별 유용형질 특이적인 functional marker와 background selection용 분자마커를 이용한 유전자 지도 작성과 육종년한을 단축할 수 있는 세대단축 시스템을 개발해야 한다. functional marker를 이용한 벼 분자육종 시스템의 구축은 육종목적에 따라 교배모본의 선정 및 육종단계별 분자마커를 이용한 선발 전략을 수립할 수 있을 것으로 판단되며, 전통육종보다 더 구체적이고 예측가능한 육종이 이루어질 것으로 기대된다.

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CB-0002

Investigation of Gene-Gene Interaction in Soybean

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The crop breeding program have been dramatically developed by integrating marker-assisted selection (MAS) into conventional plant breeding method based on the quantitative genetics. For the best practice of MAS, precise and solid molecular markers, which are tightly linked to the target traits, should be secured. Recent development of analytical techniques, such as next generation sequencing technology and genome-wide association studies (GWAS), a large number of single nucleotide polymorphic markers (SNP) could be landed on the chromosome and utilized for the downstream genetic analysis and breeding program. However, classical quantitative genetics methods are still limited to the aggregate statistical effects of alleles and cannot investigate the different modes of gene action, such as epistatis, that is the interaction between different genes. In this study, to evaluate and investigate the epistasis in plant, multifactor dimensionality reduction (MDR) is employed. Since this non-parametric method could classified multi-dimensional genotype data into one dimensional binary data, population QTL or GWAS analysis tools could be applied without further modification. With speed breeding technique, this approach could contribute accelerate the crop breeding program and develop the noble cultivars.

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CB-0003

Identifying hidden genetic determinants of carotenogenesis for improving fruit quality in tomato and pepper

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Carotenoids and apocarotenoids function as pigment and flavor volatiles that improve attraction value to consumers in addition to the health benefits. Using positional cloning and an introgression line of *Solanum habrochaites*, we identified a carotenoid cleavage dioxygenase 4 (CCD4) as the responsible factor for controlling the dark-orange fruit color. *ShCCD4b* expression in ripe fruits of the IL8A was ~8,000 times greater than that of wild type presumably due to 5′ *cis*-regulatory changes. Phytoene, ζ-carotene, and neurosporene levels were increased in *ShCCD4b*-overexpressing ripe fruits, whereas *trans*-lycopene, β-carotene, and lutein levels were reduced. Using solid-phase microextraction-gas chromatography-mass spectrometry analysis, increased levels of geranylacetone and β-ionone were determined in *ShCCD4b*-overexpressing ripe fruits. In carotenoid-accumulating *Escherichia coli* strains, ShCCD4b cleaved both the ζ-carotene and β-carotene at the C9-C10 (C9′-C10′) positions to produce geranylacetone and β-ionone, respectively. The loci *c1*, *c2*, and *y* have been widely reported as genetic determinants of various ripe fruit colors in pepper, however, *c1* is not well understood. Two cultivars showing peach or orange fruit in *Capsicum chinense* 'Habanero' were found to have *c2* mutation and were hypothesized to segregate *c1* locus in the F_2 population. Habanero peach (HP) showed the reduced pigmentation, and smaller chloroplasts and less stacked thylakoid grana in fruits. To identify the genomic region of the *c1* locus, bulked segregant analysis combined with genotyping-by-sequencing was employed and *Pseudo-Response Regulator 2* (*PRR2*) was cosegregated with the peach fruit color. Our findings will be helpful to enhance the esthetic and nutritional value of tomato and pepper, and to understand complex regulatory mechanisms of carotenoid.

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CB-0004

Assembly of chromosome-level genome to accelerate octoploid strawberry breeding

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Strawberry is a vital horticultural crop worldwide which encompass diverse color, shape and taste. The genus *Fragaria* consists of 22 wild species, ranging from diploid to decaploid. Cultivated strawberry is an octoploid (*F.* × *ananassa*) with high genome heterozygosity and complexity which makes it difficult to implement molecular breeding approaches. To overcome the difficulties, more than 100 homozygous inbred lines derived from ten cultivars have been generated in National Institute of Horticultural and Herbal Science. One of the inbred line, 'Wongyo 3115', was sequenced for reference genome assembly. 'Wongyo 3115' is an highly homozygous inbred line with pink-colored and high-firm fruits. Using long- and short-read sequencing technologies, chromosome-level genome was assembled. Genome size was 805.6 Mb and 151,892 genes were annotated by IsoSeq data together with *ab initio* approach. High-density linkage map of F_2 population showed higher collinearity between genetic map and 'Wongyo 3115' genome than the genome of heterozygous cultivar 'Camarosa'.

Based on 'Wongyo 3115' genome, we carried out quantitative trait locus (QTL) mapping for fruit firmness, color and leaf chlorophyll content. Linkage map of two F_2 populations were constructed using an Axiom 35K strawberry chip and genotyping-by-sequencing. Candidate genes including *expansin*, *MYB10*, and *Glutamyl-tRNA reductase* for fruit firmness, fruit color and leaf chlorophyll content, respectively. In addition to these traits, we are mapping QTLs for fruit quality related traits like sugar content, fruit shape, and cavity. Overall, chromosome-level genome and further genetic analysis will facilitate molecular breeding of strawberry in Korea.

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CC-0001

영상식물학 기반 디지털육종의 방향

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영상식물학(plant image science; 식물표현체학(plant phenomics))은 식물영상을 기반으로 식물의 다양한 측면을 연구하는 학문으로 식물의 영상 획득-처리-분석-해석을 통해 식물의 생리적 상태, 형태적 특징, 생장반응 등을 연구하는 융합학문이다. 영상식물학은 식물의 형태관련 영상정보에 기반한 식물의 동정(identification)과 분류(classification), 생물적 & 비생물적 요소에 대한 식물의 영상반응에 기반한 진단(diagnosis) 및 검정, 식물의 형태적 & 양적형질관련 영상정보에 기반한 표현형 검정과 선발(screening) 등에 폭넓게 활용될 수 있다. 작물의 유전적요인(G) × 환경적요인(E) × 재배적요인(M)의 상호작용에 의해 발현되는 작물의 복잡한 표현형질 정보의 획득과 분석에 있어 전통적인 작물 표현형분석의 한계를 극복하고 발전시키는데 영상식물학이 큰 역할을 담당하고 있으며 디지털육종으로의 전환에 핵심기술이 되고 있다. 이미 세계적인 다국적 농업기업들(Bayer CropScience, BASF, Corteva, Syngenta 등)은 작물육종에 영상식물학적 기술을 육종플랫폼의 한 축으로 활용하고 있다. 다양한 후대종 창출을 위한 방법(교배, 돌연변이, 형질전환, 유전자편집 등)을 통해 확보된 후대종의 검정단계에 파종전 종자에서 추출한 DNA를 이용한 유전체분석을 실시하고, 종자에서 비롯된 개별 후대 개체의 표현형 영상정보를 자동화된 표현체분석장비(plant phenomic system)를 활용하여 생애전주기에 걸쳐 확보 분석하는 표현체분석을 실시하고 있다. 이를 통해 유전체정보와 영상기반 표현형정보의 상호연관성 비교를 통해 작물육종의 목적 형질 선발에 효과적으로 활용될 수 있는 분자표지 개발이나 계통선발 등에 폭넓게 활용하고 있다. 특히 목적 형질을 갖는 우수한 계통선발의 효율성 및 효과성을 제고하고 비용을 절감시켜 작물육종의 효율을 혁신적으로 발전시키고 있다. 최근에는 작물의 영상정보와 인공지능(AI)을 결합함으로써 획득한 영상정보 big data를 보다 효율적이고 혁신적으로 처리 분석하기 위한 활발한 연구와 응용이 이루어지고 있다. 따라서 본 발표에서는 영상식물학의 개념과 농업적인 다양한 활용 가능성을 소개하고, 영상식물학의 주요 핵심기술을 설명하고, 영상식물학 기반 작물육종 현황을 검토하고, 향후 영상식물학 기반 디지털육종의 방향과 전략을 제시하고자 한다.

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CC-0002

GWAS analysis for heading date and seed shape traits using image-based phenotyping in North Korean rice population

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The North Korean (NK) rice collection is a unique source of breeding materials since the NK rice collection has not been extensively utilized for genetic analysis. This study used 190 NK rice varieties selected from the NK rice collection for non-precocious flowering and normal growth in the low-latitude Philippines. First, we performed GWAS and haplotype analyses using the selected NK rice population and proposed significant genetic loci associated with heading date (Hd) regulation and the genetic composition of this population by analyzing the allelic combination of the major Hd genes. The geographical distribution of these Hd allelic combinations was also discussed with respect to regional adaptation. Second, we also performed GWAS analysis for seed shape such as seed length, width and area. Since it is difficult to measure the seed area by the manual method, the image-based phenotyping was also applied. Three programs (Image J, Grainscan and KR-image) were used and compared in terms of convenience and accuracy for phenotyping. As it was difficult to identify an individual seed by Grainscan, the other two program was used to phenotype NK rice varieties. GWAS analysis for seed morphology using both manual and image-based methods identified several known genes (*BRD2*, *GS3*, *OsBZR1*, *OsALDH2B*, *GS6*, and *OsAGSW1*) and novel genes associated with seed morpholoty. Further haplotyping analysis revealed that haplotypes of the genes significantly contributed to the seed development. In conclusion, phenomics approach would be a useful method enhancing the phenotyping efficiency by increasing accuracy and speed compared to the manual method.

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CC-0003

Exploring the various phenotypes of seeds and GWAS using images

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A seed is a basic part in any plant that maintains human life in the form of food, pharmaceuticals, cosmetics, industries, and many others. Therefore, developing advanced seed management methods are inevitable in agricultural industries. In that sense, Agricultural Sciences adapted the automated analysis technology to enhance seed quality management using the Image J, open source program. This method allows the analysis of seed feature data, such as shape and color, in a precise quality and quick performances. Using it, seeds of 62 species, including strawberries, soybeans, rice, barley, wheat, carrots, radishes, and cabbages were analyzed for validity verification with eight morphological indicators including area, width, height, circularity, etc. in order to explore the location of chromosomal gene candidates via genome-wide association studies. Since those digital-data could provide more diverse traits than manually obtained data in a reliable and accurate manner, they would enable researchers to study unknown traits and their related genes. Furthermore, such data using the method in the current study can be generated a lot more to be “big data”, which could be utilized for artificial intelligence technology for further investigation to enhance seed quality in the near future.

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CC-0004

센서를 활용한 노지 밭작물 생육정보 진단 기술

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최근 집중호우와 폭염 등 급변하는 기후변화로 작물 스트레스가 다양하게 발생하고 있으며 발생패턴이 불규칙적이다. 센서를 활용하여 작물의 생물학적 및 비생물학적 스트레스를 진단 기술은 원예분야에서 다양한 연구가 이루어지고 있다. 그러나 농업에서 큰 부분을 차지하고 있는 노지 밭작물에서는 센서를 활용한 진단연구는 미비한 상황이다. 최근 노지 밭작물에 스마트팜 기술의 적용이 확대되고 페노믹스와 캐노피 시스템 활용이 증가하고 있으나 장비구축 소요 경비가 높아 국내 노지작물에 적용이 어렵다.

본문에서는 1) 노지 밭작물의 생물학적 및 비생물학적 스트레스 조기진단 방법, 2) 노지 밭작물 생육정보 실시간 측정 방법 및 3) 센싱기반 데이터 수집을 통한 실시간 모니터링 및 의사결정 지원 통합관제시스템 모델을 제시하였다.

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CD-0001

Roles of ABC transporters for root and seed development in rice

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Although the super family of ATP-binding cassette (ABC) proteins plays key roles in the physiology and development of plants, the functions of members of this interesting family mostly remain to be clarified, especially in crop plants. Using genome-wide transcriptome data for anatomy samples in rice, we identified 17 root-preferred and 16-shoot preferred genes at the vegetative stage, and 3 pollen, 2 embryo, 2 ovary, 2 endosperm, and 1 anther-preferred gene at the reproductive stage. Of them, we performed the functional characterization of one root-preferred genes and one shoot and seed-preferred gene. In case of the former, mutation of the gene using the CRISPR/Cas9 system and T-DNA insertion resulted in poor development of the lateral roots and root hairs. RNA sequencing and HPLC/MS experiments revealed that the mutation of this gene reduced the accumulation of feruloylputrescine at the intracellular level compared to wild type, suggesting a potential substrate of this ABC transporter. In case of the latter, T-DNA insertional mutant showed segregation ratio of 1:2:0 for wild type: heterozygotes: homozygotes, indicating the lethal phenotype during the seed development. Gene editing mutant for this gene using CRISPR/Cas9 system generated the homozygous mutant having defects in early embryo development right after fertilization in the primary generation. RNA sequencing and micro-dissection analyses for fertilized embyro of the gene edited mutant were carried out to find out potential substrate and downstream regulatory pathways for the further applications. Detailed data analysis and discussion will be presented.

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CD-0002

Future development of smartbreeding in response to ZERO HUNGER in rice

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The world population has exceeded 7.5 billion and is approaching 8 billion and the world population continues to increase. The goal of the smart breeding strategy with 5Gs for sustainable agriculture is to increase yield for ZERO HUNGER in the world. To achieve this goal, breeder need to develop crops that can achieve consistent yields at least twice that harvested now. However, in breeding, the development of crop cultivars requires consideration of several stages such as crossing, selection, and field testing, normally it can take about 16 years. However, in order to solve the food shortage, cultivars with improved traits must be breeding rapidly and precisely. Recently, the advances of genome editing (GE) technology have opened a new breeding era and are the most promising technology for achieving ZERO HUNGER. In the last decade, GE using the CRISPR/Cas9 system has revolutionized the field of agriculture by improving yields based on reducing damage from biotic and abiotic stress. To solve the ZERO HUNGER and improve crop yield in the world, we analyze the effects of biotic and abiotic stress, breed the crops with improved traits using GE technology. And we present a smart breeding strategy that is useful for ZERO HUNGER by introducing the anther culture method to quickly fasten crop traits.

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CD-0003

Improvement of Soybean Nutritional Values by Using Genome Editing Technology

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Soybean [*Glycine max* (L.) Merr.] is a major economic crop and is used as food, animal feed, and biofuel because of its high contents of oil and proteins. Soybeans contain approximately 40% protein and 20% oil. Soybean protein is used mostly in food and feed. Soybean oil is utilized in food, feed, and some industrial applications. However, to further expand the utilization of soybean, some problems need to be addressed, including the identification of the appropriate ratio of fatty acids, pest resistance, and the issues of anti-nutritional factors, such as allergenic proteins, phytic acid, and nondigestible saccharides including raffinose and stachyose. Especially these anti-nutritional factors limit the extensive use of soybean in the food and feed industry. The use of genome editing technologies, such as ZFN, TALEN, and CRISPR/Cas9, for the genetic manipulation of soybean has revolutionized the study of genetic variations, as well as soybean improvement, over the past few years. In this talk, I will introduce the development of genome edited soybeans having the reduced anti-nutritional factors, especially P34 allergenic seed protein and phytic acid, using CRISPR/Cas9 system. In addition, we are developing genome edited soybeans having shorten growth period to improve agricultural productivity. The elimination of various anti-nutritional factors in soybean seeds and the increase of productivity using gene editing will lead to advances in the soybean-based food industry and feed manufacturing.

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CD-0004

In vivo haploid induction system in dicotyledonous plant

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Haploid embryo induction system can considerably shorten the time required to create pure homozygous lines, which is the basis of doubled haploid technology. The *in vitro* haploid induction system has long been used to produce haploid embryos using maternal or paternal germlines. The *in vitro* methods, typically tissue culture-based, are labor intensive and genotype dependent. However, a seed-based *in vivo* haploid embryo induction system can overcome the limitations of the *in vitro* methods. So far, two main types of *in planta* haploid-inducing lines that trigger either maternal or paternal haploid embryo through seeds have been reported. One of them is the CENH3 (centromeric variant of histone 3)-based induction system, in which the modification of a CENH3 allows the creation of haploid inducer lines that generate viable seeds containing a paternal haploid genome. The other is the monocot-specific maternal haploid induction system, which is based on the mutation of *ZmPLA1*/*MTL*/*NLD* (*ZmPHOSPHOLIPASE-A1*/*MATRILINEAL*/*NOT LIKE DAD*). The *ZmPLA1*-based haploid inducing system is reported to produce viable seeds containing a maternal haploid genome in only monocotyledonous plants such as maize, rice, wheat, and foxtail millet. The genetic alteration of *ZmPLA1* homolog in dicotyledonous plants has not yet been reported. Herein, we report that *ZmPLA1* homolog is actively involved in the creation of haploid seeds in *Arabidopsis*. This discovery indicates that the genetic manipulation of *ZmPLA1* is also functional in dicotyledonous plant.

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CE-0001

How do cytokinin and sucrose control flowering time in rice?

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Floral induction is mediated by the FLOWERING LOCUS T (FT) or it's homologs as florigen. Interestingly, before FT was identified, cytokinin and sucrose have long been proposed as floral signals. Therefore, in this study, we focused on why these substances were proposed as floral signals and how they control flowering time in rice (*Oryza sativa*). The level of *trans*-zeatin, an active cytokinin, was high in the leaves during the vegetative growth stage and decreased rapidly to the minimum when floral signals were generated, suggesting that the hormone maintains the vegetative phase. To elucidate whether exogenous cytokinin influences the length of vegetative phase, we applied 6-benzylaminopurine to plants at various developmental stages. This treatment delayed flowering time by 8 to 9 d when compared with mock-treated plants. We also observed that cytokinin delays flowering by inhibiting Ehd1's function by inducing two type-A response regulators (OsRR1 and OsRR2). Meanwhile, sugars are major photosynthetic products and play pivotal roles on growth and development as central components reflecting internal energy status in plants. Here, we demonstrated that the contents of soluble sugars in leaf blades were high during the floral transition stage in rice. Flowering time was accelerated by external sucrose or glucose treatments by 4 to 6 days when compared with mock treated plants. We observed that a major floral repressor protein was degraded by sucrose treatment in rice. This study is expected to increase our understanding of the molecular mechanisms of how cytokinin and sugar control flowering time in rice.

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CE-0002

Genotype study for heading date using GWAS and genomic selection in wheat core-set

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Hexaploid wheat (*Triticum aestivum*. L) has a large genome size of 17 Gb and many repeated nucleotide sequences, making it difficult to conduct breeding studies. To overcome the above challenges, we constructed a wheat core-set consisting of 614 germplasm and obtained the SNP information of the core-set using 35K SNP chip. We are investigating major agricultural traits, tolerance against abiotic stresses, and quality traits for end uses of the core-set. The first trait among many traits is heading date in Korea wheat cultivar environment. Early flowering time with high grain yield has been the most important selection target trait in various agronomy characterizations, because the rainy seasons and rice transplantation time is overlapped with the harvest time of wheat. Genome-wide association study (GWAS) were performed using 35K SNP chip data set to find the domestic wheat cultivation environment suitable HD genotype. Several SNPs were identified in genes encoding phytochelatin synthetase, Kinases, and potassium channels in genome 5A and 5B by GWAS. In addition, we performed genomic prediction for HD trait, and the genomic prediction accuracy was more than 80%. This study demonstrates that genomic prediction of the HD can be key to speed breeding of wheat suitable for domestic growth. However, in order to construct a genome selection system for other traits, precise phenotypic investing methods such as the HD trait will be required.

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CE-0003

Genotyping-by-Sequencing Derived Single Nucleotide Polymorphisms Provide the First Well-Resolved Phylogeny for the Genus *Triticum* (Poaceae)

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Wheat (*Triticum* spp.) has been an important staple food crop for mankind since the beginning of agriculture. The genus Triticum L. is composed of diploid, tetraploid, and hexaploid species, majority of which have not yet been discriminated clearly, and hence their phylogeny and classification remain unresolved. Genotyping-by-sequencing (GBS) is an easy and affordable method that allows us to generate genome-wide single nucleotide polymorphism (SNP) markers. In this study, we used GBS to obtain SNPs covering all seven chromosomes from 283 accessions of *Triticum*-related genera. After filtering low-quality and redundant SNPs based on haplotype information, the GBS assay provided 14,188 high-quality SNPs that were distributed across the A (71%), B (26%), and D (2.4%) genomes. Cluster analysis and discriminant analysis of principal components (DAPC) allowed us to distinguish six distinct groups that matched well with *Triticum* species complexity. We constructed a Bayesian phylogenetic tree using 14,188 SNPs, in which 17 *Triticum* species and subspecies were discriminated. Dendrogram analysis revealed that the polyploid wheat species could be divided into groups according to the presence of A, B, D, and G genomes with strong nodal support and provided new insight into the evolution of spelt wheat. A total of 2,692 species-specific SNPs were identified to discriminate the common (*T. aestivum*) and durum (*T. turgidum*) wheat cultivar and landraces. This study demonstrated that GBS-derived SNPs could be used efficiently in genebank management to classify *Triticum* species and subspecies that are very difficult to distinguish by their morphological characters.

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CE-0004

Development of waterlogging tolerance corn variety using wild corn Teosinte

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Waterlogging tolerance of corn is one of the important factor for cultivate in paddy soil condition to increase cultivation area and self-sufficiency of corn in Korea. In order to develop elite waterlogging tolerance corn, the new corn lines bred by crossing wild corn, Teosinte, and cultivated corn inbred lines. Five accessions among the 2 species, *Zea mays subspp. mexicana* and *Zea parviglumis*, of 81 Teosinte were selected through the waterlogging treatment. The waterlogging treatments were implemented for 7 days at the seedling(V3) stage. The inbred lines were developed by crossing 5 teosinte accessions and cultivated corn lines and they were estimated waterlogging tolerance. We selected 21 elite lines of 101, and performed to analysis of agronomic traits, cytological characteristics, transcripts and metabolites in corn roots related waterlogging stress using these lines. The roots were 2.5-fold thickened with additional aerenchyma formation in the cortex under the waterlogging condition. We selected five genes, *WIP1*, *PMIP2*, *EXPA1*, *TPS1* and *MAS1*, through the microarray and RT-PCR analyses using B73. It was screened and analyzed the metabolites extracted from roots of 19KT-32(KS141 x teosinte) that was treated waterlogging. We selected 8 of 180 metabolites like as γ-aminobutyric acid, putrescine, citrulline, Gly, and Ala that expression was remarkably changed over 2.5-times, 7 metabolites increased and 1 metabolite decreased in waterlogging, respectively. Most of metabolites were related to abiotic stress in plant that it regulated to pH, osmotic pressure K^+/Ca^{++} and ATPase activity. We are analyzing the association using these results for increase breeding efficiency.

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CE-0005

벼 전분 합성 유전자 *SBE3*와 *GBSS1*의 상호작용에 의한 아밀로스 함량 증대 및 전분 이화학적 특성 변화

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벼는 세계적으로 가장 중요한 작물로 많은 아시아 국가에서 주식으로 이용되며, 벼의 전분은 우리 식단의 중요한 에너지원으로 사용되고 있다. 본 연구에서는 고아밀로스 품종인 '도담쌀'과 '화영벼'를 교배하여 얻은 네 개의 근동질 계통을 사용하여 아밀로스 함량과 전분 이화학적 특성에 대하여 분석하였다. 네 개의 근동질 계통은 도담쌀(*sbe3/Wx*^{hv})과 화영벼(*SBE3/Wx*^{b})에서 유래한 서로 다른 조합의 *SBE3*와 *GBSS1* 대립유전자를 갖고 있으며, 종자의 형태, 전분 구조 및 결정성, 아밀로펙틴 사슬 길이, 소화도 등에서 서로 다른 특징들을 나타내었다. 또한, 회귀분석 결과 두 유전자가 아밀로스와 저항성 전분 함량을 조절하는데 통계적으로 유의미한 상호작용을 보이는 것을 확인할 수 있었다. 개화 후 15일 이삭을 이용하여 전분 합성 관련 유전자들의 발현을 관찰한 결과 근동질 계통 간에 유의미한 차이가 관찰되었고, 이러한 유전자들의 발현 변화가 아밀로스, 저항성 전분 함량, 전분 이화학적 특성 변화에 영향을 주었을 것으로 사료되었다.

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CF-0001

이상기상 대응 고추, 토마토 안정생산을 위한 고온 및 저온내성 품종개발

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채소 생산은 기후 의존성이 높아 기후변화에 매우 취약하며, 특히 잦은 고온 또는 저온은 채소 작물의 생장과 발달 과정에, 생리장애, 낙화, 낙과, 기형과, 수확량 감소 등에 영향을 미친다. 따라서, 증가하는 이상기상에 대응하여 고추, 토마토 안정생산을 위한 고온 및 저온내성 품종개발이 요구된다. 고온 및 저온내성 고추, 토마토 품종개발 연구를 위하여, 엽장, 엽폭, 초장, 경경 등 영양생장을 포함한 형질과 꽃수, 착과율, 과중, 과장, 수확량 등 생식생장에 관련된 특성을 조사하였다. 또한, 생리-생화학적 특성과 내서성 및 내저온성 품종 간 상관성 구명을 위하여, 고온 및 저온내성 고추, 토마토 자원들의 광합성률, 엽록소 함량, 프롤린 함량, 전기전도도를 측정하였다. 고추 시판종 '뉴비가림'(NB) 및 '청양'(CY) 품종의 유묘기 광합성률은 고온을 처리한 'CY' 품종에서 유의하게 감소하였다. 기공 전도도, 증산율, 프롤린 함량은 'CY' 품종보다 'NB' 품종에서 더 높았으며, 'NB' 품종은 'CY' 품종에 비해 고온 스트레스 후 빠른 회복을 보였다. 토마토의 경우, 고온에서 생리-화학적 특성(광합성, 전해질 전도도, 프롤린 함량) 및 영양생장 형질(초장, 지상부 생체중, 지하부 생체중)을 조사하였다. 고온 스트레스 기간 동안 토마토 '대프니스'(Dafnis) 품종과 '미니찰'(Minichal) 품종의 유묘기 광합성률, 엽록소 함량, 프롤린 함량, 전기 전도도는 품종에 관계없이 다양하였다. 토마토 'Dafnis' 품종의 과중(31.9%), 과장(14.1%), 과경(19.1%), 과실경도(9.1%) 등의 특성들이 감소하였다. 'Minichal' 품종의 과장(7.1%)과 과경(12.1%)은 감소하였으나, 과중(3.6%)과 과실경도(8.3%)는 증가하여 'Dafnis' 품종보다 고온에 더 내성이 있는 것으로 추정되었다. 고추와 토마토를 저온처리(최저온도 10℃)와 정상관리(최저온도 15℃)구를 두고 시험처리 하여, 주요 원예적 형질들을 상관분석, 주성분 분석(PCA) 및 계층적 클러스터링을 통해 분석하였다. 저온 처리된 39개 고추 자원들의 과실 수확량은 꽃수, 과중, 과폭, 과장과 양(+)의 관계를 보였고, 계층적 군집 분석에 의해 7개 그룹으로 클러스터링 되었다. 저온 처리된 35개의 토마토 자원들은 4개의 주요 그룹으로 분류되었고, 선발된 토마토 자원은 생식생장과 영양생장 지표와 양(+)의 관계를 보였다. 본 시험의 결과들은 고온 및 저온내성 고추, 토마토 자원들의 스크리닝을 위해서는 생식 생장관련 지표와 함께 영양생장기 지표들도 같이 평가되어야 한다는 것을 보여준다.

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CF-0002

Transcriptional analysis of differentially expressed genes related with disease resistance in Vitis species for grape breeding

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Grapevines and berries are exposed to disease including ripe rot, anthracnose, crown gall, gray mold, downy mildew, and powdery mildew in the vineyards. Although diverse strategies were applied to control diseases, breeding and cultivation of varieties with high quality-grapes resistant to diseases, pests, and to stresses are the most important steps for pest control in viticulture. From the advent of next-generation sequencing (NGS) technology, molecular breeding technology has resulted in improving the efficiency for grape breeding. The completion of the genome sequencing in various Vitis species provided the way to discover the novel genes and to analyze their functions. In addition to genome-wide association study (GWAS), genome-wide transcriptomic resulted in selecting relatively reliable candidate genes related with responses resistant to foreign stresses in grapevines. Various resistance (R)-related loci to diseases were identified in domesticated and wild grapevine species through transcriptome analysis. Dynamic gene regulation pathways in grapevines susceptible and resistant to pathogens were found by transcriptome analysis. Networking analysis of clustered genes in co-expression module showed the enrichment of the most common plant-pathogen interaction pathways, such as signaling pathway, ROS production and biosynthesis of secondary metabolites. A comprehensive database from RNA-seq. focused on the collection, evaluation, treatment, and data sharing of grape RNA-seq data sets and classified into 25 conditions can be accessed worldwide by users. Results from genome-wide transcriptomic analysis can open the new way to study functional analysis of genes for molecular breeding of grapevines resistant to pathogens and other stimuli.

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CF-0003

Implementation of *C. sticuspe* genome information to the cultivated K-Chrysanthemum breedings.

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Chrysanthemums are one of the most industrially important cut flowers in the domestic floral industry. However, polyploidy and self-incompatibility have been critical impediments to applying genetic analyses and modern breeding tools. Recently, the advent of the chromosome-level genome sequence of Chrysanthemum sticuspe such as Gojo-0, which shares many similar properties to cultivated hexaploid Chrysanthemums, may open up a new way for the information-based improvement programs of this hexaploid crop. To test the possibility, we performed various genetic and genomics analyses for allelic mining(AM)- and experimental cross(EC)-populations for the cultivated Chrysanthemums by implementing Gojo-0 genome information as a reference. We first profiled the chrysanthemum genomes using the genotyping by sequencing (GBS), based on one enzyme(ApeK1) and two enzymes(Pst1-Msp1). For the genomes in the AM population, comprising 96 diverse Chrysanthemum cultivars, we found that 83.2% of reads produced from the one- and two-enzyme-GBS were mapped to Gojo-0 genome on average, resulting in 131,509 SNPs across the genome. We then conducted a genetic diversity study and genome-wide association study(GWAS) for AM population and QTL study for EC population to find beneficial alleles underlying key agricultural traits. Thus, this study provides practical insights into efficiently applying genetic and genomics tools, accelerating the improvement programs for Chrysanthemums and other horticultural crops with complex genomes.

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CF-0004

Plant Organelle DNA editing with Programmable Deaminases

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Plant organelles including mitochondria and chloroplast contain their own genomes, which encode many genes essential for respiration and photosynthesis, respectively. Plant organelle gene editing has been hampered by the lack of suitable tools for targeting DNA in these organelles. Here, we present a DddA-derived cytosine base editor (DdCBE) plasmids composing of bacterial cytidine deaminase fused to transcription activator-like effector (TALE) array proteins, which induce targeted C-to-T editing in chloroplast and mitochondria. Our organelle editing system induced base editing at frequencies of up to 25% (mitochondria) and 38% (chloroplasts) in lettuce or rapeseed calli. We also established DNA-free base editing in chloroplasts by transferring DdCBE pair mRNAs to avoid off-target effects. Furthermore, we generated antibiotics-resistant lettuce calli and plantlets with edit frequencies of up to 99% by introducing a point mutation in the chloroplast 16S rRNA gene.

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CF-0005

사과 아조변이에서 발생한 retrotransposon 삽입과 deletion이 과실숙기 지연에 미친 영향

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과수에서 발생한 아조변이는 원품종과 비교하여 과일 색깔, 크기 및 수확시기와 같은 과실특성의 차이가 관찰된다. 사과 품종 Gala의 아조변이인 가을 갈라(AGala)는 Gala보다 수확시기가 약 4주 가량 늦다. 이와 같은 수확시기 지연의 분자생물학적 메커니즘을 이해하기 위해 과실발달 기간 동안 Gala와 AGala에서 주기적으로 샘플링된 과일들을 사용하여 RNA-seq 분석을 수행하였다. 23,372개의 differentially expressed genes(DEGs)에 대한 Weighted gene co-expression network analysis(WGCNA) 결과 25개(Mod1-Mod25)의 co-expression 그룹으로 분류되었다. 이 중 AGala 특이적으로 down-regulated된 Mod1(r=-0.98, p=2E-21)과 Mod2(r=-0.52, p=0.004)는 과실 수확시기와 통계적으로 유의미한 상관관계를 보였다. 특히 Mod1의 152개 유전자 중 77개는 6번 염색체의 2.8Mb 지역에 밀집해 있었는데, 이 부분을 타겟으로 염기서열을 AGala와 Gala에서 확보해본 결과, AGala의 7번 염색체에서 10.7kb 크기의 집시 유사 레트로트랜스포존(Gy-36)이 삽입되며 AGala의 6번 염색체 삽입되며 2.8Mb 크기의 결실을 초래한 것으로 해석된다. 77개의 해당 유전자 중 식물 발달에 필수적인 것으로 알려진 Arabidopsis ACT7과 유사한 MdActin7이 Gala에서 두가지 형태로 존재했는데, mdactin7은 exon 3번째 transposon의 삽입으로 구조가 변형되어 있었다. AGala는 이 두 개의 대립유전자중, 구조가 변형된 mdactin7만 보유하고 있었다. Arabidopsis act7 계통에서 대립유전자 MdActin7 및 mdactin7의 과발현중 MdActin7은 성장 부진을 크게 복구하고 초기 개화를 촉진할 수 있지만 mdactin7은 그렇지 못했다. 따라서 Gy-36 삽입과 관련된 2.8Mb의 결실은 AGala의 과일 성숙 지연에 대해 유전적으로 인과 관계일 가능성이 높으며 기능적 대립유전자 MdActin7의 손실이 숙기지연 표현형에 기여했을 수 있다.

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CG-0001

Applications of Molecular Breeding in Medicinal Crops and Future Prospects

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The improvement of next-generation sequencing has made it possible to analyze the genetic information of medicinal crops, which was difficult to obtain in the past. In medicinal crops such as bellflower and ginseng, standard genome sequence information was established and in many other medicinal crops, including *Angelica, Codonopsis, Schisandra,* and *Atractylodes,* several types of molecular markers were developed and group structure analysis of genetic resources was performed. Species identification of medicinal crop is a big issue to be solved because there are many similar species in the same genus or in the same family. For more efficient breeding of medicinal crops, it is necessary to accumulate large amounts of phenotype data as well as genome data. Phenotype data colection is mainly focused for the observation of above-ground parts, so it seems that some methods for the phenotype data collection of medicinal crops mainly using roots is needed. In medicinal crops, efficacy as well as quantity is important. Therefore, research on ingredients related to efficacy along with genotype and phenotype should be conducted together.

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CG-0002

DNA super-barcoding for managing plant bioresource and breeding

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Since the Nagoya Protocol entered into force in 2014, 137 countries have ratified this protocol on access and benefit-sharing. Interest in native plant resources has increased worldwide due to preparing for the impact of this protocol. DNA barcoding uses the genetic information of an organism as a barcode for identification and is an efficient tool for the authentication of herbal materials, from raw ingredients to final products. To date, more than 11,000 plastid genomes have been stored in NCBI, and the number is steadily increasing owing to technology improves. Therefore, DNA super-barcoding, a concept of using whole plastid genome information as a barcode itself rather than small universal regions, has been tried to improve the identification and classification of plant materials. Once polymorphic regions are discovered from multiple alignments of plastid genomes from related species, they are converted into molecular markers, which is called the mini barcode. However, plastid-derived markers often cause false detection of targeted species because of genome complexity, such as mitochondrial plastid DNA or intraspecific diversity. Therefore, an integrated DNA barcoding system based on multiple plastome information together with 45S rDNA is necessary in order to manage our plant bioresources considering their heterogeneous nature in the wild. This will contribute to preparing for upcoming issues caused by access and benefit-sharing at the national level and managing the new breeding candidates for medicinal and industrial crops. This work was carried out with the support of "Cooperative Research Program for Agriculture Science and Technology Development (Project No. PJ017134)" Rural Development Administration, Republic of Korea.

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CG-0003

Comparative transcriptomic analysis of *Pinus densiflora* and *Pinus strobus* to find resistance candidate genes to Pine wood nematode (*Bursaphelenchus xylophilus*)

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Pine wood nematodes (*Bursaphelenchus xylophilus*) are nematodes that infect pine trees and cause pine wilt disease. *Pinus densiflora*, a native pine tree species in Korea, is susceptible to pine wood nematode and easily killed by pine wilt disease. In contrast, *Pinus strobus* is an introduced pine species from North America and has resistance to pine wood nematode. *P. strobus* ias expected to have resistance genes to pine wood nematode, but the identity of the resistance genes are still unknown. In this study, we compared transcriptome of *P. densiflora* and *P. strobus* to detect resistance candidate genes to pine wood nematode. Three biological replicates of *P. densiflora* and *P. strobus* were inoculated by 10,000 pine wood nematodes per tree. Cambium samples of trees were collected on 0, 2, 4 weeks after inoculation. RNA samples were extracted from the cambium and sequenced by Novaseq 6000 (Illumina, USA). Using Trinity (v.2.13.2), *de novo* transcriptome assembly for both species was conducted from the clean reads of sequenced RNA. We selected the differentially expressed genes (DEGs) showing P-value $\leq$ 0.05 and fold change $\geq$ 2. Total 1,041 million reads of RNA were assembled to 37,533 genes of *P. densiflora* transcriptome and 36,550 genes of *P. strobus* transcriptome. Among 163 upregulated DEGs (0 vs 2 weeks) of *P. strobus*, 13 DEGs which had no homology genes in *P. densiflora* were selected as resistance candidate genes. Further study for the transcriptome of both species would give us a hint about the resistance genes to pine wood nematode.

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CG-0004

Status and prospects of tree improvement research in industry 4.0 era

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Integration of advanced technologies in diverse disciplines by industry 4.0 is expected to bring a big leap forward in industries and research fields. Precision forestry, a shifted paradigm from traditional forestry, is emerging as a new smart approach for advanced forest management. Tree improvement is one of the promising fields by precision forestry's technology. It also demands the advanced technology simultaneously to overcome intrinsic challenges arising from dealing long living and large materials in heterogeneous environments. The extrinsic threats of climate change even urge the adoption of the innovative technologies aiming advanced tree improvement. In this study, the accomplishment, current status, challenges and future prospects of tree improvement research will be discussed. Tree improvement program so far has been contributed to forestry by supplying genetically improved forest resources with increased economic and ecological values. The programs are continuously ongoing toward the next breeding generation in major timber species around the world including Korea. Current studies in tree improvement are grafting up-to-date technology in detail research fields of omics, phenotyping combined with the environmental analysis. The subsequent challenges are being identified in this trial phase in each field. The advantage of newly adopted technologies would be gained by increasing their accuracy, reproducibility and efficiency for the purpose of promoting tree improvement on Industry 4.0.

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CH-0001

Identification and application of genetic factors in pepper and strawberry breeding

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Pepper (*Capsicum* spp.) is one of the most valuable vegetable crop and shows enormous variation in plant architecture, flower-, leaf-, and fruit related traits. Also it is the only crop synthesizes the pungent metabolite, capsaicinoid. As these horticultural traits are controlled by multiple genetic factors and highly affected by environment, there were limited studies to figure out the genetic factors.

For quantitative trait loci (QTL) mapping of morphological traits, a total of 18 horticultural traits were evaluated from more than three different environments. Then we set sliding-window approach to overcome missing data problem of low-coverage sequence. Using an ultra-high density bin map and phenotype data obtained from multiple environments, significant QTL were identified. Genetic map, phenotype data and QTL information of this study were used for further studies including fine mapping locus for fruit orientation and genomic selection of fruit-related traits.

To identify the candidate genes controlling capsaicinoid biosynthesis, we conducted QTL mapping and genome-wide association studies (GWAS). By QTL-GWAS, five candidate genes known to be involved in capsaicinoid biosynthesis were identified and proposed to regulate pungency level. In addition, one MYB transcription factor was predicted as a novel locus, *Pun3*, controlling presence and absence of pungency. These results could be helpful to understand the genetic control and breeding of pungent peppers.

We are applying genome-based genetic mapping approach to octoploid strawberry (*Fragaria* × *ananassa*). Candidate genes controlling fruit color, firmness and leaf color were identified and that for fruit sugar content, flavor, and maturation will be searched by QTL analysis. Furthermore, we are planning GWAS of strawberry core collection using array-based genotype and image-based phenotype.

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CH-0002

Mutation of light signal transduction machinery affects pericarp pigmentation and embryo development in rice grain

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Light is a crucial signaling component that controls a variety of physiological and developmental processes in morphogenesis, germination, metabolic alterations, and flowering in plants. Here, we identified four *yellowish-pericarp embryo lethal* (*yel*) mutants from four different *japonica* cultivars of rice (*Oryza sativa* L). Mutant seeds had yellowish pericarps and exhibited embryonic lethality, with significantly reduced grain size and weight. Genetic analysis and mapping revealed that the phenotype of the *yel* mutants was controlled by an ortholog of *Arabidopsis thaliana CONSTITUTIVE PHOTOMORPHOGENIC 1* (*COP1*) or *DE-ETIOLATED 1* (*DET1*). Seeds of the rice *cop1* and *det1* knockout mutant, generated via CRISPR/Cas9-based gene editing, displayed the *yel* mutant phenotype. Moreover, the knockout seeds of CONSTITUTIVE PHOTOMORPHOGENIC 10 (OsCOP10) and UV-DAMAGED DNA BINDING PROTEIN 1 (OsDDB1) which form the COP10-DET1-DDB1 (CDD) complex together with OsDET1 also showed the *yel* phenotype. Comparative transcriptome analysis revealed that genes involved in the *C*-glycosyl flavone biosynthesis pathway, including transcription factor, *OsP1*, were activated, whereas anthocyanin biosynthesis genes showed no significant change in expression. Consistent with these results, the level of *C*-glysocyl flavones such as isoorientin and isovitexin was dramatically increased in the *yel* grain. In addition, transcript levels of embryo development-related genes, especially homeobox and auxin regulation genes, as well as somatic embryogenesis-related genes, were significantly downregulated in the developing seed of *yel* mutant. Taken together, these results indicate that *OsCOP1* and *OsDET1* play a crucial role in regulation of flavonoid biosynthesis and embryo development, and the alteration in the light signal transduction could have a significant effect on pericarp pigmentation and embryogenesis in rice seed.

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CH-0003

Flavonoid metabolic changes regulated by UV lights in a soybean seedling model

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Controlling the content of target compounds and improving the bioactivity in crops are the important goals of plant breeding. Evaluation of metabolite destination during the crop cultivation is a valuable indicator for breeding strategy. In this study, flavonoid metabolic changes regulated by UV lights were evaluated in a soybean seedling model. Firstly, the accumulation pattern of 12 isoflavone types in soybean seedling was investigated responded to different UV-B irradiation period. The results showed that six isoflavones were maximally increased in the seedlings irradiated with UV-B for 24 and 36 hours. In particular, malonyl genistin did not increase in dark grown sprouts compared to the seeds, but significantly increased in UV-B grown sprouts. The *GmCHS6-8* genes were found to be specifically relevant to UV-B response as their expression was up-regulated by UV-B. Prolonged UV-B irradiation caused some damage to the cotyledons. Thus, secondly, the organ-specific compartmentalization of flavonoid was investigated using UV-A. The isoflavone content increased in the root-specific manner, while the kaempferol glycoside content increased only in shoot compartment by UV-A. Mainly increased isoflavone type was genistein-type with 6.3-fold higher content compared to the dark condition. High *GmUGT9* expression in the root by UV-A clearly demonstrate the UV-A-induced isoflavone accumulation. Regulating and optimizing the target compounds through environmental control can be a valuable strategy to expand the diversity and utilization of breeding lines.

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CH-0004

GWAS 분석을 통한 유묘기 및 출수기 내재해성 QTL 탐색

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품종 및 Inbred 12개, 65개 Intro, 60개의 Korean landrace를 포함하는 137개의 KRICE Core Set을 이용하여 저온에서 상대발아율(RGP)과 지연된평균발아율(DMGT), 유묘기에서 저온과 냉수 저항성 그리고 출수기에서 고온과 저온의 저항성 GWAS 분석을 통해 연관된 QTLs를 발견하고 bioinformatic방법과 haplotype 분석을 통해 후보유전자와 대립유전자를 밝혀냈다.

저온 상대발아율과 관련된 23개, 지연된평균발아율과 관련된 18개 SNP를 발굴하였으며, 유묘기 저온 저항성과 관련하여 염색체 1, 4 그리고 5에서 각각 Os01g0357800: encoding a pentatricopeptide repeat (PPR) domain-containing protein, Os05g0171300: encoding a plastidial ADPglucose transporter, Os05g0400200: encoding a retrotransposon protein을 유묘기 저온 저항성 관여 유전자로 특정하였다. 유묘기에 냉수를 처리한 경우에는 7개의 QTLs가 염색체 1, 3, 6, 7, 10 그리고 12에서 발견되었으며, 유묘기 냉수저항성과 관련된 유전자로 Os01g0228600에서 cytosolic hydroxypyruvate reductase, Os03g0115000에서 cupredoxin domain containing protein, Os06g0612800에서 stress-associated protein (SAP) gene family, Os12g0552500에서 universal stress protein (USP), 그리고 Os10g0482900에서 thioredoxin fold domain containing protein를 특정하였다. 출수기 GWAS 분석은 고온과 저온에서 임실율을 표현형으로 분석하였다. 고온에서 임실율과 연관된 Os10g0177200의 EF-HAND 2domain containing protein이 밝혀졌고, 저온에서 임실율과 연관된 QTLs이 염색체 3, 6 그리고 7에서 표현형 11 ~ 19% 설명되었다.

GWAS 분석을 통해 다수의 저온발아성, 유묘기 저온 및 냉수 저항성 그리고 출수기 고온 및 저온 저항성 QTLs를 밝혔으며, bioinformatic과 haplotype 분석을 통해 후보유전자를 특징하고 대립유전자의 변이서열을 밝혀 환경저항성 관련 유전, 육종에 기여할 수 있는 유전자원을 발굴하였다.

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CH-0005

The discovery of novel SNPs associated with group A soyasaponin biosynthesis from Korea soybean core collection

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Soyasaponin is a type of glycoside such as steroids, steroidal alkaloids or triterpenes, which enhance the body immunity. In order to efficiently identify genes and markers related to the soyasaponin, we used a 180K Axiom® SoyaSNP array and whole genome resequencing data from the Korean soybean core collection. As a result of conducting GWAS for group A soyasaponins (Aa and Ab derivatives), sixteen significant common markers associated with Aa and Ab derivatives were mapped to chromosome 7. Glycosyltransferase (GT) family protein (Glyma.07g254100) and UDP-glycosyltransferase superfamily proteins (Glyma.07g254600 and Glyma.07g254900) involved in the group A soyasaponin biosynthesis pathway were detected at the range of 43.1 Mb. To determine the causal candidate genes affecting the group A soyasaponin, the derivative content was compared and analyzed through the genotype combinations among markers (AX-90360369, AX-90322128, and AX-90314028) of three candidate genes. The contents of Aa and Ab derivatives were mainly determined by the allele of AX-90322128, a marker of Glyma.07g254600, and 14 novel SNPs variants closely related to Aa and Ab derivatives were identified through functional haplotypes for the genomic sequence of Glyma.07g254600. This study is meaningful in that it effectively predicted and identified genetic factors for soyasaponin using both 180K Axiom® SoyaSNP array and whole genome resequencing data. We plan to convert and verify novel SNPs associated with group A soyasaponins into KASP markers to develop functional markers applicable to all soybean varieties.

Key words: 180K Axiom® SoyaSNP array, Whole genome resequencing, Soyasaponin, Genome-Wide Association Studies, Functional haplotype

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Poster Session

PA-0001

Metabolomic and transcriptomic analysis of mungbean (*Vigna radiata*) sprout under salinity stress

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Mungbean (*Vigna radiata*) sprouts are consumed globally as a healthy food with high nutritional values. Under mild salinity stress, plants accumulate more secondary metabolites to alleviate oxidative stress. Therefore, the treatment of NaCl has been considered as a prominent approach for greater secondary metabolites in many vegetables. In the present study, metabolomic and transcriptomic changes in mungbean sprouts treated with 50 mM NaCl solution were studied to understand the regulatory mechanisms of secondary metabolites in response to salinity stress. Using Ultra Performance Liquid Chromatography, a total of 19 compounds were identified. In general, the contents of phenylpropanoid-derived metabolites, including catechin, chlorogenic acid, isovitexin, p-coumaric acid, syringic acid, ferulic acid, and vitexin, significantly increased under salinity conditions, while contents of isoflavones decreased. Through RNA sequencing, 728 differentially expressed genes (DEGs) were identified under salinity conditions and, 151 and 577 DEGs were down- and up-regulated, respectively. In phenylpropanoid and flavonoid biosynthetic pathway, 31 DEGs were detected. Among them, 10 DEGs encode key enzymes involved in the biosynthesis of the secondary metabolites significantly increased after NaCl treatment. All 10 DEGs were significantly up-regulated. Notably, *MYB*, *WRKY*, and *bHLH* family transcription factors were also identified as up-regulated DEGs. In conclusion, we confirmed that NaCl treatment enhanced the expression of genes associated with phenylpropanoids and flavonoids metabolism and can be considered an appropriate approach to enhance the health-promoting compounds in mungbean sprouts. Furthermore, these findings will provide valuable information for molecular breeders and scientists interested in improving the nutritional quality of legumes.

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PA-0002

Metabolic profiling of mungbean (*Vigna radiata* L.) sprout of 57 genotypes

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Mungbean (*Vigna radiata* L.) is one of major legume crops in Asia, containing high contents of protein and carbohydrate. Mungbean sprouts have higher functional substances, such as flavonoid and isoflavonoid than sprouts of other legumes. Since mungbean was first domesticated in India, diverse genotypes have been cultivated mainly over Asia, and there are variations in the contents of secondary metabolites according to genotypes. In this study, metabolic profiling of mungbean sprouts of 57 genotypes originated from nine countries were performed, including phenylalanine, flavonoid and isoflavonoid by Ultra Performance Liquid Chromatography (UPLC) analysis. In total, 21 compounds were qualified and quantified, such as biochaninA, caffeic acid, catechin, chlorogenic acid, coumestrol, daidzein, daidzin, formononetin, gallic acid, genistein, genistin, glycitein, glycitin, isovitexin, myricetin, neochlorogenic acid, p-coumaric acid, quercetin, resveratrol, t-ferulic acid and vitexin. In most genotypes, chlorogenic acid had the highest contents, followed by catechin. In Sunhwa (VC1973A), a reference genotype, gallic acid was the highest, while chlorogenic acid was not detected. In wild mungbeans with black seedcoat, high amount of isoflavonoids were detected, including coumestrol, daidzin and genistin. Out of 21 secondary metabolites, chlorogenic acid, glycitein, catechin and quercetin had the most variations in order among 57 genotypes. In this study, we conducted metabolic profiling using 57 mungbean genotypes and provided an overview of secondary metabolites in mungbean sprouts.

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PA-0003

Metabolic profiling of seed coat and whole sprout of 10 mungbean (*Vigna radiata*. L) genotypes using Ultra-Performance Liquid Chromatography

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Mungbeans (*Vigna radiata*. L) are one of major legume crops with high contents of carbohydrates and proteins. In this study, antioxidant activity and the contents of individual secondary metabolites of whole sprout and seed coat were evaluated using 10 mungbean genotypes with diverse seed colors and origins. The contents of total phenol and total flavonoid and antioxidant activity had no significant correlation with seed coat color and/or origin, while there were significant variations in each value among genotypes in both seed coat and whole sprout. In total 23 secondary metabolites, including biochanin A, caffeic acid, catechin, chlorogenic acid, coumestrol, daidzein, daidzin, formononetin, gallic acid, genistein, genistin, glycitein, glycitin, isovitexin, kaempferol, myricetin, neochlorogenic acid, p-coumaric acid, quercetin, resveratrol, syringic acid, t-ferulic acid and vitexin were used as standard materials. Out of 23 polyphenols, flavonoids (catechin, isovitexin, myricetin, quercetin and vitexin), isoflavonoids (biochanin A, coumestrol, daidzein, daidzin, genistein, genistin, glycitein and glycitin), phenylpropanoids (caffeic acid, chlorogenic acid, neochlorogenic acid, p-coumaric acid and t-ferulic acid), and others phenols (gallic acid, resveratrol and syringic acid) were identified and quantified. Glycitin and syringic acid were detected only in the seed coat, and chlorogenic acid, coumestrol, genistein, glycitein and t-ferulic acid were detected only in sprouts. We conducted metabolic profiling of seed coat and whole sprout in mungbean. Our study showed the accumulation of individual polyphenolic compounds had tissue- and genotype- specificity. These findings will provide valuable information for molecular breeding to develop mungbean cultivars for sprout production with high contents of polyphenols.

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PA-0004

The effect of hormone (6-BA, ETH, and 2,4_D) treatments on morphological and biochemical traits of mungbean (*Vigna radiata* (L.) Wilczek) sprouts

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Phytohormones have been well known to affect morphological traits in plants. In mungbean, the effect of hormone has been studied on physical traits, but the effect on biochemical traits remain unknown. To investigate biochemical changes in response to hormones (cytokinin (6-BA), ethylene (ETH), and auxin (2,4_D)), the contents of polyphenolic compounds were measured using Ultra Performance Liquid Chromatography (UPLC) under different concentrations of the hormones. After the treatment of three hormones, the thickness of hypocotyl was increased than control, and the length of hypocotyls and roots were decreased. Under the treatment of ETH, the thickness of hypocotyl significantly increased ($p < 0.05$), as the concentration increased. Under the treatments of 6-BA and 2,4_D, the number of lateral roots significant decreased. The contents of total phenols and total flavonoids decreased as the concentration of hormones increased. However, under 2,4_D treatment, total phenols and flavonoids increased as the concentration increased until 10 ppm. Antioxidant capacity also significantly increased only under 2,4_D treatment until 10 ppm. In total, 17 compounds were quantified, including Caffeic acid, Catechin, Chlorogenic acid, Coumestrol, Daidzein, Daidzin, Gallic acid, Genistin, Glycitein, Glycitin, Isovitexin, Myricetin, Neochlorogenic acid, p-Coumaric acid, Quercetin, Resveratrol, and Vitexin. Glycitein was detected only when hormone was treated, while p-coumaric acid was significantly decreased under the treatments. Under high concentration of ETH, coumestrol showed dramatic increase. In this study, we showed morphological and biochemical effect of hormones on mungbean sprout. The results will help to improve food quality of mungbean sprout.

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PA-0005

The Utility of Next Generation Sequencing for Single Event Molecular Characterizations and Stacked Event Product Analysis

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The molecular characterization of genetically modified products has historically relied on Southern blot analysis. However, current Next Generation Sequencing (NGS) technology can efficiently characterize the incorporated transgene (T-DNA) by sequencing the entire plant genome. By generating NGS data with sufficient coverage depth, followed by mapping the sequence read to the transformation plasmid, T-DNA and flanking DNA sequence are identified. Similar to Southern blot analysis, the analysis of mapped reads, over multiple breeding generations, can determine the T-DNA copy number, absence of transformation plasmid backbone and generational stability of the event.

Once characterized, single events are often combined into a stacked trait product through conventional breeding. This conventional breeding process does not affect the stability of the T-DNA, preventing the need for a repeated characterization of the events. Instead, the presence and intactness of the stacked events can be confirmed by comparing the sequence of the characterized single event and the sequence of the event in the stacked product. NGS, specifically NGS of event specific amplicons, is well suited for this purpose.

NGS is an efficient and accurate way of characterizing genetically modified products and determining the presence and intactness of T-DNA in stacked event products. The conclusions drawn from NGS are similar to those historically provided by Southern blotting with the addition of a nucleotide by nucleotide overview of the DNA sequence being investigated.

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PA-0006

Two Different cultivars of *Pyrus ussuriensis* Are Evolutionary Originated in Oriental Pears by Complete Chloroplast Genome Sequences

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Pears are an economically important temperate crop, largely produced by natural and artificial interspecific hybridization, as they are self-incompatible. Due to their long cultivation history, dating back more than 3000 years, predicting their breeding history remains difficult. Therefore, in this study, we sequenced the complete chloroplast genomes of 18 *Pyrus* species and used these sequences for divergent analysis. The length of the genomes ranged from 159,885 to 160,153 bp. All the *Pyrus* species showed an equal number of genes (127 genes) including 83 protein-coding genes, 36 tRNA genes and 8 rRNA genes. We analyzed for divergence among *Pyrus* species and found that most of the genome sequences, gene contents and gene structures are highly conserved with a lower degree of variation. The 1 *Malus* and 18 *Pyrus* cp genomes commonly possessed 17 intron-containing genes (5 tRNA genes, and 12 protein-coding genes). Fifteen genes have one intron, while the *ycf3* and *clpP* genes have two introns. Five intron-containing genes, namely, *ndhB*, *rpl2*, *rps12*, *trnA-UGC* and *trnE-UUC*, are located in IR regions, and one gene, *trnL-UAA*, located in the LSC region appears to have the same intron lengths as those found in *Pomoideae* conserved sequences. We clarified intron length polymorphic sequences over than 10 bp differnces in *clpP*, *ndhA*, *petD*, *rpl22*, *rps16* and *trnK-UUU* genes and designed primers. They could amplify the polymorphic intron regions in these genes. Two *Pyrus ussuriensis* cultivars, Doonggeullebae and Cheongdangrori showed the polymorphisms in all intron length polymorphisms even though they classified with same species. Oriental pear has 5 primary wild species: *P. betuleafolia*, *P. calleryana*, *P. pashia*, *P. ussuriensis* and *P. pyrifolia*. This study suggests that cp genes polymorphisms in a *P. fauriei*, two *P. calleryana* and *P. ussuriensis* and a bunch of *P. pyrifolia* could assign the anticipating evolution process in *Pyrus*.

Keywords: chloroplast genome; *Pyrus ussuriensis*; *Pyrus pyrifolia*; phylogeny; next-generation sequencing

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PA-0007

Transcription factors regulated by LEAFY COTYLEDON 2 in triacylglycerol accumulation

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Triacylglycerol (TAG), used as an energy source for seed germination, is accumulated in the cotyledon during seed development. LEAFY COTYLEDON 2 (LEC2) is known as a master regulator that controls downstream transcription factors (TFs) and genes for seed maturation and TAG biosynthesis. However, the TFs regulated by LEC2 in TAG biosynthesis have been little studied. Here, we identified new seed-specific TFs upregulated by LEC2. The 25 TF candidates up-regulated by LEC2 were decided using microarray analysis in LEC2-expressed leave. Each 25 TFs overexpression in *Nicotiana benthamiana* leaves by Agrobacterium infiltration showed various changes in TAG accumulation. Out of them, the 5 TFs, *ARABIDOPSIS RESPONSIVE REGULATOR 2* (*ARR21*), *AINTEGUMETA-LIKE 6* (*AIL6*), *ETHYLENE RESPONSIVE FACTOR 55* (*ERF55*), *WRKY DNA-BINDING PROTEIN 8* (*WRKY8*), *ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 38* (*ANAC038*), used to analysis of TAG contents. Their overexpression accumulated high TAG contents and were expressed in different seed developing process, respectively. They were transactivated directly or indirectly by LEC2 in transcriptional activity assay. The discovery of novel TFs regulating TAG accumulation with LEC2 will be very helpful in improving the seed oil content.

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PA-0008

Assembly and Analysis of the Complete mitogenome of *Silybum marianum*

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Silybum marianum (known as Milk Thistle) in group of Asteraceae is native to the Mediterranean. The seed of *S. marianum* is known well for antioxidant and therapy of liver disease. Mitochondria which is organelles related to energy generation and synthesis, and degradation involved in numerous metabolic processes. Plant mitogenome varies considerably in size (varying from 200 to 700 kb mostly), gene order, and gene content. Angiosperm mitogenome experience remarkably high rates of gene loss and concomitant transfer to the nucleus and of intron acquisition by horizontal transfer. We assembled the mitogenome to study molecular biology of *S. marianum.* To support this study, we used Oxford Nanopore long-reads sequencing data. Self-looping contig was selected based on high identity contig to result of BLASTn with plant reference mitogenomes. In the result of assembly and annotation, the mitogenome of *S. marianum* size is 407,123bp and 26 protein coding genes, 3 ribosome RNA genes, and 41 tRNA genes were identified. We found five protein-coding genes (ccmFc, cox2, nad2, nad7, rps3) harboring introns and two genes (nad6, nad7) duplicated. Reference mitogenomes of 11 Asteraceae in BLASTn result to high matched hit and 4 outgroups contain 16 orthologous mitochondrial protein coding genes compared with the mitogenome of *S. marianum*. The mitogenome of *S. marianumis* close to these mitogenomes of *Arctium tomentosum* and *Arctium lappa* in the phylogenetic tree analysis using protein coding sequence of the orthologous genes. In this study, we can identify mitogenome of *S. marianum*, and utilize the mitogenome to phylogenetic analysis in Asteraceae.

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PA-0009

Genetic variation among accessions of *Perilla* crop and their weedy types collected from Korea using new developed SSR markers

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Understanding of the genetic variation among crop germplasm is the basis for conservation of genetic resources and breeding programs, however the SSR markers for analyze the genetic diversity and genetic relationship of *Perilla* crop is still lacking. In this study, 17 new SSR primers were developed from RNA sequences, and these new primers were used to analyze the genetic diversity, population structure and genetic relationship between 90 accessions of *Perilla* crop. A total of 100 alleles were detected with an average of 5.9 alleles per locus. The number of alleles per locus ranged from 2 to 14, ranging from 130-315 bp. Genetic diversity (GD) ranged from 0.164 to 0.831, with an average of 0.549. The average PIC was 0.507 and ranged from 0.153 to 0.817, The average GD values were 0.331, 0.588 and 0.389 from the cultivated and weedy types of var. *frutescens*, weedy types of var. *crispa*, respectively. The GD value of the both weed type accessions was higher than cultivation type accessions. According to the analysis results of population structure and genetic relationship, it showed that the genetic relationship between accession of weedy var. *frutescens* and var. *crispa* is closer than the accession of cultivated var. *frutescens*. This study illustrated that the availability of the new SSR primer sets in analyzing the genetic variation between *Perilla* crop accessions, and also could be applied to cultivar identification, conservation of *Perilla* germplasm accessions, genetic mapping analysis, and the designation of important genes / QTLs in *Perilla* crop breeding programs.

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PA-0010

Functions of ARR21 and ARR13 transcription factors in seed fatty acid synthesis

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Type-B ARABIDOPSIS RESPONSEREGULATORS 21 (ARR21) is a seed-specific transcription factor (TF), and They regulate other genes due to cytokinin signals. During seed development, Fatty acid biosynthesis is regulated by many of TFs. Based on previous research, Tobacco leaves overexpressing ARR21 increases triacylglyceride. Therefore, ARR21 is related to fatty acid synthesis. In this study, Loss of function mutant generated by clustered regularly interspaced short palindromic repeats-CRISPR-associated protein 9 (CRISPR-Cas9) system and overexpression lines generated by overexpressing (OX) of ARR21 under the control of 35S cauliflower mosaic virus promoter (CaMV) are obtained. In the quantitative analysis using gas chromatography, the Total fatty acid methyl ester (FAME) of 35S ARR21 is increased. Total FAME of arr21 shows a decreasing tendency. Also, in qualitative analysis, the Component of FA is changed. Type-B ARRs known has gene redundancy, so ARR13 very similar to ARR21 needs to be researched. Accordingly, it seems necessary to produce each arr21, arr13 single mutant, and arr21/arr13 double mutant. Through this study, the genotypic and phenotypic characterization of new TFs involved in the Fatty Acid synthesis is characterized, and the changes in the function of ARR21 and ARR13 with and without cytokinin.

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PA-0011

Transcriptome Analysis Reveals Contributioins of MVA and MEP for Specific Terpenoid Biosynthesis in *Rehmannia glutinosa*

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Terpenoids are naturally occurring compounds involved in respiration, photosynthesis, membrane fluidity, and pathogen interactions and are classified according to the structure of their carbon skeleton. Although most terpenoids possess pharmacological activity, knowledge about terpenoid metabolism in medicinal plants is insufficient. *Rehmannia glutinosa* (*R. glutinosa*) is a traditional herb that is widely used in East Asia and has been reported to contain various terpenoids. In this study, we performed a comprehensive transcriptome analysis of terpenoid metabolism in *R. glutinosa* using two RNA sequencing platforms: Illumina and PacBio. The results show that the sterol, saponin, iridoid, and carotenoid pathways are active in *R. glutinosa.* Sterol and saponin biosynthesis was mevalonate pathway-dependent, whereas iridoid and carotenoid biosynthesis was methylerythritol 4-phosphate pathway-dependent. In addition, we found that homologous genes of key enzymes involved in terpenoid metabolism were expressed differentially and that differential expression of these genes was associated with specific terpenoid biosynthesis. The different expression of homologous genes encoding acetyl-CoA acetyltransferase, 3-hydroxy-3-methylglutaryl-CoA reductase, mevalonate kinase, mevalonate diphosphate decarboxylase, farnesyl pyrophosphate synthase, squalene synthase, and squalene epoxidase was associated with sterol and saponin biosynthesis. Homologous genes encoding 1-deoxy-D-xylulose 5-phosphate synthase were also differentially expressed and were associated with carotenoid and iridoid biosynthesis. These results suggest that biosynthesis of specific terpenoids can be regulated by homologous of key enzymes involved in plant terpenoid metabolism.

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PA-0012

CRISPR/Cas9-multiple guide RNAs construction and case study for targeting the *FAD2* and *FATB* multi-genes in soybean

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CRISPR/Cas9 is a commonly used technique in reverse-genetics research to knock out a gene of interest. However, when targeting a multi-gene family or multiple genes, it is necessary to construct a vector with multiple single guide RNAs (sgRNAs) to knock out. In this research, newly modified Golden Gate cloning method was used to generate multiple sgRNAs-Cas9 vector and save procedure time. Using this vector, Fatty Acid Desaturase 2 (FAD2) and Fatty Acyl-ACP Thioesterase B (FATB) in *Glycine max* were targeted for multiple knock out. The used vectors were pHEE401E_UBQ_Bar and pBAtC_tRNA for *Glycine max* transgenic T0 generation. The genomic DNA were extracted from T0 generation leaves and analyzed by deep sequencing. By the result, hetero lines which has various in/del ratio were obtained and for fatty acid examination, Gas Chromatography was done using most highly edited T1 generation seeds. The GC results showed maximum 84% increased Oleic acid (18:1) and 11% decreased saturated fatty acid (16:0, 18:0). These lines were propagated and confirmed the fixation of hetero genotype to homo genotype and T2 seeds were harvested to measure fatty acid content. In this presentation, combinations of indel mutations in *FAD2* and *FATB* multiple genes and changes in oleic acid and saturated fatty acids will be discussed.

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PA-0013

The transcription factor ERF55 regulates seed triacylglycerol synthesis

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Seed triacylglycerol (TAG) is useful as food and industrial raw material. Transcription factors that promote seed TAG synthesis are useful for oil crops. The purpose of this study is to investigate whether ERF55, a transcription factor regulated by LEC2, a master transcription factor of seed development, regulates TAG synthesis metabolism. To identify the function of ERF55 in TAG metabolism, knock-out mutants were generated with CRISPR/Cas9. The seed TAG of the *efr55* knock-out mutants were reduced than that of the wild-type. Conversely, the TAG of the seeds overexpressed with *ERF55* under the control of the β-conglycinin promoter was enhanced. These results suggest that ERF55 is involved in the regulation of TAG synthesis in seeds. We are going to explore target genes of ERF55 controls the TAG metabolism of seeds.

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PA-0014

Detection of SNPs variations in the seed storage protein gene involved in β-conglycinin

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β-conglycinin is a trimeric glycosylated protein with a molecular weight of about 150-200 kDa. It has a high content of aspartic acid, glutamic acid, leucine, and arginine, and accounts for 34% of the total protein in soybean. Protein composition (*eg.*7S and 11S) can affect the nutritional quality and functional properties of soy protein products. Many cupins, including soybean 7S globulin (β-conglycinin), are known to be major plant food allergens. Therefore, genetic studies on storage proteins such as β-conglycinin are important to reduce soybean allergens and to develop functional varieties with improved quality. SNPs variations in the soybean core collection were detected by functional haplotype analysis for cupin 7S vicilin-like N domains of β-conglycinin subunit (α', β) genes. Glyma.10g246300 is an α' subunit gene of β-conglycinin, and the soybean core collection was classified into two groups in the cupin 7S vicilin-like N domain. An amino acid was substituted from Arg^{427} to His^{427} at the 47.4 Mb of coding sequence. Glyma.20g146200 was classified into 5 groups as a β subunit gene, and 7 non-synonymous and 1 synonymous SNPs were identified at the 38.4 Mb. Soybean varieties with major or minor alleles for both α' and β subunit genes were selected based on SNPs variation information. Genetic information about storage protein in soybeans would be useful in selecting varieties for food manufacturing or utilizing protein components in a variety of applications.

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PA-0015

Genome-wide association study and selective sweeps reveal genetic variations associated Chip Processing clones selected over sixty years in global potato breeding programs

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Although with booming potato chip industry, distinct chip processing clones have been released over the past 60 years, the genetic architecture of their chip processing characteristics remains largely unknown.

The case-control genome-wide association studies with SolCAP SNP array data for Chip Processing clones versus all other market class in the 359-line potato diversity panel (Jo et al 2022) were performed to detect significant signals on chromosome 10. The signals were reproduced in the GWAS test using the strata-corrected 190-line panel and also genomic scans employing selective sweep approaches such as XP-CLR and PCAdapt. Hundreds of regions across the genome that had been differentially selected were those involved in carbohydrate-related genes or loci and various transcription factors, indicating to be associated with the improvement of chip processing performance of potato cultivars. The results could have implications for genomics-assisted breeding for the improved chip processing characteristics in potato.

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PA-0016

Analysis of genetic diversity and population structure among cultivated potato clones from Korea and global breeding programs

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Characterizing the genetic diversity and population structure of breeding materials is essential for breeding to improve crop plants. The potato is an important non-cereal food crop worldwide, but breeding potatoes remains challenging owing to their auto-tetraploidy and highly heterozygous genome. We evaluated the genetic structure of a 110-line Korean potato germplasm using the SolCAP 8303 single nucleotide polymorphism (SNP) Infinium array and compared it with potato clones from other countries to understand the genetic landscape of cultivated potatoes. Following the tetraploid model, we conducted population structure analysis, revealing three subpopulations represented by two Korean potato groups and one separate foreign potato group within 110 lines. When analyzing 393 global potato clones, country/region-specific genetic patterns were revealed. The Korean potato clones exhibited higher heterozygosity than those from Japan, the United States, and other potato landraces. We also employed integrated extended haplotype homozygosity (iHS) and cross-population extended haplotype homozygosity (XP-EHH) to identify selection signatures spanning candidate genes associated with biotic and abiotic stress tolerance. Based on the informativeness of SNPs for dosage genotyping calls, 10 highly informative SNPs discriminating all 393 potatoes were identified, converted into KASP markers to validate. Our results could help understanding a potato breeding history that reflects regional adaptations and distinct market demands.

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PA-0017

Complete chloroplast genome of *Atractylodes japonica* (Asteraceae) and problems in species identification of *Atractylodes*

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Atractylodes japonica Koidz. ex. Kitam. (Asteraceae) is a perennial plant and its rhizome has been used as traditional herbal medicine in Korea, China, and Japan. Susceptibility to ionizing radiation is observed in *A. japonica* that suggested doses of 50 - 60 Gy gamma rays and 15 - 25 Gy proton beams has been reported for mutation breeding. We assembled the complete chloroplast genome sequence of *A. japonica* native to Korea. The total length of the circular genome was 153,207 bp, which comprised a large single-copy (84,265 bp), a small single-copy (18,657 bp), and a pair of inverted repeat (25,147-bp each) regions. Similarity-based gene annotation predicted 132 genes which included 87 protein-coding genes, 37 transfer ribonucleic acid (RNA) genes, and eight ribosomal RNA genes. Phylogenetic analysis based on multiple alignments of 78 protein-coding sequences in CP genomes using the maximum likelihood method using 13 genomes from six *Atractylodes* species previously reported showed intermingled clustering of five species, *A. macrocephala*, *A. chinensis*, *A. koreana*, *A. lancea*, and *A. japonica*. This indicates ambiguous species identification based on morphological characters in *Atractylodes.*

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PA-0018

High quality genome assembly of *Brassica tournefortii*

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Saharan mustard (*Brassica tournefortii*) is an invasive plant species in the Brassicaceae family that exhibits remarkable abiotic stress resilience. Originating from the Mediterranean basin, North Africa, and Asia, *B. tournefortii* is a rapid-cycling oilseed species well adapted to semi-arid and arid habitats as well as poor soils. The oil has a high erucic acid (C22:1⊿9) content that is ideal for industrial products, such as biofuels, due to its superior ignition performance and oxidative stability. As a drought-avoidant winter annual, *B. tournefortii* possesses a quicker life cycle and greater harvest index than its commercial counterpart, canola (*Brassica napus*). Water availability is the primary factor that constrains the cultivation of bioenergy crops and an ideal biofuel feedstock will not compete with established agricultural demands for food or other resources, such as water availability and arable land. *B. tournefortii* spontaneously grows in desert regions, making the plant particularly well suited to serve as an alternative crop that can be grown using seasonal moisture with very limited or no supplemental irrigation. Here we report a high-quality, 358.4 Mbp assembly for the *B. tournefortii* genome constructed from PacBio, Illumina, and Hi-C sequencing data. The final assembly comprises eleven scaffolds corresponding to the eleven chromosomes, with a scaffold N50 value of 34.5 Mbp. We investigate the possibility of biofuel utilization in this species and ways to improve the agronomic performance of other *Brassica* oilseed crops. Our analysis provides insight into the molecular basis of invasion and strengthens our understanding of adaptations to arid environments.

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PA-0019

Investigating salt tolerance in cowpea germplasm using genome-wide association study

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Cowpea (*Vigna unguiculata* L.) is one of the most important grain legumes; it is well-adapted to various abiotic stresses and is cultivated worldwide. However, increased soil salinity due to climate change is reducing crop yields despite increasing food demands. For cowpea, high soil salinity causes the accumulation of ion chloride content and protein degradation in leaves. In this study, we evaluated cowpea salt tolerance and identified candidate genes related with salt tolerance. Four traits (LSS; leaf scorch scale, LCC; leaf chlorophyll content, ion chloride content, ion sodium content) were investigated to evaluate the salt tolerance. A total of 401 cowpea germplasms were genotyped with the Cowpea Iselect Consortium Array containing 51,128 single nucleotide polymorphism (SNP) markers. Association analysis between phenotypic traits related with salt-tolerance and genotypes was conducted using Mixed Linear Model (MLM) in QTLmax (www.qtlmax.com). According to the GWAS results, a total of 12 SNP markers were associated with salt-tolerance in three different chromosomes (Chr. 6, 7, and 10). As a result of haplotype analysis, we founded that the SNP markers founded in LSS and LCC traits move in association with neighboring SNP markers. These results of our study can enhance the understanding of salt-tolerance in cowpea and can be used to select salt-tolerant parents for breeding programs.

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PA-0020

Species delimitation within subgenus *Anguinum* (genus *Allium*) inferred from complete plastid genome and nuclear ribosomal DNA sequences

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Allium ochotense and *A. microdictyon* belonging to subgenus *Anguinum*, are commonly known as 'Siberian garlic' or 'Alpine leek', and widely used as edible and medicinal plants due to their medicinal properties. These two *Allium* species are taxonomically unclear, and often misidentified into a species, *A. victorialis*. Here, this study attempted to reveal species delimitation between two *Allium* species using complete plastid genome and nuclear ribosomal DNA sequences for identifying these species by molecular markers. Based on sequence variations and phylogenetic results of complete plastid genome and ribosomal DNA, six individuals of *Allium* species collected from different locations could be divided into two types, Ulleung- and Heungjeong-types. By comparison of sequences between two types, over 170 single nucleotide polymorphisms (SNPs), and over 80 Insertion/Deletion (InDels) were observed in their plastid genome sequences, and twenty SNPs and one InDel were observed in their 45S ribosomal DNA sequences. Phylogenetic analyses using plastid genome and ribosomal DNA sequences also indicated that *Allium* individuals of the Ulleung-type formed an independent clade from other *Allium* species. In addition, sequence depth analysis of ribosomal DNA sequences revealed that individuals collected from Jinbu and Seoraksan had both two types (Ulleung- and Heungjeong-types) of ribosomal DNAs. Consequently, molecular markers were developed using sequence variations to identify these two types. We believe that newly developed markers in this study will contribute to identify these species and their genotypes for molecular breeding, and will be helpful for understanding the interspecies relationship of *Allium* species. This research was supported by a research grant from KIST ORP program (BlueBell Research program 2E30650).

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PA-0021

Identification of noble candidate gene associated with sensitivity to phytotoxicity of etofenprox in soybean

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Phytotoxicity is caused by the interaction between plants and a chemical substance, which can result in critical damage to plants. Understanding the molecular mechanism underlying plant-chemical interaction is essential to manage pests in crop fields and avoid phytotoxicity of plants by insecticides. Some Korean soybean cultivars including Danbaek and Kwangan showed sensitivity to phytotoxicity of etofenprox (PE), resulting in leaf shape shrinkage damage and finally critical yield loss. Genomic region responsible for sensitivity to phytotoxicity of etofenprox (PE), controlled by a single dominant gene, was detected by constructing high density genetic map using recombination inbred lines (RILs) in soybean. The genomic region of ~80 kbp containing nine genes was identified on chromosome 16 using high-throughput single nucleotide polymorphism (SNP) genotyping system using two different RIL populations. Using re-sequencing data of 31 genotypes, nonsynonymous SNPs were identified in three genes, encoding glycosylphosphatidylinositol - anchored protein (GPI-AP), resulted in critical structure disruption on active site of the protein. This structural variation of GPI-AP may change various properties of the ion channels which are the target of pyrethroid insecticide including etofenprox. This is the first study to identify the candidate gene and develop SNP markers associated with PE. This study would provide genomic information to understand mechanism of phytotoxicity in soybean and functionally characterize the responsive gene.

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PA-0022

콩에서 화분매개곤충 유인형질 연관 유전자 탐색

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최근 이상기후와 과도한 해충 방제 등으로 인해 꿀벌의 서식지가 사라지면서 꿀벌의 개체수가 급격하게 감소하는 '군집 붕괴 현상'이 일어나고 있으며 이 현상으로 국내 약 60억 마리의 꿀벌이 사라져 전국 양봉농가 곳곳에서 피해가 속출하고 있다. 국내 과수 및 채소작물의 연간 생산액 약 12조원의 절반 정도 꿀벌 화분 매개를 통해 파생된 것으로 추정되어 꿀벌 개체수의 감소는 농업 경제 전반에 큰 영향을 미칠 것으로 예상되어 대체 밀원지 연구가 필요하다. 콩은 자식성 작물로 화기구조상 낮은 타식율을 보이고 있으나 매개충 이용 시 타식을 증가시키며 꿀벌이 화분 매개로 가장 효과가 컸다. 벌들은 당 함량 25% 이상인 꿀을 선호하는데 콩은 그 이상의 함량을 보유하며 벌이 선호하는 꿀의 형태를 가지고 있어 꿀벌이 꽃에서 꿀을 채집하는 정도는 화기 내 꿀의 양, 성분과 연관이 있고 특히 당 조성과 연관이 높음이 보고되고 있다. 본 연구에서는 콩에서 화분매개곤충(꿀벌) 연관 유전자탐색을 위해 콩 핵심집단 396자원을 활용하여 콩 화기내 유리당조성을 분석하고 관련 유전자탐색을 위해 Genome wide association study (GWAS)분석을 실시하였다. 콩 화기 내 꿀의 유리당 조성 분석을 위해 콩의 Nector를 추출하여 HPLC로 당 분석(Glucose, Fructose)을 실시하였고, 유전자탐색을 위해 고밀도Single Nucleotide Polymorphism (SNP) array Chip을 이용한 유전체 정보를 GAPIT3활용하여 GWAS분석을 실시하였다. 결과, Glucose 함량에 대한GWAS 분석 결과 9번 염색체 및 12번 염색체에서도 연관성 높은 QTL을 확인하였다. Fructose의 경우 9번 염색체에서 2개의 SNP가 높은 연관성을 보였는데 이 중 하나는 Glucose의 결과에서 나타난 SNP와 일치하였다. 추가적으로 Linkage Disequilibrium (LD) 분석을 통해 확보된 영역 내에서 후보유전자를 탐색하고 추후 검증을 통해 최종적으로 화분 매개 곤충 유인 연관 유전자를 탐색할 경우, 자식성 식물에 화분매개충을 유인하는 인자를 도입으로 수정률 증대에 따른 수량 증가와 향후 대체 밀원용 품종 개발에 활용할 수 있을 것이다.

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PA-0023

Identification of novel annexin gene in rye (*Secale cereale* L.) and observation of the gene expressions under abiotic stresses

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Rye (*Secale cereale* L.) is one of the most cold-tolerant cereal crops and also known to be tolerant to diverse abiotic stresses. Due to the large and highly repetitive genome of rye, utilization of rye genome has been very limited. However, with help of sequencing and bioinformatic technologies, as well as recently available draft genome sequence many studies have been conducted, Plant annexins are components of calcium-signaling networks. They are encoded by multigene families and implicated in the regulation of plant development as well as protection from abiotic stresses. The annexin gene family has been identified in multiple plant species but none of them have been investigated in rye. In this study, we identified 12 novel rye annexin genes through investigating recently published rye genome and classified them into five groups according to phylogenetic analysis with other plant species. Protein motif analysis, chromosomal localization, and analysis of *cis*-element in promoter have been conducted. The plant tissue-specific gene expression was observed using public RNA-seq data. Furthermore, the expression of rye annexin genes under diverse abiotic stresses, including cold, heat, NaCl, and polyethylene glycol (PEG), were observed via real-time PCR analysis. The results of this study will provide a basis for further functional characterization of rye annexin genes in response to abiotic stresses.

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PA-0024

SNP detection and map construction in wild chrysanthemum using genotyping-by-sequencing

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Chrysanthemum (*Chrysanthemum morifolium* Ramat.) is one of the most important ornamental and medical plant belonging to Asteraceae family. It is believed to be first cultivated in China around the 15th century BC and has a long history of cultivation. Wild chrysanthemum species serve as a good genetic resources because they are known to harbor a various favorable resistance genes that can be introduced into chrysanthemum cultivars via intergenic or interspecific breeding. Therefore, understanding the genetic basis of wild chrysanthemum is necessary to identify agronomically important genetic factors or genes. In this study, we performed genotyping-by-sequencing (GBS) to detect genetic variation in the 152 F_1 progenies derived from a cross between two diploid and wild *Chrysanthemum* species *C. boreale* (‘CWT-2’) and *C. makinoi* (‘CWT-8’). As a result, 80.92% of raw reads were mapped to the genome of *C. boreale* (unpublished data by S. Y. Won) with an average of 3,180,142 mapped reads per sample. A total of 2,589 single nucleotide polymorphisms (SNPs) were detected among the population, and the final SNPs after removing redundant genotypes were assigned into nine linkage groups and used to construct genetic linkage map. We observed high level of collinearity between the linkage map and the genome assembly, supporting their high quality. Based on this map, further study for additional genetic analysis will provide important information of genome structure and functional genomics, and reveal insights for further research in chrysanthemum breeding.

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PA-0025

Plastid Phylogenomics and Evolution of Araliaceae

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Using maternally inherited plastid genome data, phylogenetic reconstruction and divergence time estimation were performed to explore the evolutionary trajectory of Araliaceae species. A total of 89 plastid genome sequences were used, 12 of which were newly assembled in this study. Gene order and genome structure were highly conserved in the Araliaceae plastomes, even at the boundaries of IR and single-copy regions. Phylogenetic reconstructions using four different datasets indicated phylogenetic discordances within the Asian Palmate group. Divergence time estimation indicated that the split between Araliaceae and Apiaceae occurred after the K-Pg extinction, and two subfamilies within Araliaceae diverged in the Middle Eocene. Within the subfamily Aralioideae, divergence times of five major groups were estimated at around 22 Ma during the Late Oligocene to the Early Miocene, and most clades diverged around 14 Ma in the Middle Miocene. Splits of two subfamilies and most clades in Araliaceae occurred at two climatic optima, the Mid-Eocene Climatic Optimum (40 Ma) and the Mid-Miocene Climatic Optimum (14 Ma), indicating that global warming events have triggered the divergence of Araliaceae species as adaptive radiation, especially in the Middle Miocene. This implies that the adaptive radiation in the Middle Miocene results in phylogenetic discordances within the Asian Palmate group. Our results provide the evolutionary trajectory of Araliaceae and advance our current understanding of the evolution of Araliaceae species.

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PA-0026

CRISPR/Cas9-mediated *Arabidopsis FBN3* mutants and their function in high light stress

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Fibrillins (FBNs) are lipid-associated proteins present in chloroplast. They present as structural proteins in thylakoids, stroma, and plastoglobule (PG). In higher plants, *FBNs* consists of a small gene family and play important roles in plant growth, development, responses to hormone and stresses. The main functions of FBNs studied are related to chloroplast development and resistance to highlight stress, acting as an inhibitor of jasmonate-induced senescence, and related to osmotic stress to function of seed germination and cotyledon formation. The function of FBN3 under abiotic stress including high-light stress has not yet been identified. Interestingly, *FBN3* exists singly in rice or tomato, but in Arabidopsis, tandem duplicated as *FBN3a* and *FBN3b* exist on the same chromosome. In this study, in order to investigate whether there is a single function or overlap of functions between these, a homozygous mutants, which lost *FBN3a* and *FBN3b* function by inserting T-DNA, was obtained and homozygous *fbn3a 3b* double knockout mutants was constructed using CRISPR/Cas9 system. It was confirmed that the photosynthetic capacity of wild-type and T-DNA single mutants was restored to a certain level at 48 hours under high light stress, but CRISPR *fbn3a 3b* double knockout mutant lines #10-8 and #21-11 did not. These results suggest that *FBN3a* and *FBN3b* function redundantly and are involved in protection against light stress.

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PA-0027

Analysis of transcriptome between GM soybean and Non-GM soybean using RNA sequencing and qRT-PCR

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Transcriptome studies have been mainly used to discover specific genes expressed in plants under certain conditions and environmental variations. this study was carried out for analysis of transcriptome between with GM soybean overexpressing *PfFAD3-1* and Non-GM soybean. we selected three transgenic soybeans lines with a copy of T-DNA and analyzed the integration site, The omega-3 content of each GM soybeans increased by about four times compared to control soybean(Non-GM). In order to analysis the expression patterns of the genes related to the fatty acid biosynthesis pathway in transgenic soybeans, we designed primers to amplify fatty acid-related endogenous genes such *GmFAD3* and transgenes. As a result of analyzing the expression of the transgenes in plant tissues, the genes expression was the highest in the seed. this confirm the influence of the seed-specific expression promoter. RNA-seq analysis is under way to identify differently expressed genes between comparative crops. theses comparative analysis can provide more scientific information for safety assessment of GMOs along with omics such as genome, metabolome, but more research and reliable data will be needed.

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PA-0028

Novel allele of *fad2-1a* from an EMS induced mutant soybean line, PE529 produced elevated oleic acid

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Soybean seed oil typically contains approximately 23% oleic acid. Increased oleic acid is beneficial for cardiovascular system and oxidative stability of oil. Therefore, increased oleic acid has been a primary goal of the soybean breeders to improve oil quality. Soybean seed with both mutant alleles of *FAD2-1A* (*S117N* from 17D) and *FAD2-1B* (*P137R* from PI 283327) genes has been reported to produce more than 80 % of oleic acid in oil. To find out a new mutant allele of *FAD2-1A*, a mutant population was developed from the ethyl methanesulfonate (EMS) induced soybean cultivar Pungsannamul. Mutant lines with an elevated oleic acid were selected to discover a new allele of *FAD2-1A* with targeting induced local lesions in genomes (TILLING) method. A mutant line, PE529 carrying a novel allele of *FAD2-1A* gene has been identified. A SNP in PE529 induced conversion of amino acid from a tryptophan to a premature stop codon at position 293 in the *FAD2-1A* gene, we designated this mutation as *W293stop*. F_2 seeds from a cross of PE529 and PI 283327 were analyzed for oleic acid levels. The result showed that seeds with greater than 80 % oleic acid were identified, indicating that a novel allele from PE529 can be used to produce soybean oil with more than 80 % oleic acid content. Soybean with a novel allele could be a useful genetic resource for developing the quality of oil in breeding programs.

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PA-0029

Genome-wide association study (GWAS) for seed starch content in soybean

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Soybean (*Glycine max* (L.) Merr.) is one of the most important food resources. As soybean are an excellent source of diets, they are used as an ingredient for nutritious foods and various traditional foods. Starch is an important nutrient as an energy source for humans and animals. Legumes such as mung beans, common beans and peas have about 34 to 55% starch content, while soybeans contain less than 1% of starch content in the seed. The high starch content in the seed is related to taste, flavor, and the softer texture, which improve the quality of processed foods. In this study, we identified the genomic regions associated with starch content by genome wide association study (GWAS) with 409 cultivated soybean collections. Cultivated soybean accessions were grown over two years to determine starch content by the enzymatic assay and genotyped with the 180k Soya SNP array. The mean starch content was 1.5% with a range of 0.4-4.6% in 2020. The starch content averaged 1.3% with a range of 0.7-2.5% in 2021. The starch content of core collections across two years averaged 1.4% and ranged from 0.4 to 4.6%. As a result of GWAS, the most significant SNPs were located on chromosomes 8 and 10 for the averaged starch content across two years. Further researches will be required to identify the candidate genes for starch content in soybean. The information in this study will help to promote uses of soybean starch in breeding program and food industry.

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PA-0030

Genomic editing of rice Late Pollen specific expressed genes(LP) using CRISPR/Cas9 system

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In flowering plants, studies of pollen germination and post-germination development are significantly important for understanding plant reproduction and crop yield. However, little is known about the molecular mechanisms of pollen germination and pollen tube growth in rice. Here, based on microarray data analyzed for developing anthers and pollen grains, we propose four rice genes such as *OsGNL2*(GNOM-Like 2), *OsSKS*(SKU5 similar family), *OsCNGC4/5*(Cyclic nucleotide-gated ion channel 4/5), and *OsFBO16*(Cyclin-like F-box domain containing protein), showing late pollen-preferred expression in anatomical expression analysis. To identify whether these genes are involved in the key processes of late pollen development, we generated transgenic plants containing CRISPR/Cas9 vector targeting exon 1 or exon 2 of candidate genes using the pRGEB32 vector. Sequencing revealed CRISPR/Cas9 system specifically causes nucleotide deletions, insertions, or frameshift mutations in the target region, resulting in a premature stop codon. We examined the expression levels of candidate genes by qRT-PCR in genome-edited plants and found that the transcript levels of target genes significantly decreased in mutant lines compared to wild type. Moreover, we evaluated that these candidate genes play important roles in fertilization by assessing spikelet fertility. The rice grain yield was greatly affected by the CRISPR/Cas9 system. Especially, *OsSKS* and *OsCNGC4/5* genome-edited mutants exhibited extremely low frequencies on fertility which are consistent with their genome-edited pattern and expression levels. Therefore, our results strongly suggest that these genes could be associated with important functions on pollen development and fertility in rice.

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PA-0031

Insight of Haplotype Effect on the Candidate Genes Related to Preharvest Sprouting

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The dormancy of seeds is a property related to the direct survival of plants. Seed dormancy is characterized by environmental conditions that are difficult for plants to live in or prevent seeds from germinating without development. Genetic information can be preserved to date without extinction under adverse environmental conditions related to these characteristics. The sudden climate change caused by global warming is fatal to these less bred varieties. The seeds germinate during the harvest season while the crops depend on the panicles of typhoons and floods called pre-harvest sprouting (PHS). We detected candidate genes by designing genomic data-based testing, such as genome-wide association studies (GWAS). PHS-related phenotype values were measured and used in GWAS in mid-southern Korea. It also incorporated GWAS and Linkage disequilibrium to correlate the amino acid levels of several genes through the Haplotype of candidate genes explored. This study suggests a method to efficiently extract genetic factors from agricultural properties where many other noisy factors, such as environmental factors, operate.

Keywords: Pre-harvest sprouting, Linkage disequilibrium, GWAS, Haplotype

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PA-0032

Comprehensive analysis of LTR-RT activation in *Panax ginseng*

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Activation of long terminal repeat retrotransposons (LTR-RT) by environmental change and stress influence not only gene structure but gene expression regulation in plants. However, LTR-RTs activation of *Panax ginseng* in response to stress has not been studied in detail. Here, for the first time, we investigated whether heat and Methyl jasmonate (MeJA) treatment induces stress-specific LTR-RT activation in *P. ginseng*. To conduct a comprehensive analysis of LTR-RTs throughout the complete genome, we initially characterized intact LTR-RTs using the high-quality reference genome in pseudochromosome level (TYP1; Unpublished). A total of 13,311 intact LTR-RTs, 11,388 *Gypsy* type (85.6%) and 1,923 *Copia* type (14.4%), were identified in *P. ginseng* reference genome sequence. Using these LTR-RT datasets, we discovered that heat treatment led to hypermethylation of the LTR-RTs, especially in the CHH sequence context. Integrated transcriptomic and epigenomic analysis identified that one *Retrofit* element was transcriptionally active under MeJA treatment. Moreover, amplification LTRs of eclDNAs followed by sequencing (ALE-seq) detected that one *Sire* element is likely active in response to MeJA treatment. Our findings indicate that MeJA treatment has the largest impact on LTR-RT activation in *P. ginseng*.

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PA-0033

Transcriptome analysis of two germplasms sweetpotatoes with different taste characteristics according to storage period

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The taste characteristics of sweetpotato are one of the most important factors for consumers. Sweetpotato is known to increase sugar content due to starch degradation during storage after harvest. However, the degree of this change varies depending on the germplasm, and the mechanism and related factors have not been clearly known. In this study, starch content, moisture content, free sugar content, and RNA-seq analysis were performed according to storage period using germplasm of high sugar content (‘Sodammi’) and germplasm of low sugar content (MI2018-20-09). The starch content of the two germplasms decreased with the storage period, and MI2018-20-09 was higher than that of ‘Sodammi’. The moisture content showed a tendency to increase in MI2018-20-09, but the ‘Sodammi’ was higher than in MI2018-20-09. Total soluble sugar content increased in ‘Sodammi’ of fresh type. In addition, the maltose content showed the highest in ‘Sodammi’ of steam type. Transcriptome analysis of the two germplasms showed different trends. In ‘Sodammi’ and MI2018-20-09, there were increased DEGs of 310 and 270, respectively, during the storage period. In increased DEGs of ‘Sodammi’, there were genes related to glycolysis/gluconeogenesis and fatty acid degradation. On the other hand, increased DEGs of MI2018-20-09 contained genes related to ribosome and protein processing in the endoplasmic reticulum. The results of this study will be used as basic data contributing to the breeding of varieties with excellent taste through related genes according to the storage period in two germplasms showing different textures after harvest.

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PA-0034

Transcriptome analysis by RNA-seq reveals genes related to flower coloration in *Dendrobium* mutants

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Dendrobium is widely used in herbal medicine containing many kinds of active ingredients, mainly grown in tropical and subtropical and Asia and eastern Australia. In this study, we performed RNA-sequencing to obtain comprehensive trascriptome analysis and identified putative genes involved in flower coloration in RB008A (Cont), RB008A-S29 (yellow broad stripe type), RB008A-S30 (white type), and RB008A-S34 (yellow marginal stripe type). A total of 86.9 Gb reads were generated for one control (RB008A) and three mutants (S29, S30, and S34) and finally yielded 70,653 representative transcripts having an average length of 1,590 bp, of which 59,171 (83.75%) were annotated against various databases. Expression profiling of trancripts identified the lowest 1,231 (C_vs_S34) and the highest 10,593 (S29_vs_S34) differentially expressed genes (DEGs) among in the six groups. Those DEGs estimated that the representative pathways were “biosynthesis of secondary metabolites”, including phenylpropanoid biosynthesis, and anthocyanin biosynthesis by KEGG enrichment analysis. Thus, we investigated genes related to flavonoid and anthocyanin pathway, which counted 46 DEGs. Our results provide a resource for understanding gene functions and should also be useful in the further studies of flower coloration in *dendrobium*.

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PA-0035

밀 핵심집단의 주요 농업형질에 대한 전장유전체연관분석

이명희, 김경민, 김경훈, 이고은, 최준용, 강천식, 고종민, 최창현*

전라북도 완주군 이서면 혁신로 181 국립식량과학원

밀 핵심집단(Core-set)의 구축은 유전적 다양성이 확보된 유전자원을 보다 효율적으로 사용하고 관리할 수 있으며, 복잡한 형질의 표현형 및 DNA 다형성의 유전형을 포함하여 자연 변이에 대해 집중적으로 조사하는 효율적인 방법이다. 본 연구에서는 아시아, 유럽, 아메리카, 아프리카, 유라시아, 오세아니아 등 약 60여 개국의 1,969개 germplasm으로부터 614개의 한국형 밀(*Triticum aestivum* L.) 핵심집단을 구축하였다. 2018년부터 2021년 동안 국립식량과학원(완주군) 밀연구포장에서 주요 농업형질(출수기, 성숙기, 초장, 수량구성요소 등)을 조사하였으며 'Axiom Wheat Breeder 35K Genotyping Array'를 사용하여 SNP data base를 확보하였다. 밀 핵심집단의 표현형 및 유전자형 정보를 활용하여 Genome-wide Association Studies (GWAS)를 수행함으로써 6 배수성 밀의 농업적 특성과 관련된 유전자좌를 식별하였다. 유전자형과 표현형 간의 상관관계는 Blink, MLM, MLMM의 각 모델별로 수행하였으며, -log10(p)>5인 GWAS 결과에 유의한 SNP를 선발하였다. 유전형 분석 결과 약 35,000개의 SNP 중 94개가 수확량 구성 요소 및 생육 특성을 포함한 여러 농업적 특성과 관련된 SNP로 선택되었다. 선택된 SNP 마커는 앞으로 품종개발을 위한 도구로서 활용될 것으로 기대된다.

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PA-0036

Genetic diversity of plastid genome and 45S rDNA sequences in genus *Ligularia* (Asteraceae)

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Ligularia fischeri and *L. stenocephala* belonging to genus *Ligularia* (Asteraceae), are recognized as a useful biological resource due to their pharmacological efficacy. However, *Ligularia* species distributed in South Korea have trouble in classification and identification because of their ambiguous morphological characters. In this study, plastid genome and 45S rDNA sequences of 6 individuals from two *Ligularia* species were newly assembled using the dnaLCW (*de novo* assembly of Low Coverage Whole-genome sequencing) method, and were used for sequence comparison and phylogenetic reconstruction. Sequence variation and phylogenetic result indicated that three individuals of *L. stenocephala* were distinguished from other *Ligularia* species, and formed their own clade.

In contrast, *L. fischeri* and its closely related taxa formed three clades, but phylogenetic relationships between them remain uncertain. All *Ligularia* species included in this study were classified into five groups based on phylogenetic results, and molecular markers for identifying genotypes of these five groups were developed. We believe that developed molecular markers in this study will be useful for identifying genotypes of *Ligularia* species, further contribute to the molecular breeding of these species.

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PA-0037

Combination of Chromosome-level Assembly of Agaricus bisporus and Comprehensive Transcriptome Analysis on Mechanical Stress Condition Reveals Browning Correlated Genes

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The edible button mushroom *Agaricus bisporus* is a popular food worldwide including South Korea. We performed de novo genome assembly with South Korean white-colored cultivar of *A. bisporus*, KMCC00540. After generating scaffold level genome sequence, we inferred chromosome level assembly by genomic synteny analysis with representative *A. bisporus* strain H97 and H39. KMCC00540 genome had 13 pseudochromosomes with 33,030,236 bp covering both strains mostly. Comparative genomic analysis with cultivar H97 indicated most of genomic regions and most of annotated proteins were shared (over 90%), ensuring our cultivar to be used as one of representative cultivar. Meanwhile, *A. bisporus* suffers from browning even by small mechanical stimulus during transportation which significantly lowers its commercial values. To identify which genes are responding to mechanical stimulus and inducing browning, we performed time-course transcriptome analysis based on our de novo assembled genome data. Mechanical stimulus induces long fatty acid ligase activity related genes were highly up-regulated by mechanical stimulus while melanin biosynthetic genes were up-regulated especially in early time point. In summary, we assembled chromosome level genome information of *A. bisporus* of Korean strain and identified which genes are responding to mechanical stimulus, which are key hints to improve post-harvest control of *A. bisporus* by any biological methods.

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PA-0038

Comparative genomic analysis of *nucleotide-binding leucine-rich repeat* (*NLR*) genes reveals the structure of resistance gene clusters in pepper (*Capsicum* spp.)

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Nucleotide-binding leucine-rich repeat (NLR) domain is important for plant disease resistance genes by recognizing pathogens or turning on the plant immune system against external stress. Even its importance for breeding resistant crops, highly repetitive NLR gene structure and hundreds of homologous NLR genes make it difficult to fine-map the resistance gene in crops. Here, we comprehensively identified NLR genes using twelve pepper genomes combined with resistance gene enrichment sequencing (RenSeq) approaches. A total of eleven pepper accessions, six *Capsicum annuum*, and five other *Capsicum* species accessions, were used for RenSeq analysis. All RenSeq reads were aligned to twelve pepper genomes and predicted an average of 765 intact NLR genes. These predicted genes were used to construct the pan-NLRome in *C. annuum.* In addition, RenSeq reads were aligned to the most high-quality pepper genome, 'Dempsey', and used to extract SNPs and small indels on a genome-wide scale. These two genomic datasets, pan-NLRome and genome-wide variants in pepper genome were applied to the NLR clustered region compared with other pepper genomes. These methods could reveal the genomic differences and clarify the candidate resistance genes in *Phytophthora* root rot (*Pc5.1*) and root-knot nematode resistance locus (*Me7*). Combined with bulked segregant analysis (BSA) RenSeq method, we found one strong candidate gene for root-knot nematode resistance in the *Me7* locus. These genomic approaches could be helpful to reveal the NLR resistance gene in crops that have complex genome structures, such as peppers.

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PA-0039

Genetic Diversity of *Adenophora verticillata* (Pall.) Fisch. using SSR Markers

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Adenophora verticillata (Pall.) Fisch. has been used food and medicinal purposes in Eastern Asia including Republic of Korea. To date there are no studies on the genetic diversity of *A. verticillata*. The present study aimed to study the genetic diversity of *A. verticillata* variants using genome-wide Simple Sequence Repeat (SSR) markers. The genetic diversity of 40 variants of *A. verticillata* habitats and cultivated in of different areas, was analyzed using 8 genome-wide SSR markers by Park *et al*(2017). The results revealed that the genetic variants were very diverse, and genetic analysis using the 8 genome-wide SSR markers revealed high diversity among the variants. In addition, differences in external morphological characteristics such as stem color, leaf shape, and flower color were confirmed for each clade, and the results of the 8 genome-wide SSR marker were supported. It is expected that the development of the true *A. verticillata* cultivar, by studying the system and group selection, can be achieved by genetic analysis using the developed markers, for generating a genetically fixed lineage and group selection.

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PA-0040

한국콩 핵심집단의 100립중 관여 전장유전체연관분석

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전라북도 완주군 이서면 혁신로 181 국립식량과학원

콩 종실의 100립중은 수량구성요소의 하나로서 우리나라 용도별 콩 이용에서 매우 중요하여, 소립종은 나물용콩으로, 중대립종은 두부 및 장류용으로 그리고 대립종은 밥밑용으로 종실의 크기에 따라 이용하여 왔다. 본 발표에서는 우리나라 콩 핵심집단 430자원의 종실의 무게를 좌우하는 유전적 요인을 해석하기 위하여 2021년 전주에서 재배생산된 콩 종실과 각 자원의 180k soybean array의 SNP 유전자형을 이용하여 종실중의 변이에 관여하는 유전체상의 요인을 분석하였다. 분석에 사용한 핵심집단은 4개의 집단으로 구성됨을 확인하였고, 종실의 무게에 관여하는 유전체 상에서 8개 영역이 고도로 유의하게 종실의 무게에 관여하는 것으로 나타났다. 8개의 영역을 기존에 보고된 GWAS-QTLs 영역과 비교한 결과, 6개의 영역은 기존 보고와 0.3~2 M bp의 거리에 한국 콩 핵심집단의 종실 무게 관여 유전요인이 존재하는 것으로 나타났고, 2개 염색체 (8번, 17번)에서는 신규한 GWAS-QTLs일 것으로 추정되는 결과를 얻었다. 이러한 결과는 추후 1~2년간의 연차변이 데이터를 축적하여 연차간 변이를 보정한 결과 분석으로 발전시켜 한국콩 육종과 이용에서 기초자료로 이용될 예정이다.

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PA-0041

콩에서 SYMMV 저항성 유전인자 연관분석

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전라북도 완주군 이서면 혁신로 181 국립식량과학원

콩을 가해하는 바이러스중 SMV(*Soybean Mosaic Virus)*는 우점종의 위치에서 최근 10여년 동안 내병성 품종의 육종 보급에 따라서 SYMMV(*Soybean Yellow Mild Mosaic Virus*)로 급격히 대체되고 있다. 그러나, SYMMV에 대한 장려품종들의 저항성은 낮고, 저항성 유전에 대한 연구가 상대적으로 저조한 실정이다. 본 연구에서는 430 자원으로 구성된 한국 재배종 콩 핵심집단을 대상으로 국립식량과학원에서 보유중인 SYMMV isolate를 이용하여 저항성과 감수성 정도을 5점 척도로 접종잎과 상부 잎별 증상을 조사한 후, 13만개 SNP 마커로 연관분석을 수행하였다. 그 결과, SYMMV에 대한 저항성 반응의 광의의 유전력은 0.90으로 매우 커서 주동 유전자가 저항성에 작용하는 것으로 나타났다. 연관분석 결과, 염색체 6번에 $-\log_{10}P$ 값이 14 정도의 매우 유전력이 높은 유전체 영역을 확인하였다. 이러한 결과는 향후 SYMMV 저항성 육종에 기여할 것으로 예상한다.

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PA-0042

Natural variation in *OsCCA1* regulates flowering time and contributes to rice cultivation at a wide range of latitudes

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The timing of flowering is a crucial factor for successful grain production at a wide range of latitudes. Domestication of rice (*Oryza sativa*) included selection for natural alleles of flowering-time genes that allow rice plants to adapt to broad geographic areas. Here, we describe the role played by natural alleles of *CIRCADIAN CLOCK ASSOCIATED 1* (*OsCCA1*) in cultivated rice based on our analysis of single nucleotide polymorphisms deposited in the International Rice Genebank Collection Information System database. Rice varieties harboring japonica-type *OsCCA1* alleles (*OsCCA1a* haplotype) flowered earlier than those harboring indica-type *OsCCA1* alleles (*OsCCA1d* haplotype). In the japonica cultivar 'Dongjin', a T-DNA insertion in *OsCCA1a* resulted in late flowering under long-day and short-day conditions, indicating that *OsCCA1* is a floral inducer. RT-qPCR analysis showed that the loss of OsCCA1a function induces the expression of the floral repressors *PSEUDO-RESPONSE REGULATOR 37* (*OsPRR37*) and *Days to Heading 8* (*DTH8*), followed by the repression of the *Early heading date 1* (*Ehd1*)-*Heading date 3a (Hd3a)-RICE FLOWERING LOCUS T 1* (*RFT1*) pathway. Binding affinity assays indicated that OsCCA1 binds to the promoter regions of *OsPRR37* and *DTH8.* Naturally occurring *OsCCA1* alleles are evolutionarily conserved in cultivated rice (*O. sativa*). *Oryza rufipogon*-I (Or-I) and Or-III type accessions, representing the ancestors of *O. sativa indica* and *japonica*, harbored *indica*- and *japonica*-type *OsCCA1* alleles, respectively. Taken together, our results demonstrate that *OsCCA1* is a likely domestication locus that has contributed to the geographic adaptation and expansion of cultivated rice.

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PA-0043

Molecular characterization of KIX domain proteins related to organ size regulation in Soybean (*Glycine max* (L.) Merr.)

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Soybean (*Glycine max* (L.) Merr.) is one of the most important crops worldwide used as protein and vegetable oil source for human food and animal feed. Soybean seeds are mainly used as food sources, whereas whole organs are utilized as animal feed. As a result, organ size is important for plant yield and biomass. Research related to plant organ size is continuously being studied. Recently, it has been reported that the plant organ size is regulated by various protein interactions, including KIX domain protein. The purpose of this study is to identify all KIX domain proteins encompassed in soybean genome and characterize the ones that regulates plant organ size. KIX base and Soybean database were used to investigate KIX domain genes in soybean. We identified the 11 GmKIX genes with conserved KIX domain in soybean genome. Three paralogs of KIX8 and two paralogs of KIX9, which are expected to be related to organ size were isolated through comparative analysis of amino acid sequences. The paralogs of KIX8 and KIX9 were conserved in N-terminals region, and were separated into similar groups as a result of phylogenetic analysis. In addition, expression of GmKIX genes was analyzed by RNA-Seq in three stages of seed development. it was confirmed that there was a relatively large amount of expression of GmKIX genes in the early stages of seed development. These results will be useful for understanding the functions of these 11 GmKIX genes in organ size regulation of soybean.

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PA-0044

Haplotyping and Evolutionary Studies on Trehalose-6-Phosphate Phosphatase 7 (*TPP7*), Anaerobic Germination 1 (*AG1*) Tolerance Gene (*Os09g0369400*) in KRICE_CORE

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Anaerobic germination (AG) is an important trait playing as an essential role in submergence resistance, especially for rice production in flood-prone lowland areas. Among the trehalose-6-phosphate phosphatase (*TPP*) gene family, *TPP7* is responsible for the germination vigor under submergence. *AG1* gene that encodes *TPP7* can enhance the coleoptile elongation in seeds. AG tolerance enables robust seedling establishment through the rapid and sustained coleoptile elongation under flooded situations. Here, we used a core set of 475 rice accessions, KRICE_CORE (Korean World Rice Collection) and conducted haplotype and genetic variant analyses to provide comprehensive information on functional SNPs and InDels based on the *TPP7* (*Os09g0369400*) gene. We observed 18 haplotype groups and found ten functional SNPs in exons 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 deletion (intron-5) was found in haplotype 12 including six indica and four temperate japonica accessions. In the genetic diversity analysis of the *TPP7* (*Os09g0369400*) gene, we found that the indica group revealed the highest nucleotide diversity (π) value, and the fixation index (F_{ST}) between tropical japonica and aus was higher than those of other sub-groups. We also observed that japonica types showed a higher anaerobic germination tolerance than the different rice types. A combination of these findings related to the *AG1* gene, encoding *TPP7* with their functional SNPs and their genetic diversities can be useful and applicable in future rice breeding programs.

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

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PA-0045

The Complete Chloroplast Genomes of Two Medicinal Citrus Landraces, *Citrus sunki* and *Citrus erythrosa* (Rutaceae) in Jeju Island, Korea

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Twelve citrus landraces naturally grow in Jeju island, Korea, including Jinkyul (Citrus sunki Hort. ex Tanaka) and Dongjeongkyool (C. erythrosa Hort. ex Tanaka). Fruit peel and young fruit of many citrus species including these two landraces have long been used as oriental medicinal materials due to their gastric protective, antiulcer, cholesterol lowering and anti-cancer effects. Here we assembled and annotated the complete chloroplast (Cp) genome sequences of C. sunki (Voucher no. IT233734, GenBank accession no. MT767776). and C. erythrosa (Voucher no. IT233658, GenBank accession no. MW722946) to provide taxonomic information with other species in the genus Citrus. The complete Cp genomes of C. sunki and C. erythrosa were 160,699 bp and 160,120 bp in length, respectively, and composed of four distinct regions: a large single copy (87,918 bp vs. 87,731 bp), a small single copy (21,355 bp vs. 18,393 bp), and a pair of inverted repeats (each 25,713 bp vs. each 26,998 bp). The Cp genomes of two Citrus species contained a total of 134 genes (89 protein-coding, 37 tRNA, and 8 rRNA genes) and 133 genes (88 protein-coding, 37 tRNA, and 8 rRNA genes), respectively, missing orf56 gene in C. erythrosa. The phylogenetic analysis using Cp genome sequences revealed that C. sunki forms a clade with C. reticulata, whereas C. erythrosa is a sister group to the clade of species including C. maxima and C. reticulata within the genus Citrus. The complete Cp genomes in this study will give us a valuable information for DNA super-barcoding and phylogenetic origin analysis of the genus Citrus.

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PA-0046

*Agastache rugosa*의 유전체 정보를 기반으로 한 SSR marker 개발 및 종간의 Cross-species transferability

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배초향은 꿀풀과에 속하는 다년생 초본식물이다. 배초향은 다양한 폴리페놀 화합물이 함유되어 있어 항산화능 평가, 항염 및 항균 등의 연구가 진행되어왔으나, 분자 유전학적 연구는 부족한 실정이다. SSR 마커는 높은 다형성과 재현성을 가지는 공우성 마커로 유전적 다양성 분석, 유전자 연관 지도 작성 등에 유용하다. 본 연구는 *Agastache rugosa* 유전체를 기반으로 유전적 다양성 평가를 위한 SSR 마커를 개발하였다. *A. rugosa* 게놈에서 249,746개의 SSR이 탐색 되었으며 그중 100,219개에 대한 primer 제작이 가능하였다. 제작된 primer 중 SSR repeat type 별 개수는 dinucleotide가 51,626개(51.51%)로 가장 많았고 tetranucleotide가 20,449개(20.40%), trinucleotide가 16,259개(16.22%) 순으로 확인되었다. 250개의 primer를 선발 후 *A. rugosa* 4 자원을 사용하여 PCR 조건을 확립하였고, 이 중 112개의 primer가 증폭되었으며 1개의 primer를 제외한 111개의 primer가 다형성을 나타냈다. polymorphic primer에 대한 다양성 분석 결과, 대립유전자 수(NA)의 범위는 2에서 19개로 확인되었으며, 평균 대립유전자 수는 6.5개로 확인되었다. 주요 대립유전자 빈도(MAF)는 0.11에서 0.95로 평균 0.467이며, 이형접합체(Ho)는 0에서 0.89로 평균 0.177로 나타났다. PIC 값의 범위는 0.09에서 0.92로 평균 0.617로 나타났다. 배초향종 간의 Cross-species transferability를 확인한 결과, *A. foeniculum*은 83.6%, *A. urticifolia*는 79.1%였으며, 평균 81.38%로 관찰되었다. 계통수를 이용하여 *A. rugosa* 종 내 19 자원을 대상으로 군집분석을 진행한 결과 4개의 주요 군집으로 분류되었다. Group 1에는 2 자원(KOR 2 자원)이 분포하였으며, Group 2에는 3 자원(RUS 1, KOR 2 자원)이 분포하였다. Group 3에는 10 자원(USA 2, POL 1, FIN 1, KOR 1, CAN 2, NLD 3 자원)이 분포하였고, Group 4에는 4 자원(PRK 1, FIN 1, RUS 2 자원)이 분포하였다. 111개의 polymorphic SSR marker 중 80% 이상 PCR된 79개의 marker를 사용하여 배초향 3종 47 자원의 군집분석을 진행한 결과 3개의 군집으로 분류되었다. Group I에는 *A. rugosa* 19 자원이 포함되었으며, Group II에는 *A. foeniculum* 14 자원이 포함되었고, Group III에는 *A. urticifolia* 14 자원이 포함되었다. 배초향 47 자원의 집단구조 분석 결과 3개의 집단(K=3)으로 구분되었다. Pop. 1에는 *A. rugosa* 19 자원이 포함되었으며, Pop. 2에는 *A. foeniculum* 14 자원이 포함되었고, Pop. 3에는 *A. urticifolia* 14 자원이 포함되어 군집분석과 유사한 결과가 나타났다. 본 연구에서 개발된 SSR 마커는 향후 배초향 유전자원의 품종 구분, 유전적 다양성 분석 및 육종 연구 등에 활용될 수 있을 것이다.

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PA-0047

Newly developing cDNA-SSR markers and genetic diversity in Amaranth

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Amaranth is a highly worthy crop worldwide because of its large amounts of essential micronutrient contents and excellent adaptability to a variety of unfavorable environments. Evaluation of genetic diversity is essential for the preservation of species and the selection of strains for developing new varieties. cDNA-SSR markers are highly transferable to related species and are useful in genetic diversity evaluation, variety identification, and genetic map construction. A total of 46,896 SSRs were identified and utilized for designing primer pairs. Among identified SSR motifs, trinucleotide repeats (21,503) were most abundant followed by tetranucleotide repeats (8,455). A set of 100 primers was synthesized and screened using PCR amplification products. Among designed primers, 16 primer pairs were successfully amplified, and the remaining 84 primers failed to generate PCR products at various annealing temperatures. Sixteen polymorphic markers were selected and used to evaluate genetic diversity among 120 accessions of 9 *Amaranthus* species. The major allele frequency ranged from 0.17 to 0.67, and the number of genotypes and the number of alleles ranged from 9 to 91, and from 8 to 90, respectively. The observed heterozygosity and the expected heterozygosity ranged from 0.00 to 0.73, and from 0.51 to 0.90, respectively. The polymorphic information content value ranged from 0.46 to 0.89. Those 16 markers were found to be transferable among the 9 *Amaranthus* species. The cluster analysis using the UPGMA algorithm showed that 120 *Amaranthus* accessions were classified into four main clusters. The model-based structure analysis suggested that the optimum number of subpopulations was two (K=2). This study could provide a valuable resource for breeding programs and genetic diversity analysis in amaranth.

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PA-0048

Development of fragrance gene (*OsBADH2*) mutagenesis in rice (*Oryza sativa*) engineered by CRISPR/Cas9 technology

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Rice grain quality is a complex and powerful tool for its value chain by a specific user reflected in a variety of perceptions. The fragrance is a key quality trait in high-price marketability as well as for consumers' preference, and consequently attractive to geneticists in high interest of its substantial development through genome mining societies. The CRISPR system is the most recently updated and applies gene editing technology in quality rice improvement. In this study, the fragrance controlling gene (*OsBADH2*) was targeted to edit its mutagenesis by using CRISPR/Cas9 technology, and the demonstration was successfully performed on the rice cultivar, Dongjin. As result, the average mutation rate was 83.8%, representing each targeted gene by more than 70%. BAR-strip analysis of the selected T-DNA free plants reconfirmed their basta resistance or sensitivity. The observed grain features and amylose content (AC) of the edited lines were slightly reduced compared to the wild type (WT). A clear description of 2AP contents were detected in all nine edited homozygous lines developed by CRISPR/Cas9 system, exhibiting their stable inheritability in T2 generations. Our study of *OsBADH2* gene expression in edited lines also guaranteed a high and specific efficiency of CRISPR-targeted mutagenesis, and these mutants can be of great outcomes for desired crop improvement.

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PA-0049

Development of middle-amylose rice varieties using CRISPR/Cas9 edited lines by marker-assisted backcrossing (MABc)

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Plant breeding is a useful and purposeful principle manipulating new species with desired characteristics. Altering the desired trait targeted by CRISPR/Cas9 system can modify its genetic functions for crop improvement. The premium cooking and eating quality (ECQ) rice were mostly determined by its fragrance and amylose content (AC). In this study, we used such special rice cultivars as Miho, Wolbaek, Samgwang and Koshihikari for the CRISPR-targeted *OsBADH2* mutagenesis, which will also be backcrossed by themselves. The *OsBADH2* mutagenesis was successfully targeted by CRISPR/Cas9 with an average mutation rate of more than 75%, and selected T-DNA free T2 generations confirmed Basta resistance. The edited *OsBADH2* mutant lines were backcrossed for their background specialty like waxy/sticky rice (very low AC). The F1 plants were applied by markers-assisted genotyping, and then will be backcrossed till to their high background recovery (>95%). The phenotypic characteristics (fragrance/2AP content, grain dimension, amylose content, etc.) of backcrossed lines will be analyzed in comparison with positive and negative controls. A clear description of 2AP and AC contents is expected to be in the backcrossed lines. Our study, marker-assisted backcrossing (MABc) of the CRISPR-targeted *OsBADH2* edited lines with AC-specified recurrent parents, will be effective in using quick and precise editing of targeted desired traits. The outcomes can be expected to be of useful parental lines for future breeding programs of desired ECQ rice improvement.

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PA-0050

Haplotyping and Evolutionary Analysis of Novel *HPPD INHIBITOR SENSITIVE 1* (*HIS1*) Gene in Korean World Rice Collection

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HPPD INHIBITOR SENSITIVE 1 (*HIS1*) is a rice-specific gene, and the loss of function of *HIS1* can affect HPPD herbicide sensitivity. It can also cause the bleaching of young foliage tissues and eventual plant death. Weeds are crop pests, and their infestations are a ubiquitous annual threat, reducing crop yield. We used the 475 Korean Rice Accessions and investigated the genotypic and haplotypic variations of the *HIS1* (*Os02g0280700*) gene to unveil their functional properties. The evolutionary relatedness was estimated based on the classified populations using single nucleotide polymorphisms (SNPs) and insertions/deletions (InDels). Forty-two haplotypes, including 43 nonsynonymous SNPs, were observed within the *HIS1* gene region. The predominant functional haplotypes were Hap_2 (22 *indica accessions*), representing a functional SNP (fSNP) T/G detected on exon 4, and Hap_5 (41 *indica* accessions), indicating an InDel allele, 28-bp deletion, found in exon 3. Hap_3 marked bi-allelic fSNPs, G/T, and G/A, representing eight *indica* and one wild rice accession. *Japonica* types showed higher resistance than *indica* types under screening using Tefuryltrione (TFT) herbicide. In comparing six ecotypes or four variety types for nucleotide diversity (π) analysis, the wild type showed a lower value (π = 0.00032) than others in the *HIS1* gene. The significant deviations of positive (*indica*, *aus*, and admixture under balancing selection) and negative (*japonica* and wild under purifying selection) Tajima's D values can be informative about the selective sweeps of *HIS1* genome insight. Our findings of fSNPs and genetic diversity information of the *HIS1* gene can be applicable for future breeding of herbicide-resistant rice varieties.

Keywords: *HPPD INHIBITOR SENSITIVE 1* (*HIS1*), Haplotype, SNP, Genetic Diversity

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PA-0051

Functional Haplotypes and Evolutionary Analysis of *HPPD INHIBITOR SENSITIVE 1* (*HIS1*) Gene for Selection Events in Different Rice Groups

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HPPDi activates plants by blocking 4-Hydroxyphenylpyruvate dioxygenase which is a plant enzyme in breaking down the amino acid (Tyrosine) into molecules. Weed interference is a severe problem in any agricultural system because they aggressively compete with the crops for nutrients, light, and other essential resources. Their infestation imposes an extreme challenge to crop yield, productivity, and survival of plants. Herbicides are vital constituents of a modern integrated weed management system. To investigate the haplotype variation and evolution of the *HIS1* gene (*Os02g0280700*), a total of 451 rice accessions were classified into four different varietal groups, namely landrace, weedy, bred and wild. We found 42 haplotypes, including SNPs and InDels sites, in the *HIS1* gene. The major haplotype, same as a reference sequence, was observed in Hap_1, and 28 bp deletion occurred in Hap_2, representing 25 bred, four landrace, and eight weedy accessions. The functional SNPs (fSNPs): T/G and G/A were observed in Hap_3 (27 accessions) and Hap_5 (8 accessions). The most variation haplotypes (Hap_9 to Hap_42) were found in wild types. In the PCA plot, despite the bred group showing clear separation in some portions, it was also admixed with the weedy group in some range. The wild group was in separated association with other varietal groups. In structure analysis, the bred, landrace, and weedy showed the admixture pattern, but a clear separation from the wild was observed at K=2 and K=5. The higher F_{ST} values were identified between the wild group and any other groups. In both nucleotide diversity (π) and Tajima's *D* analyses, the highest mean value was observed in the weedy group, and the lowest was found in the wild. The findings of fSNPs and InDels and evolutionary information will be useful in the breeding program. They can promote further studies in varietal selection with desired traits activated by the *HIS1* gene.

Keywords: *HPPD INHIBITOR SENSITIVE 1* (*HIS1*), Haplotype, SNP, Evolution

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PA-0052

The Evolutionary and Haplotype Analysis of *Gamma-Tocopherol Methyltransferase (γ-TMT)* Gene Involved in Tocopherol Accumulation in Korean Rice Accession

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Gamma-tocopherol methyltransferase (*γ-TMT*) is an important gene in the vitamin E biosynthesis pathway and regulates the accumulation of tocopherols, which are a key factor of rice nutritional quality. We estimated the haplotype variations and evolutionary analysis (e.g., genetic diversity and population genetic structure) of *γ-TMT* gene in the 475 Korean rice accessions. We observed 19 nonsynonymous SNPs across the coding gene region, representing 16 haplotypes. We noticed only one functional haplotype (Hap_18) belonging to the cultivated rice accessions. Hap_18 is the only major cultivated haplotype while all the remaining were under the wild rice accessions. The only predominant and functional cultivated (88 indica, four aus, and two admixture) haplotype, Hap_18, held two functional alleles interfered by G/A SNP in exon two and A/G SNP in exon 4, which appeared to be the determinants of vitamin-E content between japonica and indica. Higher nucleotide diversity in indica (π=0.0156) can be of supportive information to predict the evolutionary relationships with other populated groups, especially with japonica, within *γ-TMT* gene region. Sudden population contraction by significant positive Tajima's *D* value (2.0985) of indica also provided selection signature of *γ-TMT* domestication under balancing selection. Significant differentiation by higher F_{ST} value was observed between two major populations (indica and japonica), indicating higher genetic diversity that cannot be shared. Our findings on functional *γ-TMT* haplotypes can be useful for the selection of varieties in the future breeding program. The evolutionary studies can also be applicable in functional studies of *γ-TMT* gene into deeper genomic insights.

Keywords: *gamma-Tocopherol Methyltransferase*, Tocopherol, Vitamin E, Haplotype Analysis

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PA-0053

Genetic Analysis and Evolutionary Relationship of Starch Synthase IVA (*SSIVA*) Gene in 475 Rice Accessions

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Starch synthase proteins in rice and other cereals are classified into major components, the soluble starch synthases (*SSI, SSII, SSIII* and *SSIV*) and the granule-bound starch synthase (*GBSS*). In rice, there is only one gene for *SSI,* three isoforms for *SSII*, and two each for *SSIII*, *IV*, and *GBSS*. The starch synthase IVA (*SSIVA*), a homologous isoform of *SSIVB*, is one of the least characterized genes involved in the starch biosynthesis pathway. The importance of *SSIVA* for starch granule formation remains to be established due to its less known, unclear and limited functional analyses. To investigate the genetic information of this gene, we used 475 different rice accessions belonging to different subgroups of origins. We then performed bioinformatic analyses through resequencing, haplotyping, and characterizing the detected variations. The results indicated 76 non-synonymous SNPs along 12 different exons of chromosome 1. There were 50 haplotypes, of which 3, 8, 39, and 42 showed the highest accumulation of rice accessions. Such haplotypes from Hap-38 to Hap-45 belonged only to cultivated rice accessions. The highest F_{ST} value (0.95) was found between the Temperate Japonica and Aroma groups, followed by the Temperate-Tropical Japonica group (0.84). A considerably high F_{ST} value between Temperate and Tropical Japonica indicates great genetic isolation from each other, indirectly meaning no genetic variations to be shared.

Keywords: *SSIVA*, Starch synthase proteins, Haplotype, Rice

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PA-0054

Extensive Genome, Transcriptome, and eQTL Analysis of *Xa39* Gene (*OS11g0588600*) Unraveling A Novel Gene through Haplotype and Evolutionary Analysis in KCore Rice

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Bacterial Leaf Blight (BLB) caused by *Xanthomonas oryzae* pv. *oryzae (Xoo)* is one of the major diseases in rice. BLB is a severe disease during the monsoon season and occurs in high-yielding varieties under high nitrogenous fertilizers, especially in irrigated and rainfed lowland ecosystems. It attacks most rice cultivating areas such as Africa and Asia, causing a loss of 20-80% yield. Growing BLB resistance variates is the most promising way to protect rice from BLB infection. This study used 475 core collections of Korean rice germplasms with seven different ecotype groups. eQTLs analysis of specific *Xa39* gene was carried out, and haplotype, haplotype diversity, and F_{ST} among ecotypes of *Xa39* gene were analyzed using genetic information. In the Cis-regulatory element, 22,319,757 bp, the expression level was high with the high -log10 *p*-value for eQTL analysis of the *Xa39* gene. The genetic variance for the *Xa39* gene was observed by 94.7 %, while that of residual variance occurred at 5.3 %. As a result of haplotype analysis, a total of 171 haplotypes with 133 polymorphic sites (24 InDels and 109 SNPs) were identified in the coding region. For the F_{ST} analysis of the *Xa39* gene, the highest mean weighted value was observed between japonica and aus and the lowest value between indica and admixture. In eQTL analysis of the *Os11g0588600*, *Xa39* gene, we found that SNP upstream 9kbp of *Xa39* which T to C substitution, significantly reduced the expression of *Xa39*, and our findings will provide vital information in variety selection for future breeding research of resistant rice varieties.

Keywords: rice, Bacterial leaf blight (BLB), haplotype diversity, eQTL, *Xa39*

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PA-0055

Transcriptome analysis of *Ligularia fischeri* using long-read sequencing technology: From determining the entire gene set to developing molecular markers

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L. fischeri is distributed in Korea, northeast China, Japan, eastern Siberia and in Himalayan regions. In Korea commonly known as Gom-chi, it grows in wet woodlands or damp shady areas besides mountains and sloping fields. Its leaves have a unique aroma and taste, making it a popular vegetable side dish or used in tea preparations. Moreover, it exhibits a broad range of pharmacological effects including protection against chronic alcohol use and hepatotoxicity by preventing cell damage, useful in treating jaundice, scarlet fever and rheumatoid arthritis. The leaf extracts possess anti-inflammation, anticancer, antigenotoxic, antimicrobial, antimutagenic and antioxidant activities. The medicinal activities of *L. fischeri* are mainly attributable to the secondary metabolites such as Terpenoids, flavonoids and phenolic compounds which can act as a template for drug designing to cure various diseases. Regardless of its economic and pharmacological value, research for plant-derived products in *L. fischeri* is limited to understanding its chemical nature rather than revealing its genetic information, there are no transcriptome/genome sequences available in the public database limiting its research at molecular level. To address this issue, *L. fischeri* leaf transcriptome was sequenced using Pacific Biosciences single molecule long-read isoform sequencing platform. This is the first detailed transcriptome analysis of *L. fischeri.* The resulting transcriptome along with the identified alternative splicing events provides insights into the biological process including the genes related to biosynthesis of characteristic secondary metabolites. This data will be valuable resource as transcriptome reference for further studies in the genetics and breeding of *L. fischeri.*

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PA-0056

Identification of candidate gene for floury endosperm phenotype of rice mutant by analysis of whole genome resequencing

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Recently, floury endosperm mutants with weak and fragile endosperm property has been used as breeding materials for development of rice cultivars suitable for dry-milling. Through irradiation breeding method, we developed new floury endosperm mutant 'Z106' which was derived from the callus of *japonica* cultivar Dongan irradiated by gamma ray. In phenotypic characterization, this mutant showed a white opaque endosperm phenotype along with increased culm length and brown rice length, and reduced 1000-grain weight compared with Dongan. To identify candidate gene, we performed comparative analysis of whole genome sequence between Dongan and Z106 mutant. A total of 196 variations including 174 SNPs and 11 InDels were detected in the genic region of genome. Through variations screening in 18 genes related to compound granule formation and starch synthesis, we identified that three variations (i.e. one SNP and two InDels) are located in *FLO4* gene encoding pyruvate phosphate dikinase. Considering the positions of these variations, it was estimated that the SNP (G2948A) occurred in 3' splice site of 20th intron could induce changes of amino acid sequence. The SNP was validated by sanger sequencing confirmation, and the results of mRNA sequencing showed that the SNP induced alternative splicing of *FLO4* gene, resulting in premature stop codon by frameshift within coding region. These results suggest that *FLO4* is the most suitable candidate gene for floury endosperm phenotype of Z106 mutant, and this mutant and genetic information obtained in this study are expected to be utilized for breeding new floury rice varieties.

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PA-0057

Evolution and diversity of *Peucedanum japonicum* inferred from enormous inverted repeat exansion in plastome

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Peucedanum japonicum is a promising plant resource as its diverse application, including oriental medicine and vegetables. We newly assembled complete plastid genome and 45S rDNA sequences of six *P. japonicum* accessions. According to the assembly results, plastid genome of *P. japonicum* is divided into two types; long-type and short-type, each with 17kb length differences. Long-type plastid genome is almost 164kb while short-type is 147kb. Phylogenetic analysis derived from plastid genome clearly separated long-type *P. japonicum* and short-type *P. japonicum* into different groups, while 45S rDNA tree formed monophyletic group. One of the short-type *P. japonicum* showed relatively far genetic distance from other *P. japonicum*, implying that long-type *P. japonicum* evolved from short-type. We developed 16 molecular markers based on SNPs that were derived from plastome variations. These markers also adapted to 55 *P. japonicum* collection. Assembly results and marker validation reveals that long-type plastid accessions have lower intra-specific diversity than short-type. Furthermore, we could detect accessions with different genotypes from sequenced accessions. This study will provide insight and basic information for *P. japonicum* breeding program.

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PA-0058

Characterization of Flavonols and Sequence Analysis of the Flavonoid *3´-Hydroxylase* Genes in Legumes

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Flavonols are major flavonoid components of legume leaves. The composition of flavonol glycosides (FGs) is varied among genotypes and involved in pod pubescence color. In soybean (*Glycine max* (L.) Merr.), dominant and recessive alleles of the *T* locus are responsible for brown and gray pubescence, respectively, encoding flavonoid 3'-hydroxylase (F3'H) as a cytochrome p450 (CYP450)-dependent monooxygenases. The objectives of this study were to characterize flavonols in leaves of soybean and mungbean and to investigate nucleotide variants in the *flavonoid 3´-hydroxylase* (*F3´H*) genes. The flavonols types and their contents of 16 genotypes, including 13 soybeans and 3 mungbeans, were separated and identified by high performance liquid chromatography. Soybean and mungbean genotypes with tawny pubescence showed more diverse flavonols and higher contents than ones with gray pubescence. The total flavonol content (TFC) was highest at the reproductive stage, especially after pod formation. Among soybean genotypes, SS2-2 showed the highest TFC of 12201.6 ± 368.9 mg/kg dry weight (DW). The TFC of the mungbean genotype VC1973A was 137787.3 ± 5167.6 mg/kg DW, containing quercetin-3-O-rutinoside of 132518.8 ± 5019.3mg/kg DW. The soybean genome has 16 *F3'H* genes expanded by twice whole-genome duplication events and tandem duplication, suggesting their sub- and neo-functionalization based on expression differences and sequence variations in CYP75B43-specific conserved motifs. We also identified that the frame shift in the *T* locus (Glyma.06g202300) was only associated with the pubescence color and flavonol composition, consistent with the previous study.

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PA-0059

Using Instrumental cooked rice texture measurement as a phenotyping tool in Genome-Wide Association Study

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Texture is considered as a multidimensional sensory attribute experienced by humans. Textural property can be an indicator of high-quality rice and it is a principal consideration in its consumer acceptance and palatability. Thus, understanding underlying genetic basis is important for the genetic improvement of preferred textural properties in crop improvement programs. Phenotypic variations of texture properties in cooked rice are expressed in terms of their hardness or firmness, tenderness and adhesiveness by texture assessments. We investigated diverse cooked rice texture properties that includes hardness (HRD) and adhesiveness (ADH) of 268 *japonica* rice accessions, including improved varieties and landraces. A set of 1,254,682 high quality single nucleotide polymorphism (SNP) dataset derived from the panels were retained for marker-trait associations of textural properties using genome wide association studies (GWAS). We identified significant SNPs on chromosome 3, 4, 6, 10, 11, 12 for HRD. In case of ADH, the lead SNPs were detected on chromosome 1, 2, 6, 8. The results of this study could contribute to our understanding of texture analysis of cooked rice and provide rice industry and breeding programs with basic information to develop varieties with textural properties.

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PA-0060

Genome-Wide Association Study of Rice Grain Size Traits Using micro-CT Phenotyping

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Rice grain size is one of the most valuable breeding targets contributing to yield, appearance, and eating quality. However, the difference in grain size among cultivars is minuscule, and highly accurate measurements of hundreds to hundreds of thousands of samples are required. X-ray micro-computed tomography(μCT) can visualize and quantify two-dimensional (2D) and three-dimensional (3D) structures to the sub-micron level, allowing precise quantification. The 2D traits, such as length, width, thickness, and length-width ratio, and the 3D volumetric data, were evaluated in the collection of 236 japonica rice accessions. Phenotypic evaluation of all the traits showed normal distribution, and volume was positively correlated with width(0.76) and thickness(0.73). Then GWAS analysis was conducted using 1,254,682 single nucleotide polymorphisms (SNPs) to identify loci controlling the variation for the size-related traits. A total of 197 lead SNPs were detected on chromosomes 3 and 5, of which 35 were associated with more than one trait. The quantitative trait loci (QTL) gw3.1 and cloned gene GS3 showed powerful effects on grain length in this study. These results show that GWAS using phenotypic data from micro-CT is an effective method for identifying genetic loci associated with rice grain size and shape.

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PA-0061

Construction of High-contiguity reference genome sequences of two *Hibiscus syriacus* accessions (Gangneung and Baekdansim)

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Rose of sharon (*Hibiscus syriacus*) one of the most widespread garden shrubs in the world, showed a complexed structure of genome generated by multiple number of polyploidization during its diversification and evolution. We constructed two reference genome assemblies for *H. syriacus* accessions (Gangneung and Baekdansim) with long read sequencing and Hi-C scaffolding, resulting in 1.87 Gbp and 1.82 Gbp size of assembly. Total 88,741 and 87,438 gene models were predicted from Gangnueng and Baekdansim genome assemblies respectively. To identify genetic varieties putatively associated to horticultural traits of the *H. syriacus*, we re-sequenced 10 accessions showed different phenotypes related to cold-resistance and floral architecture. As a result, we identified total 4,339,048 SNPs based on the reference genome of Gangneung. The phylogenetic trees drawn by four-fold degenerate sites (4D SNPs) clustered accessions corresponding their known origins and crossing information. Total 1,051 number of SNPs were located on 268 number of cold-related genes(CRGs) searched by sequence similarity against 114 *A. thaliana* CRGs, resulting in detection of 19 cold-resistant accession/group specific SNPs. The reference genome will serve as a platform for developing cold-tolerance varieties and improved floral traits in the *H. syriacus* breeding program.

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PA-0062

LegExpress: A bioinformatic web-based interface for re-analyzing cross-legume gene expression profiles

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Genome-wide transcriptome analysis is one of the most powerful means to gain a broad and deep insight into the molecular mechanisms that underlie dynamic interactions among numerous genes in organisms. Although several bioinformatic platforms for gene expression profiling have been developed for individual species, platform for cross-species transcriptome analysis is not currently available. We employed the technical concept of translational genomics between different species and aimed to build the platform in user-friendly manner. This DB-linked platform, named LegExpress, harbors wide array of transcriptome data for three representative species with relatively the most comprehensive gene expression information, including Glycine max, Medicago truncatula and Arabidopsis thaliana. All these expression data were collected from publically available ArrayExpress(http://www.ebi.ac.uk/arrayexpress/)DB and composed mainly of Affymetrix GenChip data. Raw data were processed to select high-quality transcriptome data and normalized by the RMA standardization method. We developed a program for visualization of the data and organized the user interface according to suitable criteria, such as organs, developmental stages, time courses and different stimuli (e.g., hormones, biotic/abiotic stresses). It is anticipated that LegExpress may play a useful role for breeder/researcher-friendly transcriptome analysis platform and can be applied to design breeding programs through helping breeders discover trait-associated genes.

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PA-0063

GWAS-driven identification of genomic loci associated with phenotypic traits of seed pigmentation in soybean

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Soybean (Glycine max [L.] Merr.) is the most important crop among all cultivated legume crops in the world. Seed coat has been significantly influenced during the period of domestication in that it is linked to seed dormancy, seed viability and cost factors in processing seeds for oil and soy foods. To identify loci linked with seed pigmentation, we collected the resequencing data of 438 accessions. A genome wide association study using all possible combinations of three traits revealed four loci (designated as 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.

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PA-0064

Web interface for breeding design focused on pedigree-linked phenotype information of soybean cultivars

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For breeding design, parental information of any domesticated species is an important source because it's an indicator of the genetic relationship among bred lines. As the accumulation of genome and phenome data on cultivars rapidly increases, well-structured pedigree and system to utilize it have played a key role. For this reason, we intended to construct a pedigree-based web interface to link the phenotypic information and genealogical relationship of soybean cultivars. A well-structured pedigree of 178 korean soybean cultivars and its phenotype information were used as key data for database construction. Three submodules consisting of pedigree-, tabular- and single cultivar-based search pages constitute the web interface. Single Page Application (SPA) makes users to quickly switch between pedigree and tabular list mode still on a same filter status. Furthermore, comparison of the parental information and a SNP-based phylogeny from cultivars in its pedigree presented that there is a certain degree of correlation between them. Our web page is developed as an intuitive auxiliary system for breeding design in the future and plans to expand itself to a global database by integrating international soybean data. This web interface is available at https://tgil.donga.ac.kr/SoyPedi/index.html.

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PA-0065

Identification of novel loci for flowering time in mungbean [*Vigna radiata* (L.) R. Wilczek] using genome-wide association study

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Flowering time is one of the important agricultural traits in crops. Since mungbean does not flower simultaneously, especially, it leads to asynchronous pod maturity and laborious multiple harvests per individual. The objective of this study was to discover new quantitative trait loci (QTLs) for days-to-first-flowering (DFF) in mungbean by genome-wide association study (GWAS). In total, 206 mungbean accessions collected from 20 countries were sequenced using genotyping by sequencing. Principle component analysis and the population structure showed that these accessions were divided into two sub-population, wild and cultivated ones. GWAS using 3,596 single nucleotide polymorphisms (SNPs) identified seven significant SNPs associated with DFF. Based on the linkage disequilibrium (LD) decay distance, LD block was determined to be 768 kb genomic region surrounding each SNPs. The SNPs sharing LD block were merged into same locus, resulting in five DFF QTLs on Chr01, Chr02, Chr08 and Chr09. A novel locus, *DFF2-2* was identified by a leading SNP (Chr2_51229568) with the highest *p*-value of 5.32 and Chr2_51229546 with *p*-value of 4.17. In *DFF2-2* locus, Chr2_28317065 was detected in genic region of *Vradi02g00001828*, a homologous gene of soybean *E1*. The *DFF2-2* locus was found to be syntenically conserved with two blocks on Chr13 and Chr20 of soybean, harboring three and five QTLs associated with flowering time, respectively. Syntenic blocks of the other four loci for DFF were also found in soybean genomic regions containing flowering-related QTLs. These findings provide genomic information for understanding the flowering time in mungbean.

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PA-0066

RNA genome sequence of soybean mosaic virus was not affected by temperature stress

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Recently, the study on pathogenicity depending on the temperature of plant viruses is drawing attention because of climate change. In a previous study, we found that the symptoms and viral accumulation vary with temperature when soybean mosaic virus (SMV) and soybean yellow mottle mosaic virus (SYMMV) is infected with soybeans. The genome sequence of a virus can be mutated by temperature. Such mutations are called temperature-sensitive (ts) mutations. We hypothesized that ts mutation generated by low- or high-temperature stress induces the mild symptoms of SMV on soybeans. Therefore, we performed RNA-seq to search for the gene and to investigate the frequency of mutations of SMV that mutated by temperature. The RNA-seq results showed that the mutation in the viral genomic RNA almost does not exist in soybean infected with SMV depending on the temperature. The symptoms on soybean leaves caused by SMV at low- or high-temperature are milder than the symptoms induced at 25℃. These results suggested the pathogenic change of SMV according to the temperature is not related to the mutation of the nucleotide sequence of the virus. Our results are thought to be applicable to breeding varieties resistant to soybean virus disease.

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PA-0067

Investigation of a pathogenesis-related gene for breeding the viral-resistant soybean

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Pathogenesis-related (PR) proteins are produced in plants as a defense response against plant pathogens. The expression level of the PR gene is up-regulated or down-regulated by biotic stress and abiotic stress. There are many diseases in soybean caused by plant pathogens. Among them, soybean mosaic virus (SMV), soybean yellow mottle mosaic virus (SYMMV), and bean common mosaic virus (BCMV) is the major causal agents of viral disease in soybean in Korea. During the viral infection, molecular interactions between soybean and viruses determine the development of resistance in soybean plants. The soybean has a lot of PR genes, including GmCYB5-1, GmEXPA1, GmEXPA2, GmMPK4, GmKR3, and GmPR2, associated with immune responses to virus attacks (Widyasari, 2020). Our previous studies show that the symptoms of soybean induced by SMV and SYMMV have changed depending on growth temperature. So, we applied temperature stress to soybean plants and investigated the change in the expression level of PR protein through RT-qPCR. As a result, it was confirmed that the expression of PR genes in soybean can be regulated by abiotic stress such as temperature. Soybean is most important crops cultivated in worldwide. If we can understand the correlation between virus temperature-dependent pathogenicity and plant PR protein, it will be helpful in selecting suitable soybean cultivars according to climate change.

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PA-0068

Identification of QTLs related to (-)-epicatechin contents and hilum color in soybean (*Glycine max*) seeds

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(-)-Epicatechin (EC) is one of the primary forms of flavan-3-ols and a building block of proanthocyanidins (PAs; also known as condensed tannins) responsible for the brown pigmentation of seed. These polyphenolic compounds are the most potent antioxidants and free radical scavengers that have multiple health benefits upon consumption. Here, quantitative trait loci (QTLs) associated with biosynthesis of EC and hilum color in 235 recombinant inbred lines (RILs) of Jinpung (cultivar) and IT109098 (landrace) were identified via high-resolution single nucleotide polymorphism (SNP) linkage map. Hilum color was classified in four grades upon observation, and EC contents of mapping parents showed Jinpung with 0.00 ± 0.00 μg/g and IT109098 with 1186.62 ± 448.96 μg/g. For both hilum color and EC contents, bimodal distributions were shown for the progeny. Seed coats with only brown color showed EC contents, but levels not in a linear fashion based upon principal component analysis (PCA) and linear regression.

Major QTLs for EC contents, *qEP06*(Chr06 18555043-18864382) and *qEP08*(Chr08 8,771,172-9,214,678bp), were identified with significant logarithm of odds (LOD) scores of 8.63 and 12.24, and with percentage of phenotypic variance (PVE) of 10.5 and 15.16, respectively. *qEP06* spanned known T Locus, and closely located *I* locus (~200kb apart) in Chr08 (Chr08 8,380,000-8,520,000bp) to *qEP08* was not relevant to EC contents according to QTL regions of allele stacking. RILs with alleles of *qEP06* and *qEP08* both from IT109098 showed high EC contents within the seed. To isolate a causal gene for *qEP08*, further study, such as fine mapping and cloning, would be necessary.

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PA-0069

반송(*Pinus densiflora* f. *multicaulis* Uyeki) 구화의 성전환 단계에 따른 전사체 비교

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반송(*Pinus densiflora* f. *multicaulis* Uyeki)은 소나무의 독특한 품종 중 하나로 한국과 일본에 분포한다. 반송은 다른 소나무속 수종들보다 생식기관 발달 시 수구화에서 암구화로 변하는 성전환이 더 빈번하게 관찰된다. 본 연구에서는 수구화에서 암구화로 성전환이 일어나는 양성구화를 대상으로 성전환 시작단계부터 마지막까지 5단계로 구분하여 전사체를 해독하였으며, 이를 성전환이 일어나지 않은 암구화와 수구화의 전사체 분석결과와 비교하였다. 각 시료별, 성전환 단계별로 발현된 모든 유전자를 동정하였으며, 유전자의 발현 차이를 비교하고 특이적으로 발현하는 유전자들을 탐색하였다. 분석결과 총 2,796개의 유전자를 동정하였으며, 유전자 발현 패턴에 따라 동정한 유전자들을 18그룹으로 분류하였다. 수구화에서는 LEA gene family와 cyplp029 gene, WRKY transcription factor *ZmWRKY17*, dhn_ESK2 등이 특이적으로 발현하였으며, 성전환 시작단계에서는 Ethylene을 조절하는 *PtLTP1*, Auxin을 수송하는 PIN1, 질소를 수송하는 NPF7.3가 높게 발현하였다. 성전환 마지막 단계에서는 다른 단계에서는 발현하지 않은LINE-1 retrotransposable element를 동정할 수 있었다. 암구화에서는 조직에 상시 특이적으로 발현하는 지베렐린과 브라시노스테로이드 생합성에 관여하는 CYPs, gibberellin metabolism genes 등 호르몬의 전구체들을 동정하였다. 이처럼 구화의 형태와 발달 단계에 따라 유전자들의 발현량에 많은 차이가 있었으며, 단계별로 특이적으로 발현하는 유전자들을 확인하였다. 본 연구 결과는 향후 반송의 성전환 메커니즘을 밝히는 연구에 도움이 될 것이다.

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PA-0070

고구마(*Ipomoea batatas* L.) 카로티노이드 대사 관련 AP2 전사인자 확인

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고구마(*Ipomoea batatas* L.)에서 카로티노이드는 기능성 성분으로 중요한 역할을 하여 최근 많은 연구가 이뤄지고 있다. 고구마에서 몇몇 카로티노이드 대사 유전자는 확인되었지만 이에 관여하는 전사인자는 아직 밝혀지지 않았다. 이를 확인하기 위해 고구마 Taizhong 6 품종의 코딩 서열을 대상으로 전사인자를 탐색하였다. 사과 과실에서 MdPSY2-1의 프로모터에 결합하는 전사인자 MdAP2-34의 상동유전자, g51968을 고구마에서 확인하였다. g51968은 MdAP2-34에 비해 두 번째 AP2 도메인 시작 부위에 아미노산의 결실이 존재한다. 실제로 결실이 존재하는지 확인하기 위해 약 2.9Gb의 고구마 진율미 품종의 롱리드 조립 유전체와 고구마 Xushu 18 품종의 RNA 시퀀싱 SRA 데이터를 이용하여 발현되는 서열을 확인하였다. Exonerate로 확인한 g51968의 위치 6곳에서 RNA 리드 매핑을 확인한 결과, 모든 위치에서 g51968에서 결실된 서열이 별도의 엑손으로 존재하였으며, 첫 번째 AP2 도메인 내에 아미노산 3개의 삽입이 확인되었다. 이러한 결과는 g51968 유전자 영역에서 alternative splicing이 일어났을 가능성이 있음을 시사한다. 두 개의 AP2 도메인의 서열이 MdAP2-34와 고구마의 상동유전자 서열 간 다를 수 있다. 이를 확인하기 위해 고구마에서 MdAP2-34 상동유전자의 mRNA를 목적으로 한 RT-PCR 산물의 시퀀싱을 진행할 계획이다. 또한 과발현 시 카로티노이드 함량 증가를 확인하는 등의 기능 검정을 통해 고구마의 카로티노이드 대사 관련 전사인자를 밝힐 수 있을 것으로 기대된다.

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PA-0071

Identification of QTLs Conferring Flavanol Contents in Soybean Seeds

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(-)-Epicatechin and its dimer, procyanidin B2 are forms of flavanols commonly found in plants, responsible for brown coloration in seeds, and they have various health benefits, such as anti-oxidation and anti-cancer. Compared to isoflavones, genetics on (-)-epicatechin and procyanidin B2 retain less uncovered in soybean. The present study was performed to identify quantitative trait loci (QTLs) conferring (-)-epicatechin and procyanidin B2 contents in soybean seeds using high-resolution single nucleotide polymorphism linkage map of a recombinant inbred line population of IT109098 (greenish brown seed coat) x K7-113 (black seed coat). Both of the mapping parents showed high (-)-epicatechin and procyanidin B2 and the progeny showed normal distribution. The value of L*, a* and b*, color components in seed coat had bimodal distribution in the progeny.

We identified the same two QTLs conferring (-)-epicatechin and procyanidin B2 contents in seeds on Chr02 and Chr10 in 2020 and 2021. As a major QTL, *qECPABB10* on Chr10 explained 23.5-44.4% of phenotypic variation, showing high LOD of 15.4-44.3. Additional QTL for (-)-epicatechin was close to a QTL for seed coat color on Chr09. Among 47 genes in *qECPABB10*, *Glyma.10G210000* and *Glyma.10G210600* encoding phenylalanine ammonia-lyase 2 and auxin response factor 16, respectively, are likely to be candidate genes based on variants annotation and seed-specific expression.

Consequently, the major QTL, *qECPBB10* regulates flavanol contents in soybean seeds independently from seed coat color. This study will provide primary insight to improve our understanding of flavanols biosynthetic pathway in soybean and breeding of high-flavanols cultivars.

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PA-0072

Traces of the *Gentianales*-to-*Apocynaceae* evolution from the genome sequences of three *Cynanchum* species

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The various pharmaceutical effects from the Apocynaceae family are reported, and their industrial and academic importance is growing. The most well-known Apocynaceae species in Korea, *Cynanchum wilfordii*, *C. auriculatum*, and *C. rostellatum*, are medicinal plants that have long been used for traditional medicine in North-east Asia. The various medicinal effects, including anti-inflammatory, antioxidant, and relieving hyperlipidemia, have been reported from these plants, and the significance of the breeding for stabilization of supply and guarantee of quality. However, cultivars of these plants have not been developed, nor has research been conducted on the breeding system. Therefore, genome data is necessary to support this. The draft genome sequences of three *Cynanchum* species were assembled using a hybrid assembly strategy that includes Oxford Nanopore Technology, Pacbio HIFI, and DNase Hi-C. The BUSCO values of three draft genomes are more than 99 percent, and every chromosome is scaffolded into the telomere-to-telomere structure. Using RNA sequencing data and NRDB for gene annotation, approximately 25,000 protein-coding genes were predicted for each of the three species. The orthologous gene array of the *Coffea canephora*, which belongs to the *Rubiaceae*, was similar to *Cynanchum* genomes. The trace of *Gentianales*-to-*Apocynaceae* structural genome rearrangement is predicted through these conserved genome sequences. This information can be used to study the evolution and digital breeding of *Cynanchum* species.

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PA-0073

Genome-wide association study of agronomic traits related to grain yield in rice (*Oryza sativa L.*)

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To meet the ever-increasing demand for food, these shortages have become a serious problem, because of population growth and improved living standards. Especially, the production through improved plant varieties of major crops such as rice is one of the methods to solve these requirements to increase yield. In this study, a genome-wide association study (GWAS) was performed to detect candidate quantitative trait loci (QTL) related to grain yield traits (no. of panicles per hill, no. of spikelets per panicle, 1,000-grain weight, rate of ripened grains, and panicle length) utilizing core collection (137 rice accessions including 62 temperate japonica, 19 tropical japonica, 43 indica, 8 aus, and 2 admixture). In these results, every two QTLs were confirmed from four traits (no. of panicles per hill, 1,000-grain weight, rate of ripened grains, panicle length), respectively. and three QTLs were detected from one trait (no. of spikelets per panicle).

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PA-0074

Genome-wide Association study to Detect Candidate QTLs Related to Flooding Tolerance in rice (*Oryza sativa* L.)

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Direct seeding is considered an efficient cultivation technology that reduces water use and labor costs. Flooding damage to rice was reported as one of the major problems to direct seeding in rainfed lowland areas where the water remains. This study assessed the performance of core collection (137 rice accessions including 62 temperate japonica, 19 tropical japonica, 43 indica, 8 aus, and 2 admixture) when directly seeded in flooded soils using dry seeds. Also, the genome-wide association study (GWAS) combined with a principal component analysis (PCA) and a kinship matrix analysis was performed to identify quantitative trait loci (QTL) for flooding tolerance. Through this GWAS analysis, seven significant SNPs on chromosome 3, 6, 11, and 12 were confirmed to be associated with flooding tolerance, and a linkage disequilibrium (LD) decay analysis identified the 230 kb exploratory range for the detection of QTLs and candidate genes. Seven QTL were detected, on chromosome 3 (*qAG3-1*), 6 (*qAG6-1*), 11 (*qAG11-1*, *qAG11-2*, and *qAG11-3*), 12 (*qAG12-1* and *qAG12-2*). The results of this study provide associated SNPs in candidate genes for flooding conditions and strategies for developing direct seeding in breeding programs.

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PA-0075

Genome-Wide Association Study and Haplotype Analysis of Alkaline Tolerance at the Rice Germination Stage

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Alkaline stress is the one of major abiotic stress, similar to saline stress in rice, it performed serious damage to rice growth, yield, and quality. Although there has a diverse study for saline stress, but still showed a poor understanding of alkaline tolerance in rice seedling stage. In this study, a set of alkaline tolerance-related traits were measured, including germination energy, germination ratio, relative root length, and shoot length. The integrated populations were participated, which based on Japonica-Indica core-collection and breeding varieties. Genome-wide association study was performed, based on 1.57 million high-quality single nucleotide polymorphisms and 279 varieties. Totally 71 individual or overlap loci were identified in whole panel, Japonica, and Indica panel. In combination with RNA-seq data, gene and GO annotations, and significant SNP position, 12 genes were selected as candidates for alkaline tolerance in rice seeding stage. Through qRT-PCR verification, three genes showed different expression changes in tolerance and susceptible varieties. Haplotype analysis showed the 3 genes contained diverse haplotypes that significantly related to the alkaline tolerance index. SNP-haplotype analysis results showed that some key SNP could be performed crucial functions between Japonica and Indica sub-populations. Haplotype-haplotype interaction analysis indicated that co-hap1 is the favorable haplotype combination for improved alkaline tolerance in the current study.

Our results identified multiple novel loci and 3 candidate functional genes for the basic research for alkaline tolerance at the rice germination stage, haplotype results implied the pyramid haplotype could be helpful for future variety selection and breeding research.

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PA-0076

Genome-wide Association Study for the Resistance to the Brown Spot in Rice (*Oryza sativa L.*)

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Rice brown spot (BS), caused by *Cochliobolus miyabeanus*. The disease affects both rain-fed and upland rice production, causing losses in both yield and grain quality. In this study, 137 rice cultivars were used and measured brown spot disease infection levels. The main objective of the present study was screening rice germplasm collection for brown spot resistance after artificial inoculation with a virulent isolate of *C. miyabeanus.* Genome-wide association study (GWAS) and RNA-sequencing allowed the identification of 8 candidate genes in chromosome 6, according to previous research, there are two genes (*OsBS1* and *OsBS2*) among them related to rice disease resistance. In order to further verify that *OsBS1* and *OsBS2* are associated with resistance rice BS, 15 rice cultivars (9 resistants and 6 susceptible) as materials infected *C. miyabeanus* and extracted RNA of rice leaves in 0,2 and 6 days respectively in order to measure *OsBS1* and *OsBS2* genes expression by use qRT-PCR. The result showed after infected BS, *OsBS1* gene expression generally decreased. In the contrast, *OsBS2* gene expression appeared to increase, and compared with the susceptible group, the resistant group showed higher gene expression on the 6th day after being infected. According to this research results, *OsBS1* and *OsBS2* probably play an important role in the aspect of rice BS resistance.

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PA-0077

Validating the reference genome assembly of *Panax ginseng*

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Panax ginseng, a member of the family Araliaceae, is a well-known medicinal plant known for its excellent pharmacological properties. A reference genome for *P. ginseng* had previously been constructed, but there was still opportunity for improvement due to limitations from the plant's large and complicated genome structure as well as its growth characteristics. In order to improve the genome assembly, we utilized cutting-edge sequencing technologies in a hybrid assembly of a *P. ginseng* resource. The final genome assembly was 3.2 Gbp in size, with the 24 longest super-scaffolds reflecting the 24 chromosomes of *P. ginseng*. Calculating BUSCO values, mapping raw reads onto the final assembly, and other methods were used to validate the assembly. Comparative analysis was done with other publicly available genome sequences of *Panax* species to cross-validate the assembly and evaluate polyploid characteristics within the *Panax* genus. Moreover, cytogenetic approaches were implemented to validate the assembly. Thousands of oligoprobes were generated from single copy regions within each chromosome of the diploid species' genome, which could hybridize to the relevant chromosome via fluorescence in situ hybridization (FISH). The high-quality reference genome can be used in a variety of breeding programs and also serve as a benchmark for other genomic studies.

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PA-0078

Anisotropic Hydrogel Microparticles conjugated Universal Mismatch DNA Probes for Highly Specific Nucleic Acid Multiplex Detection of SNPs

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Crop genome mutation testing is receiving increasing attention in the field of crop breeding and origin inspection. Especially, hydrogel microparticle-based nucleic acid assays are an attractive detection platform based on their multiplexing capabilities with high sensitivity and specificity. A particular area of interest is single-nucleotide polymorphism (SNP) sensing, where multiple SNPs should be identified in a highly reliable yet economical manner. However, hydrogel microparticles leveraging probe-target hybridization as a key mechanism are hampered by small duplex stability differences arising from single base-pair mismatch. We have developed anisotropic hydrogel microparticles with DNA probes tailored for multiplex SNP detection. Within the DNA probes, we adopt a widely used base analog (5-nitroindole) so that it substitutes one of the base sequences among DNA probes. The effects of the modification of the probes' structure on SNP sensing has been tested from multiple perspectives, such as specificity, sensitivity, and available assay temperatures at a given ionic strength. We have validated that our hydrogel microparticles exhibit much higher specificity for a single base-pair mismatch with minimal reduction in sensitivity. Our particles can also detect multiple SNPs located in different target strands, which is a significant challenge for conventional particles.

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PA-0079

Detection of multiple SNPs in ginseng genome based on encoded hydrogel microparticles

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Hydrogel microparticle-based nucleic acid assays are an attractive detection platform based on their multiplexing capabilities with high sensitivity and specificity. A particular area of interest is sensing single-nucleotide polymorphism (SNP), a substitution of a single nucleotide at a specific position in the genome. As it is closely related to target traits, the SNP sensing was often utilized in a breeding industry of plants, where multiple SNP sensing in a reliable yet economical manner has been highly required. However, the microparticle-based SNP sensing has been impossible due to the small pore sizes of the particles compared to the genome sizes of plants. Herein, we present the process that enables the extraction of multiple short target DNA (~50 bp in length) containing SNP sites from the genome of ginseng and the multiplexed detection of the extracted target DNA based on encoded hydrogel microparticles. The chloroplast DNA of ginseng was used as the target genome. The SNP associated with the country of origin were detected using graphically encoded hydrogel microparticles labeled with fluorescence or color. We successfully detected 8 SNP sites simultaneously and distinguished the country of origin of ginseng.

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PA-0080

감자에서 전게놈연관분석법 (GWAS) 및 선발씨그니쳐법 (Selective sweeps) 을 이용한 칩가공특성의 유전변이의 해석

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감자칩가공산업의 발전과 더불어 칩가공성감자품종들을 최신게놈학의 기술을 적용하여 전게놈수준에서 해석하는 것은 디지털분자육종법으로 새로운 칩가공감자품종들을 효율적으로 육성하는데서 중요한 의의를 가진다. 한국과 세계적인 감자육종프로그램을 통하여 육성된 칩가공감자품종들에 있어서 전게놈수준에서 칩가공성과 관련된 유전변이를 GWAS 및 4가지 Selective sweep 방법을 이용하여 분석하였다.
휠터링된 4배체모델의 3977개의 SNP 마커를 이용하여 359개의 4배체 감자클론에 대한 case-control GWAS를 GWASpoly를 적용하여 진행한 결과 염색체 10 우에서 통계적으로 유의한 GWAS signals 를 찾을수 있었다. GWAS에서 발견된 유전변이는 XP-CLR 및 PCAapt 방법을 이용한 전게놈스캔에서도 재발견되었다. 가장 유의한 SNP 마커 (lead SNP)와 칩가공특성과의 상관이 분석되였다. 4가지 Selective sweeps 방법으로 탄수화물대사와 관련된 유전자자리, 전사인자 등에서 칩가공성과 관련된 breeding signatures 를 찾을수 있었다. 이 연구는 감자에서 칩가공특성의 분자적 이해를 깊이하고 향후 칩가공성이 좋은 감자를 genomics-guided breeding 에 의해 육성하는데 기여할수 있다.

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PB-0001

Research on resistance breeding using non-phenotypic trait data (HPLC data) for rice BLB disease (*Oryza sativa* L.)

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Bacterial leaf blight (BLB) is caused by *Xanthomonas oryzae* pv. *oryzae* and is a major cause of rice yield reductions around the world. When diseased, plants produce a variety of metabolites to resist pathogens. In this study, the various defense metabolites were quantified using high-performance liquid chromatography (HPLC) after *Xoo* inoculation in Cheongcheong/Nagdong double haploid (CNDH) population. Quantitative trait locus (QTL) mapping was conducted using the concentration of the plant defense metabolites. HPLC analyzes the concentration of substances according to the severity of disease symptoms. Searching for BLB resistance candidate genes by applying this analysis method is very effective when mapping related genes. These resistance genes can be mapped directly to the causative pathogens. A total of 17 metabolites were detected by means of HPLC analysis after *Xoo* inoculation in the CNDH population. QTL mapping of the metabolite concentrations resulted in the detection of the BLB resistance candidate gene, *OsWRKYq6*, in RM3343 of chromosome 6. *OsWRKYq6* has a very high homology sequence with WRKY transcription factor39, and when inoculated with *Xoo*, the relative expression level of the resistant population was higher than that of the susceptible population. Resistance genes have previously been detected using only phenotypic change data. In this study, resistance candidate genes were detected using the concentration of metabolites produced in plants after inoculation with pathogens. This newly developed analysis method can be used to effectively detect and identify genes directly involved in disease resistance for future studies.

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PB-0002

국내 밀 품종의 종자 영상 이미지 분석

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국산 밀 품종의 순도 관리에 필요한 기초 자료 제공을 위하여 국산 밀 50 품종에 대해서 종자 영상 이미지를 분석하였다. 영상이미지는 digital camera α6000 (Sony Co., Japan)에 30 mm MACRO 렌즈와 무선 리모컨을 설치해 100개 종자를 ImageJ (Abràmoff et al. 2004) 프로그램을 이용하여 분석하였다. 조사 항목은 종자 길이, 폭, 둘레, 면적, 길이와 종자 폭의 비율과 원형률을 3회 반복하였고, ImageJ 프로그램을 이용하여 분석하였으며, 분산분석은 PROC GLM을 이용하였고, 군집분석은 R 통계프로그램을 이용하였다. 종자의 영상 이미지 분석 결과, 국산 밀의 평균 값은 각각 종자 길이 6.8 mm(6.0-7.7 mm), 종자의 폭 3.4 mm(3.1-3.8 mm), 종자의 평균 면적 18.5 mm^2(14.8-22.9 mm^2), 종자 길이와 폭의 비율 2.00(1.79-2.39), 원형률 0.75(0.69-0.79)이었다. 국내 품종에서 종자가 길수록 종자 폭과 둘레가 큰 것으로 나타났고, 종자의 면적은 종자의 길이, 폭, 둘레와 정의 상관을 나타내었다. 군집분석 결과, 영상 이미지의 분산분석을 99.6% 설명이 가능했으며, 2개의 군집으로 나눌 수 있었다. 군집 Ⅰ과 군집 Ⅱ에 각각 21개와 29개 품종이 속했으며, 군집 Ⅰ의 종자 길이, 폭, 둘레와 면적이 군집 Ⅱ에 비해 높은 것으로 나타났다. 군집 Ⅰ은 2000년 이전에 육성된 종자가 큰 적립계 품종이 주로 속하였고, 군집 Ⅱ는 2000년 이후 육성된 백립계 품종과 적립계 품종 중에 비교적 종자 크기 적은 품종이 속한 것으로 분류되었다.

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PB-0003

국내 밀 품종의 종자 외관 특성 및 유전자 분석

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국산 밀 품종의 순도 관리에 필요한 기초 자료제공을 위하여 국산 밀 50 품종에 대해서 종자의 화학적 외관검사와 종실 특성 관련 유전자 분석을 실시하였다. 화학적 외관검사로 NaOH와 Ninhydrin를 통해 50개 품종은 백립계(26%)와 적립계(74%)로 구분되었으며, L-DOPA assay를 통해 PPO 활성이 높은 품종(48%)과 낮은 품종(52%)로 구분되었다. 종피색 관련 유전자인 *Tamyb-10* 분석 결과, 백립계 품종은 *Tamyb-A1a/Tamyb-B1a/Tamyb-D1a*를 지녔으며, 적립계 품종에서는 4가지 유전자형(*aba, abb, baa, bba*)이 나타났다. 백립계 품종에서는 *Tamyb-10* 유전자 조성에 따른 적색 정도 구별이 가능하였지만, 적립계 품종에서는 구별이 불가능하였다. 국내 품종에서 종자 크기와 관련된 유전자 *TaCWI-4A, TaGW2-6A*와 *TaSus2-2B*를 검정하였는데, *TaCWI-4A* 유전자형에 따른 종실 특성은 차이가 없었으며, *TaGW2-6A*와 *TaSus2-2B*에서 *Hap-6A-G*와 *Hap-L*을 지닌 품종이 *Hap-6A-A*와 *Hap-H*를 지닌 품종보다 천립중이 컸다. 또한 PPO 활성이 높은 품종은 *Ppo-A1a/Ppo-B1b/Ppo-D1b*의 비율이 높았으며, 낮은 품종은 *Ppo-A1b/Ppo-B1a/Ppo-D1a*의 비율이 높았다. L-DOPA assay에서 착색이 되지 않고 밝았던 26개 품종의 *Ppo-1* 유전적 조성을 비교해보면, PPO 활성이 낮은 *Ppo-A1b*와 *Ppo-D1a*를 지닌 품종은 각각 13개와 24개로 한백을 제외한 12 품종은 *Ppo-A1b/Ppo-D1a*를 지닌 것으로 나타났다.

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PB-0004

QTL analysis for rice BLB (bacterial leaf blight) with micro-trait data by using OCT (optical coherence tomography) technology (*Oryza sativa* L.)

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With rapid population growth and global food security. This makes the efficiency and accuracy of the current manual screening mode of traditional breeding face a serious challenge. So the Non-invasive investigation of rice leaf specimens to characterize the morphological formation and particular structural information that is beneficial for agricultural perspective was demonstrated using a low coherence interferometric method called swept source optical coherence tomography (SS-OCT). The acquired results non-invasively revealed morphological properties of rice leaf, such as bulliform cells; aerenchyma, parenchyma, and collenchyma layer; and vascular bundle. Beside aforementioned morphologic characteristics, several leaf characteristics associated with cytological mechanisms of leaf rolling (leaf inclination) were examined for the pre-identification of inevitable necrosis and atrophy of leaf tissues by evaluating acute angle information, such as angular characteristics of the external bi-directional angles between the lower epidermis layer and lower mid-vein, and internal angle of lower mid-vein. To further assist the pre-identification, acquired cross-sections were employed to enumerate the small veins of each leaf specimen. Since mutants enlarge leaf angles due to increased cell division in the adaxial epidermis, healthy and abnormal leaf specimens were morphologically and quantitatively compared. Therefore, the results of the method can be used in agriculture, and SS-OCT shows potential as a rigorous investigation method for selecting mutant infected rice leaf specimens rapidly and non-destructively compared to destructive and time consuming gold-standard methods with a lack of precision.

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PB-0005

Molecular characterization of high linoleic acid mutant and *FAD3* genes in perilla

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Perilla (*Perilla frutescens* var. *frutescens*) is a tetraploid that is one of the oilseed crops grown mainly in South Korea and Asia. Perilla seed has a high polyunsaturated fatty acid in triacylglycerol (TAG), which is composed of 64% α-linolenic acid (18:3) and 14% linoleic acid (18:2). However, it is considered to reduce the polyunsaturated fatty acid to prevent oil has turned rancid. For this reason, Gamma irradiation treatment was carried out in the perilla and found the high linoleic acid mutant, referred to as *110-18#15*. Compared with wild type, which produced linoleic acid at 14%, linoleic acid contents increased 37% in seeds of *110-18#15* line. Because FATTY ACID DESATURASE 3 (FAD3) synthesizes α-linolenic acid from linoleic acid, we isolated two *PfFAD3a* and *PfFAD3b* from perilla and performed the complementation analysis in Arabidopsis *fad2-3* mutant. As a result, complemented lines showed that linolenic acid was increased from 1.2% to 35% in seeds. Finally, we tried to analyze the sequence difference between *PfFAD3a* and *PfFAD3b* in the *110-18#15* line. The *PfFAD3b* sequence was no different compared to the wild type, but the *PfFAD3a* gene was not amplified by PCR. Therefore, it was expected that the *PfFAD3* gene was changed by gamma irradiation.

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PB-0006

A novel resistance gene for bakanae disease in rice, *qBK4T* identified by GWAS

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Bakanae (foolish seedling) disease caused by *Gibberella fujikuroi* causes serious problems in the majority of rice growing countries. The discovery and deployment of durable resistance genes for Bakanae disease is an effective and sustainable mean to mitigating production losses. In this study, Genome-Wide Association Study (GWAS) approach was employed on 145 $BC_1F_{7:8}$ NILs population derived from a crossing between Ilpum × Tung tin wan hien1, recurrent and R-donor parents, with the latter carrying a new R gene conferring a broad spectrum resistance to Korean Bakanae disease races. A GWAS analysis was conducted to identify genes/loci conferring bakanae resistance in rice. Results identified uncovered genomic regions highly associated with the observed phenotypic variation for response to bakanae infection on the long arm of chromosome 4 (named as $qBK4^T$). A localization of $qBK4^T$ was delimited at an approximate 324kb interval in the physical map between AX-116847364 (33.12 Mb) and AX-115752415 (33.44 Mb). Previous studies reported QTLs controlling Bakanae disease on chromosome 4 but different loci, such as *qBK4.1* and *qBK4_31750955*. Therefore, this study provides new insights for R-gene-specific marker development, which could be useful for downstream Bakanae disease-resistant breeding and R-gene pyramiding. Further characterization of the R-gene would be helpful to unveil the mechanism underlying Bakanae disease resistance in rice.

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PB-0007

Gene integration approach detected QTLs Associated with Bakanae disease resistance in rice

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Bakanae (foolish seedling) disease caused by *Gibberella fujikuroi* causes serious problems in the majority of rice growing countries. In this study, we attempted to investigate quantitative trait loci (QTLs) conferring Bakanae disease resistance in rice. Therefore, a rice population comprising 200 $F_{6:7}$ lines, developed from a cross between MY299BK (resistant) and Saenuri (moderately resistant), harboring *qBK1* and *qFfR6*, respectively, was used. The mapping population was employed to perform QTL analysis, using Kompetitive Allele-Specific PCR (KASP) markers. Unlike previous reports, we could not detect *qFfR6*-specific QTLs on chromosome 6. Rather, two QTLs were detected on the long arm of chromosome 1, designated as $qBK1^{S1}$ and $qBK1^{S2}$. The major effect QTL designated both $qBK1^{S1}$ (Logarithm of the odds, LOD: 3.2, phenotypic variation explained, PVE: 8.22%) was flanked by Os01_KJ01_051 and Os01_KJ01_057 (2.05Mb), while $qBK1^{S2}$ (LOD: 3.6, PVE: 3.22%) was flanked by Os01_KJ01_107 and Os01_KJ01_125 (6.07Mb). This study identified two novel QTLs that could be utilized as new potential targets for the development of Bakanae disease resistance in rice through the gene integration effect.

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PB-0008

Genetic variation of five fatty acid components and two seed characteristics in Korean *Perilla* germplasm using SSR markers

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Perilla seed oil of *P. frutescens* var. *frutescens* of *Perilla* crop has been used in foods such as cooking oil like sesame seed oil. Five fatty acids of 280 *Perilla* accessions were identified as follows: palmitic acid (PA) (5.30-8.66%), stearic acid (SA) (1.60-4.19%), oleic acid (OA) (9.60-22.5%), linoleic acid (LA) (8.38-25.4%), and linolenic acid (LNA) (52.7-76.4%). In a correlation analysis among the five fatty acids of the 280 *Perilla* accessions, the combinations of PA and SA (0.794**), PA and OA (0.502**), PA and LNA (0.507**), SA and OA (0.724**), and SA and LNA (0.564**) showed comparatively higher positive correlation coefficients than the other combinations. A total of 224 alleles with 29 simple sequence repeat (SSR) primer sets were detected segregating in the 280 *Perilla* accessions. By using an association analysis of the 29 SSR markers and the five fatty acids in the 280 *Perilla* accessions, we found 13 SSR markers (KNUPF2, KNUPF4, KNUPF10, KNUPF16, KNUPF25, KNUPF26, KNUPF28, KNUPF55, KNUPF62, KNUPF74, KNUPF85, KNUPF89, and KNUPF118) related to the five fatty acids. Among these SSR markers, eight SSR markers were associated with the SA trait, six SSR markers were associated with the PA trait, six SSR markers were associated with the OA trait, two SSR markers were associated with the LA trait, and two SSR markers were associated with the LNA trait. Therefore, these SSR markers are considered to be useful markers for selecting useful accessions related to content of the five fatty acids from native Korean germplasm accessions of *Perilla* crop.

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PB-0009

Response of Hulless Oat (*Avena nuda* L.) Spikelets Under Different Temperature Conditions

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Oats (*Avena sativa* L.) is well adapted to low fertile soil and adverse growing environment. Because of its high nutritional contents and yields, hullless oat (*Avena nuda* L.) is becoming increasingly popular. Numerous favorite traits such as early-maturing genotypes with enhanced yields, superior agronomic qualities, disease resistance, high energy value and protein contents have been added to the hullless oat. Although, increasing acreage due to these advantages, abiotic stresses directly limit the growth of hulless oat, which restricts the effective use and development of the oat. In this study, to reveal the growth phenomena especially in the spikelets during grain filling periods under the different temperatures, physiological, transcriptional and proteomic analysis were performed. Oats were exposed to five different temperatures at grain-filling stage. Those temperature ranges are in accordance with different altitudes in Northern parts of Korean peninsula. Numerous abiotic stress related parameters were measured at different grain developmental stages as well as different location of inflorescences in each plant. The obtained results showed different response of reproductive organ to diverse temperatures, which can propose possible optimum temperature ranges to get maximum grain yield. Since high temperature during grain filling period is now considered as a major interference on yield potential, we expect that obtained results allow us to classify optimal temperature for oat grain yields.

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PB-0010

Analysis of *DA1*-like gene family in oat (*Avena sativa* L.) and functional characterization of *AsDA1*-2D heat tolerance

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Ubiquitin receptor of *DA1* gene has been known to play an important role in regulating grain size *via* ubiquitin-proteasome pathway. However, *DA1* gene has not yet reported in oat (*Avena sativa* L.). Based on BLASTP search in *Avena* database, a total of three *AsDA1* genes, *AsDA1*-1D, *AsDA1*-2D, *AsDA1*-5A, which located in 1D, 2D and 5A were identified, respectively. From the phylogenetic relationships with other plant species, all *DA1* family genes exhibited having a common structure containing conserved motifs and *AsDA1* proteins. To confirm the expression of each *AsDA1*-1D, *AsDA1*-2D, *AsDA1*-5A gene in response to heat stress, qRT-PCR was performed. Among the three genes, only *AsDA1*-2D showed gradually high expression under heat stress. *AsDA1*-2D showed up-regulated expression level under other abiotic stresses. Through thermotolerance yeast assay *AsDA1-2D* transgenic yeast maintained the growth ratio compared to empty vector yeast under high temperature stress. Analysis of correlation between *AsDA1*-2D gene express and degree of heat stress will be helpful for enhancing oat tolerance under the abiotic stresses.

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PB-0011

Development of multi-stress tolerant temperate rice variety using multi-omics breeding

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Some high-quality japonica varieties exhibited intolerance to low fertilizer application and high temperature. MS11-*Pup1* showed good yield performance under low phosphorus application and possibly high temperature. We therefore used MS11-Pup1 as the donor to improve multiple abiotic stress tolerance in Golden Queen3 and its derivative. We have been utilizing the rapid marker-assisted backcrossing (MABC) program aiming to produce BC_2F_2 seeds with minimum introgression from the donor in the successful breeding line using our own pseudomolecules to elucidate the genomic constitution of high-quality rice varieties in a precise manner. Additionally, the genes linked to the chromosomal introgression during the breeding process using *Pup1*(nutrition uptake), *Sub1*(submergence tolerance), *AG1*(anaerobic germination), and *Pi9*(rice blast) might be linked to poor grain quality. We therefore utilized whole genome sequence data to generate breeding lines that are more attractive to consumers by analyzing the alleles associated with some poor traits in MS11-*Pup1* and CSA-*Pi9* (Ciherang+*Sub1*+*AG1*+*Pi9*). We used pseudomolecules generated from long read amplicons generated by Nanopore technology to elucidate promising genomic regions useful for genome editing. *In silico* PCR was conducted using primers spanning gene regions known to causal phenotypic variations. Preliminary data showed allele differences in *Badh2*, *GS3* and *waxy* genes among high quality varieties, CSA, CSA-*Pi9*, MS11, and MS11-*Pup1*. We therefore have a meaningful case that these regions are useful sites for targeted mutation towards a more favorable allele type. The combination of allele modification by genome editing team followed by MABC could be the one of proof-of-concept workflows for rapid breeding for climate-ready rice.

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PB-0012

Natural variation in *qTA8* regulates tiller angle by affecting gravitropic response in rice

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Tiller angle, a major component of rice plant architecture, affects planting density, photosynthetic efficiency, and disease resistance in population, thus determining the rice yield per unit area. Shoot gravitropism has a large effect on tiller angle by contributing to asymmetric growth of two sides of tiller bases. Here, we identified a major locus *qTA8* which was simultaneously associated with gravitropic response and tiller angle using genome-wide association analysis and QTL-seq. *qTA8* allele causing narrow tiller angle exhibited immediate response to gravistimulation with a simultaneous elevation of H_2O_2 levels at early stage. Furthermore, *qTA8* affected the expression patterns of transcripts involved in reactive oxygen species (ROS) generation and response to excessive ROS. Evolutionary analysis revealed that *qTA8* alleles for narrow tiller angle originated from wild progenitors and were positively selected independently in *temperate japonica* and *indica* subspecies during domestication. Allelic combinations of *TAC1*, another major gene controlling tiller angle, and *qTA8* implied that two loci act additively in modulating tiller angle in both natural population and NILs. These findings provide understanding of the genetic mechanism of tiller angle control in rice and *qTA8* could be used to develop rice varieties with ideal plant architecture.

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PB-0013

Comparative transcriptome analysis of Soybean development in weedy and cultivar growth types

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In cultivated plants, shoot morphology is an important factor that influences crop economic value. However, the effects of gene expression patterns on shoot morphology are not clearly understood. In this study, the molecular mechanism behind shoot morphology (including leaf, stem, and node) was analyzed using RNA sequencing to compare weedy (creeper) and cultivar (stand) growth types obtained in F7 derived from a cross of wild and cultivated soybeans. A total of 12,513 (in leaves), 14,255 (in stems), and 11,850 (in nodes) differentially expressed genes were identified among weedy and cultivar soybeans. Comparative transcriptome and expression analyses revealed 22 phytohormone-responsive genes. We found that *GIBBERELLIN 2-OXIDASE 8* (*GA2ox8*), *SPINDLY* (*SPY*), *FERONIA* (*FER*), *AUXIN RESPONSE FACTOR 8* (*ARF8*), *CYTOKININ DEHYDROGENASE-1* (*CKX1*), and *ARABIDOPSIS HISTIDINE KINASE-3* (*AHK3*), which are crucial phytohormone response genes, were mainly regulated in the shoot of weedy and cultivar types. These results indicate that interactions between phytohormone signaling genes regulate shoot morphology in weedy and cultivar growth type plants. Our study provides insights that are useful for breeding and improving crops to generate high-yield soybean varieties.

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PB-0014

농업용 승인 유전자변형생물체의 국경감시 체계 구축에 필요한 품목 특이적 검정 및 비의도적 혼입량 측정방법 확립

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전라북도 전주시 덕진구 농생명로 370 국립농업과학원

LMO가 상업화되면서 국가간 이동시 환경에 미치는 영향 및 위해성 관리의 필요성이 대두되어 국제 협약인 카르타헤나 의정서가 발의되었다. 이에 따라 국내의 경우 「유전자변형생물체의 국가간 이동 등에 관한 법률」(이하 LMO법)이 제정되어, LMO 수입 승인 절차 및 유통 과정 전반의 관리, 감독의 근거가 마련되었다. 해당 법률에 의거 국립농업과학원 생물안전성과에서는 농림축산업용 LMO의 위해성 심사 시 제출되는 LMO표준품의 보관, LMO검정법의 심사 및 LMO 검정 방법의 표준화 등 농림축산업용 LMO의 검정체계 전반에 관한 업무를 수행한다.

LMO법 통합고시 제 3-13조(비의도적 혼입등의 기준 및 확인 절차)에 의거 국내 Non-LMO 수입 시 인정되는 비의도적 LMO혼입 비율은 3% 이하로 규정하고 있는 바, LMO의 삽입유전자를 증폭하는 PCR 검정 방법을 이용한 정성 분석을 통하여 Non-LMO와 LMO를 구분하고, LMO로 확인되면 특이적 이벤트만을 증폭하는 분자 마커를 이용하여 해당 이벤트의 포함여부를 검정한다. 검정된 이벤트의 LMO 함량을 확인하기 위하여 Real time PCR을 이용한 표준 검량곡선을 구하고, 이를 통해 시료의 내제 유전자로 전체 DNA량, 삽입유전자로 LMO DNA량을 정량 한다. 정량 된 시료의 DNA량을 통하여 LMO 함량을 구하고, 시료의 LMO 함유량이 3% 초과시 국내에 Non-LMO로 수입이 불가로 판정한다.

국내 LMO 수입량은 점차적으로 증가하여 2018년 기준으로 1천 만 톤 이상 증가하였다. 21년 기준 1,114.5톤이 수입되었고, 그중 대부분이 사료 및 사료 가공용 LMO로 84.2%를 차지하고 있다. 이에 국립농업과학원 생물안전성과 LMO 검정평가실에서는 해당하는 70개 이벤트 (옥수수 25개, 콩 17개, 면화 16개, 카놀라 7개, 감자 3개, 알파파 2개)에 대한 정량 및 정성 분석법에 대한 표준화 및 검정 기술을 확립하였고, 관련된 전반적인 연구 및 지원 업무를 수행하고 있다.

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PB-0015

QTL analysis and mapping of *qBBR11*, related to field resistant to bacterial blight in rice

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Rice is used as a staple food by half of the world's population and is responsible for most of the calories. Bacterial blight (BB) disease caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) is a major cause of severe yield loss in rice mainly in Asia and is one of the most devastating diseases. BB diseases in rice caused various damage throughout the growing period of rice, and the degree of damage varies. rice has established complex molecular mechanisms to respond to *Xoo*. Here, *qBBR11*, a resistance QTL against BB disease, was detected in KJ11_067 to KJ11_068 on chromosome 11 in a population derived by crossing JJ623 and HR27195 with a similar genetic background but different degrees of resistance to BB disease. *qBBR11* was narrowed down chromosome 11 to 200 kbp segment franked. Sixteen candidate genes were included in this region. In particular, high-impact variations were detected in *Os11g0517800* which encode the domain region of GCN2 which is the eIF-2-alpha kinase associated with the resistance of abiotic/biotic stress in rice. In JJ623, which is moderately resistant to BB disease, a stop codon was created due to single nucleotide polymorphism (SNP). Therefore, compared with HR27195, JJ623 has weaker resistance to BB disease, though the two have similar genetic backgrounds. The results suggest that variation in the *qBBR11* region regulates an important role in improving resistance to BB diseases, and *qBBR11* is useful in providing an important resource for marker-assisted selection to improve mechanisms of resistance to BB disease.

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PB-0016

Expression of OsF3H enhances Bacterial Leaf Blight (BLB) stress tolerance in rice by induction of antioxidant flavonoids, defense genes and hormones

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Efficient accumulation of flavonoids is important for increased tolerance to biotic stress. Although several plant defense mechanisms are known, the roles of many pathways, proteins, and secondary metabolites in stress tolerance are unknown. We generated a flavanone 3-hydroxylase (F3H) overexpressor rice line and inoculated *Xanthomonas oryzae* pv. *oryzae* and compared control and wild type inoculated plants. In addition to promoting plant growth and developmental maintenance, the overexpression of F3H increased the accumulation of flavonoids and increased tolerance to bacterial leaf blight (BLB) stress. Moreover, leaf-lesion length was higher in infected wild type plants compared with infected transgenics. Kaempferol and quercetin, which scavenge reactive oxygen species, over-accumulated in transgenic lines compared with wild types in response to pathogenic infection, detected by scanning electron microscopy and spectrophotometry. The induction of F3H altered the antioxidant system and reduced the levels of glutathione peroxidase and lipid peroxidase in transgenic lines compared with wild types. Downstream gene regulation analysis showed that the expression of F3H increased the regulation of FLS, DFR, and SLR1 during BLB stress. The analysis of SA and JA signaling revealed an antagonistic interaction between both hormones and that F3H induction significantly promoted SA and inhibited JA accumulation in transgenic lines. SA-dependent NPR1 and Xa1 showed significant upregulation in infected transgenic lines compared with infected control and wild type lines. Thus, the overexpression of F3H is essential for increasing BLB stress tolerance.

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PB-0017

Identification of rice seed germination related genes under low different temperature conditions using QTL analysis

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Recently, unusual temperature by global warming affects the crop yield and quality. Adverse conditions such as low temperature, high temperature, drought, and salinity affect on the physiological processes and induce changes related to genetic mechanisms. In particular, rice is a sensitive crop at low temperatures compared with other main crops. The low temperature causes harmful influences in the overall process of rice growth such as uneven germination and the establishment of seedlings. Especially, low temperature at the seed germination stage affects the germination percentage (GP) and germination delay. In general, the optimum temperature of germination is around 30℃. Below the optimum temperature of germination, it causes the delay of germination, early seedling growth and also impacts low GP. Therefore, high GP at low temperature is a primary trait to elucidate stable seedlings. In this research, we figured out the genes related to rice seed germination under low different temperature conditions by analyzing the quantitative trait locus (QTL). Total 4 QTLs were detected in chromosomes 3, 6, and 8. Among them, twenty-five germination related genes mapped in RM7197-RM15063 on chromosome 3. Finally, *OsGPq3* gene which is related to endosperm development was selected as a target gene. *OsGPq3* can be used as basic data in further studies associated with seed germination.

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PB-0018

Effect of insect-resistant genetically modified (Bt-9) rice on above-ground non-target arthropods in Korea

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Insect-resistant genetically modified (Bt-9) rice shows resistance against rice leaf roller (*Cnaphalocrocis medinalis*) by expressing a toxic protein (mCry1Ac1) mediated from the soil bacterium *Bacillus thuringiensis*. Environmental risk assessment of Bt-9 event, in addition to the parent variety Dongjin and cultivar Ilmi, was performed during the rice cultivation seasons of 2016 and 2017 at LMO quarantine fields in Jeonju and Gunwi, Korea. Non-target arthropods (insects and spiders) were captured using an aspirator from the three rice ecosystems of both locations, and in total 40,817 individuals of 62 families and 11 orders were collected. The numbers of individuals collected from the Bt-9, Ilmi, and Dongjin rice ecosystems were 13,982, 14,105, and 12,730, respectively, which did not differ significantly among rice ecosystems. The dominance, diversity, evenness, and richness indices of the collected insects were not statistically different among the rice ecosystems, but significant variations between the two locations and survey years were detected. Principal component analysis showed that insects and spiders in the Bt-9, Dongjin, and Ilmi rice ecosystems were separated by the study locations and years irrespective of rice variety. In conclusion, results obtained in two consecutive years from two non-genetically modified rice ecosystems and a Bt-9 rice ecosystem showed that the Bt-9 rice had no significant negative impacts on the above-ground insect and spider communities.

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PB-0019

Risk assessment of TRX (Thioredoxin) genetically modified soybean on associated non-target insects and arachnid

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The effects on the biodiversity of above-ground insects and spiders in agroecosystem by the cultivation of genetically modified crops was evaluated. In this study, we assessed the effects of genetically modified soybean events TRX (expressing the human thioredoxin gene under the control of the β-conglycinin promoter with tolerance to the herbicide glufosinate) on plant-dwelling non-target insects and arachnids compared with those of a non-GM parental cultivar, Gwangan soybean. Field surveys of soybean fields were carried out at Jeonju and Ochang, Korea, in 2016 and 2017. We found that the number of captured individuals was higher at Ochang in 2017 on both TRX and Gwangan soybean plants. From 2016 to 2017, the average population density of the insect pests and natural enemies decreased; however, in the case of other insects, the population density remained unchanged. The dominance index of the captured non-target insects and arachnids decreased, whereas the diversity and richness indices increased over time on the genotypes at both regions. The evenness index of non-target insects and arachnids decreased at Jeonju but showed no change at Ochang, regardless of the genotype. Hemiptera, Hymenoptera, and Diptera were the most dominant orders of the insect pests, natural enemies, and other insects, respectively. The score from PROXSCAL multidimensional scaling using combined data showed that insects and arachnids in different natural environments differed due to their cultivation regions and years, irrespective of soybean cultivars. Overall, the results indicated that the TRX soybean did not negatively affect the community of plant-dwelling non-target insects and arachnids.

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PB-0020

Deciphering the Anthocyanin Biosynthesis in Different Colored Taproot Radish Plants

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Radish (*Raphanus sativus* L.), belonging to the *Brassicaceae* family is an economically important taproot vegetable crop grown globally. Radish taproots have diverse colors depending on the accumulation and distribution of anthocyanins and chlorophyll. Anthocyanins, belonging to class of flavonoid-derived secondary metabolites, act as visual attractants for pollinators or seed dispersers and help to protect plants against various biotic and abiotic stresses. In addition, they have human health benefits due to their strong antioxidant properties in preventing certain cancers, chronic human diseases, and cardiovascular diseases.

To elucidate the anthocyanin biosynthetic mechanism, analysis of anthocyanin-related genes and metabolites was performed with different taproot colored radishes. Depending on the cultivars, it exhibited the different level of anthocyanin composition and content. The white radish cultivar did not accumulate the any kind of anthocyanins, consistent with the visual appearance, but the red, purple, and dark purple cultivars mainly accumulate pelargonidins, cyanindins, and delphinidins in differing densities. Transcript level of RsMYB1 and RsTT8, which were member of active anthocyanin promoting complex was highly expressed in pigmented radish cultivars, but barely in white radish, consistence of the expression level of flavonoid biosynthetic genes. Interestingly, the transcript level of RsF3'H of red colored radish cultivar was very low compared to that of purple, and dark purple colored radish cultivar. Based on the nucleotide variation of anthocyanin biosynthesis related genes, we developed the molecular marker to discriminate the root skin color of radish. This result indicated the expression of anthocyanin biosynthetic genes was responsible for the root color development in radish.

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PB-0021

Transcriptome Analysis of Differentially Expressed Genes Involved in Flavonoid Biosynthesis in Ray Florets of *Chrysanthemum morifolium* under Different Temperature Cultivation

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Chrysanthemum (*Chrysanthemum morifolium*) belongs to the *Asteraceae* and is an economically important floricultural crop as well as a medicinal plant species. Flower color is a key trait for commercial value with a differential accumulation of secondary metabolites such as anthocyanins and carotenoids determining the ray floret color. Anthocyanins, a class of flavonoid compounds, can be accumulated or degraded under cold or high temperatures for protecting plant tissues. While the mechanism of anthocyanin biosynthesis in chrysanthemum according to cultivation temperature remains largely unknown. To investigate this mechanism, we performed the RNA-seq analysis with white and red ray florets cultivars under different cultivation conditions. As a result of visual appearance, the white ray floret cultivar increased anthocyanin contents under low temperatures, but the red ray floret cultivar reduced anthocyanin contents under high temperatures. Expectedly, the transcript levels of anthocyanin biosynthetic genes well coincided with the anthocyanin accumulation pattern of two chrysanthemum cultivars. According to the comparison of differentially expressed genes, we selected the genes involved in flavonoid biosynthesis and validated the gene expression pattern by quantitative real-time PCR. Among them, the expression level of F-box protein was the opposite pattern between white and red cultivars. Now, we are investigating the role of F-box protein in anthocyanin biosynthesis in chrysanthemum. These results will provide meaningful information for anthocyanin biosynthetic mechanism in ray florets of chrysanthemum under different temperature cultivation.

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PB-0022

Toward fine-mapping of a QTL for pre-harvest sprouting resistance with Korean *japonica* rice varieties

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Pre-harvest sprouting (PHS) causes serious economic losses because of reductions in yield and quality in rice. In a previous study, we found QTLs for PHS resistance on chromosome 3, 4 and 11 with 160 recombinant inbred lines derived from a cross between the Korean temperate *japonica* varieties Odae (moderately resistant to PHS) and Unbong40 (susceptible to PHS) under two different environmental conditions - field (summer) and greenhouse (winter) environments. Among the QTLs, the QTL on chromosome 11 (*qPHS11*) showed stable effects in the two environments and we proceeded toward fine-mapping of this QTL. Through backcross between Odae (donor parent) and Unbong40 (recurrent parent), we made 14 BC4F1 plants, and genotyped them with 180 kompetitive allele-specific PCR (KASP) and 14 cleaved amplified polymorphic sequence (CAPS) markers distributed across whole rice genome. We selected a BC4F1 plant with the highest recurrent parent genome recovery rate. Then, we planted 210 F2 progeny plants from the selected BC4F1 plant and genotyped them with 10 KASP and 6 CAPS markers located on chromosome 11. The PHS rates of the plants were measured. By QTL mapping with the genotype data and PHS rates of the BC4F2 plants, the *qPHS11* was delimited to the interval of *KJ11_091* - *OUC11_11310* (23.55 - 24.04 Mbp). This QTL can be used to improve the PHS resistance of Korean temperate *japonica* varieties.

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PB-0023

Molecular characterization of the Plant U-box proteins in the Poaceae involved in low temperature stress response

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The plant U-box (PUB) proteins function as E3 ligases to poly-ubiquitinate the target proteins for their degradation or post-translational modification. PUBs also play important roles in regulating diverse biological processes, including plant response to environmental stresses. Nevertheless, their functional roles regarding cold response in the Poaceae have not been fully investigated. In this study, we identified cold-responsive PUB proteins in the Poaceae and suggested their roles in cold response. Cold-responsive PUB proteins were screened via RNAseq analysis using public RNAseq data of rye, wheat, and barley. Cold treatment was conducted to three-leaf stage seedlings of the three Triticeae crops and oat. The cold response of each species was examined by measuring proline and soluble sugar content. Next, real-time PCR was conducted to validate the gene expressions and only two genes represented altered expression levels in all the species. One of the two proteins, PUB6, was further investigated in this study. Yeast-two hybrid screening was performed to identify PUB6-interacting proteins and four putative proteins were obtained. Yeast co-transformation and bimolecular fluorescence complementation (BiFC) were performed and their subcellular location was observed through GFP-tagged vectors. The functional role of PUB6 was verified through *in vitro* ubiquitination assay and cell-free degradation assay. The results of this study will provide some evidence for revealing the PUB-mediated cold stress tolerance mechanism.

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PB-0024

Genome-wide analysis of the U-box E3 ubiquitin ligase enzyme gene family in winter crop

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Biological and cellular processes in plants are regulated by many mechanisms, such as controlled gene expression, protein synthesis, protein modification, protein degradation, and interactions among molecules. E3 ubiquitin ligases are a central modifier of plant signaling pathways that act through targeting proteins to the degradation pathway. U-box E3 ligases play crucial roles in regulating plant development, reproduction, cellular protein degradation and responses to biotic and abiotic stresses. We have identified a total of 265 U-box genes in wheat genome and their orthologous gene in winter crop, such as barley, oat, and rye, and these genes were further divided into various subgroups based on specific domains. Gene ontology, KEGG, and KOG analysis of U-box genes were investigated. Transcriptome analysis showed differential expression patterns of U-box genes of inter- and intra-species of winter crops specifically expressed in cold stress condition. The genome-wide analysis of U-box genes provides new opportunities for characterization of candidate U-box genes and elucidation of biological roles in winter crop under cold stress responses.

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PB-0025

Genome wide association study reveal the casuative factors underlying isoflavone content in a mutant soybean population derived from radiation breeding

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Isoflavones are major secondary metabolites that are exclusively produced by legumes. Soy isoflavones play important roles in human health as well as in the plant defense system. The isoflavone content is influenced by minor-effect quantitative trait loci, which interact with polygenetic and environmental factors. It has been difficult to clarify the regulation of isoflavone biosynthesis because of its complex heritability and the influence of external factors. Here, using a genotype-by-sequencing-based genome-wide association mapping study, 189 mutant soybean genotypes were genotyped on the basis of 25,646 high-quality single nucleotide polymorphisms (SNPs) without missing data and minor allele frequency of < 0.01. All lines were phenotyped by determining the contents of 12 isoflavones in the soybean seeds in two consecutive years (2020 and 2021). Then, quantitative trait nucleotides (QTNs) related to isoflavone contents were identified and validated using multi-locus GWAS models. A total of 152 and 72 QTNs related to isoflavone contents were detected by multiple MLM-based models in 2020 and 2021, respectively. Of these, 30 and 10 QTNs were related to more than two types of isoflavones in 2020 and 2021, respectively. Forty-four QTNs were detected within the 441-Kb physical interval surrounding Gly05_38940662. Of them, four QTNs were located at Glyma.05g206900 and Glyma.05g207000, which encode glutathione S-transferase 1 (GmGST1), as determined from previous quantitative trait loci annotations and the literature. We validated substantial differences in the transcript levels of *GmGST1* and two other core genes (*IFS1* and *IFS2*) in the isoflavone biosynthetic pathway between the original cultivar and its mutant.

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PB-0026

Gene expression profile of gamma-ray irradiated sorghum (*Sorghum bicolor* L.) mutants under salt treatment conditions

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Sorghum (*Sorghum bicolor* L.) is one of the C4 crop and the species which most suitable for marginal land including salinity soil. Moreover, It is spotlighted as an important resource for food, feed and biofuels. In this study, we constructed sorghum mutant pool induced by gamma-ray (100 ~ 400 Gy). The 28 elite mutant lines were chosen through agronomic traits and to evaluate salt tolerance, ten mutant lines showing phenotypic variation compared to the original accessions were selected. Based on germination rate, shoot length, and root length, three mutants (B5, SY6 and SY7) were shown significant difference with increased shoot length (1.3 ~ 2.2 fold) and root length (1.5 ~ 2.5 fold) compared with original accessions under saline conditions (150 mM NaCl). We determined that the transcripts level of 20 genes closely related to abiotic stress such as heat shock protein, ROS scavenging system, aquaporin, and transcription factors genes. Fifteen-five causal genes showed different transcription levels between salt treatment and no-treatment in B5. The expression levels of Sb03g045840 and Sb03g030750 showed significantly different in B5 compared with control by salt treatment, and it is speculated that this is the most important gene for the mechanism of salt tolerance. In conclusion, We prove the simple method could identify causal genes underlying mechanism of salt tolerance.

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PB-0027

Towards the Development of Rice with Low Fertilizer Usage by Utilizing Genomics & Phenomics Approaches

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Increasing fertilizer cost is one of the challenges being faced by rice farmers worldwide. Nitrogen (N) and phosphorus (P) are among the critical nutrients needed by rice plants to reach maximum yield potential. Recent advances in molecular breeding have paved way to the development of high-yielding rice varieties. However, often, these varieties require high level of fertilizer inputs especially N and P. Our breeding pipeline aims to take advantage of genomics and phenomics approaches to develop rice varieties efficient in terms of N and P utilization. First, using a diverse set of Korean rice varieties in conjunction with pseudomolecules generated from long read genomic sequences (Nanopore technology), haplotype-based identification of core variety sets will be conducted for genes related to P-uptake. These core sets will be tested in several temporal and spatial field experiments in different fertilizer regimes. The next step involves the development of precise phenotyping methods to elucidate important traits as biological markers to evaluated N and P uptake in rice. Important P-related genes such *OsPSTOL1* will be introgressed to varieties with high nitrogen-use efficiency (NUE) to develop rice with improved N-P uptake. Simultaneous to this breeding pipeline will be the development of mapping populations to identify QTLs related to NUE. Additionally, we have analyzed a core set of Korean rice varieties for *OsPTF1*, one of the most important genes related to P-uptake. Based on *OsPTF1* haplotypes, we have identified donor lines to develop NILs with both *OsPTF1* and *OsPSTOL1*.

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PB-0028

High-density linkage mapping of causative QTLs underlying isoflavone content in gamma-ray mutant soybean (*Glycine max* L.)

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Soybean [*Glycine max* (L.) Merrill] is a rich source of secondary metabolite including isoflavone as well as edible protein and oil, which could be used as cosmetic and medicine for human health, and defense system for themselves. However, since isoflavone content is quantitative trait affected by environmental effects, the information of its genetic basis was limited. Herein, to unveil stable QTLs for individual and total isoflavone content in soybean seeds, 190 segregating mutant-based F_2 population was crossed between original cultivar with low isoflavone conetent (Dandeak; 1580.51 μg g^{-1}) and its mutant soybean (DB088; 6393.36 μg g^{-1}). Fine linkage map of 2812.01 cM was constructed by using high-density Axiom ® 180k SoyaSNP array. Based on isoflavone content, 39 quantitative trait loci were mapped into nine chromosomes. Of these, seven single nucleotide polymorphism markers (Gm02_12248842, Gm04_34123994, Gm10_44764983, Gm11_10573890, Gm11_5859806, Gm15_19072693 and Gm20_26501680) were detected for a minimum of two types of isoflavone content, it means that these markers were closely involved in biosynthesis of isoflavone in soybean seed. Furthermore, the correlative analysis was demonstrated that several isoflavone contents were negatively/positively correlated with agricultural traits such as days to flowering, days to maturity, growth type, plant type, plant habit, number of nodes. Therefore, these mutant alleles derived from DB-088 would be beneficial for marker-assisted selection in soybean with high isoflavone content. This result will make a breakthrough on genetic basis underlying isoflavone content in soybean seed using both the high-density SNP array and mutant-based mapping population.

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PB-0029

An emerging toolbox for optimizing gene expression of plant biotechnology traits

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Biotechnology-enabled crops have been globally commercialized for many years, and new approaches such as smart technologies are emerging in the development of such crops. Machine learning has created new opportunities in the area of agriculture. It has been used for crop management, livestock management, weed management and soil health management. And now it has been used to generate molecular tools, such as Optimized Expression Elements (OEEs). OEEs are defined as naturally-derived expression elements generated from natural sources (eg. Arabidopsis or maize) through computational algorithms to provide an optimized expression profile. OEEs include promoters, 5′ untranslated regions (5′ UTRs), introns, and 3′ UTRs so that they are neither genes nor expressed as gene products. It was shown via a peer-reviewed publication[1)] that OEE function is similar to that of natural expression elements. Specifically, OEE promoters precisely initiate transcripts, OEE introns are effectively spliced, and OEE 3′ UTRs enable predictable processing of transcript 3′ ends. As a result, OEEs enable expression of genes in the right tissue and the right time which is desirable for future biotechnology plants. Similar to endogenous expression elements, multiple science-based analyses (eg. next generation sequencing-based molecular characterization, bioinformatics) are conducted to ensure absence of unintended effects from OEEs as well as assuring the safety of biotechnology plants developed using these elements.

Therefore, it is expected that OEEs are equivalent to natural sequences applied in biotechnology plant development to express traits. More importantly, OEEs will expand the toolbox of expression elements to create more opportunities for optimizing gene expression of future plant biotechnology traits.

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1) To J. P. C. *et al*. (2021). Expression Elements Derived From Plant Sequences Provide Effective Gene Expression Regulation and New Opportunities for Plant Biotechnology Traits. https://doi.org/10.3389/fpls.2021.712179

PB-0030

Morphological Characteristics of Interspecific Hybridization between *Brassica rapa* L. ssp. and transgenic *B. napus*

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Interspecific hybridization between transgenic crops and their wild relatives is a major concern for transgene dispersal in the environment. Hence, under controlled conditions, artificial hand pollination experiments were performed in order to assess the hybridization potential of *Brassica rapa* and genetically modified (GM) *Brassica napus*. Yet, the morphology of their hybrids and selfing progenies is still a matter of conjecture. Thus, this study explored the morphological characteristics of six subspecies of *B. rapa* that hybridized with GM *B. napus* through hand pollination. In the resulting F_1 hybrids, the combination of *B. rapa* ssp. *narinosa* (♀) x GM *B. napus* (♂) had the highest crossability index (16.9±2.6). However, the F_1 selfing progenies of *B. rapa* ssp. *rapa* (♀) x GM *B. napus* were found to be more effective in producing viable future generations with the highest crossability index (1.6±0.69) than other subspecies. Consequently, they were used for the generation of F_2 and F_3 progenies. The 18 different morphological (vegetative and generative) characteristics among the parental cross combinations (PCC) revealed five clusters. Whereas F_1 hybrid progenies have been inferred, three clusters were measured and visualized through hierarchical clustering. Different generations were found to be grouped based on their different morphological characteristics. The study concluded that the clusters 3 of PCC and the interspecific hybrids (FFF) had strong reproductive fitness, implying a good fitness of generative agricultural features that can help us assess future generations.

Keywords: *Brassica napus*, *Brassica rapa*, genetically modified crops, interspecific hybridization, morphological characteristics.

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PB-0031

Genetic approaches for Interspecific Hybridization using microsatellite markers in between *Brassica rapa* ssp. *rapa.* and transgenic *B. napus*

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Transgene dispersal in the environment is hampered by interspecific hybridization between transgenic crops and their natural counterparts. Under controlled greenhouse conditions, artificial hand pollination experiments were conducted to evaluate the interspecific hybrids between *Brassica rapa* ssp. *rapa* and genetically modified (GM) *Brassica napus*. Initially, observed the nuclear DNA contents/chromosome numbers of the parental genotypes *B. rapa* ssp. *rapa* (Kangwhasoonmu: KS) (2n=20), GM *B. napus* (2n=38) and non-GM *B. napus* "Youngsan" (2n=38) are used as internal control. The KSF_1 hybrid revealed that 2n=29 as (AAC; n+n) and further generated selfing progenies of 23 KSF2 and 28 KSF3 chromosome numbers varied from 2=29 to 2n=34 and 2n=31 to 2n=40, respectively. To validate those interspecific hybrids between *B. rapa* ssp. *rapa* and selfing progenies, 17 simple sequence repeat (SSR) markers were used for genetic analysis. KSF_2 (93.09%) and KSF_3 (90.23%) revealed heterozygosity in both the A and C genomes. $KSBC_1$ extended with 33 $KSBC_1$ plants revealed a heterozygous nature of 53.65%. Further, cluster analysis using the Jaccard distance matrix and UPGMA dendrogram was constructed, which revealed a good degree of fit by the values of the cophenetic correlation coefficient ($r = 0.940, p<0.001$). The study concluded KSF_2 and KSF_3 were genetically distant from the $KSBC_1$ generations and could effectively hybridize with B. rapa ssp. through artificial hand pollination in a controlled environment.

Keywords: GM *Brassica napus*, *B. rapa* ssp *rapa*, interspecific hybridization, chromosome numbers, SSR markers.

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PB-0032

Validation of molecular markers for marker-assisted selection (MAS) in strawberry (*Fragaria* × *ananassa*)

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Strawberry (*Fragaria* × *ananassa*) is a major horticultural crop worldwide. In Korea, breeding strategy for new strawberry cultivar was limited to traditional cross breeding. Also molecular markers were rarely developed and used due to its genome complexity and heterozygosity. Recently, reference genomes of cultivated octoploid strawberry have been assembled, and multiple molecular markers associated with valuable traits including disease resistance, fruit color, and volatile compounds have been developed. For marker-assisted selection (MAS) in strawberry, we introduced molecular markers for anthracnose, *Fusarium* wilt, and *Phytophthora* crown rot resistance. Genotypes of six disease-resistant markers could not explain the phenotypes of 24 core germplasm. We developed novel markers linked to *Fusarium* wilt resistance locus *Fw*1-*Fw*5. Of the 20 markers, one marker could detect the resistant genotype of “Suhong”. In addition, one marker linked to fruit aroma gene could detect the peach-like aroma of “Misohyang”. Further validation and development of markers will greatly increase breeding efficiency for disease-resistant and high-quality cultivars.

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PB-0033

Multi-locus genome-wide association study for seed protein and oil content using soybean mutant diversity pool (MDP) lines

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Soybean (Glycine max) is a globally important legume crop that provides a primary source of high-quality vegetable protein and oil. Seed protein and oil content is two major quantitative traits in soybean breeding, is controlled by multiple genes with relatively small effects. To identify quantitative trait nucleotides (QTNs) controlling oil and protein content, we performed a multi-locus genome-wide association study (GWAS) to dissect the genetic architecture of seed protein and oil content in 192 soybean mutants of gamma-irradiated soybean mutant pool, exhibiting a wide range for seed protein content (40.91 - 43.14%) and seed oil content (14.96 -18.54%). A total of 37,249 single nucleotide polymorphism (SNPs) with a missing data percentage <10% were genotyped using genotype-by-sequencing (GBS) technology. Using five multi-locus GWAS methods, a total of 58 significant QTNs located on 18 of the 20 soybean chromosomes were identified related to seed protein and oil content. 24 QTNs for protein content and 10 QTNs for oil content has been previously identified to the same location and potential candidate genes that involved in seed protein oil synthesis and metabolism. The GWAS results also detected 14 and 10 QTNs associated with seed protein and oil content, respectively. The new well-defined QTNs will significantly improve molecular breeding program and the identified candidate gene may help elucidate the mechanism of protein and oil biosynthesis. These finding will facilitate marker-assisted selective breeding for soybean protein and oil content traits.

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PB-0034

Genome wide association study for major agronomic traits in wild soybean (*Glycine soja*)

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Wild soybean (*Glycine soja*) is the wild ancestor of cultivated soybean (*Glycine max*) and preserve valuable gene pool for improving agronomic traits in soybean. In this study, a total of 203 wild soybean accessions were cultivated in the experimental field of chonnam national university in Gwangju, and the major agronomic traits including days to flowering (DtF), days to maturity (DtM), number of pods (NoP) and one-hundred seed weight (100SW) were investigated. Wild soybean accessions were divided into 4 clusters by ADMIXTURE, principal component analysis and neighbor-joined cluster. DtM and DtF showed a negative correlation ($p < 0.01$), and DtF and 100SW also showed a negative correlation ($p < 0.01$). On the other hand, DtM and 100SW showed a positive correlation ($p < 0.01$). Genome wide association study (GWAS) identified 18 SNPs linked to DtF, 32 SNPs to DtM, and 41 SNPs to 100SW at thresholds $-\log_{10}(P) = 6$. The identification of SNP markers associated with agronomic traits are expected to be helpful for the development of molecular markers that can be used for soybean breeding.

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PB-0035

Quantitative trait loci (QTL) analysis of protein and oil contents in wild soybean (*Glycine soja*)

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Soybeans are a major crop as an important source of edible protein and oil because they are mainly composed of 40% protein and 20% oil. Wild soybean (*Glycine soja*) retains an important genetic variation for improving agronomic traits in cultivated soybeans. In this study, QTL analysis for protein and fat content was performed based on the genetic map prepared in BC_1F_2 derived from cross between Daepungkong (*Glycine max*) and GWS-1887 (*Glycine soja*). The average content of protein and oil in population was 44.25 and 12.14, respectively. QTLs related to protein (LOD=3.29 and R^2=15.8%) and oil content (LOD=3.06 and R^2=10.7%) were simultaneously detected in Gm20_27578013 on chromosome 20. A total of 27 candidate genes were found in the region, and InDels were found in 23 of them. Expression analysis of detected candidate genes is in progress, and these results can be usefully used for soybean breeding.

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PB-0036

Identification of genetic mutations in soybeans with low Kunitz Trypsin inhibitor activity

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Soybean Kunitz Trypsin inhibitor (KTi) is a non-nutritive factor that reduces the food availability of soybean processed foods and affects the digestion and absorption of nutrients in animals. KTi can be reduced through heat treatment, but there is a problem with reducing nutritional value. KTi-3 gene is involved in over 80% of KTi expression. In addition, the KTi-1 reduces trypsin inhibitor activity like the KTi-3. The purpose of this study is to find new genetic mutations that contribute to low KTi. Trypsin inhibitor activity (TIA) was measured in 908 soybean accessions by colorimetric analysis. A total of 6 soybean accessions showed lower than 60% TIA content. As a result of KTi-3 target sequencing, three soybean accessions showed the same mutations (one G to T transversion and AG deletion) of KTi-3 gene in the PI542044. The other accessions showed normal sequences in KTi-3 gene. This result indicated that low KTi soybean accessions had novel mutations in KTi genes. The identification of new KTi mutations in this study will provide useful information for the development of novel KTi molecular markers.

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PB-0037

Identification of salt tolerance genes using QTL mapping in soybean mutant

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Mutagenesis is being used as a breeding method to rapidly acquire useful traits. Especially gamma-ray mutation has been used widely in various crops such as rice and soybean. Salinity is a major abiotic stress that causes leaf yellowing and necrosis in soybeans. Known salt-tolerant QTLs were located on chromosomes 3, 7, 9, and 18. The QTL on chromosome 3 was associated with ion regulation. We generated a salt-tolerant mutant line by irradiating 250 Gy gamma-rays on 'Gwangan'. The salt-tolerant mutant line (M7) was crossed with the salt-sensitive cultivar 'Deapung' to develop the F2 population. A total of 169 F2 plants were genotyped using a 6K Illumina soybean SNP chip. QTL analysis was performed using salt-tolerant phenotypes (leaf scorch score, SPAD, Cl^- accumulation) obtained from 169 F2:3 lines. All QTLs associated with each trait were detected on chromosome 3. The results in this study will assist in the cloning of candidate genes related to salt-tolerant in soybeans and provide useful information for the development of new varieties.

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PB-0038

QTL-seq identified a locus controlling lignan content in sesame

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Sesame (*Sesamum indicum* L.) belongs to oil crops with a high oil content and contains healthy functional ingredients such as unsaturated fatty acids and lignan. Despite the steady increase in consumption and interest throughout the world, there is still a lack of interest in genetic research or the use of molecular breeding. The same generation of individuals from the same background is a suitable material for examining quantitative traits affected by multiple genes, and QTL-seq is an efficient mapping strategy to compare the association of phenotypes with polymorphic markers by comparing the phenotypes of both extremes. In this study, the F_7 RIL population was derived from a cross between Goenbaek and Gomazou, which had a large difference in lignan content, and 10 individuals with high lignan content and 10 individuals with low lignan content were pooled with respective bulk to perform QTL-seq. A significant SNP-index region was found in chromosome 1, designated *qLignan1*, by comparing the SNP frequency of the two extremes. Analysis of variants in *qLignan1* based on the reference genome, Goenbaek, found nonsynonymous SNPs affecting coding-sequence in a total of nine genes, and this result confirmed a novel QTL distinct from previous reports related to the lignan content regulators in sesame. Functional research on the genes identified in this study should be conducted, but it is significant to suggest genetic factors that affect the mechanism of controlling the lignan content, and it will promote the use of molecular breeding of sesame as well as molecular markers.

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PB-0039

‘JJ625LG/남찬’ 벼 재조합자식계통을 이용한 수량 관련 형질 QTL 분석

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전라북도 완주군 이서면 혁신로 181 국립식량과학원

우리나라 자포니카 벼 수량성 향상을 위해 자포니카 장립・장원형 벼 ‘JJ625LG’와 소비조건에서도 수량성이 높은 ‘남찬’을 이용하여 육성된 88개 재조합자식계통(RILs)에 대한 수량 관련 형질 QTL 분석을 수행하였다. 모부본에 다형성을 보인 156개 KASP 마커와 입형 관련 유전자 *GS3* 및 *qSW5*, 내병성 관련 유전자 *Stvb-i*, *qFfR1* 등 160개 분자표지를 이용하여 일반농업형질 6개(출수기, 간장, 수장, 수수, 수당립수, 등숙률), 입형 관련 형질 5개(현미길이, 너비, 두께, 장폭비, 천립중), 이삭 관련 형질 17개(1・2차 지경 및 착생립 관련 형질 등)에 대해서 분석하였다. 출수기 QTL로 8번 염색체에서 탐색된 *qHD8*은 *Hd18* 유전자로 추정되며, 표현형 변이의 54.3%를 설명할 수 있었으며 ‘남찬’ 대립유전자형이 2.4일의 양의 상가적효과를 나타냈다. 간장 QTL로 1번 염색체에서 탐색된 *qCL1*은 *SD1* 유전자로 추정되며, 표현형 변이의 27.3%를 설명할 수 있었으며 ‘남찬’ 대립유전자형이 3.6cm의 양의 상가적효과를 나타냈다. 이삭 관련 형질에서 수당립수, 착립밀도, 2차지경수 및 착생립수, 2차지경 평균립수, 1차지경당 2차지경수 및 착생립수 등 7개 형질은 1번 염색체의 동일한 위치에서 QTL이 탐색되었는데 해당 QTL은 *Gn1a* 유전자로 추정되며, 표현형 변이를 15.4-19.4%를 설명할 수 있었고 ‘JJ625LG’ 대립유전자형이 양의 상가적 효과를 나타냈다. 추출도와 2차지경 평균립수에 대해 3번 염색체 동일 위치에서 탐색된 QTL은 입형 관련 유전자 *GS3*와 인접해 있었고, 표현형 변이의 11.8-29.2%를 설명할 수 있었으며 ‘JJ625LG’ 대립유전자형이 음의 상가적 효과를 나타냈다. 입형 관련 형질에서 길이, 너비, 두께, 장폭비 등 4개 형질은 3, 5번의 동일한 위치에서 QTL이 탐색되었는데 해당 QTL은 *GS3*와 *qSW5*의 유전자로 추정되며, 표현형 변이를 7.4-62.6%를 설명할 수 있었다. 3번 염색체에서 탐색된 QTL은 ‘JJ625LG’ 대립유전자형(*gs3*)이 길이와 장폭비에 양의 상가적 효과, 너비에는 음의 상가적 효과를 나타냈다. 5번 염색체에서 탐색된 QTL은 ‘JJ625LG’ 대립유전자형(*qSW5*)이 길이와 장폭비에 양의 상가적 효과, 너비와 두께에는 음의 상가적 효과를 나타냈다. ‘JJ625LG/남찬’ RILs의 수량 관련 형질 변이에는 주동 유전자인 *Hd18, SD1, Gn1a, GS3, qSW5*가 관여하는 것으로 판단되며, 추가 표현형 조사와 대립유전자형 분석 등을 통하여 수량성 향상에 관여하는 요인을 구명하고자 한다.

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PB-0040

Rice C3HC4-type RING finger protein, OsRFPHC-3, plays a positive regulatory role in high salinity tolerance

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Soil salinity negatively affects plant growth, productivity, and metabolism. Rice is known to have higher sensitive phenotypes than other cereal crops such as wheat, sorghum, and barley. Ubiquitins-mediate E3 ligase is closely related to enhancing salt insensitivity. We characterized the molecular functions of a rice C3HC4 really interesting new gene (RING). Oryza sativa RING finger protein HC-3 (*OsRFPHC-3*) was highly expressed at 100 mM NaCl and targeted the nucleus. *In vitro* ubiquitin assay demonstrated that OsRFPHC-3 possessed the E3-ubiquitin ligase activity; however, the negative control and mutant OsRFPHC-3^{C282A} did not show any antibody response with a polyubiquitin chain. Under salinity, transgenic plants exhibited higher chlorophyll, proline, and soluble sugar contents and lowered H_2O_2 accumulation than the wild type, supporting transgenic plants with enhanced salinity tolerance phenotypes. Additionally to identify the physiological character of *OsRFPHC-3*-overexpression plants, we measured antioxidant enzymes such as SOD, POD, and CAT. The results showed no difference between transgenic lines and WT under normal conditions, but when plants were exposed to 100 mM NaCl conditions, transgenic lines showed more enzyme activity than WT plants. Further studies need to explore interaction partner genes to understand the exact molecular mechanisms that enhance plants insensitivity to salinity stress.

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PB-0041

Molecular characterization of rice plants caused by mutations in the leucine carboxyl methyl transferase gene

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Abiotic stress is the major environmental factor negatively affecting crop growth and productivity worldwide. Rice is considered a drought-sensitive crop, and the development and yield of rice are greatly affected by the drought. The distribution of soluble sugars in the plant is altered in response to drought stress. Soluble sugars also act as signal molecules to regulate gene expression in plant growth and stress response. Using a forward genetics approach, an insensitive drought line, 200-1217(43), was selected from 150 rice mutant lines (M10) induced by gamma-ray irradiation. In the whole-genome re-sequencing of 200-1217(43) mutant, a single base adenine deletion of the LOC_Os03g56370 gene is annotated leucine carboxyl methyl transferase, was found. The original gene was named OsLCMT, and the mutant gene was named LCMTp.Thr163fs, which means that the frameshift occurred at the 163rd amino acid, threonine. Under drought treatment conditions, the 200-1217(43) mutant showed a high survival rate, fresh weight, relative water content, soluble sugar contents, and lower hydrogen peroxide(H_2O_2). In addition, the partner gene, OsSnRK1a, was found through an experiment with yeast-two-hybrid and BIFC assay, and the location of the two genes was confirmed to be cytosol through subcellular localization analysis. And the function of methyltransferase was confirmed through the invitro methyltransferase assay. The relative expression levels in WT and 200-1217(43) mutant, the expression level of the OsLCMT gene was lower in the mutant than in the WT, and the expression level of the partner gene OsSnRK1a and the expression level of the sugar signaling pathway genes were increased.

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PB-0042

Identification of Candidate Genes Controlling Capsaiciniod Biosynthetic Genes Using an EMS-induced Mutant Pepper (*Capsicum annuum* L.)

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The capsaicinoids are the unique and pungent alkaloid mixture of *Capsicum*. They 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 the 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 loss-of-function variants. 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 candidate genes controlling capsaicinoid biosynthetic genes. Expression levels of putative capsaicinoid biosynthetic genes in placental tissues between 'Yuwolcho' and '221-2-1a' indicated branched-chain fatty acid pathway regulation could be the main factor for non-pungency of '221-2-1a'. 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. The segregation ratio indicated the non-pungency of '221-2-1a' may be controlled by two genes. To identify the genetic loci, genetic mapping was performed using genome-wide markers and BSA-seq analysis, and one locus on chromosome 6 was identified and named *Pun4*. Using more SNP markers, the *Pun4* region was delimited to 655.1 kb region and 12 candidate genes were predicted. Among the genes, 9 genes expressed in the placenta were selected for TRV-mediated gene silencing using pungent pepper 'MicroPep red' and two silenced lines showed depressed capsaicinoid levels.

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PB-0043

Expression profile-based validation and comparison of sesamin contents in root and leaf tissue of two different cultivars of sesame (*Sesamum indicum* L.)

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Sesame (*Sesamum indicum* L.) is a traditional and valuable oilseed crop from the *Pedaliaceae* family. Leaves of sesamum are used as leafy vegetables in many countries like Nigeria, Japan, and the tropical region of the world. Sesamin is one of the lignan components mainly found in sesame seeds. It is considered that sesamin provides several health advantages to humans (like lowers the risk of cancer and protect heart health,etc). Typically, sesamin is found in seeds but rarely in leaves, In this study, we used the two different cultivars 'Gomazou' and 'Goenbaek' to detect the sesamin content in root and leaf tissue. The experiment was performed with the replicates, root and leaf samples collected in three different stages; (I) seedling stage (Three weeks after sowing (AS)); (II) vegetative propagation transition stage (Five weeks AS); and (III) sesame mature stage (Seven weeks AS). Based on quantitative RT-PCR analysis the expression profile of given roots and leaf samples of cultivars revealed that the expression of the sesamin *CYP81Q1* gene was much higher in cultivar 'Gomazou' than in 'Goenbaek,' in five weeks samples. It shows the confirmative results with the previous study performed by the Japanese group. Hence it is proven that the expression pattern of *CYP81Q1* gene is very critical and influences sesamin content in leaf tissue.

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PB-0044

수박 MABC 시스템을 활용한 흰가루병 저항성 연관 여교배 집단 작성

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수박(*Citrullus lanatus*)은 여러 박과채소 중에서 경제적 중요성을 지니는 대표적인 작물 중 하나이다. 차세대 유전체 염기서열 분석 기술을 통해 대량 SNP 정보를 얻을 수 있으며, 이에 기반을 둔 분자마커가 활용, 더 나아가 효율적인 육종을 위해서 분자마커에 기반한 MAS 및 MABC 시스템 활용이 높아지고 있다. 본 연구에서는 우량계통 '920533'을 반복친으로, 흰가루 저항성 계통인 'Arka Manik' 1회친으로 교배하여 BC_1F_1 집단을 작성하였다. 작성한 집단 250 개체를 foreground selection을 수행하기 위해 기존에 보고된 흰가루병 저항성 연관 분자마커(CAPS)를 활용하여 유전자형이 heterozygote인 106개체를 선발하였다. 이후 선발된 여교배 집단 개체에 대해 background selection을 수행하기 위해 기존에 개발된 Fluidigm용 MABC 마커 341개를 활용하였다. 마커검정 결과를 바탕으로 개체별 반복친의 회복률을 분석하였는데 평균적으로 74.0%의 회복률을 보였으며, 최솟값은 62.1%, 최댓값은 87.1%였다. 최종적으로 106개체 중 회복률이 가장 높으며 흰가루병에 저항성을 갖는 BC_1F_1-203 개체를 선발하였다.

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PB-0045

Comparative histological analysis of anther development in Tetep-cytoplasmic male sterility and identification of *restorer-of-fertility* gene in rice

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Cytoplasmic male sterility (CMS) is a maternally inherited trait that causes dysfunction in pollen production and anther development. CMS is caused by mitochondrial-nuclear interaction, and can be suppressed by functional nuclear *restorer-of-fertility* (Rf) gene. The Tetep-CMS/*Rf* system was developed through inter-subspecific backcrosses between *indica* and *japonica* rice accessions. Phenotypic analysis revealed Tetep-CMS was caused by abnormal anther dehiscence and inability to release functional pollen. Histological analysis of developing anthers collected from CMS plants showed connective tissue deformities and aberrant dehydration of endothecium and epidermis. Fine mapping of *Rf*-Tetep using a series of segregating population, delimited the candidate region to an approximately 109 kb genomic interval between M2099 and FM07 molecular markers. Nanopore sequencing based genome assembly, gene prediction and annotation revealed 11 open reading frames (ORFs), and suggest ORF6 annotated as pentatricopeptide repeat motif containing gene 1 (*PPR1*), as a possible candidate gene responsible for fertility restoration. Pairwise alignment Tetep-CMS revealed two non-synonymous substitutions within the *PPR1* amino acid sequences. This study will enhance our understanding of mitochondrial-nuclear genome interaction by suggesting that tissue specific dysfunction in anther is responsible for anther indehiscence, and propose that functional *Rf* gene is derived from allelic variation between inter-subspecies in rice.

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PB-0046

Overexpression of *IbMYB1a* gene induced anthocyanin accumulation in soybean seeds

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Anthocyanins are water-soluble secondary metabolites known as flavonoids that are responsible for red, purple, and blue coloring in flowers, fruits, and vegetables. They are known to be effective in protecting human body from as oxidative stress, certain cancers, cardiovascular diseases, hepatic damages, and diabetes. MYB transcription factors (TFs) play important roles in transcriptional regulation of anthocyanins. In this study, we generated soybean overexpressing the *IbMYB1a* gene under the control of two different promoters, including CaMV 35S promoter and β-conglycinin promoter, using an efficient *Agobacterium*-mediated transformation. As expected, we were able to identify black seeds with strong anthocyanin pigments after harvesting from T_0 plants. Anthocyanin phenotypes of *IbMYB1a* overexpression were confirmed in transgenic soybean lines during development. Overexpression of *IbMYB1a* in P35S:*IbMYB1a* soybean lines produced strong anthocyanin pigmentation in leaves and flowers, while a deep purple color was generated in Pβ-con:*IbMYB1a* soybean seeds. Anthocyanin phenotypes of *IbMYB1a* soybean seeds were also observed by comparing with wild-type black soybean seeds. The pigmentation was observed only in the seed coat from the wild-type black soybean and P35S:*IbMYB1a* soybean seeds (T_1), while Pβ-con:*IbMYB1a* soybean seeds (T_1) showed the distinct purple coloration on both the surface and cross section except for the seed coat. The anthocyanin content in the transgenic generation T_2 seeds was increased 8-fold in P35S:*IbMYB1a* soybean and 84 to 382-fold in Pβ-con:*IbMYB1a* compared to the wild-type soybean. Finally, *IbMYB1a* overexpression exhibited the increase of anthocyanin content in transgenic soybean seeds.

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PB-0047

Inhibition of gene expression for anti-nutritional factors and allergen in soybean seeds via RNAi-mediated co-transformation

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Soybean [Glycine max (L). Merr] is one of the major economic crops providing protein and vegetable oil. However, soybean seeds contain anti-nutritional factors, such as Kunitz Trypsin Inhibitor protein and soybean agglutinin (or lectin) protein, that reduce the quality of the protein and also the efficiency of the feed. Soybean is also classified as one of the eight major allergenic foods, and the incidence of soy-caused allergies is expected to increase. Transgenic soybean seeds with improved anti-nutritional factors and allergen were produced by introducing Kunitz Trypsin Inhibitor (TI), Lectin (LE), and P34 allergen coding sequences within RNA interference (RNAi) inducing hairpin construct via *Agrobacterium*-mediated co-transformation. Three plasmids, including pCKLSL-β-con:*TI*(RNAi), pCKLSL-β-con:*LE*(RNAi), and pCKLSL-β-con:*P34*(RNAi), were co-transformed, and a total of thirty pCKLSL-β-con:*TI*x*LE*x*P34*(RNAi) transgenic soybean plants were produced. As a result of performing the PCR analysis from well-grown twenty-eight transgenic lines, it was confirmed that twenty-five transgenic lines showed the expected amplification of transgenes *TI*, *LE*, and *P34*, the selective marker gene *Bar*, and the β-conglycinin promoter sequences. In addition, qRT-PCR was performed to confirm the gene expression of anti-nutritional factors (*TI* and *LE*) and soybean allergen *P34* from transgenic soybean seeds. Co-transformation of *TI*, *LE*, and *P34* coding sequence within RNAi exhibited the reduction of *TI*, *LE*, and *P34* gene expressions in transgenic soybean seeds compared to that of non-transgenic soybean seeds.

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PB-0048

Non-pungency of *Capsicum chacoense* is attributed to a novel non-functional allele of *pAMT*

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Capsaicinoid is an alkaloid compound responsible for the hot taste (pungency) of chili pepper (*Capsicum* spp.). To date, a few genes have been identified to be involved in the biosynthesis of capsaicinoids: *Pun1*, *Pun2*, *Pun3*, *CaKR1*, and *pAMT*. Loss of function in these genes results in loss of pungency. The non-functional *pAMT* allele results in producing capsinoids instead of capsaicinoids, which also leads to a non-pungency phenotype. Unlike other genes, *Pun2* has not been characterized yet since it was first reported as a responsible genetic factor for the non-pungency of *Capsicum chacoense*. In this study, non-pungent *C. chacoense* 'PI260433-np' and pungent *C. chacoense* 'PI260433-p' were selected to construct a mapping population to identify *Pun2*. However, it turned out that PI260433-np produced significant amounts of capsinoids, which indicated the non-pungency of PI260433-np may be due to the loss of function in *pAMT*. Through sequence analysis, the insertion of seven nucleotides was found in the 8th exon of *pAMT* in PI260433-np whereas there were no significant differences in other capsaicinoid biosynthetic genes. This insertion generates an early stop codon, leading to the lack of the PLP binding domain site that is vital for *pAMT* enzymatic activity. A KASP analysis showed that this insertion was co-segregated with the capsaicinoid and capsinoid contents in the F_2 population. Therefore, we named this novel allele $pamt^{11}$. Taken together, the non-pungency of *C. chacoense* PI260433-np is due to *pamt* and the *Pun2* encodes the *pAMT* gene.

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PB-0049

Identification and Functional Analysis of MPKKK-MKK-MAPK cascade involved in freezing tolerance in wheat (*Triticum aestivum* L.)

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Bread wheat (*Triticum aestivum* L.) is one of the major crops providing more than 20% of the calories for the world population. Freezing stress during winter damages and often kills wheat, causing dramatic decrease of grain yield. Plants have developed diverse molecular mechanism to resist certain stresses. MPKKK-MKK-MAPK cascade is one of the pathways which regulates diverse plant metabolism including growth and development, hormone signaling, and stress response via phosphorylation of target proteins. However, its role in wheat has not been widely investigated. In this study, we identified cold-responsive MAPKs through genome-wide identification and RNAseq analysis. Then, upstream MPKKKs and MKKs were also identified by RNAseq and investigating previous studies. The gene expression under cold stress was validated via real-time PCR analysis. The subcellular localization was performed through GFP-fused vectors and the interactions between MPKKK/MKK and MKK/MAPK were observed via BiFC analysis in wheat protoplasts. *MAPK20-2* overexpressing transgenic *Brachypodium* was generated and its freezing tolerance was compared to wild-type plants. Survival rate, proline content, and soluble sugar content revealed that the transgenic plants were more tolerant to freezing stress. Further, gene expression analysis of the transgenic line showed that overexpression of *MAPK20-2* altered expression patterns of stress-related genes. The results of this study will provide a basis for further understanding of freezing tolerance mechanism and MAPK cascades in wheat.

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PB-0050

Diversity Analysis of the Korean *Codonopsis lanceolata* by the Comparison of Chloroplast Genomes

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Codonopsis lanceolata is a perennial herb of the Campanulaceae family and mainly distributed in East Asia. *C. lanceolata* contains saponin and has an efficacy to prevent vascular diseases or cancer. Recently, the consumption of *C. lanceolata* is increasing as food materials as well as a medicinal plant. However, molecular breeding studies on *C. lanceolata* are insufficient. In this study, we tried to find the relationship between Korean *C. lanceolata* and develop markers to distinguish *C. lanceolata* genetic sources by the comparison the chloroplast genome. Forty three *C. lanceolata* genetic resources were collected from wild resources and the markets over the country. Next-generation sequencing analysis was performed for the *C. lanceolata* genetic sources and chloroplast genomes were assembled using Geneious Prime program. The finished chloroplast genomes were analyzed using CLC Main Workbench program, and *Codonopsis filosula* chloroplast genome was used as an outgroup. Through the comparative analysis, 1,446 polymorphism sections were found, including 1,378 single nucleotide polymorphism and 68 insertion or deletion. The systematic analysis of the chloroplast genome revealed the phylogenetic relationship between *C. lanceolata* genetic resources, but the relationship between the collected regions could not be found. Molecular markers developed based on these results would be useful for the breeding of *C. lanceolata* elite cultivars.

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PB-0051

국산밀 유전자원의 종실 크기 관련 유전자 변이 평가

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종실 크기는 밀의 수량성은 물론 제분율과 수발아율에도 영향을 미치는 중요한 특성이지만, 국내 품종에 대한 제한적인 연구만 일부 수행되었다. 본 연구는 국내 육종프로그램의 선발 효율 증진 및 유용 자원 선발을 위한 기초 자료 제공을 위하여, 국산밀 유전자원(49 품종, 126 계통, 268 재래종과 82 북한자원)의 *TaCwi-A1, TaGW2-6A*와 *TaSus2-2B*의 대립유전자를 평가하였다. 세포벽 전환효소(cell wall invertase)인 *TaCwi-A1*는 종실 무게와 상관이 있으며, *TaCwi-A1b*가 *TaCwi-A1a*에 비해 천립중이 큰 걸로 알려져 있다. *TaCwi-A1b*의 비율은 품종과 재래종에서는 각각 71%(35개)와 96%(258개)로 높았지만, 계통과 북한자원에서는 59%(74개와 48개)로 낮았다. 종실 넓이와 상관 있는 *TaGW2-6A*는 프로모터지역의 SNP를 바탕으로 *Hap-6A-A*와 *Hap-6A-G*의 2개의 대립유전자가 있으며, *Hap-6A-G*가 *Hap-6A-A* 타입보다 종자가 큰 것으로 알려져 있다. *Hap-6A-G*의 비율은 품종과 계통에서는 각각 35%(18개)와 33%(42개)로 낮았지만, 재래종과 북한 자원에서는 각각 69%(184개)와 74%(61개)로 높았다. 설탕을 전분으로 전환 시키는 효소(sucrose synthase)인 *TaSus2-2B*는 천립중이 높은 *Hap-H*와 천립중이 낮은 *Hap-L*로 구분되는데, *Hap-H*의 비율은 품종, 계통과 재래종에서는 각각 87%(41개), 73%(92개)와 83%(223개)로 높았지만, 북한 자원에서는 30%(25개)로 낮았다. 큰 종실 크기를 나타내는 *TaCwi-A1b, Hap-6A-G*와 *Hap-H*를 지녀 높은 천립중을 지닐 것으로 예측되는 자원은 재래종에서 141개(52%)로 높은 비율로 나타났으며, 품종(10개, 20%), 계통(17개, 13%)과 북한자원(10개, 12%)에서는 낮았다. *TaCwi-A1a, Hap-6A-A*와 *Hap-L*을 지녀 낮은 천립중을 보일 것으로 예측되는 자원은 7개[계통(3개), 재래종(1개), 북한자원(3개)]로 나타났다.

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PB-0052

국산밀 품종의 붉은곰팡이병(赤黴病, Scab, Fusarium Head Blight) 검정

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붉은곰팡이병에 감염된 밀은 수량 감소와 품질 저하는 물론 인축 독성의 위험이 있기 때문에 저항성 품종 육성이 매우 중요하다. 따라서, 본 연구에서는 국산밀 40품종에 붉은곰팡이병 포장 감염률 평가와 관련 4개 표지인자(*Fhb 1, Fhb 2, Fhb 3, Fhb 4*)에 대한 평가를 수행하였다. 포장 감염률 평가는 초기 곰팡이 감염에서부터 감염 확산이 완료된 성숙기에 평가를 하였으며, 3년간(2019-2021년) 조사하였다. 국산밀 품종의 평균 감염율은 43.7%였으며, 2021년은 14.3%로 제일 낮았으며, 2020년은 74.2%로 높았고 2019년은 42.5%로 연차간 변이가 크게 나타났다. 종자 초기 감염 저항성(Type I)과 관련한 표지인자 *Fhb 4*와 *Fhb 5*는 *Xgwm349*와 *Xgwm156*를 이용하였으며, 이삭 내 곰팡이 확산 저항성(Type II) 과 관련이 있는 표지인자 *Fhb 1*과 *Fhb 2*의 평가는 *TaHRC-GSM*과 *Xwmc398*를 이용하였다. Type I의 표지인자 검정 결과, *Fhb 4*와 *Fhb 5*에서 저항성을 보인 품종은 각각 24개와 28개였으며, 2개 표지인자에서 모두 저항성을 나타낸 품종은 17개였다. Type II의 *Fhb 1*과 *Fhb 2*에서 저항성을 보인 품종은 각각 13개와 7개였고, *Fhb 1*과 *Fhb 2*동시에 저항성을 가지는 품종은 5개였다. Type I에서 저항성을 보인 품종의 평균 감염률은 43.6%였고, 감수성을 보인 품종은 47.0%였으며, Type II에서는 저항성 품종이 42.3%, 감수성 품종이 45.7%로 차이가 없는 것으로 나타났다. 4개 표지인자 모두 저항성을 보인 품종은 고분, 다홍과 청계였으며, 이들 품종의 평균 감염률은 각각 40.0%, 43.3%와 46.6%로 품종의 평균 감염률과 차이가 없었다. 국내 품종에서 3년 평균 감염율이 30%이하로 낮은 품종은 밀성(20%), 백강(23.3%), 백찰(10%), 서둔(26.6%)과 태중(26.6%)이었으며, 서둔과 밀성은 *Fhb 1, Fhb 4*과 *Fhb 5*에서 저항성을 보였으며, 태중은 *Fhb 4와 Fhb 5에서*, 백찰은 *Fhb 4*에서 저항성을 보였지만, 백강은 저항성 유전자를 지니지 않은 걸로 나타났다. 이러한 결과는 재배 환경 및 출수기 등 여러 외부 요인이 영향을 미친 것으로 보이기 때문에 관련된 추가적인 연구가 필요하다.

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PB-0053

밀 고분자 단백질 Glu1-Bx7 과발현 근동질계통의 글루테닌 특성 분석

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밀은 종실에 함유되어있는 글루텐 단백질의 함량 및 조성에 따라 제분 후 밀가루에서 다양한 가공적성을 나타내는데, 보다 점탄성이 높은 밀가루를 생산하기 위해서는 많은 양의 글루텐 단백질 함량과 강력한 글루텐 단백질 질적 유전자 조성이 매우 중요하다. 글루텐 단백질 질적 조성 중에서 고분자 글루테닌 조성이 강력한 밀가루 반죽 특성에 가장 큰 영향을 미치는데, 최근에는 Glu1-Bx7 글루텐 단백질 과발현 밀에서 더욱 강력한 밀가루 특성을 나타낸다고 알려져 있다. 따라서 본 연구에서는 '금강' Glu1-Bx7 과발현 근동질계통을 육성하고 *Glu1-Bx7*과 *Glu1-Bx7*^{OE} (Over Expression) 대립유전자 변이와 글루테닌 발현 특성을 분석하였다. 먼저 608점의 유전자원에서 *Glu1-Bx7* 프로모터 지역에 43 bp가 삽입된 자원을 탐색하여 7개의 자원을 발견하였고, 그중 4개의 자원에서 Glu1-Bx7 유전자가 중복되는 것을 확인하여 *Glu1-Bx7*^{OE} 대립유전자를 보유한 자원을 선정하였다. 프로모터 지역에 43 bp가 삽입된 7개 자원의 Glu1-Bx7 단백질의 발현을 HPLC를 이용하여 분석한 결과 또한 유전자가 중복되는 4개의 자원에서만 Glu1-Bx7 단백질이 높게 증가하였다. 4개의 자원 중 고분자 글루테닌 조성이 '금강'과 비슷한 'CHISHOLM' 자원을 선택하고 인공 교배하여 F_1을 양성하였고, 이후 '금강'을 3번 더 여교배하고 세대 진전하여 금강 Bx7 과발현 근동질계통 BC_3F_3를 육성하였다. SDS-PAGE와 HPLC로 Bx7 단백질 발현을 분석한 결과 '금강'에 비해 '금강' Bx7 과발현 근동질계통이 Bx7 단백질 발현이 높았다. 이러한 결과를 통해 *Glu1-Bx7*^{OE} 대립유전자를 도입함으로써 고분자 글루테닌 단백질 질적 조성의 수준을 한 단계 높일 수 있으며, 기존보다 강력한 밀가루를 생산할 수 있는 품종을 육성할 수 있을 것으로 기대된다.

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PB-0054

제빵 적합 자원 선발을 위한 국산밀 유전자원 평가

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제빵용 품종 육성을 위하여 국산밀 525개 유전자원[품종(49개), 계통(126개), 재래종(268개)와 북한자원(82개)]에 대한 *Glu-1, Glu-A3, Glu-B3*과 *Pin-D1* 유전자를 평가하였다. *Glu-A1a/b, Glu-B1b/f/i*와 *Glu-D1d*를 지녀 *Glu-1* 점수가 10점인 자원은 51개로 자원별로는 각각 품종(8개), 계통(21개), 재래종(1개)와 북한자원(21개)로 나타났다. 이들 자원 중에서 *Pina-D1b*나 *Pinb-D1b*를 지닌 경질밀은 37개로 각각 품종(5개), 계통(18개), 재래종(1개)와 북한자원(13개)으로 나타났다. 이들 자원 외에 빵용 품종의 필수조건으로 알려진 *Glu-D1d*를 가진 자원은 각각 품종(3개), 계통(24개), 재래종(6개)와 북한자원(41개)였으며, 2000년 이후에 육성된 29 품종의 *Glu-D1d* 보유 비율은 27%(8품종)로 2000년 이전에 육성된 품종(15%, 3품종)보다 높았다. *Glu-B1*에서 빵용에 적합한 *Glu-B1b/f*를 지닌 자원 비율은 각각 품종(84%), 계통(78%), 재래종(94%)과 북한자원(70%)으로 높았고, *Glu-B1i*를 지닌 자원은 5개[품종(중모2008), 계통(IT246989, IT246973)과 북한자원(YHTRI14972, IT246982)]로 나타났다. *Glu-A1*에서 *Glu-A1a/b*의 비율은 각각 품종(51%), 계통(37%), 재래종(11%)와 북한자원(46%)으로 계통과 재래종에서 *Glu-A1c*의 비율이 높았다. *Glu-A3*와 *Glu-B3* 평가 결과, 제빵에 적합한 유전조성으로 알려진 *Glu-A3d*를 지닌 자원은 52개[품종(14개), 계통(10개), 재래종(20개)과 북한자원(8개)]였고, *Glu-B3b/g*를 지닌 자원은 77개[품종(8개), 계통(4개), 재래종(29개)과 북한자원(36개)]였으며, *Glu-A3d*와 *Glu-B3b/g*를 동시에 지닌 자원은 7개[품종(수강), 계통(IT246986), 재래종(IT159784), 북한자원(HTRI16956, HTRI14981, HTRI4487, IT246975)]였다. IT246986은 *Glu-1* 10점이면서 *Glu-A3d*와 *Glu-B3g*이고, *Pina-D1a*와 *Pinb-D1b*를 지닌 유일한 자원으로 나타났다.

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PB-0055

조숙 자원 선발을 위한 국산밀 유전자원 평가

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국산밀 유전자원에서 조숙 자원을 선발하기 위하여 525개 유전자원에 대해 포장 출수기 평가(2019-2021)와 관련 유전자인 *Vrn-1*과 *Ppd-1* 조성을 분석하였다. 본 연구에 활용된 국산밀 유전자원은 품종(49개), 계통(126개), 재래종(268개)와 북한자원(82개)을 포함하고 있다. 포장 출수기의 2년 평균은 4월 22일이었으며, 2020년이 2019년 보다 1일 빨랐고, 유전자원내에서는 품종과 계통이 4월 18일로 빨랐으며, 재래종은 4월 22일이었고, 북한자원은 4월 25일로 가장 늦었다. 국내품종에서는 조은, 조경, 조농과 조품의 출수기(4월 10일-4월 15일)가 빨랐으며, 계통의 35%(44개)는 이들 품종보다 출수기가 최소 2일이상 빨랐다(4월 8일-4월 15일). 파성에 관련된 *Vrn-1* 분석 결과, 국산밀 자원은 *vrn-A1*로 모두 추파형이었고, *vrn-B1*의 비율이 93%(품종 86%, 계통 96%, 재래종 94%, 북한자원 87%)로 대부분 추파형이었으며, Vrn-D1에서는 *vrn-D1*과 *Vrn-D1* 비율이 각각 66%과 34%로 추파형 비율(품종 59%, 계통 56%, 재래종 66%, 북한자원 82%)이 높았다. 광주기성 관련 유전자인 *Ppd-1* 분석 결과, 광에 대한 반응 둔감성을 나타내는 *Ppd-A1a*는 국내 자원에서는 발견되지 않았으며, *Ppd-B1a* 비율도 6%(품종 6%, 계통 15%, 재래종 1%, 북한자원 3%)로 낮았지만, *Ppd-D1a* 비율은 76%(품종 92%, 계통 97%, 재래종 74%, 북한자원 63%)로 높았으며, 출수기가 빠른 품종과 계통의 *Ppd-D1a*비율이 재래종과 북한자원에 비해 18%이상 높았다. 조숙인 4개 품종의 유전자 조성은 *vrn-A1, vrn-B1, Ppd-A1b, Ppd-B1b*와 *Ppd-D1a*로 차이가 없었으며, *Vrn-D1*에서 조경은 *Vrn-D1a*를 지녔고, 조품은 *Vrn-D1b*였으며, 조은과 조농은 *vrn-D1*로 나타났다. 조숙인 44계통 중 조경과 같은 조성은 18계통이었고, 조은과 조농과 같은 계통은 14계통이었으며, 12계통은 현재 평가 중이다.

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PB-0056

국내 밀 유전 집단의 붉은곰팡이병(赤黴病, Scab, Fusarium Head Blight) 검정

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국내 환경에서 붉은곰팡이병 저항성 자원 선발 효율성을 높이고자 본 연구에서는 붉은곰팡이병 저항성 정도가 상이한 2개 유전집단(F_{10})에 대한 평가를 수행하였다. 집단-1은 포장 평균 감염률이 중도저항성인 서둔(26.6%)과 안백(33.3%)의 교배 집단(146계통)이고, 집단-2는 포장 평균 감염률 높아 감수성인 다홍(43.3%)과 금강(60.0%)의 교배 집단(148계통)으로 이들 집단에 대한 포장감염률과 4개 표지인자(*Fhb 1, Fhb 2, Fhb 3, Fhb 4*)를 평가하였다. 4년동안(2016-17,2020-21) 포장 감염률을 조사하였으며, 포장감염률은 5 단계(저항성 1점-감수성 5점)로 평가하였다. 집단-1과 2의 평균감염률은 각각 3.1점과 3.3점이었지만 2016년(3.7점/4.5점)의 감염률이 높았고, 2021년(2.2점/1.9점)이 낮아서 년차간 변이가 있는 것으로 나타났다. 종자 초기 감염 저항성(Type I)과 관련한 표지인자 *Fhb 4*와 *Fhb 5*는 *Xgwm349*와 *Xgwm156*를 이용하였으며, 이삭 내 곰팡이 확산 저항성(Type II) 과 관련이 있는 표지인자 *Fhb 1*과 *Fhb 2*의 평가는 *TaHRC-GSM*과 *Xwmc398*를 이용하였다. 집단-1의 Type I의 표지인자 검정 결과, *Fhb 4*와 *Fhb 5*에서 저항성을 보인 계통은 각각 123개와 91개였으며, 2개 표지인자에서 모두 저항성을 나타낸 계통은 75개였고, Type II의 *Fhb 1*과 *Fhb 2*에서 저항성을 보인 계통은 각각 63개와 19개였고, *Fhb 1*과 *Fhb 2* 동시에 저항성을 가지는 계통은 1개였다. 집단-2에서 Type I의 *Fhb 4*와 *Fhb 5*에서 저항성을 보인 계통은 각각 139개와 16개였으며, 2개 표지인자에서 모두 저항성을 나타낸 계통은 14개였고, Type II의 *Fhb 1*과 *Fhb 2*에서 저항성을 보인 계통은 각각 6개와 3개였고, *Fhb 1*과 *Fhb 2* 동시에 저항성을 가지는 계통은 없었다. 집단-1에서 표지인자에서 저항성을 나타낸 계통의 평균 감염률은 *Fhb 1* (3.3점), *Fhb 2* (2.8점), *Fhb 4* (3.1점)과 *Fhb 5*(3.2점)이었으며, 감수성에서는 *Fhb 1* (2.9점), *Fhb 2* (3.1점), *Fhb 4* (3.0점)과 *Fhb 5* (2.8점)로 *Fhb 2*에서만 유의성이 나타났다. 집단-2에서는 저항성 계통의 평균 감염률은 *Fhb 1* (3.3점), *Fhb 2* (3.0점), *Fhb 4* (3.1점)과 *Fhb 5*(3.2점)이었으며, 감수성에서는 *Fhb 1* (3.1점), *Fhb 2* (3.1점), *Fhb 4* (3.0점)과 *Fhb 5* (2.8점)로 감염률이 높은 유전집단에서는 유전자형에 따른 차이가 나타나지 않았다.

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PB-0057

Screening of Ethyl Methanesulfonate (EMS) Mutant rice (*Oryza sativa* L.) Lines exposed to Potassium Chlorates

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Chlorates, such as potassium chlorates ($KClO_3$) are commonly used to investigate the divergence in nitrogen use efficiency (NUE) in plants. In addition, ClO_3 are reported to exert an inhibitory effect on the reducing activity of nitrate reductase (NR) of nitrate (NO_3) to nitrite (NO_2). In rice, *Oryza sativa* L. is the most cultivated species and has two subspecies, *indica* and *japonica*. These subspecies have a wide genome difference mainly attributed to their domestication history. Improving NUE in plants has been and continue to be at the center of several research programs, and has gained momentum during the last two decades with the increasing evidence of global warming caused by greenhouse gases (GHGs) from various economic sectors, including agriculture. In this study, a 0.1% $KClO_3$ solution was applied to rice ethyl methanesulfonate (EMS) M3 lines derived from the wild type Yeongjin. The screening population comprised 260 lines, the WT, and well-known $KClO_3$ sensitive and resistant rice cultivars included in the study as controls to validate the phenotype of the mutant lines. Preliminary phenotypic results identified a few Yeongjin EMS $KClO_3$ sensitive rice lines among tested lines. Sensitive Yeongjin EMS mutant lines shall be used for detection of mutations in the target genomic region, especially within NR or NRT.

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PB-0058

Identification of Candidate Genes within QTLs Conferring Bacterial Wilt Resistance in Chili Pepper

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The pathogen *Ralstonia solanacearum* causing bacterial wilt have wide host range about 300 species including pepper. The pathogen was classified into five races by host range diversity and into five biovars by physiological or biochemical differance. Therefore, resistance to *R. solanacearum* was seem to be strain specific. In the previous study, we identified QTLs conferring bacterial wilt resistance using two different isolates of *R. solanacearum*, 'HS' and 'HWA', in two F2 populations derived from the strongly resistant pepper cultivar 'Konesian Hot'. We performed bioassay during six weeks using two different isolates 'HS' and 'HWA', and disease index was scored from 0 (resistant) to 3 (susceptible). In this study, we identified candidate genes within the detected QTL regions conferring bacterial wilt resistance. The QTLs spanning between C07_223207483-HRM and C07_225182092, C09_5494783-HRM and C09_6047262, C09_6047262 and C09_4049745, and C10_231662410 and C10_231709238 was identified for resistance to 'HS' isolate. In results, a total of five candidate genes including two (*CA07g17970* and *CA07g18080*) on chromosome 7, three (*CA09g02490*, *CA09g02550* and *CA0g02600*) on chromosome 9, and one (*CA10g21300*) on chromosome 10 were identified. The QTLs spanning between C05_219987467 and C05_224297044, C09_3453876-HRM and C09_3682838 was identified for resistance to 'HWA' isolate. One candidate gene (*CA05g16160*) on chromosome 5 and two (*CA09g01260* and *CA09g01620*) on chromosome 9 were identified. In the next step, we will find gene variations by sequencing the identified genes and develop gene-based markers.

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PB-0059

Identification of QTLs for Fruit Size in Paprika (*Capsicum annuum* L.) Using Genotyping-by-sequencing Analysis

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Morphological characteristics of paprika (*Capsicum annuum* L.) are important factors that determine consumer preferences. Fruit weight, width, and height of paprika are the main breeding target traits for cultivar improvement. These characteristics are representative quantitative traits and are regulated by several QTLs. Fruit weight was measured for weight containing the pedicel. Fruit width was measured for the maximum width. Fruit height was measured for maximum length from the shoulder to the bottom of the fruit. In this study, we aimed to identify QTLs for paprika fruit size including weight, width, and height using genotyping-by-sequencing (GBS) analysis, which were performed using 94 individuals of an F2 segregating population derived from the commercial F1 paprika cultivar 'Hera Red'. A total of 4,302 SNPs was identified by GBS analysis and used for construction of paprika genetic linkage map. The map, consisting of 15 linkage groups including 12 chromosomes with 639 SNP markers, covered a total of 1365.7cM genetic distance. QTL analysis revealed a total of eleven QTLs associated with fruit weight (*qWEI-Jul6.1*, *qWEI-Jul9.1*, *qWEI-Aug11.1*, and *qWEI-Avr5.1*), fruit width (*qWID-Jul9.1*, *qWID-Jul12.1*, and *qWID-Avr9.1*), and fruit height (*qHEI-Jul10.1*, *qHEI-Aug10.1*, *qHEI-Aug11.1*, and *qHEI-Avr10.1*). This QTL information will be useful for developing commercial paprika varieties with larger fruits.

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PB-0060

고시히카리 후대 단간 내병성 조생종 우량계통 “밀양396호” 육성

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고시히카리는 일본에서 가장 많이 재배되고 있는 고품질 브랜드쌀이다, 국내에서도 브랜드 활용 상업화 전략으로 인해 고시히카리의 재배면적이 경기도를 중심으로 증가되고 있다. 그러나 고시히카리는 키가 커서 도복에 약하고, 내병성 또한 약하기 때문에 국내에서 재배하기 어려운 품종이므로 고시히카리 재배면적 증가는 농민에게 경제적 및 노동력 측면의 부담을 가중시키는 요인이 되고 있다. 본 연구는 이에 따라 분자육종과 전통육종 기술을 접목하여 고시히카리 유전적 배경을 가지면서 내병성과 내도복성이 향상된 유망계통 밀양396호를 육성하여 고시히카리 대체용 벼 품종을 개발하고자 했다.

밀양396호를 육성하기 위해 2017년에서 2018년에 밀양에서 고시히카리를 반복친, 해담쌀을 공여친으로 여교배한 고시히카리*2/해담쌀 BC_2F_1 식물체로 계통선발을 진행했다. 여교배 개체 육성 과정에서는 줄무늬잎마름병 및 도열병 저항성 유전자 관련 마커 Indel7과 RM206에 대해 이형접합체인 개체를 8개체 선발했다. 2018년 하계 BC_2F_3 세대에서 고시히카리보다 키가 작은 단간계통을 중심으로 선발하였다. 선발된 계통은 동계 세대단축을 이용한 집단육종법으로 세대를 진전하였으며, 2020년하계 생산력검정 예비선발시험 및 2021년 생산력검정본시험을 수행하여 재배안전성(내병성, 내도복성) 및 품질이 우수한 계통 YR32525-B-B-B-4를 선발하여 밀양396호로 명명하였다.

밀양396호의 출수기는 보비조건 조기재배에서 7월 16일로 고시히카리보다 14일, 해담쌀보다 2일 빨랐으며, 조기재배 표준품종인 조평과 비슷한 수준이었다. 간장은 76.7㎝으로 조평보다 3㎝ 짧다. 바이러스병인 줄무늬잎마름병에 저항성이었으며, 도열병은 해담쌀 유래의 목도열병 저항성 유전자 *Pb1*과 잎도열병 광범위저항성 유전자 *Piz*를 가지고 있었다. 잎도열병 밭못자리 검정에서도 해담쌀 수준의 저항성으로 중강 정도의 반응을 보여 고시히카리보다 개선된 내병성을 가지고 있는 것으로 확인되었다. 수량은 569㎏/10로 조평과 유사한 수준이었다. 또한 조평 대비 식미가 우수하면서 완전미율 및 윤기치가 높아, 고품질 내병성 조생종 벼 품종 육성을 가능케 할 것으로 보인다.

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PB-0061

Assessment of Mesocotyl Elongation in Doubled Haploid Rice (*Oryza sativa* L.)

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Dry-direct rice seeding is a common practice in many African countries because it saves water and reduces labour costs. However, dry-direct seeded rice suffers from poor seedling emergence and establishment, reducing the plant population and yields. Emergence of deep-sown rice is enhanced by mesocotyl elongation, hence genotypes with longer mesocotyl are suitable for direct seeding. Thus, identification of QTLs associated with mesocotyl length could accelerate breeding of rice for direct seeding. In this study, 117 doubled haploid lines and their parental lines were evaluated for mesocotyl elongation from deep sowing in moistened soil. Pre-germinated healthy-looking seedlings were sown at a depth of 6 cm in moistened soil and grown in a greenhouse. Preliminary visual observations identified promising DH lines with potential long mesocotyl. The final evaluation will be done 10 days after sowing. Phenotypic data will be used for quantitative trait locus (QTL) analysis.

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PB-0062

Isolation of soybean ARGONAUTE protein involved in seed coat color pigmentation

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Post-transcriptional gene silencing (PTGS) of *chalcone synthase* (CHS) genes controlled the soybean seed coat color pigmentation. In order to understand the PTGS in seed coat pigmentation, we screened the EMS mutant population derived in the Pungsannamul (Yellow seed coat color; *I, r, t*) 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 wild type cultivars, Pungsannamul and Jinpung, respectively. Segregation analysis revealed that the all three brown seed phenotypes are controlled by a single recessive gene. Complementation analysis among three mutants by crossing revealed that the brown seed coat color mutation of all three mutants is caused by different types of mutation in the same gene. Using the single nucleotide polymorphism (SNP) array and Next Generation Sequencing, we identified a SNP in ARGONAUTE 5 (AGO5) in PE63 (G5369A), PE407 (G3707A), and PE63 (G37979A), respectively. dCAPS analysis of three mutants revealed that the brown seed phenotype was co-segregated with AGO5 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 AGO5 plays roles in seed color pigmentation by regulating the *chalcone synthase* (CHS) genes.

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PB-0063

국내 귀리 품종 전장유전체 염기서열 분석을 통한 SSR 기반 InDel 마커 선발

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귀리(*Avena sativa* L.)는 6배체이며 염색체 개수가 42개이고 유전체 크기가 11Gb로 크기 때문에 분자유전학적 연구가 어려웠다. 그러나 차세대 시퀀싱(Next generation sequencing)기술이 발달하고 귀리 OT3098의 reference genome 염기서열이 보고되면서 분자유전학적 연구 기반이 마련되었다. 이에 귀리의 디지털 육종 기반 및 핵심집단을 구축하기 위해 국내 귀리 품종의 전장유전체를 해독하여 InDel 마커를 선발하였다. 본 연구의 식물재료는 국립식량과학원에서 육성한 '삼한(육성년도 2001)', '대양(2005)', '하이스피드(2007)'를 사용하였다. TruSeq PCR Free(550)를 이용하여 whole genome library를 구성한 후, Trimmomatic(0.39)프로그램으로 read를 확보하였다. BWA(0.7.17-r1198) 프로그램으로 OT3098의 전장유전체 염기서열에 alignment한 뒤 GATK(4.2.0.0) 프로그램으로 variant calling을 진행하였다. 1차적으로 발견한 변이 중 multi-allele variants를 제거하고 depth filtering(5≤DP≤100)한 뒤 모든 품종에서 genotyping된 변이만 선발하여 Primer3 프로그램으로 프라이머를 제작하였다. OT3098의 전장유전체에 mapping한 염기 수는 '삼한', '대양', '하이스피드' 품종별로 각각 10,329,329,326, 10,392,225,953, 10,383,743,016bp 이었으며 평균 depth는 28.3, 28.3, 28.8이었다. Variant calling 결과 세 품종에서 OT3098의 염기서열 대비 총 86,064,846개의 변이가 탐색되었다. Reference genome 기준으로 2,812,609개의 SSR 기반 InDel 영역이 분석되었다. 이 중 유전자 영역에 분포하면서 max length difference가 18 이상인 프라이머를 염색체별로 고르게 선발하여 AsInD1A-1 등 총 60개의 InDel 마커를 선발하였다. 이는 A, C, D 게놈 별로 각각 20개이며, 염색체별로는 1~4개씩 분포한다. SSR motif는 AC, AG 등의 dinucleotide에서 CCACA, TGTGT인 pentranucleotide까지 총 19종이며 repeat 수는 4~37의 범위이다. 본 연구에서 제작한 마커는 귀리 국내 품종 및 국외 유전자원으로 다형성을 확인한 뒤 핵심집단을 구축하는 데 사용할 예정이다.

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PB-0064

Isolation of Ab-γg rich saponin mutants from EMS-induced population in soybean

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Triterpenoid saponins are major components of secondary metabolites in soybean. They are divided into two groups which are group A saponins and DDMP saponins. Group A saponins are consisted of soyasapogenol A (SA) including sugar chains at both C-3 and C-22 positions, whereas DDMP saponins are made up of soyasapogenol B (SB) including DDMP moiety at C-22 and having sugar chain at C-3 position. The ethyl methanesulfonate (EMS)-induced mutant, PE1607, which has a high level of Ab-γg saponins was isolated. By LC-MS analysis, the Ab-γg saponin concentration was seven times higher than cv. pungsannamul which is the origin of PE1607 mutant. Segregation analysis showed that a high level of Ab-γg saponin is controlled by a single locus. After physical mapping, the candidate region was narrowed down to the 7-mb region on chromosome 10.

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PB-0065

변이밀집영역 기반의 Indel 마커를 활용한 국내육성 벼 품종의 계통유연관계 분석

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유전체 기반의 변이밀집영역(dVB, dense variation block)에서 선발된 112개 Indel 마커를 활용하여 우리나라 직무육성 벼 품종 216종을 대상으로 유전형을 분석하고 이들 결과를 바탕으로 structure analysis와 phylogenetic analysis를 실시한 결과, 216 품종은 3개의 Subgroup, 자포니카형(Subgroup1), 통일형(Subgroup2), 중간형(Subgroup3)과 1개의 admixture group으로 나타났다. 또한, 주요인 분석 결과, Subgroup1과 Subgroup3 사이에는 Admixture 타입의 유전형이 다양하게 분포하여 품종 간 변별력을 제공하는 것으로 나타났다. 직무육성 품종들의 유전적 유사도는 높지만 dVB 기반의 112개 Indel 마커가 변별력을 높여 유전형 식별이 모두 가능함을 의미한다고 할 수 있다. 216 품종의 유전형과 육성연도별 4년 평균수량을 비교해 본 결과 통일형 품종의 경우는 80년대부터 2010년대까지 꾸준히 수량이 증대되어 왔으나, 자포니카 품종의 경우는 수량 증대에 일정한 경향은 없었다. 이는 90년대 이후 고품질 쌀 품종개발로 방향이 전환되면서 자포니카 품종 수가 대부분을 차지하고 있으며, 통일형 벼에서 도입한 형질이 수량보다는 병충해 저항성이나 내재해성 인자를 도입해 왔기 때문으로 생각된다. 직무육성 벼 품종의 유전형 패턴이 Subgroup3의 패턴인 혼합형이 존재하는 것은 고 수량을 통한 우리 쌀의 자급 달성이 통일형 벼를 통해 이루어졌고 그 이후 고품질 쌀 품종개발로 정책방향이 전환되면서 자포니카 쌀 품종이 개발되어 왔기 때문이다. 이 과정에서 병충해저항성과 내재해성 인자 도입을 위하여 야생벼나 인디카 등을 활용하기 위한 BRIDGE 역할을 하는 품종들이 개발됨으로서 그 과정에서 혼합형 유전형 패턴이 하나의 Subgroup으로 형성된 것으로 생각된다.

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PB-0066

Genetic analysis and SNP marker development of glabrous hull trait in Asian rice (*Oryza sativa* L.)

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The glabrous hull trait in rice has the advantage of decreasing dust during threshing and saving the volume for grain storage. RIL population derived from a cross between Korean variety Boramchan and American glabrous variety Pecos was used for genetic analysis of glabrous hull trait. The segregation ratio of the glabrous hull trait was fitted to the 1:1 ratio in the RIL population, and this implies the glabrous hull trait was controlled single gene. The glabrous hull trait was mapped between two KASP markers, K05_005 and K05_011, on the short arm of chromosome 5. In this region, the *GLR1* gene, which controls glabrous traits in leaf and hull, was cloned from the American rice variety Rico No. 1. The glabrous trait in the *glr1* plant was caused not by DNA sequence difference but by DNA methylation in the promoter region (Li et al. 2012). Thus there is no functional marker for the *GLR1* gene yet. To develop a tightly linked SNP marker, SNPs in the 10kb sequence on either side of the *GLR1* gene of Boramchan and Pecos were extracted from resequencing data. A total of 14 SNPs was identified in the 10kb flanking region of *GLR1* gene between Boramchan and Pecos. Haplotype analysis using 14 SNPs was conducted using SNP information of 4,726 accessions in the RiceVarMap2 database. Five haplotypes were detected in 4,726 accessions, and hap 3 contained glabrous accessions. A unique SNP in the glabrous haplotype was identified on 4.5 kb downstream of the *GLR1* gene. An SNP marker, which was designed on the unique SNP to detect glabrous accessions, clearly distinguished non-glabrous and glabrous varieties. In addition, the SNP marker showed a perfect link with the glabrous hull trait in segregating populations derived from a cross between the non-glabrous and glabrous varieties. The SNP marker developed in this study would provide an efficient selection tool during the early stage of new glabrous variety development.

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PB-0067

Screening and identification of wheat lines missing the Omega-5 gliadin encoded on 1D chromosome

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Omega-5 gliadins are one of the main allergens involved in WDEIA, potentially life threatening form of food allergy. The use of wheat flour without omega-5 gliadins in the regular life is considered as one of the prophylactic approaches against WDEIA. In our previous study, we identified the novel type of minor omega-5 gliadin encoded on 1D chromosome with altered C- and N- terminal and repetitive central domain containing dominant epitopes of WDEIA, which are also reactive to patient sera. The protein, along with major 1B omega-5 gliadins, is an important target for development of hypo-allergenic wheat using breeding and biotechnology approaches. For this purpose, we selected and identified wheat lines lacking 1D omega-5 gliadins by PCR and CNV analysis from wheat germplasm. 2D-immunoblot analysis using monoclonal antibody to assess sensitization ability of the selected lines, showed no reactivity in the region of 1D omega-5 gliadin. The selected wheat lines will be used as breeding material to develop a double deletion mutant missing major 1B and minor 1D omega-5 gliadins as a feasible solution for the onset of wheat allergy.

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PB-0068

Development of a method for quantification of omega-1,2 gliadin genes by real-time PCR

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Wheat is a major food crop grown throughout the world that is used in a wide range of different food products because of the unique viscoelastic properties of the flour. At the same time, At the same time, it causes human health problems, including food allergies and celiac disease (CD). Alpha, gamma and omega-1,2 gliadins contain immune-dominant T-cell stimulating epitopes associated with CD. In this study, the reference wheat Chinese Spring (CS) and nullisomic tetrasomic lines of CS were used to distinguish the omega-1,2 gliadins encoded on chromosomes 1A and 1D. Omega-1,2 gliadins begin with ARQ or ARE and contain the repetitive motif PQQPFP. In the RP-UPLC analysis, it was confirmed that the peak of the ARE-type omega-1,2 gliadin protein encoded in the 1D chromosome was reduced. Probes specifically expressing ARE-type and ARQ-type omega-1,2 gliadins were designed and their expression was confirmed by real-time PCR. The expression of the designed porbe was significantly decreased in the line in which the 1A or 1D chromosomal region coding for omega-1,2 gliadin was deleted, but was significantly increased in the line in which 1A or 1D chromosome was present as tetrasomic. The data suggest that contribute to the development of wheat breeds aimed at reducing the immunogenic potential of wheat.

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PB-0069

Optimization of a fast and reproducible RP-UPLC method for HMW-GS alleles for large-scale analysis

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High-molecular-weight glutenin subunits (HMW-GS) account for only 10% of total wheat storage proteins, but play an important role in the processing quality of wheat flour. To rapidly, accurately and reproducibly identify HMW-GS, we established an optimized reversed-phase ultra-performance liquid chromatography (RP-UPLC) method. Separation parameters were optimized using an ACQUITY UPLC Protein BEH C_4 column and stepwise ACN gradient, and the separation patterns and retention times (RTs) of 22 subunits were comparatively analyzed in 16 standard wheat cultivars. All HMW-GS proteins were well separated within about 5.5 min, and all analyses were complete within 12 min. We distinguished the 16 subunits based on RT, although three subunits in 1Bx (1Bx7/1Bx7^{OE} and 1Bx17) and three subunits in 1By (1By8*, 1By9 and 1By15) had overlapping RTs; these were differentiated by SDS-PAGE. To distinguish 1Bx7 and 1Bx7^{OE}, which differ in protein abundance, RP-UPLC was combined with PCR analysis of DNA junction markers. The optimized method was successfully applied to determine HMW-GS alleles in a large collection of bread wheat germplasm (1787 lines).

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PB-0070

Analysis of allelic variation of *Gli-B1* locus encoding for Omega-5 gliadins by RP-UPLC

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Wheat (*Triticum aestivum* L.) is one of the most important staple grain crops consumed by humans worldwide and is a major source of proteins in a daily diet. In general, among the storage proteins of wheat endosperm, gliadins are known to be the most polymorphic. In addition, when considering their relevance of gliadins to wheat end-use quality and human health problems, genetic studies of gliadins are very important. Because of the complexity and heterogeneity of these proteins, resolving the genetic polymorphism remains still challenging. The aim of our study was to evaluate the profile patterns of omega-5 gliadins, which are known to have the lowest copy number among gliadin genes, in various *Gli-B1* alleles using RP-UPLC. For this purpose, we optimized RP-UPLC method for separation of omega-5 gliadin fraction using Chinese Spring and its nullisomic tetrasomic lines. Pattern analysis of omeaga-5 gliadin profiles was carried out using standard wheat cultivars of each *Gli-B1* alleles by the optimized method. Finally, the results were compared to omega-5 gliadin profiles of *Gli-B1* alleles from wheat genotypes reported in other reference.

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PB-0071

GBS 분석을 통한 국내 무(*Raphanus sativus* L.) 품종의 유전적 유연관계 분석

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GBS(Genotyping-By-Sequencing)는 전체 유전체를 Sequencing 하는 대신 제한효소를 이용해 Genomic DNA를 절단하고 그 주위 염기서열을 Sequence하는 방법으로, 기존 Whole Genome Sequencing 방법에 비해 적은 비용과 함께 불필요한 데이터를 줄일 수 있다는 장점을 가졌다. 본 실험에서는 GBS 분석을 통해 국내 무 품종의 유전적 유연관계를 분석하였다. 무 94품종을 품종군 별로 일반무 63품종, 알타리무 8품종, 열무 9품종, 소형무 5품종, 시래기무 3품종, 단무지무 4품종, 유색무 2품종으로 구분하였으며, 일반무는 재배작형에 따라 봄무 16품종, 여름무 15품종, 가을무 20품종, 겨울무 10품종으로 구분해 GBS 분석을 진행하였다. GBS 분석 결과를 바탕으로 생성된 각 품종 별 SNP genotyping 결과를 바탕으로 Unweighted Pair Group Method with Arithmetic Mean 방법으로 군집분석으로 실시하였고 Phylogenetic tree를 작성하였다. 국내 무 품종은 크게 알타리무, 소형무, 시래기무를 다수 포함한 그룹I와 단무지무, 일반무, 유색무를 포함한 그룹II로 구분되었다. 그룹II는 다시 단무지무와 일반무로 구분되었으며, 일반무 그룹에서는 봄무, 여름무, 겨울무가 가을무와 다른 군집으로 구분되어 유전적인 차이를 보였다. 본 연구 결과는 국내 무 품종의 유전적 유연관계에 대한 좋은 정보를 제공할 것으로 기대된다.

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PB-0072

유전체 정보를 이용한 초다수성 통일형 품종의 내냉성 유전자 하프로타입 분석

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경남 밀양시 점필재로 20, 농촌진흥청 국립식량과학원 남부작물부 논이용작물과

국내 벼 품종은 크게 밥쌀용 자포니카와 초다수성 통일형으로 구분된다. 국내에서 육성된 초다수성 통일형 품종은 일반 밥쌀용 품종보다 수량성이 20~40% 이상 높은 특징을 가지고 있다. 특히, 2017년에 육성된 초다수성 통일형 품종인 금강1호의 평균 쌀수량은 817kg/10a으로 세계적인 수준이다. 하지만 초다수성 통일형 품종은 밥쌀용 자포니카 품종보다 저온에 약해 재배환경에 민감하게 반응한다. 초다수성 통일형 품종의 내냉성을 증진하기 위해 현재까지 유전분석 연구 등을 통해 기능이 검정된 유전자 12종의 하프로타입을 분석하였다. 먼저 선발된 12종의 유전자에 대한 하프로타입은 벼 3K 유전체 정보를 기반으로 하는 Haplotype analysis 툴을 사용하여 분석하였다. 내냉성 유전자들의 하프로타입은 평균 13.6개 존재하는 것으로 탐색 되었다. 특히, bZIP73은 총 4 종류의 하프로타입으로 다형성이 작았으며, 하프로타입이 31개 탐색된 CTB2 유전자가 가장 다형성이 높은 것으로 분석되었다. 국내 육성 초다수성 통일형 품종이 보유한 내냉성 유전자 하프로타입 분석을 위하여 한아름4호, 금강1호 등 총 11개 품종에 대한 NGS를 수행하고 유전체 정보를 확보하였다. 국내 육성 품종이 보유한 내냉성 유전전자에 대한 하프로타입은 Haplotype analysis 툴을 통해 활용한 SNP 위치와 동일한 위치의 염기서열을 유전체에 정보에서 추출하여 분석하였다. qLTG3-1과 TCD5/TVS을 제외한 대부분의 내냉성 유전자에 대하여 초다수성 통일형 품종은 표준 품종인 Nipponbare와 국내 내냉성 품종인 진부벼와 다른 하프로타입을 보유 하고 있었다. 하프로타입 분석 정보는 SNP 특이 분자마커 개발과 내냉성 유전자 도입 계통 육성에 활용될 수 있을 것으로 기대한다.

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PB-0073

무(*Raphanus sativus* L.) 품종의 표현형적 특성과 heterozygosity 간의 상관관계 분석

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무(2n=18)는 전국적으로 널리 재배되고 있는 원예작물로 주로 잡종강세 현상을 이용한 F_1을 품종으로 이용하며, 국내 채소 종자시장에서 중요한 위치를 차지하고 있어 새로운 품종 개발을 위한 노력이 꾸준하게 지속되어왔다. 본 실험에서는 일반무 63개, 알타리무 8개, 열무 9개, 소형무 5개, 시래기무 3개, 단무지무 4개, 유색무 2개 도합 94종의 무 유전자원을 이용한 Genotyping-by-sequencing(GBS) 분석을 통해 SNP를 탐색하고 그 결과와 노지 생육조사 결과를 종합하여 무 뿌리의 표현형적 특성과 heterozygosity 사이의 관계를 파악하고자 하였다. GBS 분석 결과, 94개 무 품종은 평균적으로 106,893개의 SNP를 가지고 있으며 이중 homozygous SNP가 59,290개, heterozygous SNP가 18,356개, homozygous와 heterozygous로 구분할 수 없는 경우가 29,247개로 나타났다. 이 결과를 바탕으로 무 품종을 일반무와 기타 무(알타리무, 열무, 소형무, 시래기무, 단무지무, 유색무) 두 그룹으로 나누어 heterozygosity와 각 표현형적 특성(근중, 엽중, 근장, 엽장, 근폭, 엽수)의 상관관계를 분석한 결과, 기타 무가 근장을 제외한 모든 특성에서 고도의 상관관계를 가진 것으로 나타났다. 하지만 일반무 품종군의 경우, heterozygosity가 모든 표현형적 특성과 상관관계가 비교적 낮았으며 통계적으로도 유의하지 않았다. 이 결과는, 모본과 부본의 heterozygosity를 기반으로 한 교배조합 작성의 가능성을 제시한다.

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PB-0074

QTL Mapping for the Incidence of Flowers in Grape (*Vitis* spp.) through Genotyping-by-sequencing Analysis and SNP Marker

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Grape (*Vitis* spp., 2n = 38) is one of the most extensively cultivated fruit plants with table grapes accounting for 36% of the total world production. Breeders in table grape growing areas have been trying to develop grape cultivars with superior berry traits to those already be on the market. However, visual selection during grape breeding is time consuming and labor intensive. In the past decades, many studies were reported on the development of grape genetic linkage maps and the identification of QTLs for various fruit traits such as seedlessness, berry size, fruit ripening, fruit quality, and cluster structure. In this study, we aimed to identify QTLs for the incidence of flowers through genotyping-by-sequencing (GBS) analysis and SNP marker development. A total of 192 F_1 individuals derived from the cross between 'Tano Red' (*V. labrusca* × *V. vinifera*) and 'Ruby Seedless' (*V. vinifera*) was used for the QTL analysis and SNP marker development. In the previous study, a total of 1,336 SNPs was used for designing primer sets for high-resolution melting (HRM) analysis. HRM analysis revealed the diallelic segregation in 805 of primer sets. In results, a total of 2,267 markers consisting of 1,940 GBS-based SNPs and 327 HRM markers was mapped on grape genetic linkage map. QTL analysis was performed on seven flower incidence traits including total average short, total average long, average first short, average first short, average first long, average first third long, and availability short. A major QTL was identified on chromosome 5 in six traits including total average short, total average long, average first short, average first long, average first third long, and availability short. QTLs for total average short, average first short, and availability short were found on chromosomes 7, 17, and 10, respectively. Another QTL was identified on chromosome 18 in two traits including total average long and average first long. This QTL information and the QTL-linked HRM markers are expected to be helpful for grape breeding.

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PB-0075

콩의 다양한 재배품종에서 효율적인 원형질체 분리 및 유전자 도입

송지연, 박규태, 이상범, 박수권, 김유나, 김둘이, 문중경, 서미숙*

전라북도 완주군 이서면 혁신로 181 국립식량과학원 작물기초기반과

콩(*Glycine max* (L.) Merr.)은 식물성 기름과 단백질원으로써 경제적 가치가 높은 작물 중 하나이다. 최근 식물 생명공학 분야에서 유전자 교정 기술이 각광을 받으면서 콩에서도 유전자 교정 기술을 기반으로 하는 연구가 수행되고 있다. 하지만 콩의 경우 형질전환 효율이 낮고 재분화율 또한 낮은 것으로 알려져 있어, 유전자교정에 많은 어려움이 있는 실정이다. 본 연구에서는 콩의 원형질체를 이용하여 목적 유전자의 guide RNA를 선발하는 시스템을 개발하고자 한다. 실험을 위해, 콩의 잎과 하배축을 이용하여 원형질체를 분리하였고, 분리한 원형질체에서 외래 유전자의 도입 효율을 확인하기 위하여 pBI221-EGFP 벡터를 사용하였다. 형광현미경을 통하여 EGFP의 발현 여부를 확인한 결과 5일 간 암배양한 하배축을 이용하였을 때 유전자 도입 효율이 높다는 것을 확인하였다. 이러한 결과를 토대로 원형질체에 시범 유전자의 guide RNA를 도입하고 Deep-sequencing 분석을 통해 유전자 교정 효율을 확인 할 수 있었다. 본 연구를 통해 개발된 콩 원형질체 분리 및 유전자 도입 조건을 이용한다면, 콩의 유전자 교정 기술에 필수적인 guide RNA 교정 효율을 효율적으로 검증할 수 있으며, 이를 통해 콩의 유전자 기능 연구 및 유전자교정을 통한 새로운 품종 개발에 활용 가능할 것으로 판단된다.

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PB-0076

Expression profiling of genes involved in sugar content regulation in waxy corns : A holistic approach towards enhancement of sweetness in waxy corn kernels

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Zea mays is third most important cereal crop consumed in the world. It is eaten in various forms involving culinary and as a raw food. Various type of corns are sought for their specific eating qualities. Sweetness in maize is one of the vital attribute that attracts the consumers. However there are already various high-sugar corns such as sugary (su-1), sugar enhanced (se) and supersweet or shrunken (sh2) in vague, but they lack the unique feeling of stickiness and chewiness which is associated mainly with the waxy corns. Waxy corns are the high starch corns cultivated mainly in the East Asia region. Their stickiness comes from mutation of wx (waxy) gene in sugar to starch conversion pathway which implies nearly 99% of amylopectin accumulation. Alongside, high accumulation of amylopectin the sugar content in waxy corn stays very low. The sweetness in waxy corn along with its characteristic sticky flavor is sought by consumers. However some efforts has been made in past to enhance the sweetness of waxy corn, but the success achieved by them is below par. Additionally the genetic barriers also hinders the manipulation of sugar content in waxy corns. A holistic approach is required to uncover the sugar to starch conversion pathway related genes in tandem. In the present work we used different kind of waxy corns and selected cultivars with contrasting sugar content to setup an expression profiling of all the genes involved in sugar to starch conversion pathway.

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PB-0077

Genome-wide association study for resistance to *Heterodera sojae* in the Korean soybean core collection

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Heterodera sojae is a new soybean cyst nematode (SCN) species parasitic on soybean roots, like *H. glycines*, and harms soybean growth and subsequent yield. *H. sojae* is found in Korea and is widely distributed in the soybean fields. Unlike H. glycines, no genes related to *H. sojae* resistance have been identified. In addition, it is not known whether the markers linked with *H. glycines* resistance can also be used to screen for resistance to *H. sojae*. Here, we classified a total of 430 accessions from the Korean soybean core collection into the different *H. glycines* resistance types by using previously developed markers. Moreover, 385 soybean accessions were phenotyped for *H. sojae* resistance. Interestingly, several accessions with *H. glycines* resistant genotypes did not show resistance to *H. soja,* and it is expected that *H. sojae* resistance is associated with different genes and mechanisms from *H. glycines*. Therefore, we performed a genome-wide association study (GWAS) analysis to identify single nucleotide polymorphisms (SNPs) related to *H. sojae* resistance using the whole-genome resequencing (WGR) data of the Korean soybean core collection. Several significant SNPs associated with *H. sojae* resistance were detected, and a T-test testing the allelic effect of the resistance suggested that the SNP located at Chr 18 is associated with resistance to *H. sojae*. Candidate genes related to the resistance were identified by linkage disequilibrium (LD) block analysis.

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PB-0078

Specific sound waves promote root growth by regulating phytohormone content in *Arabidopsis thaliana*

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Sound waves affect plants at the biochemical, physical, and genetic levels. However, the mechanisms by which plants respond to sound waves are largely unknown. Therefore, the aim of this study was to examine the effect of sound waves on *Arabidopsis thaliana* growth. The results of the study showed that *Arabidopsis* seeds exposed to specific sound waves for 15 h per day for 3 d had significantly higher root growth than that in the untreated control. The root length and cell number in the root apical meristem were significantly affected by sound waves. Genes involved in cell division also were upregulated in seedlings exposed to sound waves. Root development was affected by the concentration and activity of some phytohormones, including cytokinin and auxin. Analysis of the expression levels of genes regulating cytokinin and auxin biosynthesis and signaling showed that cytokinin and ethylene signaling genes were downregulated, while auxin signaling and biosynthesis genes were upregulated in Arabidopsis exposed to sound waves. Cytokinin and auxin concentrations of the roots of *Arabidopsis* plants also increased and decreased after exposure to sound waves, respectively. The expression of the auxin marker gene DR5*rev*:GFP was significantly higher in the roots of the Arabidopsis exposed to sound waves than that in the untreated control, confirming an increase in the auxin content of the roots. Our findings suggest that sound waves are potential agricultural tools for improving crop growth performance.

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PB-0079

Specific sound waves in sprout vegetables during growth and storage affect flavonoid content and antioxidant activity

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Recent studies have shown that sound waves regulate various aspects of plant growth, plant metabolite content, and stress response. Sound waves regulate growth and development in a variety of plants, but their effects on sprout vegetables are still not well understood. The purpose of this study is to select sound wave treatment conditions to increase flavonoid content and antioxidant activity during growth and storage of sprout vegetables and to understand the mechanism. These sprouts were treated with each sound wave for 2 h per day for either consecutive (long term [LT]) or alternating days (short term [ST]) during growth and storage. The flavonoid contents of the sprouts were found to differ according to the sound frequency, exposure time, species, and growth conditions. A 16 to 88% increase in flavonoid content was induced during growth and storage in sprouts under specific sound wave conditions. Quantitative RT-PCR (qPCR) based analysis showed that the expression patterns of the flavonoid biosynthesis related genes were correlated with the flavonoid contents observed in each treatment suggesting that sound waves regulate the flavonoid biosynthesis pathway. DPPH and FRAP analyzes also showed significantly higher antioxidant effects of sprouts under specific sound wave treatment. The flavonoid accumulation was positively correlated with the antioxidant properties of the sprout vegetables. Our findings suggest that sound waves with a particular frequency could be used to improve metabolite contents of crops for functional products.

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PB-0080

Identification of a novel locus (*C2*) controlling canary yellow flesh in watermelons

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The flesh color of cultivated watermelons(*Citrullus lanatus* L.) is classified into scarlet or coral red, canary yellow, and orange due to the accumulation of specific carotenoids. Canary yellow flesh(CY) is dominant to red flesh, which is determined by the *C* locus encoding LCYB(Lycopene β-cyclase) involved in the carotenoid biosynthesis pathway. However, in some inbreds homozygous for *C*, yellow flesh mixed with red(incomplete canary yellow flesh, ICY) is observed, implying that a secondary genetic factor in addition to *LCYB* may exist in determining canary yellow flesh. In this study, whole genome resequencing(WGRS) of three CY and three ICY inbreds and mapping of an F_2 population derived from a cross between CY and ICY inbred were performed to identify the locus(named C_2) associated with the ICY. The WGRS deliminated a genomic region that is conserved in DNA sequence only among three CY inbreds. This genomic region spends 27.60-28.32Mb on chromosome 2 and carries 26 genes. A total of eight SNPs from these genes were converted to the CAPS and mapped using 131 F_2 plants. In this F_2 population, CY and ICY segregated by 3:1, indicating dominant effect of single gene for CY. In linkage mapping, the C_2 was franked by two tightly linked CAPS markers. Our results show that C_2 is a new locus that regulates canary yellow flesh along with the *LCYB*. The molecular function of C_2 and its interplay with the *LCYB* in the formation of canary yellow flesh remains to be elucidated in the future.

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PB-0081

Identification of Genomic Regions Associated with the Resistance to Black Leaf Mold Based on the Genotyping-by-sequencing of *Solanum harbrochaites* (LA1777) Introgression Lines

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Black leaf mold (BLM) caused by *Pseudocercospora fuligena* is a destructive disease in tomato. In this study, BLM resistance to Korean isolate of *P. fuligena* was evaluated in *Solanum habrochaites* introgession lines (ILs) derived from a cross between the resistant donor LA1777 and the susceptible recurrent parent LA4024 (*S. lycopersicum*). Bioassay revealed 8 ILs including LA1777 with high levels of resistance (DSI =0.0~10.0) to BLM and the rest of the ILs including LA4024 (DSI =53.0) showed a wide range of intermediate resistance and susceptibility (DSI = 10.3~53.0). These accessions were genotyped by the Genotyping-by-sequencing (GBS), which produced a total of 59,216 single nucleotide polymorphisms (SNPs). The SNPs were used to map introgressed regions (IRs) of LA1777 genome in each IL, and a total of 135 IRs were identified with an average of 1.5 regions per IL. Using 2,666 SNPs after filtering, a Genome-wide Association Study was performed on fixed and random model circulating probability unification mode, and a total of 10 significant SNPs (*P*-value <0.003) were identified from the IR of chromosome 1 (6 SNPs) and 7 (4 SNPs). Two SNPs located on genes Solyc07g045400.1.1 and Solyc07g045353.1.1 that encodes pentatricopeptide repeats and zinc finger BED domain, respectively were selected for CAPS marker conversion and genotyped on 404 tomato accessions evaluated for the BLM resistance. A high level of correlation between the marker genotype and BLM resistance was detected in these accessions, indicating strong association of these IRs with the BLM resistance.

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PB-0082

A Novel set of EST-SSR Markers for the Evaluation of Genetic diversity and Polyploidy in Persimmons (*Diospyros* spp.)

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A high level of polyploidy exist among persimmons (*D. kaki* Thunb., 2n=6x =90; 2n=9x=105) and rootstock species (*D. lotus*, 2n=2x=30; *D. virginiana*, 2n=4x=60). Allele-specific DNA markers such as EST-SSR are useful for multiple allele detection and genetic diversity study in polyploid species. In this study, a novel set of EST-SSRs was developed and used for population genetic analysis, cultivar identification, and polyploidy detection of 96 persimmon accessions consisted of three different ploidy (2x, 6x, 9x) and four cultivar groups (PCA, PCNA, PVNA, and PVA) collected from different countries. A genome-wide EST-SSRs were identified from a RNA-seq data from 'Jochu' and 'Fuyu'. The number of EST-SSRs detected from 'Jochu' and 'Fuyu' were 155K and 146K, respectively. A total of 1,783 EST-SSRs detected from 1,745 transcripts were polymorphic between these cultivars. Tri-motif (17.09%) and hexa motif (41.54%) encoding amino acid were observed at the highest frequency. A total of 120 EST-SSR primer sets were designed and tested on a 8 accession panel, and 12 primer sets showing successful PCR, high level of polymorphism, and polyploid-specific banding patterns were selected to genotype the 96 accessions. The population genetics analysis including allele frequency analysis, AMOVA, and PCoA based on the EST-SSR genotype data provided the insight for understanding genetic diversity and structure of Korean persimmon germplasm collection. In addition, these 12 EST-SSR markers could be efficiently used for identification of each accession and polyploidy detection.

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PB-0083

Genomic prediction of bacterial wilt resistance in cultivated tomato (*Solanum lycopersicum* L.)

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Bacterial wilt (BW), caused by *Ralstonia solanacearum*, is a devastating disease in cultivated tomato. Genomic selection can be an effective breeding strategy to improve BW resistance that is controlled by QTL with minor effects. In this study, we investigated prediction accuracy of genomic estimated breeding values (GEBVs) for BW resistance using two populations consisting of 191 (P1) and 161 (P2) varieties. Disease severity of each population was evaluated in three independent seedling assays following inoculation with race 1 of *R. solanacearum*. For genotyping, the 51K Axiom™ SNP array was used, and 31,330 confident SNPs were filtered as a common set for both populations. With the phenotypic and genotypic data, prediction accuracy of GEBVs was evaluated in the three training populations (P1, P2, and combined) using the ridge regression best linear unbiased prediction (RR-BLUP) model and leave-one-out cross-validation (LOOCV) method. The Pearson correlation coefficients between GEBVs and observed phenotypes ranged from 0.533 (P2) to 0.685 (combined). Furthermore, two subsets of 96 and 192 SNP markers were selected based on marker effects. The GEBVs of these marker sets showed correlation coefficients ranging from 0.588 to 0.757 in the three training populations. We found higher levels of prediction accuracy (0.652-0.805 coefficients) using additional marker sets (96 and 192 SNPs) that were selected based on both marker effects and genome distribution, relative to all of 31,330 markers as well as the marker effect-based sets. These results suggest that genomic selection facilitates development of elite cultivars with BW resistance in tomato breeding programs.

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PB-0084

QTL Analysis of Two Major Effect QTLs Controlling Awn Development in Rice

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Rice (*Oryza sativa* L) is one of the most important crop in the world and widely studied model plant. Based on actual observations and previous research results, we totally recognized that awn is unfavorable characteristic during harvest and processing, and awn was one of the target character in selection program of early farmers and breeders. However, the genetic mechanism of awn length development is still unclear. In this study, we focus on efforts to analysis the major-effect QTLs and find candidate genes for awn development in rice and by using a mapping population derived from a cross between the Korean *indica* cultivar 'Milyang23' and NIL4/9 (derived from a cross between 'Hwaseongbyeo' and *O. minuta*). As a results, two QTL *qAwn4* and *qAwn9* were mapped on chromosome 4 and 9, respectively. By comparative sequencing analyses parental lines, *LABA1* was determined as the causal gene underlying *qAwn4*. With extensive mapping efforts, the *qAwn9* was finally mapped to a 199 -kb physical region between markers RM24663 and RM24679. Within this interval, 27 annotated genes were revealed, and five genes (*Os09g0520400, Os09g0521400, Os09g0521900, Os09g0524800, Os09g0525400*) were considered as the most likely candidate genes for *qAwn9* based on their functional annotations and sequence variations. The other tests such as haplotype analysis and gene expression analysis are underway. Our results lay a foundation for further cloning of a new awn gene underlying *qAwn9*.

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PB-0085

Identification of accession-specific variants and development of KASP markers for assessing the genetic makeup of *Brassica rapa* seeds

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Most crop seeds are F1 hybrids. Seed providers and plant breeders must be confident that the seed supplied to growers is of known, and uniform, genetic makeup. This requires maintenance of pure genotypes of the parental lines and testing to ensure the genetic purity of the F1 seed. Traditionally, seed purity has been assessed with a grow-out test (GOT) in the field, a time consuming and costly venture. Early in the last decade, seed testing with molecular markers was introduced as a replacement for GOT, and Kompetitive allele specific PCR (KASP) markers were recognized as promising tools for genetic testing of seeds. However, the markers available at that time could be inaccurate and applicable to only a small number of accessions or varieties due to the limited genetic information and reference genomes available.

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PB-0086

Wheat transformation system and Korean wheat variety application using *GRF-GIF* chimeric gene cloned from cv. Keumgang

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Stable embryogenesis and *Agrobacterium*-mediated transformation(one copy transgene integration) method are very important in successful wheat transformation for wheat research. Therefore, improving the efficiency of the *Agrobacterium*-mediated transformation method for Korean wheat varieties is very essential for many research of Korean wheat. In a previous study, we reported the successful potential of a stable immature embryogenesis method applying speed breeding conditions in Korea. In this experiment, the wheat transformation was applied to immature embryos collected in Speed breeding conditions, and the efficiency of wheat transformation was confirmed by measuring the transgene integration rate. In addition, the recently reported *GRF-GIF* chimera gene was cloned from cv. Keumgang, a wheat-promoting variety in Korea, and constructed, and its ability to improve regeneration was confirmed. As a result, the transgene integration was confirmed by PCR screening for calli and one regenerated callus that had been selected for 5 weeks by G418 antibiotics. Immunostrip test results using putative transformants, stably transgene-integration efficiency was 0.15%. Finally, PCR screenings using the putative transgenic plants were confirmed that was integrated transgene. This study can be usefully used to establish a Korean wheat transformation system, and transformation technology is currently being applied to Korean wheat varieties.

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PB-0087

Efficiency Analysis of Agrobacterium Transformation of Korean Wheat Varieties By GUS System

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Wheat is one of the three major crops, and domestic consumption is steadily increasing, but its self-sufficiency rate is only 0.7% due to low quality in Korea. In particular, wheat is a hexaploid plant and has difficulty in transformation due to its large genome size of 16GB and complex of genome structure. Agrobacterium-mediated transformation can stably insert a defined segment of DNA fragment into a plant genome than the conventional hybridization method, and generally has a lower copy number and fewer rearrangements and an improved stability of expression over generations than free DNA delivery methods. In this study, a total of 43 Korean wheat were identified by the GUS assay to analyze the T-DNA integration efficiency. The transformed Agrobacterium(EHA105) was obtained by subcloning of the GUS gene into the pCAMBIA 1301 vector. For analysis, immature embryos (1.0-2.0 mm in diameter) were collected and inoculated with AGROBACTERIUM(od 0.6). For immature embryos, spikes were selected according to the size among those 13 ~ 15 days after flowering. After inoculation, immature embryos were placed on medium supplemented with acetosyringone and co-cultivated for 2 days. After resting for 5 days, GUS staining was performed for 24 hours. The expression level of the GUS gene was evaluated by visual assessment according to the blue signal intensity. As a result, GUS staining was obtained 26 cultivars. Among them, it can be seen that the stronger blue signal intensity was in Jonong, Saeol, Jopum, Sugang, and Keumgang, indicating that GUS was stable and the high expression.

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PB-0088

Identification of candidate genes and development of HRM markers related to Ripening Period of Wheat (*Triticum aestivum*) by GWAS analysis

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GWAS (Genome-Wide Association Studies) is efficient method to find related genes and SNPs through statistical analysis of the association between phenotype and genotype. Among molecular markers related to genes and related mechanisms that affect agricultural characteristics, SNP markers have the advantage of being stably used compared to existing markers, and HRM (high-resolution melting) enables quick and easy identification of SNPs. In our study, the expression of Ripening-related candidate genes obtained through GWAS analysis in korea wheat core collection was confirmed through qRT-PCR. It was confirmed that the candidate gene decreased the expression of the spikes as wheat ripened. However, the expression of the candidate gene in roots, stems, leaves, and spikes during the growth stage was confirmed opposite the ripening stage. On the 0th day of heading, it was highly expressed in stems and spikes, and on the 30th day after heading, it was highly expressed in the roots and leaves. The discovered ripening - related candidate genes are presumed to be involved in seed development, root development, cell mitosis, and flowering. In addition, the SNP of the F_1 generation of breeding combinations was analyzed with HRM markers. The breeding combination was conducted out using varieties with different ripening periods, and the possibility as a marker was confirmed by clearly showing the distinction by SNP between the breeding combination and the parent through HRM analysis. Identification candidate genes and HRM marker related to wheat ripening can be applied to a variety of agricultural traits, thus providing the basis for molecular breeding.

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PB-0089

Voltage-dependent anion channel (*VDAC*) functions in the GA biosynthesis pathway in monocot plant and affects seed germination

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Pre-harvest sprouting (PHS) damage is emerging as a major problem due to climate change. PHS and germination are regulated through various genetic mechanisms and interactions. In a previous study, we found through transcriptome analysis that the expression of *voltage-dependent anion channels* (*VDACs*) in PHS-resistant wheat was lower in PHS conditions. To identify the relationship between *VDAC* and PHS, we performed functional analysis by a monocot model plant (*brachypodium distachyon*). Functional genetic analysis was performed through an over-expression lines and gene-edited lines (deletion lines and base substituted lines) using CRISPR/Cas9. Unlike base-substituted lines and over-expression lines in the germination test, the deletion lines significantly suppressed germination but recovered during exogenous GA treatment. Expression of the GA in the early biosynthesis stage involved gene, *KS*, showed an opposite pattern to that of *VDAC* in the deletion lines. In addition, *GA2ox* expression was predicted to decrease in endogenous GA content through a reduction in normal conditions and recovery upon GA treatment. There were no significant differences in GA biosynthesis gene expression in base-substituted lines and over-expression lines. Additionally, in the deletion lines, a decrease in height and growth retarded phenotypes were observed but PHS was significantly suppressed in the spike. As a result, it was confirmed that the endogenous GA content was reduced in the seeds of the deletion lines. In conclusion, *VDAC* may play an important involvement in endogenous GA early biosynthesis pathway to regulate germination, and the target sequence region through gene editing is provide an evidence for involvement in germination regardless of the increase in expression level.

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PB-0090

Efficient CRISPR/Cas9 genome editing plant selection method using HRM

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Protoplast gene editing of monocot plants using CRISPR/Cas9 is simple and accurate. However, to select genetically modified plants, transformation verification analysis such as confirmation of reporter genes is required. In particular, verification of genome editing through sequencing is necessary. We have established a system to quickly and accurately check whether or not a gene is edited without a reporter gene system using HRM. Protoplasts were isolated using the first leaf of Bobwhite, a cultivar with high transformation efficiency. Three gRNAs were designed by targeting genes related to pre-harvest sprouting resistance. Protoplasts were transformed with PEG-mediated method and transferred to Regeneration medium. After two days of culture, gDNA was extracted from the transformed protoplast and HRM was performed. HRM primer was designed to be about 150 bp centered on the genome editing target. Gene editing was analyzed through HRM melting curve compared to wildtype. Sequencing analysis was performed on the samples selected by the HRM results to verify the editing of the gRNA target sequence. Genome editing verification using HRM analysis is available as a fast and simple selection method for various genome editing studies, including protoplast transformation.

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PB-0091

GWAS analysis revealed the genetic composition of heading date genes in the photoperiod-insensitive North Korean rice population

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Rice is a major food crop that feeds more than half the world's population. Heading date (Hd) is one of the main factors that determine rice yield and local adaptation. To identify the genetic factors involved in the wide regional adaptability of rice, we performed a genome-wide association study (GWAS) with 190 North Korean (NK) rice varieties selected for non-precocious flowering in the Philippines, a low-latitude region. By GWAS, we identified five significant loci for Hd in 2018 and 2019 trials. Among the five lead single nucleotide polymorphisms (SNPs), three were located adjacent to the known Hd genes, Heading date 3a (*Hd3a*), Heading date 5 (*Hd5*), and *GF14-c*. In contrast, three SNPs were located in novel loci with minor effects on heading. Further GWAS analysis for photoperiod sensitivity (PS) revealed no significant genes associated with PS, approving that this NK population is largely photoperiod-insensitive. Haplotyping analysis showed that more than 80% of the NK varieties harbored nonfunctional alleles of major Hd genes investigated, of which a nonfunctional allele of *Heading date 1* (*Hd1*) was observed in 66% of the varieties. Geographical distribution analysis of Hd allele combination types indicated that nonfunctional alleles of floral repressor Hd genes enabled rice cultivation in high-latitude regions. In contrast, *Hd1* alleles largely contributed to the broad regional adaptation of rice varieties. In conclusion, the identification of the genetic composition of this population would be critical for the breeding of region-specific adaptable rice.

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PB-0092

QTL-Seq Analysis for Identification of Resistance Loci to Bacterial Canker in Tomato

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Bacterial canker caused by *Clavibacter michiganensis* (*Cm*) is one of the most economically important vascular diseases causing unilateral leaf wilting, stem canker, a bird's-eye lesion on fruit, and whole plant wilting in tomato. There is no commercially available cultivar with bacterial canker resistance, and genomics-assisted breeding can accelerate the development of cultivars with enhanced resistance. *Solanum lycopersicum* "Hawaii 7998" was found to show bacterial canker resistance. A Quantitative trait loci (QTL)-seq was performed to identify the resistance loci using 909 F2 individuals derived from a cross between *S. lycopersicum* "E6203" (susceptible) and "Hawaii 7998," and a genomic region (37.24-41.15 Mb) associated with bacterial canker resistance on chromosome 6 (*Rcm6*) was found. To dissect the Rcm6 region, 12 markers were developed and several markers were associated with the resistance phenotypes. Among the markers, the Rcm6-9 genotype completely matched with the phenotype in the 47 cultivars. To further validate the *Rcm6* as a resistance locus and the Rcm6-9 efficiency, subsequent analysis using F2 and F3 progenies was conducted. The progeny individuals with homozygous resistance allele at the Rcm6-9 showed significantly lower disease severity than those possessing homozygous susceptibility alleles. Genomes of five susceptible and two resistant cultivars were analyzed and previously known R-genes were selected to find candidate genes for *Rcm6*. Nucleotide-binding leucine-rich repeat, receptor-like kinase, and receptor-like protein were identified to have putative functional mutations and show differential expression upon the *Cm* infection. The DNA markers and candidate genes will facilitate marker-assisted breeding and provide genetic insight of bacterial canker resistance tomato.

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PB-0093

The availability and implications of nSSR and cpSSR (DNA) markers for the identification of morphologically similar cultivars in *Hibiscus syriacus* L.

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In order to identify morphologically indistinguishable cultivars of *Hibiscus syriacus* L., various nuclear and chloroplast simple sequence repeats (nSSR and cpSSR, respectively) markers were used. A total of 45 nSSR and 12 cpSSR markers were used for the identification of 32 cultivars clustered into 14 groups. Among them, 12 cultivars in six groups including 'Hongtanshim' and 'Bonjoia' from the same group were identified using 41 nSSR markers. However, there was no difference for rest 20 cultivars in eight groups despite of the use of all developed markers including 12 cpSSRs. For many indistinguishable cultivars including 'Pompon rouge' and 'Amplissimus', their breeding processes were not clearly known. As well, either genetically close cultivars including 'Blue Bird', 'Natsuzora' and 'Parangsae' or cultivars selected from controlled/open-pollinated progeny with the exotic cultivars as the female parent, for example, 'Pyonghwa' and 'Bicolor' were not identified with SSR markers. To improve the management efficiency of genetic resources and to minimize the confusion in markets, reconfirmation of uncertain breeding history and development of novel and efficient markers are required in this species.

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PB-0094

Genome-Wide Association Study of Leaf Chlorophyll Content Using High-Density 50K SNP Array in Peanut Accessions

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Chlorophyll concentration, a crucial component for photosynthesis in plants, has been studied extensively across crop species. The objective of this research was to assess the genetic diversity of 453 peanut accessions. We used the Axiom Arachis array, which has 58K single-nucleotide polymorphisms (SNPs), to conduct a genome-wide association study (GWAS) of leaf color data based on chlorophyll content analyses. We identified seven SNPs significantly associated with leaf chlorophyll content on the chromosomes Aradu.A02, Aradu.A08, Araip.B02, Araip.B05, Araip.B06, and Araip.B08 in a GAPIT analysis. Across the seasons, the SNP AX-176820297 on Araip.B05 was substantially related to leaf chlorophyll concentration. The Arahy.SDG4EV gene was shown to be in linkage disequilibrium (LD) with the relevant SNPs, and its expression was found to be significantly correlated with leaf chlorophyll content. The results of the present study can provide useful information with which to assess genetic variations in chlorophyll content and might be utilized for further genetic and genomic studies and breeding programs in peanuts.

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PB-0095

Genome-Wide Association Study and Transcriptome Analysis of Salinity Tolerance in Peanuts (*Arachis hypogaea* L.)

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Soil salinity is well known to reduce crop production significantly. Although peanut is considered as a moderately sensitive species to salinity stress, however a few studies on salinity tolerance in peanut have been reported.
A total of 300 peanut accessions with 58K SNPs by Axiom_Arachis array were used for the genome-wide association study (GWAS). The enriched compression mixed linear model (ECMLM) of GAPIT package was used to conduct GWAS for several traits. Transcriptome analysis was performed with roots of each salinity tolerance and susceptible accession with 200 mM NaCl at 0h, 12h and 24h after salt treatment.
We identified 33 SNPs as being significantly associated with salt stress in GWAS analysis, and the 105 candidate genes significantly related to sodium ion content were detected. A total of 973 differentially expressed genes (DEGs) were identified, of which 342 were down-regulated and 631 were up-regulated genes, assigned to 233 GO terms and 29 KEGG groups. These 973 DEGs included candidate genes that are known to be involved in tolerance to salinity stress: transporters, MAPK signaling pathway and Cytochrome P450, etc.

Acknowledgement: The study was conducted to identify genomic regions related to salinity tolerance by GWAS and transcriptome analysis. The results from this study will provide a valuable genetic resources for the breeding of salinity tolerance accessions in peanut.

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PB-0096

Genetic diversity of *Panax ginseng* revealed by genome-wide SNP chip

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Ginseng (*Panax ginseng*) is Korea's most well-known medicinal plant. However, due to its physiological characteristics, ginseng breeding research has been hampered. Furthermore, the nature of allotetraploidy and the highly repetitive genome structure caused by two whole genome duplication events hampered the development of effective molecular markers. The genotyping-by-sequencing (GBS) method was used to overcome the limitations imposed by genome complexity and discover a large number of high-quality SNPs. SNPs found in single copy regions of the genome were obtained by strictly filtering raw variants. The 192 informative SNPs found throughout the genome were finally chosen and designed into two sets of 96 SNP chips and applied to 867 diverse ginseng germplasms. This is the first SNP chip for ginseng, and it will be a useful digital genotyping tool for identifying the genotype of diverse genetic resources on a large scale. SNP chips can be used in a variety of applications, including seed purity testing and digital breeding, by scanning the rate of fixation across the entire genome.

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PB-0097

Development of Fast Neutron-mediated Ice Plant Cultivars 'Icitol 1 and Icitol 2' with Improved Biomass and Free Cyclitol Content

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Crassulacean acid metabolism (CAM) is a specialized carbon fixation pathway that characterized by nocturnal CO2 uptake to improve water-use efficiency (WUE). Recently, a halophytes species common or crystalline ice plant (Mesembryanthemum crystallinum L.) has become a model to study CAM photosynthesis due to an adaptive mechanism of shifting from C3 photosynthesis to CAM subjected to water or salt stress conditions, which greatly enhances WUE and stress tolerance. The common ice plants are also known to have a number of health-promoting properties in type-2 metabolic syndrome and diabetes treatment due to cyclitols compounds including D-pinitol, D-chiro-inositol, and myo-inositol. These compounds have been reported to accumulate at high levels when ice plants performed CAM photosynthesis under drought and salt stresses. We have developed a total of 1,071 M1 ice plant mutant populations irradiated with 40 or 50 Gy and 368 M3 candidates were selected during the primary screen on the basis of plant biomass. Within these populations, 2 M5 mutants, Icitol 1 and Icitol 2, had significantly increased plant biomass and selected free cyclitol compounds compared to wild-type plants.

These two ice plant cultivars could be high potential sources as cyclitol-rich high-functional food and medicinal uses.

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PB-0098

Quantitative Trait Locus(QTL) Analysis for Grain Size in Rice using RILs derived from a Cross between Japonica varieties

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Grain size is an important trait that determines the weight of 1,000 seeds, and affects the appearance and eating quality. In this study, the 190 RILs derived from a cross between 'Samnam' and 'Koshihikari' were used for the quantitative trait loci(QTL) analysis of seven grain size traits using 'SmartGrain' software. A genotyping of the RIL population was constructed using 96 Fluidigm SNP markers. The QTL IciMapping 4.2 Program was used for the preparation of the linkage map and QTL mapping. Area size(AP), perimeter length(PL), and grain width(GW) showed significant differences between parents, and as a result of correlation analysis, PL and grain length showed the highest correlation with a correlation coefficient of 0.94. After constructing a linkage map with 74 SNP markers, a total of sixteen QTLs were identified for the six traits (without grain length to width ratio) were detected on six chromosomes. LODs of the QTLs identified on this study were found to 2.52 ~ 7.22 and PVEs were 4.09 ~ 11.85%. In addition, QTLs of each trait were located close to each other, so that the grain size-related traits could be controlled together. These results are expected to be as useful genetic information for adjusting the rice grain size.

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PB-0099

Development of DNA Marker for the Resistance to Bakanae Disease in Rice (*Oryza sativa* L.)

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Functional markers, which are designed using polymorphic sites in gene sequences and which result in phenotypic variation, have high efficiency in marker-assisted selection (MAS). Bakanae disease is a rice disease whose importance is considerably increasing in several rice growing countries, leading to incremental production losses. In this study, 359 Korean landrace accessions were screened for bakanae resistance, allowing the identification of accessions with high-to-moderate levels of resistance to bakanae. With genotypes of 169 accessions using a KNU Axiom Oryza 580K Genotyping Array, GWAS was conducted to detect one genomic region highly associated with the observed phenotypic variation for response to *bakanae* infection on the chromosome 9 (named as *qBK9*) with 67 candidate genes. A set of markers based on the Tetra-primer ARMS-PCR (amplification refractory mutation system polymerase chain reaction) method was developed to detect the SNP *qBK9*. The specificity and applicability of the markers were verified in 359 Korean landrace accessions. We conclude that these markers can be exploited to monitor resistant lines to detect homozygous or heterozygous resistant genotypes and homozygous susceptible genotypes. Thus they can be used for genotyping the bakanae resistance rice lines, thereby effectively used in MAS.

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PB-0100

Functional Analysis of Heat-induced RING-type E3 Ligases in Sorghum: Expression Patterns, Subcellular Localizations and Interaction Partners

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Sorghum is the fifth most important crop worldwide and is predominantly grown as a staple food in arid and semiarid regions. However, modeling of global warming trends predicts to impose great pressure on the average yield production of sorghum. Ubiquitin E3 ligases are known to play an important role in regulating plant responses to abiotic stresses by targeting degradation of misfolded proteins. We have analyzed molecular functions of four Really Interesting New Gene (RING) E3 ligases of *Sorghum bicolor*. Clear changes in relative transcript abundance for four *SbHIREL2, SbHIREL3, SbHIREL14*, and *SbHIREL19* were observed in leaf tissues when plants were subjected to various abiotic stresses. C-terminal SbHIREL2-, SbHIREL3-, SbHIREL14-, and SbHIREL19-sGFP fusion proteins were localized to the cytoplasm in sorghum protoplast. Under heat-stressed conditions, the *SbHIREL*-overexpressing lines showed significantly higher germination rates and retention of green cotyledons compared with control. Yeast two-hybrid assay showed that SbHIREL2 could interact with multiple proteins. Therefore, the SbHIREL E3 ligases could play a role in sorghum heat-tolerance mechanism that has the potential to lead to regulating protein quality via Ub/26S proteasome pathway.

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PB-0101

고아밀로스 벼'신길'의 아밀로스 함량에 영향을 주는 유전자 동정

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'신길'은 통일형 품종인'한아름'(아밀로스 함량: 16.9%)을 돌연변이 처리(MNU) 하여 선발 육성된 아밀로스 함량이 23.4%인 고아밀로스 품종이다. 하지만'신길'의 아밀로스 변이에 영향을 주는 유전자는 아직 밝혀지지 않았다. 신길의 아밀로스 변이에 영향을 주는 유전 양식 규명을 위해'한아름4호'와'신길'의 후대 F1의 적합도 검정을 실시한 결과 정상립과 opaque의 분리비가 3:1로 신길의 아밀로스 변이에 영향을 주는 유전자는 1개의 열성 유전자로 확인되었다.

유전분석을 위해'한아름4호'와'신길'의 다형성 검정을 실시한 결과 총 917개의 마커 중 37개의 마커에서 다형성(5.1%)을 보였다.'한아름4호'와'신길'의 후대 F2 집단의 유전자형과 표현형을 조사하고 RCA(Recessive class analysis)방법을 통해 후보 영역을 분석한 결과 염색체 8번 15~17Mb 위치에'신길'의 opaque 표현형과 연관된 후보 영역이 탐색 되었다.

해당 지역의 염기서열 분석을 위해'한아름','신길'을 NGS 분석하였고, 총 8,004개의 돌연변이를 확인하였다. 8,004개의 다형성 SNP를 이용 reference 서열을 기준으로 발생한 변이를 비교하여 Synonymous/Non-synonymous 분석 실행하고 생성된 자료를 토대로 후보영역을 분석한 결과 Os08g0191433을 최종 후보 유전자로 선정하였다. 이 유전자의 돌연변이 염기서열을 이용하여 마커를 제작하고 정상, 분상질 표현형을 보이는 샘플들에 마커 검정을 실시한 결과 표현이 구분되는 것을 확인하였다. 이 유전자는 ss3a로 보고되어 있으며, 전분 구조에 영향을 주어 아밀로스 함량 조절을 하는 유전자로 알려져 있다.

본 실험은 고아밀로스 품종인 신길에 영향을 주는 유전자를 동정하기 위해 실시하였다.'신길'은 ss3a에 의해 아밀로스가 조절되어 고아밀로스가 되었고, 이 실험을 통해 제작된 마커는 고아밀로스 육종 효율을 높이는데 유용하게 쓰일 것으로 생각된다.

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PB-0102

Characterization and identification of multiple pistils mutant in rice

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The floral organ number is a crucial factor for seed development and seed-setting. The multiple pistils mutant was induced by treating ethyl methanesulfonate (EMS) from Korean japonica cultivar, Ilpum. In multiple pistils mutant, 30% of spikelets showed an increase in floral organ number especially in the stigma and stamen. Histological observation investigated that the number of ovaries was determined by the number of stigmas; spikelets with two or three stigmas contained only one ovary, whereas the spikelets with four stigmas possessed two ovaries. Genetic and MutMap analysis revealed that the multiple pistils phenotype was controlled by single recessive gene and the candidate gene was located between 7.5 and 22.0 Mb region on chromosome 8. The candidate gene associate with multiple pistils phenotype was identified by calculating SNP-index and we designated this gene as floral organ number 6 (*fon 6*). A single nucleotide substitution G to A in the intron splicing donor site of *fon 6* gene causes skipping of whole exon (deletion of 144 nucleotides) and premature stop codon. Furthermore, T-DNA tagging line showed increased stigma and stamen number and this result indicated that *fon 6* gene correspond to multiple pistils. These results will be helpful in elucidating the floral organ differentiation and formation in rice.

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PC-0001

A Statistical Study of Phenotypic Diversity Based on Genetic Traits in Barley

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Barley, a functional food, has garnered attention owing to the health benefits of its molecular products, such as β-glucan, polyphenols, and anthocyanin. Thus, it is necessary to develop new varieties, based on biodiversity, to improve its functional effects. In this study, we analyzed barley biodiversity based on 25 genetic traits, characteristic features, and correlation among other genetic traits. The germplasm of 25 species from 105 origins, numbering 25,104 in total, were preserved in National Agrobiodiversity Center (NAC, South Korea). Crop biodiversity, in terms of species number and origin, and species diversity were much lower (1.174) than diversity in origin (25.223), due to the presence of a biased species, *Hordeum vulgare* subsp. *vulgare*. During clustering based on specificity, we found that barley could be mostly distributed to 1-5 clusters based on genetic traits, such as ‘normal and uzu type’, ‘rough and smooth type’, ‘degree of vernalization’, and presence of ‘loose smut’, and some germplasms were specifically clustered based on other genetic traits. Furthermore, owing to correlation among genetic traits, we identified multiple correlated genetic traits that. In particular, ‘spike type’ was found to be highly correlated with ‘number of grains per size’ (0.99), which in turn was found to be correlated with ‘infection by barley yellow mosaic virus’ (0.79). Through our studies on phenotypic diversity, we expect that our analyses can suggest useful guides to species germplasms and phenotypes that need to be collected to conserve biodiversity and aid in the development of new varieties through breeding.

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PC-0002

블루베리 잎의 초분광 반사 스펙트럼과 1차원 합성곱 신경망(1D-CNN)을 이용한 멀칭 효과 분석연구

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초분광 이미징 기술은 식물의 수분스트레스를 감지하는 것을 시작으로 작물 재배와 수확에 이용되고 있는 비파괴 기술이다. 다양한 스펙트럼 정보가 여러 식물의 생리, 생장 특성에 대해 축적되고 딥러닝 기반으로 하는 이미징 분석기술이 발달하면서 농업에 적용되고 있다. 그러나 여전히 특정 스트레스 또는 재배 처리에 따라 반응하는 식물의 특성을 분류하기에 실험적 데이터가 부족한 실정이다.

블루베리는 슈퍼푸드로 선정될 만큼 뛰어난 영양소를 가진 작물로 우리나라에서도 많이 재배되는 종이다. 블루베리는 특별한 생육환경을 요구하여 토양 산도가 낮을 때 생장이 양호한 특성을 가지고 있다. 이에 재배지 토양 산도를 낮추기 위해 일반적으로 황 처리를 하고 있다. 그러나 화학비료는 토양 오염으로 생태계를 교란할 수 있는 위험으로 그 사용을 최소한으로 줄일 필요가 있다. 이에 최근 임업의 부산물인 종자 탈종 후 남는 구과를 멀칭하여 토양산도를 낮추는 시도가 이루어지고 있으나 탈종 후 구과를 멀칭재로 사용했을 때의 블루베리 생장에 미치는 효과에 대한 과학적 검증은 미흡한 실정이다.

본 연구에서는 잣구과 멀칭이 블루베리 생육에 미치는 영향을 구명하고자 무처리를 비롯한 5가지 멀칭재(잣구과, 무처리, 솔잎, 황, 잣구과+황)를 처리하고 생장과 생리반응을 처리구별로 비교・분석하였다. 더불어 각 처리구별 초분광 스펙트럼을 수집하고 딥러닝 기법인 1차원 합성곱 신경망(1D-CNN)을 이용해 생장, 생리반응을 비교하여 식물반응 특성을 구분할 수 있는지 가능성을 연구하였다. 잎의 생육・생리특성은 엽 길이, 엽 너비, 엽록소함량(SPAD value), 엽록소형광반응(Fv/Fm), 기공전도도(Gs)를 수집하였다. 잎의 초분광 스펙트럼은 VNIR(474nm~1000nm, 간격:1nm)과 SWIR(1101nm~2300nm, 간격:3nm)에서 반사 스펙트럼을 처리구별로 2000개를 수집하였다. 1-D CNN에 적용하기 전 스펙트럼은 Savitzky-Golay 2nd smoothing과 standard normal variate(SNV)로 전처리하였다. 분류 모델 알고리즘은 LeNet-5 모델을 활용하였다.

생육 수치와 생리 반응을 종합한 결과 잣구과+황 혼합처리구가 가장 양호한 것으로 나타났다. 잎에 초분광 반사 스펙트럼 데이터를 CNN 적용한 결과 raw VNIR: 96.26%, 전처리 VNIR: 98.06%, raw SWIR: 95.83%, 전처리 SWIR:97.17%으로 생육수치와 생리반응에 따른 분류와 95% 이상 정확도를 보였다. 실험을 통해 블루베리 잎 반사 스펙트럼 데이터를 딥러닝에 적용할 때 멀칭 처리에 따른 블루베리 생장 효과 구분이 가능하였다. 그 중 전처리 스펙트럼과 VNIR에서 97% 이상의 높은 정확도를 보여 분류 모델로 사용이 가능할 것으로 생각하였다.

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PC-0003

국내 메밀 주요 품종의 가공단계별 품질 특성 및 루틴 분석

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본 연구는 메밀의 식품가공기술 개발을 통해 이용성을 확대하고 다양한 소비수요를 창출하고자 가공단계에 따른 루틴 함량과 항산화 활성 등 품질 특성을 비교 분석하였다. 국내 육성된 메밀품종 중 황금미소가 양절메밀 또는 대산메밀보다 기능성물질인 루틴 및 퀘세틴 함량이 가장 높았다. 가공과정은 총 4단계로 나누었는데, 일반메밀 '양절메밀'은 껍질이 잘 벗겨지기 때문에 침지-탈피-증제-볶음으로 처리하였으며, 쓴메밀 '황금미소'는 종실 가운데 홈이 있고 껍질이 잘 벗겨지지 않는 특성으로 인해 침지-증제-탈피-볶음 과정으로 하였다. 일반메밀의 원료-탈피-찌기-볶음 단계의 루틴 함량은 원료에서의 22에서 볶음 알곡에서 7 mg/100 g로 유의하게 감소하였다. 쓴메밀의 원료-찌기-탈피-볶음 과정의 루틴 함량은 처음 원료에서 1,680에서 볶음의 835 mg/100 g으로 감소하였으나, 퀘세틴 함량은 0, 12, 36 및 32 mg/100 g으로 가공단계가 진행됨에 따라 증가하는 경향이였다. 이는 가공단계에서 찌고 볶는 열처리 과정에서 루틴을 분해하는 플라보놀-3-글루코사이다아제 효소(flavonol-3-glucosidase, f3g)에 의해 가수분해되어 루틴이 감소되고, 퀘세틴이 증가한 것으로 판단된다. 또한, 가공 마지막 볶음과정에서의 총 폴리페놀이 유의적으로 증가시키되었다. 따라서, 본 연구에서 도출된 결과는 가공단계별 메밀의 기능성 및 이용성에 대한 결과를 바탕으로 가루, 묵, 차, 국수, 새싹, 과자 등 가공제품의 소비확대에 중요한 기초자료로 활용될 것으로 기대된다.

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PC-0004

Effects of Pre-cropping with Rice Altenative Crops on Grain Yield and Flour Quality of Winter Wheat (*Triticum aestivum* L. 'Jokyung') on the Paddy Fields

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The grain yield and flour quality of winter wheat (*Triticum aestivum* L. 'Jokyung') were investigated in the paddy fields in which the double-cropping of wheat linked to rice (*Oryza sativa* L.) and its altenative crops [black bean (*Glycine max* (L.) Merr.), sesame (*Sesamum indicum* L.), and perilla (*Perilla frutescens* (L.) Britton)] was applied. In the soils in which black bean, sesame, and perilla as pre-crops were harvested, the soil pH was higher and the electrical conductivity was lower than in the rice pre-cropped soil. In addition, the available phosphate (Av. P_2O_5), and contents of Ca^{2+} and Mg^{2+} were higher and the Na^{+} contents were somewhat lower than in the rice pre-cropped soil. Winter wheat growth characteristics such as culm length, spike length, number of spikes and grains were generally favorable in the black bean pre-cropped soil. The grain yield of winter wheat increased in the black bean, sesame, and perilla pre-cropped soils by 100 kg/10a or more than in the rice pre-cropped soil. Furthermore, protein content and SDS-sedimentation value of the flour were higher, while amylose content was slightly lower, in the black bean, sesame, and perilla pre-cropped soils than in rice pre-cropped soil. The high protein content and SDS-sedimentation value, and low amylose content of flour suggest that rice altenative crops such as black bean, sesame, and perilla are favorable as pre-crops for winter wheat. Moreover, the application of these rice altenative crops as pre-crops in the crop rotation was expected to improve the grain yield and flour quality of wheat, due to agronomic advantages improving the physical and chemical properties of the paddy soil.

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PC-0005

Developing rice leaf rolling mutants by CRISPR/Cas9-mediated genome editing of homeodomain-leucine zipper (HD-ZIP) IV subfamily genes

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Targeted genome editing is a powerful tool for understanding gene function and for developing valuable agronomic traits in crops. We previously provide a pipeline to generate a mutant population of an elite Korean rice cultivar Samgwang by CRISPR/Cas9 gene editing technology targeting for the 2,535 transcription factors. So far, we generated 11,629 rice transformants, genotyped 2,261 T_0 seedlings through NGS analysis, and obtained 1,308 gene editing mutant lines targeting for 148 TFs which possess multiple phosphorylation site for SnRK2 kinase, a key player of ABA and stress signaling. Here, we report leaf rolling mutants generated by genome editing of HD-ZIP IV subfamily. The HD-ZIP IV proteins are structurally unique in that homeodomain is associated with a steroidogenic acute regulatory protein (StAR) related lipid transfer (START) domain. Generation of mutant alleles of the START domain by single guide RNA caused either abaxial or adaxial leaf-rolled phenotypes, suggesting that this domain is important to regulate leaf rolling in rice. We evaluated water use dynamics of these leaf rolling mutants using our phenotyping platform, DroughtSpotter. Our results implicate that the rolled-leaf ideotype will be useful to reduce water loss rate of rice plants under the heat and drought combined stress.

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PC-0006

Employing hyperspectral imaging for early detection of diseases in soybean

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Soybean is an important legume crop cultivated widely for food and feed purposes, it is also an inexpensive source of plant protein. Diseases caused by bacteria, fungi and viruses infections are a major concern in soybean cultivation. These diseases occurrence leads to severe yield loss, to prevent such losses, early detection of plant diseases and management before they are spared is very essential. Researchers are using different imaging systems such as (hyperspectral, red-green-blue, 3 dimensional, near-infrared, thermal and fluorescent methods) to detect plant diseases at the early stage of infection. Here, we review and discuss important bacterial, fungal and viral diseases that occur in soybean crops, different imaging systems used in plant disease detection, our lab research case study, artificial inoculation of bacterial, fungal and viral pathogens in soybean, and detection using the hyperspectral imaging system (HIS). In addition, comparison of traditional and hyperspectral disease detection methods and prospects. We believe that the ongoing research in our lab is the primary step towards the development and testing of multiple hyperspectral sensors and can also help with future breeding selection and modernization of plant disease phenotyping. Simultaneously, this approach can pave the way for disease management and assist the soybean farming community in reducing yield loss in the future.

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PC-0007

Phenotypic analysis of citrus male sterility in F1 population ('Citrus Kiyomi' x 'Citrus Sunki')

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In the citrus breeding, male-sterility is important traits to select seedless fruits in citrus breeding. More than half of individuals in population were negatively eliminated during the selection process due to fruits with seed formation. This study was conducted to investigate the genetic pattern of citrus male sterility. In this study, 'Citrus Kiyomi', seedless, were used as seed parents and 'Citrus Sunki', with seeds as pollen parents in 1994. Male sterility in F1 population were evaluated in 519 seedlings in 2020-2021. Flower buds of 473 individuals were collected in May in 2021 before anthesis and, the stamens were evaluated visually after removing petals. In results, normal yellow anthers were observed in 347 seedlings of F1 population but very small or white anthers in 126 seedlings of them. 347 seedlings of F1 population were categorized as male fertility and 126 seedlings as male sterility and it is supported that F1 segregation ratio was 3:1 by Chi-square test. It is suggested that there are two genes controlling MS and MF exist in F1 population and it is considered to be heterozygous of two genes in 'Sunki' and homozygous reccesive in 'Kiyomi'. These data will be used as basic data for the development of gene-based selection molecular markers controlling male sterility.

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PC-0008

작물 인공지능학습용 데이터 셋 구축 및 데이터 표준화 연구

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기후변화로 인한 자연재해들은 작물의 재배환경과 생리에 급격한 변화를 초래하여 경제적, 산업적으로 많은 피해를 주고 있으며, 이에 대한 대응책 마련이 필요하다. 최근 식물 표현체(phenomics) 기술은 이러한 문제를 해결하기 위한 융복합기술로 대두되고 있으며, 데이터 수집 및 분석에 대한 신뢰도와 활용성 향상을 위해 표현체 빅데이터의 생산, 분석, 품질관리, 활용 등 전과정의 표준화 방안이 요구된다. 최근 국립농업과학원은 과기부 인공지능 학습용 데이터 구축사업에서 벼와 콩 각 100품종에서 총 30만장의 전주기 영상데이터를 생산하였다. 한 식물체 당 총 20각도의 다각도 가시광(RGB) 영상을 획득하여 벼는 유묘기, 분얼형성기, 신장기, 개화기, 등숙기로, 콩은 유묘기, 신장기, 개화기, 꼬투리형성기, 종실비대기의 5단계로 영상표준을 설정하였다. 수집된 영상을 이용해 작물 기관(organ)별 주석달기(annotation)를 하고 발달시기, 품종 구분 등의 딥러닝 학습모델을 제시하였고 데이터 수집, 가공, 라벨링, 인공지능 모델개발까지 표준화 체계를 구축하였다.

표현체 분석 전과정을 매뉴얼과 절차에 따라 추진하며 기술기준과 경영기준에 따라 운영하여 한국표준과학연구원이 주관하는 국가참조표준데이터 센터 지정을 받고자 추진하고 있다. 이와 같은 노력을 바탕으로 표현체 데이터의 정확도와 신뢰도가 크게 향상될 것으로 보여지며, 아울러 산학연 네트워크의 기술 지원 및 작물디지털 피노타이핑 시스템 구축에도 기여할 것으로 기대된다.

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PC-0009

Variation in stomatal density within and between soybean leaves in different growth stages

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Stomata regulate the exchange of carbon and water vapor between leaves and the atmosphere, and indicate plants' adaptability to climate change. Stomatal abundance is modulated on plant surfaces in different environmental conditions, resulting in variation of stomatal numbers and patterns in mature leaves. Therefore, it is vital to identify and understand the variation within and between different leaves of soybean. We assessed the variation in stomatal density of the soybean cultivar Williams 82. Ninety epidermal sections were taken from one unifoliate leaf. There is significant variation among three different positions: tip, middle, and bottom within a single leaf. The variation in stomatal density emphasizes optimizing the number of epidermal sections from a single leaf. It will be sufficient to take five epidermal sections from each position and five microscopic images from each epidermal section from both the abaxial (lower) and adaxial (upper) leaf surfaces. With this procedure we identified the variation of stomatal density between different leaves across different growth stages. There was no significant variation between two leaves of VC stage and three leaflets of V1 to V4 growth stages. We found that the VC stage had the lowest stomatal density, whereas the V4 stage had the highest density. Our findings could prove to be an effective tool for evaluating stomatal density. It would assist us in analyzing disparities in physiological performance under adverse climatic conditions, phenotyping a large-scale population to identify the genetic factors responsible for stomatal density variations in soybean.

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PC-0010

Evaluation of morphological characters, phytochemical contents and antioxidant activities of amaranth leaves

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Amaranthus are widely cultivated as dietary crops, and members of the genus *Amaranthus* are promising medicine sources of antioxidants and phytochemical compounds. To explore the nutritional and medical values of *Amaranthus*, 289 accessions collected from various continents were investigated for their morphological characteristics, total polyphenol content (TPC), rutin content, and antioxidant activities of DPPH (2,2-diphenyl-1-picrylhydrazyl) and ABTS (2,2′-azino-bis-(3-ethylbenzothiazoline-6-sulfonic acid)). The results showed wide variations in the agriculture traits, phytochemical contents, and antioxidant activities amongst 289 accessions. The phytochemical content and antioxidant activities are positive correlated with leaf length, days to 50% flowering, days to 50% heading, and days to maturity. The average level of TPC, rutin, DPPH, and ABTS exhibit highest in the accessions which had yellow flower color, which hinting yellow-flowered genotypes had a high level of phytochemical contents and antioxidant activities in amaranth leaves. The 289 accessions were clustered into three groups according to their morphological characteristics, phytochemical, and antioxidant activities. Moreover, distinctive aggregation was observed among *Amaranthus* species based on PCA analysis. Our findings provide potential information of agriculture traits and genetic variation profiles for amaranth breeding.

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PC-0011

YOLO5를 이용한 딥러닝 기반 종자 표현형 측정 시스템 구축

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높은 발아율과 발아세를 가진 고활력의 종자는 다양한 농업 환경에서 안정적인 생산량을 보장한다. 기존의 연구에 따르면 종자의 발아율은 종자의 크기에 비례해 증가한다. 종자의 크기를 키우기 위해 기존 육종 기술들에 새로운 기술들을 응용하는 연구가 진행되고 있다. 종자의 크기를 측정하는 방법은 국제표준인 UPOV기준을 따라 사람에 의한 측정방식으로 많은 시간과 노동력이 요구된다. 또한, 측정하는 연구자에 따라 주관적인 요소가 포함되어 결과가 다르게 도출될 수 있다. 따라서, 정량적이며 객관적으로 종자를 평가할 수 있는 분석 방법이 필요하다. 이 시스템은 YOLO5 모델을 활용하여 종자를 학습한 딥러닝 시스템을 웹 서버로 이용하여 스트리밍 영상에서 개별 종자 이미지를 탐색하고, 실시간으로 종자의 정량적인 크기를 측정한다. 모델 학습을 위해 콩, 벼, 팥, 녹두, 보리 5개 작물 각 200품종, 품종당 100개체, 총 10만개 영상을 활용하였고, 학습데이터의 인식률을 높이기 위하여 각 품종 개별 종자 영상을 회전과 크기 조절 방법 등으로 데이터를 증강하였다. 딥러닝 학습 결과 오차율과 정확도는 loss와 mAP를 이용해 검정하였으며, class loss 0.001, object loss 0.07, box loss는 0.006의 loss와 mAP@.5에서 99%, mAP@[.5:.95]에서 87%의 정확도를 가진 학습 결과가 획득되었다. 구축된 디지털 영상을 활용한 측정 시스템이 결과의 객관성을 높이고 딥러닝 방법을 이용해 높은 신뢰성을 가진 실시간 분석이 가능했으므로, 우리는 해당 시스템이 추후 디지털육종 기술 개발 및 연구에 있어 많은 도움이 될 것으로 기대한다.

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PC-0012

Pre-study for early detection of *Fusarium fujikuroi* via fluorescence imaging method

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Rice (*Oryza sativa*) agricultural industry confronts *Fusarium fujikuroi* well known as Bakanae disease, which derives massive damages on annual yields. This pathogen secretes gibberellin that stimulates elongation at vegetative stages, then plants eventually wither in 10~14 days. The disease control must focus on the seedling and vegetative stages due to its early infection. However, early identification before symptom occurrence has some difficulties such as technical, time, or financial issues. Therefore, we applied fluorescence digital image to investigate accessible early detection method of disease between the first and 15 days after seeding (DAS) using *F. fujikuroi* inoculated and non-inoculated, susceptible 'Junam' and resistant 'Nampyung' rice cultivars. Quantified fluorescence indicators (F_0, F_p, F_t_Lss, F_v, *QY_max*, and R_{fd}_Lss) were calculated using the images acquired from DAS 1 to 17 in an interval of 2 days. Analysis showed no differences between the treatment and control groups of 'Nampyung' ($P < 0.05$), while the 'Junam' showed significant differences between the treatment and control groups in 5 indicators except the *Ft_Lss* of DAS 7 ($P = 0.576$). All indicators of treated 'Junam' 10 ~ 20% increased at DAS 7 to 9, and then continuously decreased, while 'Nampyung' showed slight increase (< 5%) or decrease at the same date. Although the fluorescence responses were not fully identified in this research, results may allow precise explanation for the responses of susceptible host plants against *F. fujikuroi* in our further studies. We expect our suggestion will be a helpful tool for developing novel pathogen control methods.

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PC-0013

인공지능을 사용한 콩잎 검출 기술에 관한 연구

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콩잎 생장 분석은 콩잎의 성장 상태를 주기적으로 확인하여 초엽, 제1복엽, 제2복엽에서 제5복엽까지 잎의 생성 시기를 기록하고 종자별로 잎 생성 시기, 개화 시기 등을 비교하는 과정이다. 초엽에서 제2복엽까지 전개 시기를 파악하면 다음 복엽의 전개 시기를 예측할 수 있다. 이 점을 이용하여 종자별 생장 차이를 발견할 수 있고 종자별 생장에 적합한 기후, 특성들을 파악할 수 있다. 기존 콩잎 관련 연구로는 윗쪽(Top-view)에서 촬영한 영상에서 식물체와 배경을 분리하는 (Segmentation) 기법과 콩잎 영상으로 질병을 분석하는 기법 등이 있다. 본 논문에서는 신경망(Neural Network) YOLOv5를 사용하여 종자별 식물체를 시계열로 촬영한 영상에서 콩잎을 검출하는 실험을 진행하였다. 신경망(Neural Network) 학습시 여러 식물체 영상을 사용하여 종자별 생장 특성에 관계없이 콩잎을 검출하고 신뢰도(Confidence-threshold) 기준치를 0.7 이상으로 설정하여 정밀도(Precision) 95.0%, 재현율 (Recall) 75.9%, 정확도(Accuracy) 75.2%의 결과를 얻었다. 본 논문에서 제시하는 콩잎 검출 기법으로 식물체의 시계열 데이터 영상 분석을 통하여 콩잎 생장 분석을 위한 콩잎 검출이 가능하다. 추가적으로 콩잎 검출용 신경망(Neural Network) 모델의 성능을 향상시키는 연구와 콩잎 생장 분석 연구과정에 본 논문의 기법을 적용시켜 엽 생성 시기와 개화기를 예측하는 연구를 병행하여 진행할 것이다.

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PC-0014

주요 RGB 컬러 지수를 이용한 밀 군락 피복도 및 엽면적 지수 평가

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전라북도 완주군 이서면 혁신로 181 국립식량과학원

작물에 있어서 군락 피복도와 엽면적 지수는 수량과 연관되는 주요 지표 중의 하나이다. 본 연구는 국립식량과학원 (35° 84' 34" N, 127° 04' 84" E) 포장에서 금강 밀 출수 24일 전부터 출수 25일 후까지 군락 피복도, 군락 엽면적 지수 및 이미지 촬영을 하였다.

군락 피복 측정은 라인 퀀텀 센서와 포인트 퀀텀 센서를 사용하였다. 엽면적 지수는 군락 엽면적기를 사용하였다. RGB 이미지 획득은 RGB 카메라를 약 2.0m 높이에서 수직 삼각대로 촬영하였다. 화이트 밸런스는 카메라에서 사용자 지정으로 노출 프로파일 대상 판을 사용하였고, 18%의 반사율로 평균 노출값을 구하기 위해 사용하였다. 카메라의 조리갯값은 f/4로 셔터 속도 우선으로 1/60초, 1/320초, 1/640초 노출 값을 설정하였고 ISO는 수동으로 설정하여 이미지를 취득하였다. 본 연구에서 사용된 RGB컬러 지수는 ExG, ExR, GLI, NGRDI, ExGR, MExG, MExG-CIVE 이었다.

본 연구 결과 군락 피복과 ExG는 부의 상관으로 1/60s는 R^2=-0.713이고, 1/320s는 R^2=-0.729이었고, 1/640s는 R^2=-0.642이었다. MExG에서는 정의 상관으로 1/60s에서는 R^2=0.975이고 1/320s에서는 R^2=0.982, R^2=1/640s에서는 0.981이었다. 그리고 ExR, GLI NGRDI, MExG, MExG-CIVE는 셔터 속도에 따라 R^2=0.950~0.970 범위를 보였다. 한편 군락 엽면적 지수와 군락 피복률과는 정의 상관(R^2=0.935)을 보였다.

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PC-0015

밀 이모작 작부체계에 따른 밀 품종별 생리생태 변화 및 품질분석

최지수*, 오성환, 서종호, 오서영, 김태희

경상남도 밀양시 점필재로 20 국립식량과학원 남부작물부

국내 제빵시장 규모가 꾸준히 증가하면서 고품질 제빵용 밀 요구도가 증가하고 있지만 밀 수요량에 비해 자급률은 1% 정도로 낮다. 우리나라 밀은 주로 전라도, 경남지역 등지에서 벼와의 이모작 재배법에 의해 생산되고 있으며 일부 콩과의 이모작 체계로도 생산되고 있으나 작부체계가 밀 생리생태 및 품질에 어떠한 영향을 끼치는지에 대한 연구는 국내에서 거의 진행되지 않았다. 하작물 재배 전 밀의 생리생태적 특성 및 품질과 하작물로 벼, 콩, 옥수수를 심은 후의 특성을 조사하여 고품질의 밀을 생산할 수 있는 작부체계 선정을 위한 자료로 활용하고자 한다.

시험은 국립식량과학원 남부작물부 포장에서 수행하였으며, 밀 품종으로 금강과 조경, 벼는 해담쌀, 콩은 대찬, 옥수수는 광평옥 품종을 사용하였다. 시비량 등은 표준재배법에 따랐으며, 생리생태적 특성으로 월동 후 생육재생기와 성숙기 생육상황 등을 조사하였고, 밀 품질로 밀가루 특성, 전분 및 반죽특성, 신속점도측정계(RVA)를 이용한 가공적성 등을 분석하였다.

하작물 재배전후 밀 생육상황 조사결과 조경과 금강 모두 하작물을 재배하기 전보다 생육재생기가 하루 늦춰졌으나, 밀양지역 조경밀의 생육재생기와 일치하였으며 작부체계 및 품종간 차이는 없었고, 초장과 경수도 유의한 차이를 보이지 않았다. 성숙기 생육상황에서 출수기와 수장, 수수, 1수립수 역시 유의한 차이가 없었다. 간장은 이모작 전에는 조경이 금강보다 크게 나타났으나, 후에 금강이 더 큰 수치를 나타냈으므로 연차간 변이를 관찰할 예정이다. 하작물 재배 전 밀 품질 특성으로 금강이 조경보다 제분율, 단백질, 침전가, 글루텐이 높고 경도가 컸으며, 조경이 금강보다 회분함량이 많았다. 또한 금강이 아밀로스함량과 폴링넘버 수치가 컸고, 손상전분은 조경이 더 많았다. 반죽특성을 비교해 보았을 때 금강의 반죽시간이 더 짧고 흡수율과 반죽안정도가 더 높았다. 신속점도측정계를 이용한 조사로 최고, 최저, 최종점도는 금강이 조경보다 높았고, peak에 이르는 시간은 조경이 더 빨랐으며, 호화온도는 조경이 더 낮은 특성을 보였다. 하작물 재배 후 밀 품질 특성을 조사하여 재배 전과의 비교를 수행할 예정이다.

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PC-0016

RGB영상 정보를 이용한 옥수수 종자 특성 분석

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옥수수는 3대 곡물 중의 하나로 식품, 에너지,산업소재,제약원료등 다양한 소재로 이용되고 있다. 우수한 품종의 옥수수를 육성하기 위해 종자의 색상, 크기, 모양 등과 같은 질적 형질 특성 조사를 함에 있어 관행적인 측정 방법에 주로 의존하여 정밀하고 체계적인 데이터를 도출하기 어려운 실정이며 대량의 종자를 정밀하고 신속하게 처리하는데 한계가 있다. 최근 디지털 영상기술을 기반으로 한 광학 이미징 기술과 분광 이미징 기술이 개발되어 작물 표현체 분석에 광범위하게 활용되고 있다. 이 연구에서는 옥수수 종자의 표현형 특성을 분석하기 위해 디지털 이미징 및 국립농업과학원 농업생명자원부에서 개발한 종자 표현형 분석 프로그램을 적용하였다. 옥수수 육성 계통인 KW7(waxy)와 KS5(Field)의 교배에 의한 F7:8세대RILs(recombinant inbred line)립질 82개 계통 8,100 립을 디지털 카메라로 촬영하여 획득한 RGB 영상과 YUV의 색차정보를 이용하여 배경에서 종자 이미지를 분리한 후 면적(area), 둘레(perimeter), 장폭(seed length), 단폭(seed width), 원형율(roundness), 둥근정도(circularity), 표면질감(solidity) 등의 종자 표현형 분석 지표와 색상분석으로 RGB 영상의 색상 값을 추출하여 특성을 분석했다. KW7의 RGB 색상 대표값은 R62 G59 B87, KS5는 R210 G169 B101으로 RIL은 R201 G183 B153으로 추출되었다. 종자의 폭은 프로그램으로 추출된 값과 실측 값의 상관관계 분석 결과 0.95 이상으로 높은 연관성을 확인하였다. 이와같이 확보한 분석 정보를 기반으로 DB를 구축함으로써 객관적이고 효율적인 운영체계로 시간과 노력을 단축하여 우수한 육종 소재를 선발하는데 중요한 역할을 할 것으로 기대된다.

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PC-0017

Toward High Throughput Field Phenotyping (HTFP)

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High throughput phenotyping platform (HTTP) is one of very effective tools for plant phenotyping such as image acquisition and analysis from a large number of plant samples. Also, numerous traits of interest were studied with HTTP and revealed new insight of the traits. However, the insights could not readily applied in a breeding scheme or physiology study in open field due to limited environmental interaction of plant in a glasshouse. Therefore, high throughput field phenotyping (HTFP) was essential tool for plant phenomics. There are number of HTFP tools for study traits of interest and proximal sensing such as fixed tower sensor or closed image acquisition from a drone provided optimal images for plant phenomics. HTFP tools such as terrestrial laser scanner (TLS) and images from drone were utilized for comparison of two rice cultivars over eight weeks. This result showed that canopy structure derived from the TLS was statistical different in last three weeks (p=0.05). Also, canopy coverage area derived from a drone showed difference between two cultivars over time. The result indicated that feasibility utilized HTFP for growth pattern of a crop in open field. In conclusion, the HTFP was emerging field in smart agriculture and it showed possibilities to apply for study of plant physiology and plant breeding in future.

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PC-0018

남부지역 논 토양에 적합한 콩(*Glycine max* (L.) Merrill) 품종 선발 및 개화기 수분 스트레스하에서 광합성의 변화

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콩(*Glycine max* (L.) Merrill)은 전세계적으로 중요한 식량자원 중에 하나로 약 40%의 단백질과 20%의 지질로 구성되어 있으며, 우리나라에서도 용도에 따라 여러 품종들이 생산 및 소비가 되고 있다. 본 연구에서는 남부지역 논 토양에 적합한 콩 품종을 선발하고, 개화기 수분 스트레스 하에서 PSII의 광화학적 활성과 광합성적 특성을 살펴보았다. 콩 5품종(대원, 대찬, 선유, 선풍, 청자3호)을 대상으로 논 재배 시, 경장은 청자3호>대원>선풍>대찬>선유 순으로 작았고, 분지 수는 선유, 청자3호, 대찬은 3-4개, 대원과 선풍은 3개 미만으로 나타났다. 수량구성요소에서 주당협수는 대찬이 64.3개로 가장 많았으며, 3품종은 44~47개의 범위에 분포하였고, 청자3호가 33.7개로 적었다. 수량은 대원, 대찬과 선유가 480kg/10a 이상으로 많았으며, 청자3호는 306kg/10a로 적고 다른 품종들에 비하여 탈립도 많이 되었다. 개화기 수분스트레스 하에서 CO_2 고정률은 충분히 관수한 식물체와 50% 관수하였을 때에는 각각 24.6 μmol・m^{-2}・s^{-1}와 22.9 μmol・m^{-2}・s^{-1}로 높았으나, 수분스트레스를 받은 식물에서는 3.6 μmol・m^{-2}・s^{-1}로 크게 낮아졌다. 반면에 호흡률은 수분스트레스를 받은 식물에서 다소 높았으며, 기공전도와 증산률은 감소하였다. 광계II의 최대 광화학적효율(F_v/F_m)은 수분 스트레스를 받은 식물에서 감소하였으며, 이때 F_o와 F_m은 증가하는 것으로 나타났다. 또한 광계II의 전자전달 활성도 수분 스트레스 하에서는 크게 낮았으며, 비광화학적으로 소멸되는 에너지가 많은 것으로 나타났다. 개체당 꼬투리 수와 종자 무게는 수분 스트레스에 의해 크게 감소하였다. 이러한 결과는 개화기에서의 수분 스트레스가 콩의 생산성을 감소시키는 요인으로 작용할 수 있음을 나타내주고 있다. 논 재배시 콩의 안정적인 생산을 위해서는 논 토양 특성상 습해 피해뿐만 아니라 건조를 포함한 복합적인 환경 스트레스에 강한 품종을 선발하여 육성하거나 피해를 최소화할 수 있는 재배기술이 확립되어야 할 것으로 보인다.

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PC-0019

딥 러닝 기반의 Semantic Segmetation을 이용한 옥수수 포장의 잡초 밀도 평가

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잡초는 작물과 경쟁적 경합 때문에 작물의 생산량을 크게 줄이는 원인 중 하나이고, 그리고 이를 방제하는 것은 농작물의 재배에 있어서 매우 중요하다. 또한 무인 항공 기술의 발달로 무인 항공 제초제의 살포는 노동력 절감 및 경제적 이점이 있지만 과도한 제초제의 사용은 직간접적으로 작물의 약해와 환경문제를 일으킨다. 이러한 점에서 항공 제초 방제에서 제초제의 부분적 살포를 위한 잡초 밀도의 평가가 요구된다. 본 연구에서는 2021년 5월 26일부터 6월 7일까지 UVA를 사용해 약 10m 높이에서 촬영된 옥수수 포장 RGB 데이터를 수집하고 Sematic segmantation의 대표적인 모델인 DeeplabV3+와 U-net을 사용하여 이를 평가하였다. 수집한 데이터는 옥수수(Object), 배경(background)의 Binary 이미지로 이진 분류하였다. 4388개의 학습데이터와 821개의 검증데이터를 옥수수 검출을 위한 학습에 사용하였고 278개의 평가 데이터는 학습과는 독립적으로 평가에 사용되었다. 학습에 사용된 segmentation model은 DeeplabV3+, U-net을 사용하였다. 특히 DeepLabV3+ semantic segmentation 모델은 옵티마이저는 Adam, 손실 함수는 Bionary Crossentropy 그리고 0.00001의 학습률의 조건에서 98.39%의 픽셀 정확도와 81.77%의 mIoU score를 나타내었다. 이러한 학습 결과를 바탕으로 배경과 토양으로부터 녹색 영역만을 분리할 수 있는 지수(ExGR)에서 모델이 예측한 옥수수의 픽셀을 제외하는 것으로 잡초의 밀도를 평가하였다. 이러한 딥 러닝 기반의 Semantic segmentation 모델에서 작물 포장의 잡초 밀도 평가는 무인 항공기를 이용한 제초제의 부분적 방제에 대한 가능성을 제시한다.

사사: 본 연구는 농촌진흥청 연구사업(세부과제명: 콩, 옥수수 재배 시 스트레스 발생 시기 디지털영상을 활용한 영상 해석 기술 개발, PJ015103012022)의 지원에 의해 이루어진 것입니다.

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PC-0020

ToF 카메라를 이용한 옥수수 생육 측정 방법에 관한 연구

박혁진[1,2], 상완규[1], 반호영[1], 권동원[1], 백재경[1], 조정일[1], 서명철[1*]

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최근 빅 데이터를 기반으로 한 디지털 농업에 관한 관심이 증가하는 가운데, 작물의 기본적인 생육 특성을 예측 또는 모델링 하기 위해서는 기존의 수기 측정 방식이 아닌 디지털 데이터화 하는 것은 필요한 과정 중 하나이다. 또한 작물의 초장, 엽면적 그리고 임관층의 변화는 작물의 생산량을 예측하는데 중요한 지표들이지만, 측정에 사용하고 있는 기존의 방식들은 작물과 접촉하거나 파괴적인 방법으로 측정되고, 노동력 또한 많이 투입 되어야 한다. 드론을 통한 촬영, 2차원 영상을 이용한 측정 방법은 작물의 군락이 차지하는 면적은 측정할 수 있지만 작물의 초장과 같은 높이에 대한 데이터를 얻지 못하고, 높이의 데이터를 얻기 위한 측면카메라는 반대로 전체 면적에서 작물 군락이 차지하는 면적에 대한 데이터를 얻지 못하는 점이 존재한다. 3차원 깊이 카메라(ToF 카메라)는 적외선이 반사되어 도달하는 시간으로 3차원의 깊이 영상을 찍는 것으로 기존의 2차원 영상과는 다른 여러 가지 지표들을 하나의 데이터에서 비교하고 측정할 수 있다. 본 연구에서는 Microsoft Corporation의 Azure kinect를 이용하여 약 3m 높이에서 수평으로 옥수수 밭의 3차원 영상 데이터를 6월 8일부터 7월 26일까지 시계열로 획득하고 프로그래밍 언어인 python용 데이터 분석을 위한 도구인 pandas, 이미지 분석을 위해 opencv2를 사용해서 옥수수 군락의 초장, 임관층, 엽면적 등을 분석하고 평가하였다. ToF 카메라로 촬영한 옥수수 포장에서의 상위 1%와 상위 10%의 cloud point의 좌표 값의 높이를 측정하여, 옥수수의 생육 측정의 자동화를 위한 프로토콜을 평가하였고, 옥수수의 초장에서 수동으로 측정한 수치와 상위 포인트 비율에 따른 자동 측정치를 비교했을 때 6개의 포장의 평균 R^2의 값이 0.9870로 높은 상관관계를 나타내었다. 또한 3차원 데이터의 옥수수 군락의 임관층의 변화와 2차원 영상 데이터에서의 엽면적을 시계열로 분석하였다. 3차원 깊이 카메라를 이용한 작물의 시계열 생육 평가는 군집의 광합성 효율과 biomass 등을 모델링 하는 것이 가능하다고 생각된다.

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PC-0021

Construction of Deep Learning-Based Disease Detection Model in Plants

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Construction of deep learning-based disease detection model using images of diseased-healthy plant pairs and a CNN algorithm consisting of five pre-trained models. The disease detection model consists of three step classification models, crop classification, disease detection, and disease classification. In the validation test, the disease detection model classified crops and disease types with high accuracy (97.09%). The low accuracy of non-model crops was improved by adding these crops to the training dataset for model construction. Also, cropped images allow higher accuracy with more obvious disease symptoms or lesion patterns. The accuracy of the classification model depended on the depth, quality, and variety of image data for training during model construction. Thus, to apply this classification model, more high quality images of various crops are required for model construction, as well as an approach for developing a platform to apply this model to smart farming.

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PC-0022

Genome-wide association study (GWAS) identified genes controlling grain size using manual and image-based phenotyping in North Korean rice

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Rice is one of the most important food crops in the world. Seed size is a major factor in rice production. 190 North Korean varieties which have not been studied were used to identify new genetic factors related to the seed size traits. To facilitate phenotyping speed and accuracy, image-based phenotyping (IBP) was also applied with manual phenotyping (MP). Seed size related traits including seed length, seed width and seed surface area were investigated in Anseong 18 and Anseong 19 populations. IBP methods were investigated using Image J using a macro developed by the Rural Development Administration, grain scan of CSIRO, and KR image of the National Seed Resources. GWAS analysis were performed using mixed linear models (MLM). A total of 9,330,794 SNPs was identified, and only 1,048,576 SNPs that have the high quality with MAF > 0.05 genotypes were used in the GWAS. GWAS analysis for seed morphology using both MP and IBP methods identified several known genes (*BRD2*, *GS3*, *OsBZR1*, *OsALDH2B*, *GS6*, and *OsAGSW1*) and novel genes associated with seed morphology. IBP and MP produced mostly common significant loci for the seed size traits, and some of the SNP showed higher *p* value in IBP than that of MP, indicating that IBP method would be a useful tool enhancing the phenotyping efficiency. Further haplotyping and candidate genes analysis are currently in progress.

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PC-0023

Agricultural and fatty acid characteristics in doubled haploid (DH) population derived from microspore of rapeseed (*Brassica napus* L.) F_1 generation

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The present study was conducted to obtain agricultural traits data on a DH population derived from microspore culture of rapeseed F_1 generation, developed from a cross between 'EMS26' line with high oleic acid and 'J8634-B-30' line. Data for agricultural traits and seed oil quality was collected from the sixty-seven DH population, including plant size, flowering time, plant and pod growth and composition of unsaturated fatty acids etc. Wide range of plant leaf size were measured after wintering with the length of 6.0 to 17.7 cm and the width of 4.5 to 9.5 cm. The agricultural traits investigated at maturity time also showed wide changes of plant height (63.0 to 134.4 cm), panicle length (11.3 to 18.0 cm), number of 1st branch (4.3 to 8.7), number of pods per plant (23 to 75), pod length (4.3 to 7.5 cm), pod width (3.7 to 6.5 cm), and number of seeds per pod (19.6 to 34.0). The flowering time of DH population was observed in April, and the earliest lines was 'DH43' on April 8. As a result of seed oil quality analysis, the average oleic acid composition of the DH population was 72.3% and linolenic acid of them was 6.2% and linoleic acid of them was 8.0%. The DH population and agricultural traits data can be utilized for future QTL analysis as well as for a breeding for varieties with high oleic acid concentration.

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PC-0024

Application of Object Detection based on Deep Learning Model for Pest Behavior Patterns in Soybean (*Glycine max* (L.) Merr.)

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Soybean (*Glycine max* (L.) Merr.) is a representative food resource. To preserve the integrity of soybean, it is necessary to protect soybean yield and seed quality from pests and diseases. The yield of soybeans can be reduced by *Riptortus pedestris* primarily, recorded as causing greatest loss. Soybean pests cause not only direct yield reduction, but also negative impacts on plant growth. Therefore, it is important to reduce crop losses by analyzing agronomic characteristics of soybean and insect pests. Traditionally, the diagnosis of agronomic traits has been carried out through the human own eyes. However, since human vision is subjective and temporary, it spends a lot of time, required a specialist, and had the inconvenience of being labor-intensive. Therefore, in this study, the behavior patterns of *Riptortus pedestris* and agronomic traits of soybean seed were detected through the sight of artificial intelligence. Time series image data were used to analyze the movement patterns of *Riptortus pedestris* according to pheromone treatment. The manufactured model will enable to identify the number of *R. pedestris* in the field, and it could be very effective tool for insect forecasting in the early stage of pest outbreaks in crop production.

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PC-0025

Generic Diversity of Volatile Organic Compounds in Brown Rice of 157 Cultivars Bred in South Korea

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The edible quality and market price of rice are significantly affected by its flavor property, which is determined by the presence and combination of diverse volatiles organic compounds in rice. In this study, the profiles of volatiles in brown rice of 157 Korean bred varieties were investigated by using headspace solid phase microextraction (HS-SPME) coupled with gas chromatography-mass spectrometer (GC-MS). Total 161 volatiles consisting of 88 odor-active and 72 odor-inactive were identified, and among odor-active volatiles aldehydes (21.6%) and hydrocarbons (23.9%) were more frequently observed chemical groups. The five major volatiles commonly observed in all 157 varieties and their compositional percentage as determined by their relative peak area were butylated hydroxytoluene (23.98%), nonanal (8.36%), methyl salicylate (6.80%), D-limonene (5.07%), and 1-octanol (2.88%). In contrast, eucalyptol and 2-methylbutanal were volatiles rarely found in rice samples. Based on the presence of 2-acetyl-1-pyrroline (2AP), six varieties were proved as fragrant rice. Partial least squares discriminant analysis (PLS-DA) revealed that volatile profiles may effectively differentiate indica and japonica rice ecotypes. All these results showed diversity of volatiles in 157 Korean bred rice varieties.

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PC-0026

Optimization of Cooking Rice in a Headspace-vial coupled with Solid Phase Microextraction for Qualitative Profiling of Volatiles in Cooked Rice

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Qualitative profiling and quantitative determination of volatiles are critical processes for understanding the flavor-relative property of cooked rice. For a more rapid and accurate characterization of 32 flavor-determining volatiles in cooked rice, experimental conditions to cook rice directly in a headspace (HS) vial prior to extracting volatiles with a solid phase microextraction (SPME) and subsequent injection into a GC/MS were optimized. For the mixing ratio of rice weight to water, 1:1 (g/mL) resulted in the highest peak area of identified volatiles compared to ratios of 0.5:1, 0.8:1, and 1.5:1. Besides, some peaks such as 2,4-nonadienal, (E,E)- and 2,4-decadienal, (E,E)- could be detected only at 1:1 ratio conditions. Increment in cooking temperature resulted in a higher peak area of rice volatiles in that cooking rice at 90 ° C increased the total peak area by 60% compared to 60 ° C. Besides, some volatiles such as methyl nonanoate could be detected only in rice cooked at 90 ° C. The finalized optimal conditions are as followings; 1.0 g of white rice and 1 mL of distilled water are placed in an HS-vial, which is heated at 90°C for 15 min in a heating block for cooking and then directly used for SPME extraction and subsequent injection into a GC-MS. Compared to a commercial rice cooker, optimized single-step rice cooking in HS-vial coupled with direct SPME extraction increased the peak area of most target volatiles by 50%. These results strongly support the practicality and efficiency of the developed rapid cooking method for flavor-related studies of cooked rice.

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PC-0027

Rapid Discrimination of *Brassica napus* Varieties using Visible and Near-infrared (Vis-NIR) Spectroscopy

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Brassica napus is an oilseed plant that is mostly used to produce edible oils, industrial oils, modified lipids and biofuels. The number of varieties/cultivars is high for the species owing to their higher level of economic use. The aim of this study is to assess the use of visible near infrared (Vis-NIR) spectroscopy in combination with multiple chemometric methods that have been explored for the discrimination of eight *Brassica napus* varieties in Korea. In this study the spectra from leaves of the eight *B. napus* varieties were measured in the Vis-NIR spectra in the range of 325-1075 nm with a stepping of 1.5 nm in reflectance mode. The spectral data were preprocessed with three different preprocessing methods and eight different chemometric analyses were used for the effective discrimination. After the outlier detection, the samples were split into two sets, one serving as calibration set and remaining one serving as a validation set. When using multiple preprocessing and chemometric methods used for the discrimination, the maximum classification accuracy was witnessed in the combination of standard normal variate and support vector machine up to 98.2%. The use of Savitzky-Golay filter smoothing as a preprocessing method had the best and most satisfactory discrimination of all other chemometric methods. The results suggest that the use of handheld Vis-NIR spectroscopy in combination with chemometric approaches can be used as an effective toll for the discrimination of *B. napus* varieties in the field.

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PC-0028

Discrimination of Transgenic Canola (*Brassica napus* L.) and their Hybrids with *B. rapa* using Vis-NIR Spectroscopy and Machine Learning Methods

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In recent years, the rapid development of genetically modified (GM) technology has raised concerns about the safety of GM crops and foods for human health and the ecological environment. Gene flow from GM crops to other crops, especially in the Brassicaceae family, might pose a threat to the environment due to their weediness. Hence, finding reliable, quick, and low-cost methods to detect and monitor the presence of GM crops and crop products is important. In this study, we used visible near-infrared (Vis-NIR) spectroscopy for the effective discrimination of GM and non-GM *Brassica napus, B. rapa*, and F1 hybrids (*B. rapa* X GM *B. napus*). Initially, Vis-NIR spectra were collected from the plants, and the spectra were preprocessed. A combination of different preprocessing methods and various modeling approaches was used for effective discrimination. Among the different combinations, the Savitzky-Golay and Support Vector Machine combination was found to be an optimal model in the discrimination of GM, non-GM, and hybrid plants with the highest accuracy rate (100%). The use of a Convolutional Neural Network with Normalization resulted 98.9%. Later, phenolic acid concentration among the different plants was assessed using GC-MS analysis. Partial least squares regression analysis of Vis-NIR spectra and biochemical characteristics showed significant correlations in their respective changes. The results showed that handheld Vis-NIR spectroscopy combined with chemometric analyses could be used for the effective discrimination of GM and non-GM *B. napus, B. rapa*, and F1 hybrids. Biochemical composition analysis can also be combined with the Vis-NIR spectra for efficient discrimination.

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PC-0029

Vis-NIR Spectroscopy and Machine Learning Methods for the Discrimination of Transgenic *Brassica napus* L. and Their Hybrids with *B. juncea*

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The rapid advancement of genetically modified (GM) technology over the years has raised concerns about the safety of GM crops and foods for human health and the environment. Gene flow from GM crops may be a threat to the environment. Therefore, it is critical to develop reliable, rapid, and low-cost technologies for detecting and monitoring the presence of GM crops and crop products. Here, we used visible near-infrared (Vis-NIR) spectroscopy to distinguish between GM and non-GM *Brassica napus*, *B. juncea*, and F1 hybrids (*B. juncea* X GM *B. napus*). The Vis-NIR spectra were preprocessed with different preprocessing methods, namely normalization, standard normal variate, and Savitzky-Golay. Both raw and preprocessed spectra were used in combination with eight different chemometric methods for the effective discrimination of GM and non-GM plants. The standard normal variate and support vector machine combination was determined to be the most accurate model in the discrimination of GM, non-GM, and hybrid plants among the many combinations (99.4%). The use of deep learning in combination with Savitzky-Golay resulted in 99.1% classification accuracy. According to the findings, it is concluded that handheld Vis-NIR spectroscopy combined with chemometric analyses could be used to distinguish between GM and non-GM *B. napus*, *B. juncea*, and F1 hybrids.

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PC-0030

Identification of *Amaranthus* Species Using Visible-Near-Infrared (Vis-NIR) Spectroscopy and Machine Learning Methods

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The feasibility of rapid and non-destructive classification of six different *Amaranthus* species was investigated using visible-near-infrared (Vis-NIR) spectra coupled with chemometric approaches. The focus of this research would be to use a handheld spectrometer in the field to classify six *Amaranthus* sp. in different geographical regions of South Korea. Spectra were obtained from the adaxial side of the leaves at 1.5 nm intervals in the Vis-NIR spectral range between 400 and 1075 nm. The obtained spectra were assessed with four different preprocessing methods in order to detect the optimum preprocessing method with high classification accuracy. Preprocessed spectra of six *Amaranthus* sp. were used as input for the machine learning-based chemometric analysis. All the classification results were validated using cross-validation to produce robust estimates of classification accuracies. The different combinations of preprocessing and modeling were shown to have a classification accuracy of between 71% and 99.7% after the cross-validation. The combination of Savitzky-Golay preprocessing and Support vector machine showed a maximum mean classification accuracy of 99.7% for the discrimination of *Amaranthus* sp. Considering the high number of spectra involved in this study, the growth stage of the plants, varying measurement locations, and the scanning position of leaves on the plant are all important. We conclude that Vis-NIR spectroscopy, in combination with appropriate preprocessing and machine learning methods, may be used in the field to effectively classify *Amaranthus* sp. for the effective management of the weedy species and/or for monitoring their food applications.

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PD-0001

Radiosensitivity and the influence of gamma-rays irradiation in wheat according to different exposure time

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Ionizing radiation is a commonly used approach to generate useful mutations in plants, although it can cause direct or indirect damage to the plants. Gamma-rays have been extensively used in mutation breeding to induce useful mutants because of their availability and penetration power. The aim of this study was to investigate the biological response on wheat to different gamma irradiation doses and exposure times. We irradiated Keumgang wheat seeds with 100-, 300-, and 500-Gy gamma-rays either for short (8 h) or long (2 weeks) exposure times, resulting in equal final dosages but different dose rates per hour. We investigated oxidative stress, seed percentage germination, plant growth, chlorophyll content, antioxidant enzyme activity, and gene expression levels to compare how gamma irradiation affects the plants depending on the irradiation dose and exposure time. We recorded that significantly more ESR radicals were generated upon long-term exposure to gamma irradiation compared with those upon short-term exposure of the same dosage. Short-term exposure resulted in slightly shorter shoots and roots compared with the controls, whereas long-term exposure led to severe growth inhibition. Antioxidant- and DNA repair-related gene expressions significantly decreased upon long-term gamma-ray exposure, also leading to higher radiosensitivity than short-term exposure. This study provides direct information on various effects on wheat mutagenesis through the comparison of short- and long-term irradiation. These results could be used to select the appropriate gamma irradiation dose to induce mutations in wheat for mutation breeding.

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PD-0002

Multigene Engineering for High Production of Hydroxy Fatty Acid in Oil Crops

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Castor (*Ricinus communis* L.) seeds contain unusual fatty acid, hydroxy fatty acid (HFA) used as a chemical feedstock for numerous industrial products. Castor cultivation is limited by the potent toxin ricin in its seeds and other poor agronomic traits, so it is advantageous to develop a suitable HFA-producing crop. Significant research efforts have been made to produce HFA in model Arabidopsis, but the level of HFA produced in transgenic Arabidopsis is much less than the level found in castor seeds which produce 90% HFA in seed oil. We designed a transformation construct that allowed co-expression of five essential castor genes (named *pCam5*) involved in HFA biosynthesis, including an *oleate 12-hydroxylase* (*FAH12*), *diacylglycerol* (*DAG*) *acyltransferase 2* (*DGAT2*), *phospholipid: DAG acyltransferase 1-2* (*PDAT1-2*), *phosphatidylcholine* (*PC*): *DAG cholinephosphotransferase* (PDCT) and *Lyso-PC acyltransferase* (*LPCAT*). Transgenic Arabidopsis *pCam5* lines produced HFA counting for 25% in seed oil. By knocking out Arabidopsis *Fatty acid elongase 1* (*AtFAE1*) in pCam5 using CRISPR/Cas9 technology, the resulted *pCam5-atfae1* lines produced over 31% of HFA. In addition, castor *WRINKLED1* (*RcWRI1*) was introduced into *pCam5-atfae1* lines and produced HFAs to 42%. Our results provide not only insights for future research uncovering mechanisms of HFA synthesis in seed, but also metabolic engineering strategies for generating safe HFA-producing crops.

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PD-0003

Genome-wide identification, *in silico* analyses, and expression profiling of *DOMAIN OF UNKNOWN FUNCTION 679* (DMP) gene family in soybean

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The DMPs (DUF679 membrane proteins) are plant-specific membrane protein family. In *Arabidopsis*, ten members of the DMP family displayed distinct tissue- and development-specific expression patterns, particularly in tissues undergoing senescence (AtDMP1, AtDMP3, and AtDMP4), dehiscence (AtDMP7), and abscission (AtDMP2, AtDMP4, AtDMP7). While AtDMP8 and AtDMP9 have been demonstrated to facilitate gamete fusion during double fertilization. Loss of function mutations in orthologues of these two genes induced maternal haploids in maize, *Medicago truncatula, Brassica napus*, tobacco, and tomato. However, the biological functions of several DMP family members are not fully understood in other crops. Therefore, we conducted genome-wide characterization of DMPs in soybean [*Glycine max* (L.) Merr.], a most widely grown commercial legume and oilseed crop. Here, we comprehensively analysed the physiochemical properties, subcellular location, conserved sites, and phylogeny of soybean DMPs family members using different bioinformatical tools. The *DMP* gene family encodes proteins that range from 136 amino acids (Glyma.09G237500) to 222 amino acids (Glyma.07G253500), with protein isoelectric points (PIs) ranging from 4.86 (Glyma.13G235100) to 9.27 (Glyma.17G020800). In subcellular localization predictions, most proteins are predicted to be located in the plasma membrane except for protein Glyma.17G020800, which is predicted to be located in the endoplasmic reticulum membrane. An expression analysis using available databases showed that *DMP* genes are expressed differently in different tissues and at different stages of plant development. Further validation of *in silico* analyses of this study will provide more comprehensive information on the biological functions of the *DMP* gene family in soybean.

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PD-0004

A *Panax ginseng* R2R3 MYB transcription factor *PgMYB123*, regulates proanthocyanidin biosynthesis in *Arabidopsis thaliana* when overexpressed

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Proanthocyanidins (PAs) are flavonoids with important defensive roles against biotic, and abiotic stress in plants. The compounds are also used extensively by humans in various industries including cosmetics, pharmaceuticals, food, and beverages. Molecular regulation of PA biosynthesis has been extensively studied in other plants such as tobacco, and *Arabidopsis* thaliana. But in a high-value medicinal plant *Panax ginseng*, PA biosynthesis regulation remains unknown. Here, we report that PA biosynthesis in *P. ginseng* is mediated by a R2R3 MYB transcription factor *PgMYB123*. Phylogenetic analysis clusters *PgMYB123* with PA biosynthesis transcription factors from other plants including *AtMYB123/TT2* from A. thaliana. *PgMYB123* was localized in the nucleus of the cell, indicating its role as a transcription factor. When overexpressed in *A. thaliana*, *PgMYB123* led to an increased PAs accumulation in siliques, and in mature seeds. Additionally, transcript level analysis in *PgMYB123*-overexpressing transgenic *A. thaliana* plants, showed upregulation of the structural genes involved in PA biosynthesis. Together, these results indicate *PgMYB123* codes for a protein that activates the genes involved in PA biosynthesis.

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PD-0005

Maize phospholipase A1 homolog, a new candidate of in vivo haploid inducer in rice

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Doubled haploid (DH) breeding is a technology that allows rapid fixation of the loci of useful traits through artificial or spontaneous chromosome doubling. The DH technology allows breeder to produce an inbred line within two generations, whereas traditional breeding takes more than seven generations. For this reason, great efforts have been made over the past few decades to establish efficient methods for haploid production. Although various haploid induction methods have been suggested in the literature, there is no reliable haploid induction system for many crops. To date, most haploid plants have been produced through in vitro culture of female or male gametes. However, the tissue culture-based methods are typically labor-intensive, and genotype-dependent. In contrast, in vivo haploid induction is genotype independent. Recently, it has been demonstrated that ZmPLA1 (NOT LIKE DAD, MATRILINEAL), a pollen-specific phospholipase in maize, is involved in haploid induction in vivo. This finding was a starting point for the understanding of the mechanism of haploid induction in vivo and for the development of efficient DH techniques in many crops. Here, we report the function of a ZmPLA1-homolog that can be used as an in vivo haploid inducer in rice. We will discuss the potential applications of the newly identified ZmPLA1-homolog and the functional differences between known haploid-inducer genes.

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PD-0006

간척농지 범용화를 위한 화옹간척지 밭작물 재배 기반기술 연구

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우리나라 간척농지는 밭작물 재배 실적이 매우 적고, 토양제염이 된 간척지라도 밭작물 재배의 가능성과 대규모 영농 시 경제성이 있는지에 대한 실증이 부족한 실정이다. 제염이 된 간척농지라도 저평지 대구획(장변 100m) 농지로 강우 시 고랑에 물고임 등 지표배수가 불량하므로 경지 내 지표배수 촉진기술의 도입이 필요할 것으로 판단된다. 또한 간척농지는 비옥도가 낮으므로 저비용 토양비옥도 증진기술의 도입, 논농사와 달리 밭작물은 담수재배가 어려우므로 대구획 간척농지에 적합한 새로운 관개방법의 도입이 필요하겠다. 따라서 본 연구에서는 화옹 간척지에서 실증재배를 통해 경지 내 시비, 배수, 관개, 밭작물 재배기법 등 가이드라인 제시하고자 한다. 특히 간척지 적합 품종 선발을 위해 밀(백강, 조경 등)과 콩(대찬, 선풍 등)을 대상으로 다양한 품종에 대해 실증재배 연구를 수행할 계획이다. 본 실증연구를 통해 간척농지를 활용한 밀・콩 기초식량 전문 생산단지 구축 및 국내 기초식량 자급 기반 마련을 도모하고자 한다.

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PD-0007

Development of an SNP-genotyping platform in rice using target capture sequencing technology

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For crop genetics and breeding, development of efficient, robust and high-throughput SNP genotyping platforms is required. Recently, target capture sequencing technology, which is very flexible in increasing the number of SNP markers, has been applied to develop SNP-genotyping platforms for maize, cassava, and fava bean. The purpose of this study was developing a target capture sequencing SNP-genotyping platform for rice. We developed a target capture sequencing panel containing 2565 SNP markers, including 1225 SNPs informative for *japonica* and 1339 SNPs informative for *indica*. We performed diversity analysis with 50 rice varieties using this panel. Of the 2565 SNP markers, 2341 (91.3%) produced useful polymorphic genotype data, and a phylogenetic tree of the 50 varieties was produced. The mean number of markers polymorphic between any two varieties was 854. We performed QTL mapping of preharvest sprouting (PHS) resistance in an F8 recombinant inbred line population derived from the cross Odae × Joun using this platform. A genetic map comprising 475 markers was constructed, and two QTLs for PHS resistance were found on chromosomes 4 and 11. This platform will be a powerful tool for rice genetics and breeding facilitating QTL or gene mapping, germplasm diversity analysis, and marker-assisted selection.

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PD-0008

팝콘 · 칼라찰옥수수 육묘일수에 따른 생육 및 수량특성

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강원도 홍천군 두촌면 장남길 26 강원도농업기술원 옥수수연구소

옥수수연구소는 찰옥수수, 종실용옥수수, 팝콘옥수수, 색소옥수수 등 용도에 따른 다양한 품종을 개발하고 있다. 강원도는 전국의 찰옥수수 재배면적의 34%를 차지하는 주 생산지로써 등숙기 중 일교차가 높아 단맛인 풍부하여 소비자 반응이 좋은 장점이 있다. 이런 강원도의 지리적 장점을 이용하여 다양한 옥수수를 특화시켜 특산단지를 조성중이다. 특히 팝콘옥수수는 2017년에 11h에서 2020년에는 68ha로 재배면적이 증대되고 있는 작목으로 지역 특화작목으로 육성가능하다. 팝콘옥수수는 전통육종방식으로 품종을 개발하였으며, 현재 오륜팝콘 등 4품종이 개발되었다. 농가 보급종은 오륜팝콘, 오륜2호, 기찬팝콘이 보급되고 있다. 팝콘 원료인 알곡의 저장온도, 저장방법, 저장기간 등 환경적 요인에 의해 팝콘품질이 변화며, 알곡이 가지고 있는 적정 수분대는 11~13%내로 유지될 때 최상의 튀김부피(30~33㎤/g)을 보인다.

칼라찰옥수수는 최근 소비 트랜드인 건강기능성 성분이 강화된 품종이다. 기존의 흰찰옥수수에는 없는 안토시아닌이 고함유된 품종으로써 새롭게 지역특화품종으로 육성중에 있다. 현재 '미홍찰', '미현찰', '부농찰'이 개발되어 있으며, 강원도 정선, 동해 지역에 시범적으로 특산단지를 조성중이다. 따라서 본 연구는 팝콘 · 칼라찰옥수수를 지역특화 작목으로 육성하여 안정적으로 수량 확보를 하기위해 재배시험을 수행하였으며 육묘일수에 따른 생육과 수량성을 비교하였다. 시험재료는 팝콘옥수수는 '오륜팝콘', 칼라찰옥수수는 '미홍찰'을 각각 이용하였다. 파종은 2021년 4월 8일에 포드파종을 하였다. 육묘일수는 20일, 30일, 40일, 50일 4처리를 하였다. 조사항목은 '오륜팝콘'은 출사일수, 간장, 착수고, 이삭길이, 이삭폭, 웅수 지경수를 조사하였으며, 육묘일수별 튀김부피를 측정하였다. '미홍찰'은 출사일수, 간장, 착수고, 간경, 웅수 지경수, 이삭길이, 착립길이, 이삭폭, 생세치삭중, 상품비율을 조사하여 육묘일수별 비교를 하였다. '오륜팝콘'은 육묘일수가 길수록 출사일수가 늘어났으며, 간장은 20일 육묘에서는 182cm, 50일 육묘에서는 95cm로 간장이 줄어들었다. 웅수 지경수는 20일 육묘에서는 14.9개였으나, 50일 육묘에서는 3.5개로 76% 줄어들었다. 육묘일수에 따른 팝콘옥수수의 튀김부피는 20일 육묘에서 34.0㎤/g, 50일 육묘에서는 33.1㎤/g로 차이가 없었다. '미홍찰'의 육묘일수별 비교에서는 '오륜팝콘' 생육과 비슷한 결과를 나타내었다. 간장은 20일 육묘에서 177cm, 50일 육묘에서는 89cm로 50% 작아졌으며, 웅수 지경수도 20일 육묘에서는 6.6개, 50일 육묘에서는 0.2개로 97% 줄어들었다. 이삭길이 18cm이상 비율로 나타내는 상품성 비교에서는 20일 육묘에서는 상품성 비율이 88.3%였으나 50일 육묘에서는 3.3%비율로 나타나 상품성이 거의 없었다. 따라서, 팝콘 및 칼라찰옥수수에서 육묘일수는 20일 이상 육묘는 피하는 것이 안정적 수량 확보 및 상품성 있는 이삭을 수확 할 수 있을 것으로 판단된다.

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PD-0009

Development of CENH3-mediated haploid induction system in tomato

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As the world's population increases, the demand for food worldwide is also increasing. Increasing crop productivity through crop breeding is a major concern. Recently, a lot of research is being done on double haploid (DH) technology for efficient crop breeding. The doubled haploid (DH) is the fastest method to fix genetic trait from maternal or paternal, reducing the breeding time required to fasten homozygous lines compared to traditional breeding. Among the haploid induction factors, Centromere histone H3 (CENH3), a protein located in the centromere, induced haploid in dicot and monocot plants. When CENH3 is impaired, the cell division process malfunctions and consequently a haploid cell is induced. CENH3-mediated haploid induction was reported only in tomato cultivar micro-tom by ethyl methanesulfonate mutagenesis. Gene editing of *CENH3* using CRISPR-Cas9, was performed to induce knock-out mutants in tomato cultivar sweet 100 to confirm haploid induction. We obtained three independent lines and showed two types of editing in a single allele with '-G' and '-GCT' deleted, respectively. Overall, fruit and seed size decreased in the mutant line. This phenomenon is considered to be a null mutation caused by deletion of 1 bp and 3 bp in *CENH3*.

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PD-0010

Study on the interaction between embryo and endosperm in rice seed development

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Rice grains comprise specialized tissues, embryos, endosperm, and maternal tissues. The embryo is located in the ventral bottom region, and it takes part in only 2-3% of the total grain weight, but has enriched different nutrients. The endosperm is the central part of the grain, and it is rich in starch and protein, which are the vital nutrient source of human food. Embryo-endosperm interaction is vital for regulating grain filling, thus being critical for grain yield and quality in major cereals. In rice, the *enl2* mutant has defects in endosperm development and enlarged embryos compared with WT seeds. To understand the early interaction of embryo and endosperm development, transcriptome analysis was performed at three and 24 HAP (hours after pollination) in WT and *enl2* mutants. GO enrichment analysis showed that genes in functional groups of response to auxin stimulus, chromatin assembly or disassembly, and regulation of transcription were significantly reduced in the mutant compared with the WT. In KEGG analysis, genes related to nucleic metabolism for purine and pyrimidine biosynthesis were downregulated. To identify the critical genes for seed development, especially those related to the interaction between the embryo and endosperm, mutant lines of interest genes were screened or generated based on our transcriptome analysis. Among them, a line showing smaller seed size, lower fertilization rate, and particularly smaller embryo was isolated. The gene encodes a receptor-like kinase and was named *Small Embryo 1* (*SE1*). It is expected to be related to signal transmission during early seed development.

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PD-0011

Functional study of CTP synthases during early seed development in rice

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Cytidine triphosphate (CTP) plays an important role in the biosynthesis of DNA, RNA, and phospholipids. Such CTP is catalyzed by CTP synthase (CTPS). Despite the presence of six similar *OsCTPS* genes in rice, only the *OsCTPS1* plays an essential role in the early seed development of rice. However, little is known about how the other *CTPS* genes, rather than *OsCTPS1*, function in the early seed development of rice. Therefore, this study focused on how other CTPS genes affect early seed development. *OsCTPS1, OsCTPS2, OsCTPS5*, and *OsCTPS6* indicated ubiquitous expression in all tissues, whereas the expression of *OsCTPS3* and *OsCTPS4* was very low. To determine the functions of the *OsCTPS* gene expressed during seed development, the mutant individuals of those genes were generated using the CRISPR/Cas9 method. *OsCTPS2, OsCTPS5*, and *OsCTPS6* null mutants displayed defects in seed development but showed a milder phenotype than the *OsCTPS1* mutation lacking the endosperm. Meanwhile, overexpression (OX) of *OsCTPS5* increased seed weight and size, similar to *OsCTPS1* OX. Interestingly, *OsCTPS2* or *OsCTPS6* OX plants displayed decreased seed weight and size. Particularly, when the *OsCTPS5* overexpression line was observed with a cross-section, a pattern of increased nucleic acid was observed, and the endosperm was packed tighter than the WT. These results indicate that other *CTPS* genes, including *OsCTPS1*, also affect rice seed development. Currently, a more detailed study of the molecular mechanisms of how each CTPS regulates seed development in rice is ongoing.

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PD-0012

Study on Ehd1-independent flowering pathway in rice

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Flowering is induced by Florigens (Hd3a and RFT1), and they function downstream of Ehd1 in rice. Ehd1 merges various upstream flowering signals and acts as a signal integrator under inductive conditions. To determine the function of Ehd1, *ehd1* mutants were generated using the CRISPR/Cas9 system. The *ehd1* mutants flowered late under paddy field conditions, approximately 20 d compared with the WT. To investigate the *Ehd1*-independent flowering mechanism, we performed SD treatment on 40-d-old WT and *ehd1* mutants grown under long-day conditions. WT and *ehd1* mutants flowered 40 d and 56 d after SD treatment, respectively. Leaf blades were collected at 2-3 d intervals to observe the floral transition during the treatment. Expression of florigen genes was promoted eight days after SD treatment in WT. In contrast, the expression of florigen genes started 14 d later than WT. Then, transcriptome analysis was conducted at critical sampling points to compare the genes that are differently expressed between WT and *ehd1* mutants. The analysis showed that *Ehd1, HDAC3*, and *OsSFL1* were significantly upregulated in the *ehd1* mutants than the WT, regardless of floral transition. OsSFL1-HDAC complex reduces histone H3 acetylation and suppress transcription of target genes, and OsSFL1 is already known as a flowering activator under SD conditions. This suggests that OsSFL1 suppresses upstream flowering repressor genes of *Ehd1* or another repressor that directly controls florigen expression. Based on these observations, rice has an *Ehd1*-independent flowering pathway and OsSFL1 seems to be involved in this pathway under inductive conditions.

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PD-0013

Research Advances in Improving Biotic and Abiotic Stress Tolerance Using CRISPR/Cas9 Genome Editing in Rice

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Rice is a major crop, which is influenced by both biotic and abiotic stresses that threaten its stable production due to climate change. In breeding, genome editing through CRISPR/Cas9 technologies provide a very efficient tool, complementing the shortcomings of traditional genome editing as well as conventional breeding methods. In this review, we analyzed the research trends of CRISPR/Cas9 in rice, and present example papers in which the mentioned technology was implemented for enhancing biotic stress resistance and abiotic stress tolerance. PubMed and Web of Science databases were used to filter papers containing “rice” and “CRISPR” as keywords in the title and published between the year 2013-2021. The extracted 209 papers were classified by field of research, i.e., protocols (49%), breeding (27%), gene functional research (18%), and others (6%). Among a total of 56 papers classified as breeding, 10 (18%) and 5 (9%) papers focused on biotic stress and abiotic stress tolerance improvement, respectively. Further literature search using additional keywords identified 9 and 5 more papers for biotic and abiotic stress tolerance improvement, respectively. Studies on biotic stress resistance included blast, bacterial leaf blight, and tungro virus. Abiotic stress tolerance studies covered topics on drought, salinity, cold temperature, and alkaline toxicity. In conclusion, CRISPR/Cas9 technology is actively used in the field of biotic and abiotic stress tolerance, and it is expected that its utilization in breeding will provide unprecedented opportunities to rapidly develop rice varieties responding to biotic and abiotic stresses caused by climate change.

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PD-0014

Development of Chinese cabbage (*Brassica rapa*) for TuMV viral resistance using CRISPR/Cas9-mediated gene editing

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CRISPR-Cas9 has emerged as an invaluable genome-editing approach able to alter DNA sequences precisely at targeted site. This influential tool enable significant advancement in plant traits improvement particularly for disease resistance compared to the traditional breeding. In crop plants, many of the recessive virus-resistance genes in plants encode eukaryotic translation initiation factors (eIFs), including eIF4E, eIF4G, and related proteins. In this study, we used CRISPR/Cas9-mediated directed mutagenesis to test whether novel sequence-specific mutations at eIF4E1 in *Brassica rapa* (Chinese cabbage) cv. 'Seoul' could confer enhanced resistance to potyviruses. We detected heritable homozygous mutations in the T_1 generation. The eIF4E1 sequence analysis of T_0 transgenic plants expressing Cas9 and eIF4E-sgRNA transcripts revealed chimeric mutations (in/del) ranging from 1 to 8 bp. Further, genotyping of the eIF4E1-edited lines in T_0 and T_1 transgenic Chinese cabbage plants indicated that the mutations were transferred to succeeding generation. When mutant lines were tested for resistance to the potyvirus Turnip mosaic virus (TuMV), they demonstrated resistance against virus. These results show that site-specific mutation of Chinese cabbage eIF4E1 effectively conferred resistance to TuMV. Consequently, this study reveals the possibility of the use of CRISPR/Cas9 technique to expedite breeding for trait improvement in Chinese cabbage plants.

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PD-0015

In vivo haploid induction system in dicotyledonous plant

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Haploid embryo induction system can considerably shorten the time required to create pure homozygous lines, which is the basis of doubled haploid technology. The *in vitro* haploid induction system has long been used to produce haploid embryos using maternal or paternal germlines. The *in vitro* methods, typically tissue culture-based, are labor intensive and genotype dependent. However, a seed-based in vivo haploid embryo induction system can overcome the limitations of the *in vitro* methods. So far, two main types of *in planta* haploid-inducing lines that trigger either maternal or paternal haploid embryo through seeds have been reported. One of them is the CENH3 (centromeric variant of histone 3)-based induction system, in which the modification of a CENH3 allows the creation of haploid inducer lines that generate viable seeds containing a paternal haploid genome. The other is the monocot-specific maternal haploid induction system, which is based on the mutation of *ZmPLA1/MTL/NLD* (*ZmPHOSPHOLIPASE-A1/MATRILINEAL/NOT LIKE DAD*). The *ZmPLA1*-based haploid inducing system is reported to produce viable seeds containing a maternal haploid genome in only monocotyledonous plants such as maize, rice, wheat, and foxtail millet. The genetic alteration of *ZmPLA1* homolog in dicotyledonous plants has not yet been reported. Herein, we report that *ZmPLA1* homolog is actively involved in the creation of haploid seeds in *Arabidopsis*. This discovery indicates that the genetic manipulation of *ZmPLA1* is also functional in dicotyledonous plant.

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PD-0016

Reverse genetic study on saddle seed color phenotype of soybean seed via introduced mutation of Argonaute5 gene by CRISPR/Cas9

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Soybean [Glycine max (L). Merr] is one of the significant sources of vegetable oil and protein for both human consumption and animal feed. Most soybean seeds have a yellow seed coat with a tiny dark fleck at the hilum. It has been known that this distinct yellow color results from the *chalcone synthase* (*CHS*) gene silencing by RNA interference (RNAi) due to the presence of *I* or I^i alleles. Moreover, it has been identified that *k1* allele has a 129-bp deletion in a gene encoding Argonaute5 (AGO5), a member of the Argonaute family of proteins, affects the distribution of *CHS* siRNAs in the seed coat. AGO proteins, as essential components of the RNA-induced silencing complex (RISC), play the central role in RNA silencing processes. In this study, reverse genetic approach was used to verify the soybean seed coat phenotype of *AGO5* gene by *Agrobacterium*-mediated transformation. We attempted to perform the *GmAGO5* gene editing using the CRISPR/Cas9 system to introduce mutations into the *GmAGO5* gene with guide RNAs in soybean (cv. Kwangankong). As a result, *GmAGO5* gene was disrupted by CRISPR/Cas9 system with sgRNA-2 and sgRNA-5 targeting the 2nd exon. Several soybean *GmAGO5* gene-edited lines were obtained in T_0 generation at editing frequencies of 0.2 % - 99.8%. Soybean lines with saddle seed color patterns showed low indel frequencies. In soybean lines showing high indel efficiency, no patterns were found in the seed coat in T_0 generation, but a saddle pattern was shown in T_1 generation, which is expected due to the segregation. Finally, we could created saddle phenotype by *GmAGO5* mutation with genome editing and confirmed the proposed molecular mechnism and function of *GmAGO5* by reverse genetic way.

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PD-0017

Mutation of *GmIPK1* Gene using CRISPR/Cas9 Reduced Phytic Acid Content in Soybean Seeds

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Phytic acid (PA) acts as an anti-nutrient substance in cereal grains which disturbs the bioavailability of micronutrients such as iron and zinc in humans, causing malnutrition. *GmIPK1* encodes inositol 1,3,4,5,6-pentakisphosphate 2-kinase enzyme, which converts *myo*-inopsitol-1,3,4,5,6-penta*kis*phosphate (IP_5) to *myo*-inositol-1,2,3,4,5,6-hexa*kis*phosphate (IP_6) in soybean (*Glycine max* L.). In this study, for developing low PA soybean, we attempted to perform the *GmIPK1* gene editing using the CRISPR/Cas9 system to introduce mutations into the *GmIPK1* gene with guide RNAs in soybean (cv. Kwangankong). As a result, *GmIPK1* gene was disrupted by CRISPR/Cas9 system with sgRNA-1 and sgRNA-4 targeting the 2nd and 3rd exons, respectively. Several soybean *GmIPK1* gene-edited lines were obtained in the T_0 generation at editing frequencies of 0.1 %- 84.3 %. Sequencing analysis exhibited various indel patterns with deletion of 1-9 nucleotides and even insertion of 1 nucleotide in several soybean lines (T_0). Finally, we obtained two sgRNA-4 GmIPK1 gene-edited homozygote soybean T_1 plants (line #21-2: 5 bp deletion; line #21-3: 1 bp insertion) by PPT leaf painting assay and PCR analysis. Analysis of soybean *Gmipk1* gene-edited lines led to the reduction of PA content in soybean T_2 seeds but did not show any defects in plant growth and seed development.

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PD-0018

TRV-mediated Genome Editing of eEF1Bγ in *Nicotiana benthamiana*

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More than half of the known virus resistance genes in plants are recessively inherited, implying that these resistance genes could have originated from a loss of function of host factors required for virus infection. In a previous study, we showed that other host factors such as *eEF1A* and *eEF1B* are also required for virus infection like tobacco mosaic virus (TMV) or potato virus X (PVX). The recent development of genome editing (GE) tools using CRISPR/Cas9 system provides unprecedented opportunities to develop virus-resistant plants by targeted knockout of host factors. Previously, GE via RNA virus such as tobacco rattle virus (TRV) to deliver single guide RNA (sgRNA) was developed to avoid time-consuming tissue culture in *Nicotiana benthamiana* and *Arabidopsis thaliana*. Here, we showed that host factor could be edited via TRV-mediated GE in *N. benthamiana*. To test TRV-mediated GE, we delivered sgRNA targeting *phytoene desaturase* (*PDS*) genes using TRV into transgenic *N. benthamiana* plants overexpressing *Cas9*. We compared U6 and Pea early browning virus (PEBV) promoters and introduced mobile sgRNA containing *FLOWERING LOCUS T* (*FT*) or tRNA-Isoleucine sequence at the 3' of sgRNA to increase GE efficiency. As a result, the U6 promoter showed up to 6.3 times higher efficiency and mobile sgRNA dramatically increased editing efficiencies especially in the systemic leaves. So, Mobile sgRNA targeting *eEF1Bγ* homologs (TRV-*eEF1Bγ*-sgRNA-tRNAIle) was delivered to generate virus-resistant plants. 20.7 - 34.5% of regenerated shoots from systemic leaves were edited in each homolog. Currently, we are developing all homologs-edited line to test virus resistance.

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PD-0019

Expression of colorectal cancer antigenic protein fused to IgM Fc for plant cell factory system using Chinese cabbage (*Brassica rapa*)

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Chinese cabbage (*Brassica rapa*) is the most important horticultural crop, grown East Asia. In this study, this vegetable was selected to develop an edible vaccine due to the high protein expression rate. EpCAM (epithelial cell adhesion molecule), a cell-surface glycoprotein highly expressed in colorectal cancer is a tumor-associated antigen (TAA) considered as a target for a tumor vaccine. The immunoglobulin M Fc (Ig M Fc) and J-chain KDEL were fused to the EpCAM to desing the an efficient edible vaccine fusion protein for colorectal cancer. *Agrobacterium*-mediated transformation was carried out using a vector harboring EpCAM fused to IgM Fc and J-chain KDEL genes, respectively. Transgenic plants expressing each protein were confirmed through PCR and Western blot. F_1 seeds were obtained through the corss-fertilization of EpCAM-IgM Fc and J-chain KDEL transgenic plants. F_4 plants were obtained through each generation and high expression level of plants were selected through PCR and western blot. The phenotype of selected transgenic plants was not different from the wild type. The selected high-expressing plants were induced to callus, and it was intended to be used as a plant cell factory system material. Thus, the present study will aid the development of plant cell vaccines factory system.

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PD-0020

High Efficient Transgene-free Genome Editing in *Solanum lycopersicum* using Potato Virus X

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Genome-editing using CRISPR-Cas is a powerful tool for plant science and crop improvement. Conventional transgene-mediated CRISPR-Cas methods were limited at the time of commercialization: generational progress is required to separate foreign DNA and regulatory restriction remains on transgenesis. Therefore, DNA-free delivery has been developed by transfecting CRISPR-Cas9 ribonucleoproteins into protoplasts. However, these wall-less cells were difficult to regenerate for most crop species. Here, we described a method for Transgene-free genome editing technology in *Solanum lycopersicum* cv. Micro-Tom through the expression of Cas9 and single-guide RNA (sgRNA) using Potato Virus X (PVX) vector. We designed and cloned sgRNAs targeting *Phytoene desaturated* that induce white-shot phenotypes on PVX vectors. Genome editing efficiency was confirmed in inoculated cotyledon through the targeted-next-generation sequencing (NGS) method. The editing efficiency of 31.1 percent was confirmed through NGS analysis of inoculated cotyledon. In order to increase the editing efficiency, 37°C heat was treated for 24 h on the 7th and 9th days after inoculation and the editing efficiency increased 1.2 times. This simple and high efficient virus-mediated delivery of CRISPR-Cas9 will contribute to genetic function research and develop the breeding materials in *S. lycopersicum*.

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PD-0021

스피드 육종 시스템과 MABC를 이용한 조경밀의 *Glu-B1* allele 치환 계통 육성

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조경은 국내 주요 백립계 제빵용 밀 품종 중 하나로 고분자글루테닌 조성(HMW-GS) 중 *Glu-B1b* allele을 가지고 있다. 본 연구에서는 캐나다 적립계 경질밀 품종인 Garnet이 가진 *Glu-B1i*를 도입하고자 최근 개발된 Speed breeding (SB)과 speed vernalisation (SV) 시스템, 그리고 marker-assisted backcross (MABC)를 이용해 여교배 및 세대진전을 수행하였다. 2019년 4월~2021년 10월까지 조경과 Garnet을 교배한 후대계통을 SV 또는 SB 조건에서 2회 여교배하고 BC_2F_4 세대까지 육성하였다. 2021년 11월 BC_2F_5 세대를 포장에 전개하여 그 농업적 특성을 평가하였다. 각 세대에서 cauBx642 마커를 이용해 *Glu-B1i* allele이 heterozygous 하거나(BC_1F_1, BC_2F_1), homozygous한 (BC_2F_2, BC_2F_3, BC_2F_4) 개체를 선발하였다. BC_2F_2, BC_2F_3 세대에서는 출수일수와 종피색 중심의 표현형 선발을 하였다. BC_2F_4 세대에서 27개 계통에 대해 총 120개의 KASP assays를 이용하여 background selection을 수행하였으며, 그중 조경 반복친 회복률이 90.0%인 YW3215-2B-1 계통을 선발하였다. YW3215-2B-1의 출수기는 4월 15일로 조경과 같았고, 성숙기는 5월 30일로 조경보다 1일 늦었다. YW3215-2B-1의 농업 특성은 간장 67 cm, 수장 10.7 cm, 주당수수 19개, 일수립수 53개로 모두 조경과 통계적으로 유의한 차이가 없었으며, Garnet과는 주당수수를 제외한 모든 농업 특성에서 5% 유의수준에서 차이를 보였다. 향후 YW3215-2B-1의 품질 관련 이화학적, 물리적 특성을 분석하여 *Glu-B1i* allele 도입이 제빵 특성에 미치는 영향을 분석할 예정이다.

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PD-0022

Identification of GM soybean using visible near infrared spectroscopy

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Despite many benefits, including herbicide tolerance, improved resistance to plant diseases and pests, and increased yields, GM crops raise concerns about adverse food safety and environmental impacts. Therefore, it must be possible to quickly and accurately identify GM crops imported from abroad to ensure the safety of consumers. In this study, using Gwangan soybean and beta-carotene-enriched GM soybean, the normal leaf of soybean leaves was photographed with a SENOP HSC-2 camera, and then spectral information in the visible and near infrared (VNIR) region was collected in the wavelength range of 650-950 nm to create a database. We tried to distinguish GM crops from non-GM crops by building and applying machine learning algorithms.

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PD-0023

Gene editing in Korean commercial wheat to reduce Omega-1, 2 gliadin Content

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Omega-1, 2 gliadin is one of the gluten protein types in wheat flour. One of the reasons for developing reduced omega-1, 2 gliadin is that it is the antigen that causes celiac disease. Since the gliadin genes are spread throughout six loci of wheat genome, it is difficult to develop hypo-allergen wheat through traditional breeding and random mutation. In this study, a Korean commercial wheat (cv. Keumkang) was transformed using a CRISPR/Cas9 gene editing system. We designed sgRNA that complementarily binds to four genes expressing omega-1, 2 gliadin, and inserted into a GE vector containing the CRISPR/Cas9 gene which is a gene editor. GE vectors containing omega-1, 2 gliadin sgRNA were introduced into immature embryos (15 DPA) of Korean commercial wheat through particle bombardment. Among the regenerated plants, the phenotype of omega-1, 2 gliadin protein was analyzed by RP-UPLC in half of T_1 seeds, and individuals with reduced omega-1, 2 gliadin were identified. Four individuals with reduced omega-1, 2 gliadin in the T_2 generation were selected through the RP-HPLC, and it was confirmed that they were transgene-free using the structural gene of the GE vector. Also, several lines with changes in the phenotypes of other types of gliadin protein were also observed. The results of our study will help utilization of transformation in Korean wheat varieties through gene editing system.

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PD-0024

Identification of GM rice using Near-infrared spectroscopy

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Although the cultivation of GM crops is increasing for food productivity, the importance of the risk management of GM crops is increasing accordingly. Therefore, a rapid detection technique is needed to prevent unintended environmental release or mixing of GM crops. PCR or lateral flow test, which is commonly used for the detection of GM crops, is time- or cost- consuming, so it is hard to test a large number of samples rapidly. Near-infrared spectroscopy is a technique for measuring intermolecular bonds, research of quality control of food or identification of crop varieties has been conducted. This technique has the advantage of being able to make non-destructive measurements, saving time and cost by minimizing sample preprocessing. In this study, we tried to develop a GM crop discrimination technique using near-infrared spectroscopy. To distinguish between drought-tolerance resistant rice and its counterpart, Ilmi, collected near-infrared spectrum in the 650-950 nm range was analyzed using machine learning algorithms.

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PD-0025

Modification of delayed flowering cabbage mutants at low temperature using a CRISPR system

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Brassicaceae crops such as cabbage (*B. oleracea var. capitata*) start to bloom after exposing to low temperatures, which recently resulted in significant economic loss in Korea. The cabbage has been known to contain three *FLC* homologous genes (*BoFLC1, BoFLC2, BoFLC3*) and one pseudogene (*BoFLC5*) that respond to low temperature for flowering. We isolated three *BoFLC* encoding genes from early, mid- and late-flowering cabbage. The *B. oleraceae FLC* genes typically have 7 exons, 6 introns and range in size from 3,361 to 4.384 bp, but some InDels in the first intron were evident between early and late flowering genotypes. As a result of *BoFLC* gene expression in samples grown in a greenhouse (control) and cold room (chilling treatment), it was significantly decreased after about 7 weeks under low-temperature conditions. Conversely, expression of *BoVIN3* increased from 7 weeks. Based on the above facts, we focused on *BoVIN3*, a gene that suppresses the BoFLC gene, in 'Ohgane' cultivar, an early-flowering cabbage. The 'Ohgane' *BoVIN3* gene has 5 exons and 4 introns, with a total length of 2,545 bp. Three sgRNAs were designed and synthesized and RNPs were delivered to cabbage protoplasts by PEG-mediated transformation. Targeted deep sequencing indicated that a InDels frequency of 7.4 to 29.1% was shown in *BoVIN3*. Here, we provide molecular characterization and differences in *FLC* homologue expression between early-flowering and late-flowering cabbage, with the expectation of promoting the breeding of late-flowering cabbage through CRISPR-CAS9 technology targeting *BoVIN3*.

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PD-0026

Enhancement of Oil Content by Genetic Modification of *FAD* genes in Peanut(*Arachis hypogaea* L.)

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Peanut, also known as ground nut, is one of the important oilseed crops in the world. So, one of the main goals of peanut breeding is to improve the fatty acid composition. Peanut is an allotetraploid with A and B subgenomes, which makes breeding peanuts difficult. The objective of this study is to enhance oil quality of peanut by genetic modification. We conducted overexpression and Knock-Out of *FAD* (fatty acid denaturease) genes to regulate high oleic acid($\omega-9$) and high α-linolenic acid($\omega-3$) contents using 2 Korean elite peanut cultivars. We used two different methods; 1) high oleic acid peanut through ahFAD2A, ahFAD2B Knock-Out, and 2) high α-linolenic acid peanut through pfFAD3 overexpression. We have constructed three different vectors; CaMV35S promoter with pfFAD3-1 overexpression, peanut seed specific promoter with pfFAD3-1 overexpression, and CRISPR/Cas9-mediated ahFAD2A, ahFAD2B simultaneous Knock-Out vectors. Binary vectors were also used for agrobacterium-mediated transformation of half mature cotyledons, respectively. After antibiotic selection stage, putative transgenic plants were confirmed by PCR amplification using T-DNA region specific primer sets. Peanut transformation using agrobacterium tumefaciens has not been reported in the South Korea. Therefore, the results from the present study will provide useful information for peanut gene-editing research groups and breeders.

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PD-0027

밀 Cystein protease 유전자 발현과 수발아와의 연관성 분석

최준용, 이명희, 강천식, 김경민, 김경훈, 이고은, 고종민, 최창현*

전라북도 완주군 이서면 혁신로 181 국립식량과학원 밀연구팀

밀은 수확 시기에 강우로 인한 품질 저하가 문제시 되고 있다. 따라서 국내 밀 품종 육성 시 수발아 평가를 수행하고 있다. 그러나 많은 집단의 평가가 이루어져야 하는 문제가 있기 때문에 정밀한 분자 마커 개발이 요구된다. 최근 국내자원을 포함한 해외 60여 개국 자원의 2,000여점의 모집단으로부터 614점의 밀 핵심집단을 구축하여 수발아 특성 평가를 수행하고 있다. 본 연구에서는 색차계를 활용하여 수발아와 연관된 종피색의 특성을 분석함으로써 수발아 특성을 평가하였다. 이 표현형 정보와 35K SNP Chip 정보를 이용하여 전장유전체연관분석(Genome Wide Association Study, GWAS)을 수행함으로써 수발아 내성이 강한 적립계밀의 종피색과 연관된 유전자를 찾았다. GWAS 결과 3A 염색체에서 -log10(p)이 5 이상인 2개의 SNP를 찾았고 그 중에 하나는 Cysteine protease (CP) 유전자의 exon에 위치하였다. 이 CP 유전자는 영국의 수발아 RIL 집단 mapping 결과에서도 *Phs-A1* 수발아 내성 locus와 연관되어 있으며, 종자의 발아 초기에 종자 호분층 및 배반 주변에서 발현하여 종자 저장단백질을 분해하는 것으로 알려져 있다. 특히 이 CP 단백질은 글루텐 형성에 필수적인 gliadin을 분해함으로써 종자 발아에 중요한 역할을 한다. 따라서 본 연구에서는 국내 밀 품종의 수발아 저항성 정도와 CP 유전자의 발현과의 연관성을 분석하고자 등숙기 종자에서 발현하는 CP 유전자의 발현 양상을 qRT-PCR을 수행하고 있으며, CRISPR/Cas9 system을 이용해 CP 유전자를 교정하고자 수발아에 약한 백립계밀 품종의 CP 유전자의 염기서열을 확보하여 CRISPR/Cas9 벡터를 구축한 후 미성숙배에 particle delivery system으로 유전자 교정을 수행하고 있다. 이 연구를 통해 적립계 밀이 수발아 특성이 우수한 원인을 규명하고, 아울러 국내 백립계 보급종의 수발아 내성을 향상 이용할 수 있을 것으로 기대한다.

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PD-0028

Analysis of a missense mutation in Dicer-like III gene among soybean germplasm from nine different countries

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DNA methylation, which epigenetically silences genes to control their expression, is generated by the RdDM (RNA-directed DNA Methylation) pathway in plants. DCL3 (Dicer-like III) is a key enzyme of the RdDM that cuts dsRNAs from 21 nt to 24 nt long siRNAs, but most of them have 24 nt lengths. Among the various lengths of siRNAs, 24 nt siRNAs act as substrates of AGO4 protein and activate the downstream process to reinforce DNA methylation. In angiosperms like *Arabidopsis thaliana*, most of the siRNAs diced by DCL3 have a 24 nt size. However, soybean (*Glycine max*) generates a relatively larger number of 21 nt and 22 nt siRNAs than 24 nt siRNAs. Even closely related Legume species such as *Medicago truncatula*, *Phaseolus vulgaris*, and *Arachis hypogaea* produce more 24 nt siRNAs than 21 nt and 22 nt. In previous research, we have suggested that a missense mutation in soybean DCL3 may cause the RNase III domain to lose its activity that dices dsRNAs to 24 nt siRNAs. To see if this trait broadly occurs not only in cultivars but also in other biological types of soybean, we analyzed the genetic resources of landrace and wild soybean (*G. soja*) germplasm from nine different countries.

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PD-0029

Potato virus X-mediated genome editing in *Capsicum annuum*

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Genome editing is a powerful tool for plant science and crop breeding. Plant genome editing is mostly achieved by conventional transgene-mediated delivery of CRISPR-Cas9 reagents. However, pepper (*Capsicum* spp.) is known to be recalcitrant for *Agrobacterium*-mediated transformation. In this study, we described a method for *Potato virus X* (PVX) -mediated genome editing in *C. annuum* which could deliver Cas9 and single-guide RNA (sgRNA) simultaneously. We used three cultivars that could be regenerated efficiently: *C. annuum* cv. Ferrari and *C. annuum* cv. Fiestar are *Brassica napus BABY BOOM* transgenic plants that can induce somatic embryo and *C. annuum* cv. C15 is an inbred line. sgRNA was designed to target the *Phytoene desaturase* gene, of which the knock-out mutant can be identified through the albino phenotype. Cotyledons and true leaves were inoculated with *Agrobacterium* including PVX vector that contained Cas9 and sgRNA. Mutations were detected in inoculated leaves through the targeted-next-generation sequencing. Cotyledons and true leaves of Ferrari showed 0.2% and 0.25% mutation near the target cleavage site, respectively. In the C15 cotyledon, 0.46% mutation was confirmed. In order to increase the editing efficiency, 37°C heat was treated for 24 h on the 9th day after inoculation and the mutation rate increased to 0.5%-0.74% (1.6-2.5 times). Among the elongated shoots, 130 shoots were acclimatized and will be subjected to mutation detection. This simple and efficient virus-mediated CRISPR-Cas9 delivery method is expected to contribute to the genetic function research and the development of breeding materials by establishing genome editing technology in peppers.

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PD-0030

Functional analysis of *Solanum lycopersicum MALE STERILITY 1* and its application in the resistance breeding against *Tomato yellow leaf curl virus* infection

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Meiosis, tapetum development and pollen coat formation are prerequisite for male fertility. Especially, tapetum placed between the sporangenous tissue and the anther wall is important for the nutrition, pollen development, and a source of precursors for pollen coat. Sporophytic pollen coat proteins (sPCPs) derived from the tapetum are deposited into pollen wall cavities and indispensable for the interaction between pollen and stigma, pollen hydration, and environmental protection. The expression of sPCPs is under the regulation of tapetum transcription factor MALE STERILITY 1 (AtMS1). We found *Solanum lycopersicum MALE STERILITY 1* (*SlMS1*) orthologous with *AtMS1* and produced T_0, genotypically *SlMS1*/*slms1*, in the cultivar Micro Tom through *SlMS1*-targeted CRISPR/Cas9 vector construction and its introduction via agrobacterium-mediated transformation. Phenotypically this genotype was almost identical with its wild type. Further, 16 among 60 T_1 plants didn't produce pollen. Sanger sequencing and deep sequencing for the PCR products amplifying CRISPR/Cas9 targeted regions revealed that all 16 plants harbored *slms1*/*slms1* genotypes but their mutation patterns were diverse. We chose three *slms1*/*slms1* lines commonly sharing deletion of single nucleotide C in the exon because these plants were phenotypically identical with Micro Tom except pollen production. We crossed these male-sterile plants with *Tomato yellow leaf curl virus* (*TYLCV*)-resistant cultivar to accumulate disease resistance and male sterility. In addition, primer pairs able to amplify 90 bp regions harboring single C deletion were designed for the efficient genotyping via high resolution melting (HRM) technique. HRM analysis confirmed that all the F_1 generation plants harbored *SlMS1*/*slms1*.

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PD-0031

Effects of temperature alteration on the NSm-mediated hypersensitive responses in the interaction between *Tomato spotted wilt virus* and *Solanum lycopersicum*

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Tomato spotted wilt virus (*TSWV*) is involved in Bunyavirales, Tospoviridae and invades more than 1000 plants belonged to solanaceous, fabaceous, cucurbitaceous plants and other agriculturally important ornamental and medicinal plants. Introduction of resistant germplasm has been the most ideal *TSWV* management method, however, its resistance was frequently broken down by the emergence of new races and lack of commercially available resistant varieties further intensify the yield losses. *Sw-5b* is the most popular resistant gene against *TSWV* infection and its protein-protein interaction with the non-structural protein, NSm necessary for intra- and intercellular *TSWV* movement, resulted in hypersensitive response (HR) and disease protection. In the interaction between *TSWV* and resistant gene Tsw-harboring pepper, *Tsw*-mediated HR was significantly affected by physiological condition of pepper plants and environmental conditions including temperature. To investigate the effect of temperature alteration on the HR development in tomatoes, we compared the disease development in the compatible interactions between SwTo2 strain and tomato cultivars Seogwang, SuperDotaerang and in the incompatible interactions between SwTo2 and cultivars Tory, Lucky. Four tomato cultivars were inoculated with SwTo2 strains and disease development was observed for 10 days under the LED and at 25°C and 30°C, then the upper systemic leaves were harvested and the amount of viral RNA was evaluated via real time PCR. In addition, we cloned *NSm* of SwTo2 into the pEarlyGate 101 to express NSm-YFP fusion protein through Gateway cloning. The construct was introduced into *Agrobacterium tumefaciens* strain GV2260 to analyze the effect of NSm on the HR expression directly.

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PD-0032

Targeted replacement of *PhcA* encoding transcription factor regulating multiple virulence genes in *Ralstonia solanacearum* infecting *Solanum lycopersicum*

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Bacterial wilt, caused by *Ralstonia solanacearum* species complex (RSSC), is devastating disease in tomato. *R. solanacearum* is the well-studied organisms, however, gene deletion or replacement still remained as a major obstacle for efficient functional analysis of genes of interest. Establishment of stable and streamlined vector construction for gene deletion is indispensable for massive functional analysis. Primers able to amplify fixed lengths of up- and downstream of PhcA, transcriptionally regulating multiple virulence genes, were designed. Therefore, their annealing temperatures and PCR conditions were highly variable. *ExTaq* polymerase-mediated gradient PCR supplemented with betaine hydrochloride and dimethyl sulfoxide stably overcame amplification problems. After PCR product purification, fusion product was generated through overlap-extension PCR using upstream fragment harboring 5'-end of downstream and downstream fragment. After amplification, the fusion product was cloned into pGEM-T easy vector and the fragment was isolated through *Bam*HI/*Xba*I digestion and cloned into the same sites of suicide vector, pEX18Tc. The construct was directly introduced into *R. solanacearum* via electroporation and primary merodiploid was screened in the presence of tetracycline and further counter-selected on the TYS10 agar. Targeted replacement was finally confirmed through PCR and sequencing. The same method also went sweetly in the functional analysis of *RSc2365* and *RSc0672*. Developed knockout vector construction method was able to precisely and stably delete genes of interest necessary for functional analysis. The vector was constructed within a week without any special instruments or reagents, therefore, this method will be a cornerstone for efficient and massive functional analyses.

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PD-0033

Digital Tools for Rice Genomics and Phenomics to Accelerate Breeding

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The voluminous increase in rice genomics and phenomics data has created the need for efficient analytical gene discovery tools for breeding applications. Hence, we have developed a number of web tools, databases, and standalone applications. In 2014, we founded the International Rice Informatics Consortium (IRIC) to support, develop, and promote such community resources. Our first SNP-Seek database (https://snp-seek.irri.org) for rice genomic diversity was released in 2015; V2 now curates SNPs, indels, and large SVs on the 3K RG and other datasets, with tools for access, exploration, and discovery. V3 release (upcoming) has a refreshed interface with logon access to freemium and premium (paid) versions. Early release data and tools (depending on donor mandates) will be available first to premium users followed by roll-out to freemium access twice yearly. Haplotool (https://gdm-haplo.irri.org/haplotool/) is an Rshiny stand-alone and web app for haplotype analysis for user-specified datasets. Crop Galaxy (http://cropgalaxy.excellenceinbreeding.org) is a web-based, open access platform with tools for data manipulation, genomic prediction, ML, and GWAS methods. We are adapting ImageBreed (https://imagebreed-irri.sgn.cornell.edu/) from the Mueller team at BTI/Cornell for UAV data from HTP field-based experiments and analysis. We have also developed a web-based Streamlit app that implements linear regression, Keras NN, and SVR based ML methods to model UAV phenomics data and predict genotype-phenotype associations (https://share.streamlit.io/songwan/htpps/develop/app.py). While we focus on rice, all of these public, open source tools are adaptable to other crops. Further development and additional tools will enable breeding to become more and more digitized and its process accelerated.

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PD-0034

작물 생리장해 수집 스마트폰 앱 개발

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전라북도 전주시 덕진구 농생명로 370 국립농업과학원 농업생명자원부 유전자공학과

최근 인공지능 기술의 발달로 의료, 제조, 서비스업 등 산업 전반에서 영상 이미지 빅데이터를 이용해 기존 방법보다 더 빠르고 정확하게 문제를 진단하고 평가하는 일들이 가능하게 되었다. 특히 농업분야에서는 선진국을 중심으로 농업 환경 정보와 작물 영상을 생육단계별로 수집하여 질병을 사전에 예측하고 최적의 작물 관리를 통해 생리장해 피해를 최소화 하는 연구를 활발히 진행중이다. 이와 같은 정확하고 신속한 생리장해 평가를 위해서는 먼저 다양한 대량의 데이터 수집이 선행되어야 한다. 우리는 스마트폰으로 실험실, 노지, 시설에서 작물생리장해 영상이미지와 재배 환경정보를 체계적이고 손쉽게 수집할 수 있는 앱을 개발하였다. 우리가 개발한 앱은 환경정보 연계(기상청 정보), 생리장해 영상 생산 가이드제공, 실험관리, 사용자별 권한관리, 다양한 조건 검색 등의 기능이 있다. 데이터베이스에 저장된 대량의 생리장해 영상정보는 인공지능 학습용 데이터셋으로 추출되어 활용될 수 있다. 현재 토마토 7개 품종에 대해 염해, 건조, 풋마름병, 토마토황화잎말림바이러스(TYLCV) 등의 생리장해 이미지를 47,000장을 생산하였고 인공지능 학습을 위해 6,800 장을 라벨링작업을 완료하였다. 앞으로 인공지능 학습을 통해 생리장해 평가를 스마트폰에서 가능하도록 고도화 할 계획이다.

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PD-0035

DNA-free genome editing of *Solanum lycopersicum* 'Heinz 1706' using optimized protoplast culture

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CRISPR/Cas9 ribonucleoproteins enable DNA-free genome editing, thus, protoplast culture is essential to develop mutant plants. However, *Solanum lycopersicum* 'Heinz 1706' that represents a model cultivar for tomato genome analysis has not yet been studied. The factors affecting the protoplast culture have been optimized including hormone combination and sugar types. To evaluate the editing efficiency using protoplasts of Heinz 1706, we have deployed the polyethylene glycol-mediated transfection for editing the TYLCV resistance gene, *ty5*. Editing efficiencies and major editing patterns were varied depending on designed sgRNAs with the highest efficiency (8.71%). These results will help to increase the efficiency of DNA-free genome editing in tomato.

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PD-0036

CAM Biodesign: Engineering Crassulacean Acid Metabolism (CAM) Photosynthesis into C_3 plants for Improving Water-use Efficiency

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A changing global climate with greenhouse gas emissions is predicted to lead to increased surface soil drying trends will lead to reduced terrestrial net primary productivity and an expansion of drylands. Yield loss risks under drought and heat conditions will increase up to 20% for major crops by the end of the 21st century. Crassulacean acid metabolism (CAM) is an adaptation that reduces water loss by shifting the diel rhythm of CO_2 fixation from day to night which results in dramatically improved water-use efficiency (WUE). CAM is widespread across the plant kingdom and is expressed in at least 343 genera in 35 families and accounts for 6~7% of vascular plant species. Introducing CAM photosynthetic machinery into C_3 plants (CAM Biodesign project) is expected to confer improved WUE to allow C_3 plant species to withstand long episodes of drought or to expand crop production into semi-arid regions. To achieve this long-term project goal, four major objectives are being pursued: 1) define and characterize the genetic basis of key CAM enzymes in 'carboxylation' and 'decarboxylation' modules; 2) engineer increased mesophyll cell volume in order to store malate in the vacuoles (tissue succulence engineering); 3) develop an effective multiple gene assembly toolkits to enable staking of a large number of transgenes into a single genomic locus to transfer fully functional 'carboxylation' and 'decarboxylation' modules from CAM species to C_3 species; and 4) analyze the effects of these modules on 'stomatal control', nocturnal CO_2 assimilation, biomass yield, and WUE. Here, progress achieved to date is presented for CAM Biodesign for improving WUE.

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PE-0001

The Suitable Soybean, Wheat and Barley Varieties for Double Paddy Cropping System in Northern Gyeonggi Province

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This experiment was conducted a three-year test from 2018 to 2020 to select a variety of soybean, wheat and barley suitable for double paddy cropping system in northern Gyeonggi-do Province by the Agricultural Resources Research Institute, GARES, Yeoncheon, Korea.

The soybean varieties that showed maturity date before mid to late October during the planting season of wheat and barley were 'Yeonpung' and 'Manpung'. When soybean varieties were sown on June 20th after the paddy cultivation of wheat and barley, the yield of 'Yeonpung' and 'Manpung' was higher than that of 'Gangpung' and 'Nokpung', which was advantageous for the double paddy cropping wheat and barley. The tofu yield was the highest in 'Manpung' at 248%, which was 10% higher than that of 'Daewon'. Taste scoring of tofu in 'Manpung' was also the highest from a taste panel. Therefore, the soybean varieties that can be harvested before the planting season of the paddy cultivation of wheat and barley in northern Gyeonggi-do Province were 'Yeonpung' and 'Manpung', especially 'Manpung' had excellent properties of tofu.

The maturity date of the barley 'Hyemi' in the first seeding time was May 31st, the fastest among the barley varieties. The rest of the barley varieties could also be harvested before June 20th, the planting season of soybeans, even if these take about a week from maturity to harvest. The yield of 'Dahyang' was the highest at 410kg/10a among the hulled barley varieties. The yield of 'Jaeanchalssal' was the highest at 354 kg/10a among the hullless barley varieties. In particular, the barley 'Hyemi' had the lowest rate of winter killing with 4.4%, indicating strong against cold injury. The maturity date of the barley 'Hyemi' in the second seeding time was June 9th, the fastest among the barley varieties and the yield of that was the highest at 325 kg/10a. The rate of winter killing of the barley 'Hyemi' was the lowest at 4.6%, which was strong against cold injury despite the late seeding time. The maturity date of the wheat 'Jojung' and 'Johan' in the first seeding time was June 3rd and June 6th, respectively. The rest of the wheat varieties could also be harvested before June 20th, the planting season of soybeans, even if these take about a week from maturity to harvest. The yield of the wheat 'Suan' and 'Joan' was significantly higher at 453 kg/10a and 448 kg/10a, respectively. In the wheat varieties the rate of winter killing ranged from 0.0 to 3.3%. That means the wheat varieties were more resistant to cold injury than the barley varieties. The maturity date of the wheat varieties in the second seeding time ranged from 9 to 12 June, allowing harvesting before the soybean sowing on June 20th. Like the first seeding time, the yield was significantly higher at 449 kg/10a in 'Suan' and 501 kg/10a in 'Joan'. The rate of winter killing of the wheat in the second seeding time was between 0.7 and 4.7 %, slightly higher than that in the first seeding time.

When the barley varieties were planted on October 19th, ‘Saechalssal’ and ‘Jaeanchalssal’ were selected among the hulled barley varieties. Among the hullless barley varieties, ‘Dahyang’ and ‘Hyemi’ were selected. The reason for the selection was that it was harvestable before the soybean sowing on June 20th of the following year and high yielding. When the barley varieties were planted on October 27, ‘Hyemi’ was selected because of resistance to cold injury. When the wheat varieties were planted on October 19th and October 27th, ‘Suan’ and ‘Johan’ were selected because of the proper maturity and high yielding for double paddy cropping soybean.

The results of economic analysis of the double paddy cropping system of soybean/unhulled-barley, soybean/hullless-barley, and soybean/wheat are as follows: It was analyzed that when soybean ‘Manpung’ and hullless barley ‘Jaeanchalssal’ were planted, their income was 153%p higher than that of single cropping rice. Income of soybean ‘Manpung’ and wheat ‘Johan’ was 101%p higher than that of single cropping rice. Income of soybean ‘Manpung’ and unhulled barley ‘Dahyang’ was 77%p higher than that of single cropping rice.

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PE-0002

The Suitable Soybean Variety for Bean Sprouts by Environment-friendly Cultivation in Northern Gyeonggi Province

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This experiment was conducted a two-year test from 2020 to 2021 to select a soybean variety for bean sprouts suitable for environment-friendly cultivation in northern Gyeonggi-do Province by the Agricultural Resources Research Institute, GARES, Yeoncheon, Korea. The tested varieties were ‘Pungsannamulkong’, ‘Pungwon’, ‘Haewon’, ‘Aram’, ‘Haepum’, ‘Bosug’, ‘Wonhwang’, ‘Wonkwang’, Sinhwa’ and ‘Joyang1’. In The 2020 experiment, the sowing time was June 5th, and in the 2021 experiment, the sowing time was June 20th. In the 2020 experiment, ‘Aram’ and ‘Sinhwa’ did not mature before October 22th, the 10-year average first frosty day in northern Gyeonggi-do. ‘The weight of one hundred seeds in ‘Pungsan’, ‘Aram’, ‘Haepum’, ‘Bosug’ and ‘Wonkwang’ were within the range of 10 to 12g, which is the appropriate for bean sprouts. The yield was high in the order of ‘Pungwon’, ‘Wonkwang’, ‘Pungsan’, ‘Haepum’, ‘Bosug’, but there was no significant difference. The occurrence of lodging was severe in ‘Pungsan’ and ‘Sinhwa’. In the 2020 experiment, anthracnose occurred severely in all varieties, and other diseases did not occur severely. The ratios of the seed diameter remaining on a 6.3mm frame in varieties excluding ‘Haewon’ was more than 2%. Except for Haewon, varieties were exceeded the government's purchasing standard which was not more than 2.0% of seed remains on the 6.30 mm frame. In the 2021 experiment, the entire variety matured before October 22th. ‘The weight of one hundred seeds in ‘Pungsan’, ‘Aram’, ‘Haepum’, ‘Bosug’, ‘Wonkwang’ and ‘Sinhwa were within the range of 10 to 12g. The yield was high in the order of ‘Wonkwang’, ‘Pungwon’, ‘Haewon’, but there was no significant difference. The occurrence of lodging was most severe in ‘Pungsan’. The occurrence of purple blotch was severe in ‘Wonhwang’ and ‘Joyang1’in 2021. The ratios of the seed diameter remaining on a 6.3 mm frame in varieties excluding ‘Haewon’ and ‘Bosug’ was more than 2%. In the processing characteristics of soybean sprouts, the yield of soybean sprouts was high in the order of ‘Joyang1’, ‘Aram’, ‘Pungwon’, ‘Wonhwang’, ‘Sinhwa’, ‘Bosug’, ‘Wonkwang’ and ‘Pungsan’. As a result of the 2020~2021 experiment, ‘Pungsan’, and ‘Wonkwang’ was selected as a sprout soybean varieties suitable for environment-friendly cultivation in northern Gyeonggi-do in consideration of the screening index.

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PE-0003

A New Soybean Cultivar, 'Jowon' Adaptable for Double Cropping System with Pod Shattering Resistance

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‘Jowon’ adaptable for double cropping system with pod shattering tolerance was soybean cultivar developed in 2021 by the Agricultural Resources Research Institute, GARES, Yeoncheon, Korea. ‘Jowon’ was first developed in 2010 from a cross between the tofu and soy-paste soybean ‘Daewon’ and ‘Yonpoong’ variety. Its characteristics are determinate growth type, erect growth habit, purple flower color, spherical seed shape, yellow testa, yellow hilum color and lanceolate leaflet shape. The flowering date of this cultivar was July 26th and the maturity date is Oct 5th in Gyeonggido Province, which were earlier than those of standard cultivar ‘Daewon’ and adaptable for double cropping system. The 100-seed weight was 26.1g, which was lower than that of ‘Daewon’(29.3g). The yield of ‘Jowon’ was 2.76MT/ha in the local adaptability tests in standard cultivation in three regions which were Yeoncheon, Hwaseong and Yeoju(Yangpyeong) from 2019 to 2021. As a result of verifying the genetic characteristics of the variety using the SNP molecular marker, the resistance to pod shattering was confirmed. Additionally, after drying it at 40℃ in a dryer, It’s pod shattering rate was 1.7%, lower than that of ‘Daewon’. As a result of the processing quality test, ‘Jowon’ is suitable for making tofu, fermented soybean lump and fast-fermented bean paste. Their yield is 6%, 3% and 3% higher than that of ‘Daewon’, respectively. ‘Jowon’ is highly adaptable to the environmental conditions of Gyeonggi Province, especially to the northern region of Han River.

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PE-0004

Genetic diversity and population structure of native South Sudan maize accessions using SSR markers

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Maize is one of the world's leading grains and covers all agricultural ecological zones of South Sudan, but farmers' field yields are very low and only certified for dependence on undeveloped landrace varieties. Small-scale farmers in South Sudan practice subsistence agriculture regarding maize. In the current study, genetic diversity and population structure were investigated among 37 landrace maize accessions collected from farmer's fields of South Sudan, using 27 SSR markers. A total of 200 alleles were revealed with an average of 3.0 alleles per locus and a range from 7.4 to 13.0 alleles per locus. The observed heterozygosity values ranged from 0.06 to 0.91with an average of 0.35. A high PIC values were identified with mean of 0.69, indicating of the benefit of the selected SSR loci. Genetic structure analysis revealed a moderate genetic differentiation within maize populations with fixation index (Fst) revealed at 0.16, while a very high genetic differentiation among Group of populations of three regions with mean Fst recorded at 0.37. The analysis of the unweighted pair group method with arithmetic mean (UPGMA) dendrogram, clustered the 37 maize accessions into three groups with 43% genetic similarity. The clustering patterns of maize accessions agrees at some extent with their source. The findings of this study will provide maize breeders with superior understanding of maize diversification as well as reservation of genetic resources to be used in the selection of advantageous and useful resources for the development of maize varieties in South Sudan.

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PE-0005

A White Waxy Hybrid Corn, 『Dodamchal』 with Good Eating Quality

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A 'Dodamchal', a new waxy corn hybrid, is a single cross hybrid developed by the crop breeding team of Crop Research & Development Division, GARES, Hwaseong, Korea in 2020. This hybrid was made by crossing between seed parent GMW0035 and pollen parent GMW0039. This variety was 71 days of growth duration from seeding and silking. Silking date had 3 days fast than Ilmichal. Ear length and ear diameter of 'Dodamchal' was 19.9 cm and 40.6 mm, respectively. The ratio of kernel set length to ear length was 96.2% and lower than Ilmichal. The number of fresh ears was more than Ilmichal however the weight of fresh ears was lower than Ilmichal in the local adaptability test in 8 areas from 2018 to 2020. This cultivar would be well adaptable to the Gyenonggi province.

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PE-0006

적색 대립으로 다수성이며, 가공적성이 우수한 팥 신품종 '홍주'

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'홍주'는 기계화적성이 우수하고 가공적성이 우수한 적색 대립 팥 품종을 육성하고자 2011년 하계에 국립식량과학원에서 쓰러짐에 강하고 담적색인 IT189429를 모본으로 하고 종자가 대립인 K275824을 부본으로 인공교배하여 계통육종법으로 선발한 품종이다.

2017~2018년 생산력검정시험에서 쓰러짐에 강하고 수량성이 높아 "밀양46호"로 계통명을 부여하였다. 2019~2021년 3년간 지역적응시험(밀양, 청원, 나주, 원주)을 실시한 결과, 가공적성이 우수하고 도복에 강한 품종으로 인정되어 2021년 농작물 직무육성 신품종 선정위원회에서 신규등록품종으로 결정되었다.

'홍주'는 개화일수 54일로 '아라리'와 비슷하나 생육일수는 102일로 3일 늦은 중만생종이다. 경장은 55㎝이며, 협수는 29개로 '아라리'보다 4개 많다. 100립중은 17.4g으로 적색의 종피색을 가진 대립 품종이다. 통팥 가공적성이 우수하고 앙금수율이 높아 팥 가공제품 제조시 품질면에서도 유리 하다. 수량성은 지역적응시험에서 평균수량이 2.21MT/ha로 다수성 품종이다. 적응지역은 강원도 산간고랭지를 제외한 전국 팥 재배 지역에서 재배가 가능하다. 기계수확이 가능한 '홍주'는 노동력과 생산비절감으로 생력화와 농가소득 증대에 기여할 것으로 기대된다.

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PE-0007

Cochlioquinone-9, a natural products, effects on damage of white-backed planthopper to rice

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The white-backed planthopper (*Sogatella furcifera*, WBPH) is a pest that causes loss of rice yield and threatens the global food supply. Excessive use of pesticides increases pesticide resistance to pests and causes environmental pollution. Therefore, it is necessary to develop natural product-based pesticides to control WBPH. Secondary metabolites act as a defense against pathogens and pests and are valuable as pesticides and breeding materials. Cochlioquinone is a secondary metabolite that exhibits various biological activities, has a negative effect on the growth and development of insects, and contributes to plant defense. In this study, WBPH resistance to cochlioquinone-9 (cq-9), a bioactive substance, was evaluated and the expression profile of related genes were analyzed. After inoculating with WBPH, the effect of cq-9 on the growth of rice was determined by measuring the length of the plant. cq-9 improved the ability of plants to resist WBPH and had an effect on plant growth. Gene expression analysis revealed that cq-9, a quinone family, interacts with plant defense genes regulating aromatic amino acid (AAA) and precursors of various plant secondary metabolites, and it plays a role in increasing the resistance of rice to WBPH. It is suggesting that cq-9 related to flavonoid compounds. Overall, this study provides insight into the mechanisms of WBPH resistance and suggests that cq-9 represents an environmentally friendly agent for WBPH control.

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PE-0008

Application CRISPR/Cas9 to accelerate early maturing-heavy panicle type breeding in rice

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Food security is essential for zero-hunger. Climate change is already exacerbating food insecurity through rising temperatures, changing precipitation patterns, and frequent extreme weather events and the impact is expected to grow over time. Especially heading date is a major factor closely associated with yield in rice. CRISPR/Cas9 system will accelerate the time to achieve zero-hunger around the world by regulating the expression of genes related to heading date and yield. Here, we applicate CRISPR/Cas9 system for demonstrated the effect of heading date and yield components under identical genetic background. As a short-day plant, rice suppresses flowering and promotes vegetative growth under long-day conditions. In this research, we generated genome-editing lines (*OsCK*q1-G) using CRISPR/Cas9 technology, and *OsCK*q1 was edited which are suppresses flowering under long-day conditions. *OsCK*q1-G was early flowered than the Ilmi which was background of genome editing rice. In genome-editing lines, only heading date was earlier than Ilmi, however all other investigated agricultural traits were same. The expression levels of genes involved in flowering, including *OsCK*q1, were investigated in Ilmi and *OsCK*q1-G. At *OsCK*q1-G, showed low expression of *OsCK*q1. While, the expression level of *Hd3a* was increased, and it was demonstrated that *OsCK*q1 is an upstream regulator of *Hd3a.* Our research demonstrates the effect of heading date gene on reproductive transition and yield components under short-day conditions. And finally, our results will provide new strategies into rice breeding contribute to a solution to the zero-hunger by securing stable rice production through the development of early maturing-heavy panicle type cultivars.

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PE-0009

Effect of different salts on nutrients uptake, gene expression, antioxidant, and growth pattern of selected rice genotypes

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The association among ion uptake, gene expression, antioxidant, biomass, and root and shoot development in rice under different salt stress are not fully understood. This study used two salts ($CaCl_2$ and $MgCl_2$) along with NaCl and analyzed their effects on mineral uptake (macronutrients and micronutrients), gene expression, seed germination, antioxidants, plant growth, and biomass in different rice genotypes. All agronomic traits among rice genotypes were drastically reduced by NaCl stress compared to other salts. Different salt stress differentially regulated ion uptake in the roots and shoots among different rice genotypes a consistent decrease in Ca^{2+}, Mn^{2+}, and Fe^{2+} ions was observed in the roots of Cheongcheong, Nagdong, and IR28. Similarly, under different salts, the stress in the shoots of Cheongcheong (Ca^{2+}, Na^{+}, and Zn^{2+}) and Nagdong (Ca^{2+}, Mg^{2+}, Na^{+}, and Zn^{2+}) and the shoots of IR28 (Ca^{2+} and Mg^{2+}) consistently increased. After 6 and 12 h, of stress, *OsHKT1*, *OsNHX1*, and *OsSOS1* gene upregulation in the shoots of Nagdong and roots and shoots of the salt-tolerant cultivar Pokkali. The glutathione (GSH) content increased in the shoot of IR28 and Nagdong by NaCl, and MgCl2 salt, whereas POD activity increased significantly by $CaCl_2$ and $MgCl_2$ in cultivar Cheongcheong and IR28 shoot. Therefore, this study suggested that Pokkali responded well to NaCl stress only, whereas the plant molecular breeding lab cultivar Nagdong showed more salt tolerance to different salts (NaCl, $CaCl_2$, and $MgCl_2$). This can potentially be used by agriculturists to develop the new salt-tolerant cultivar Nagdong-like Pokkali.

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PE-0010

Identification of a major QTL and validation of related genes for tiller angle in rice using QTL analysis

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Tiller angle, defined as the angle between the main stem and its side tillers, is one of the main target traits selected in inbreeding to achieve the ideal plant type and increase rice yield. Therefore, the discovery and identification of tiller angle-related genes can provide architecture and yield. In the present work, using QTL analysis hence a total of 8 quantitative trait loci (QTLs) were detected based on the phenotypic data of tiller angle and tiller crown width in two years. Among them, four QTLs (*qTA9*, *qCW9*, *qTA9-1*, and *qCW9-1*) were overlapped at marker interval RM6235-RM24288 on chromosome 9 with a large effect value regarded as stable major QTL. Twenty tiller angle-related genes were selected from the target region and the relative gene expression levels were checked in five compact type lines, five spreading type lines, and their parental lines. Finally, *OsSAURq9* which belongs auxin-responsive SMALL AUXIN UP RNA (SAUR) protein family was selected as a target gene. Overall, this work will help broaden our understanding of the genetic control of tiller angle and tiller crown width, and this study provides both a good theoretical basis and a new genetic resource for the breeding of ideal-type rice.

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PE-0011

Identification of quantitative trait loci for salinity tolerance in rice using Cheongcheong, Nagdong mapping population

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The soil salinity is the critical abiotic stress that limits rice production and is a major problem for rice-based farming systems in many rice-producing areas of the world. Mapping of QTLs by using molecular markers can be helpful to find salt-tolerant genes and produce some salt-tolerant cultivars. Three weeks old, 120 double haploid CNDH lines derived from a cross between the *Indica* cultivar Cheongcheong and the *Japonica* cultivar Nagdong and their parental lines were used to identify quantitative trait loci (QTLs) linked to salinity tolerance. After 2 weeks of salt stress, 8 different traits viz. shoot length (SL), root length (RL), salt injury score (SIS), chlorophyll contents (CHC), shoot fresh weight (SFW), shoot dry weight (SDW), root fresh weight (RFW), and root dry weight (RDW) were evaluated. A linkage map of 12 rice chromosomes was constructed from genotypic data DH lines using 778 SSR markers. The linkage map covered a total genetic distance of 2121.7 cM of the rice genome with an average interval of 10.6 cM between markers. Twenty-three QTLs (LOD >2) were identified on chromosomes 1,2,3,5,6,7,8,9,10,11, and 12 using composite interval mapping with trait increasing alleles coming from both parents. The QTL, *qSIS-3b* having a LOD score of 6 and phenotypic variance of 31% within the interval RM3525-RM15904 on chromosome 3 was screened to find candidate genes related to salinity tolerance. A total of 19 genes were located in this interval among them 14 candidate genes were selected on basis of different sequence annotations.

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PE-0012

Utilization of two rice populations data derived from *Indica-Japonica* cross for rice molecular breeding

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As crop improvement and biotechnology research increases, the use of more diverse rice genetic resource populations is required. In recent years, many *indica-japonica* rice hybrids have been developed and planted widely in Asia for their super-high yield potential. Accordingly by registering data from the Cheongcheong/Nagdong double haploid (CNDH) and the Samgang/Nagdong double haploid (SNDH), developed in this laboratory, it is intended to support genomics-assisted rice breeding. The cultivars Cheongcheong (IT228761, *indica*-type), Nagdong (IT006182, *japonica*-type) and Samgang (IT221837, *indica*-type) were used as the parents of the double haploid (DH) population. CNDH and SNDH population survey trait data were registered in the national data station system (Station-B) based on NCBI. The CNDH and SNDH developed double haploid (DH) mapping populations using *indica* and *japonica* rice cultivars and released at Kyungpook National University in August 2021 have been used to identify genomic regions associated with phenotypic traits of rice. Genetic maps created using genetic resource populations can be used to increase selection efficiency by using markers associated with major genes when selecting traits involved in polygene, and can be used to shorten breeding cycle and genome editing. These mapping populations and related datasets provide important insights into the rice cultivars and facilitates the practical use in rice breeding.

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PE-0013

Mapping QTLs and related genes for plant height of rice in CNDH populations

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Plant height is not only an important agricultural characteristic of crops, but also an important trait in plant factories that are being actively studied recently. In plant factories, culture beds are placed vertically to grow plants, so shorter plants are more efficient. Therefore, in this study, plant height, culm length, and panicle length from 2017 to 2021 were investigated to search for genes related to the plant height of rice in the Cheongcheong/Nagdong doubled haploid populations. As a result of the investigation, the frequency distribution of all traits showed a normal distribution for 5 years, which means that the genes related to the plant height of rice are quantitative traits. QTL (quantitative trait locus) analysis was performed based on these results. As a result of QTL analysis, a total of 32 QTLs were detected in plant height, culm length, and panicle length for 5 years. In particular, 13 QTLs were detected on chromosome 1. Among them, The QTLs of culm length detected in 2019 has a LOD score of 18.58 in RM12285-RM212 region of chromosome 1, indicating that there is a very high possibility that the QTL in this region has a gene related to the plant height of rice. In this result, there were 10 genes related to plant height of rice in the RM12285-RM212 region of chromosome 1. This result can be used as basic data to develop dwarf rice more suitable for plant factories.

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PE-0014

Data analysis and utilization through imaging of CNDH and SNDH

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Rice is 34% of the world's population used as a staple food. Many other crops have accumulated data through imaging. However data analysis on rice are still insufficient. As research policy has recently changed to a policy based on data, the importance of data management is increasing, so in this study we investigated agronomic character (culm length, panicle length, number of tillers, yield) and plant type of Cheongcheong/Nagdong double haploid (CNDH) and Samgang/Nagdong double haploid (SNDH) grown at experimental field of Kyungpook National University in Gunwi after heading stage. The average culm length of CNDH population is 66.1 ± 3.1cm, panicle length is 18.9 ± 2.5 cm, the number of tillers is 10.7 ± 1.5, moisture is 16.2%, weight is 587.4 g, and yield (kg/10a) is 398.0 kg. The average culm length of SNDH population is 69 ± 4.5 cm, panicle length is 19.4 ± 2.6 cm, the number of tillers is 11.2 ± 2.5, yield (kg/10a) is 492.0 kg. The agronomic character and the plant type, panicle of CNDH and SNDH were summarized in the order of agronomic character and plant type. The data was organized into excel and stored in station-B. Thus, other researchers can search for data through station-B. Through this, by sharing the genetic resource data of rice, it became available to anyone, industrial use of genetic resources will increase and is expected to be useful in researching rice molecular breeding.

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PE-0015

Advances in CRISPR/Cas9 and applications for short breeding strategies in rice

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Rice has been adapted to various environmental conditions for a long time, and for this reason, it is a very important staple crop worldwide. Because rice is of great economic and social importance worldwide, it is resistant to various biotic/abiotic stress, and there is a continuous demand for breeding of new cultivars with improved agronomic characteristics. Higher yield and improved organoleptic and nutritional value are also very attractive factors for breeders. The previous breeding system required a lot of time and money to develop new cultivars. However, as CRISPR/Cas9 was applied to breeding, it was possible to breed new cultivars with the traits required by people in a short time, and it is more sophisticated, faster, and more accurate than the previous breeding system. Here, drought-induced gene *OsSAP* was edited by CRISPR/Cas9. After editing, reactive oxygen species scavenging efficiency was decreased under drought stress, making the G0 plants more susceptible. This study also investigated the agricultural traits of genome editing in plants and seeds, and analyzed the expression level of *OsSAP* and *Cas9*, and the expression of *Cas9* remained stable or weakened over the course of generation advancement, but the *OsSAP* expression level was continuously removed from the G_0 plant. The coefficient of variation in both G_1 plants and G_2 seeds were lower than 5%. Taken together, our results suggest that CRISPR/Cas9 could be a novel and important tool for efficiently generating specific and inheritable targeted genome editing in rice, with short breeding cycles.

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PE-0016

Characterization of salt tolerance cultivar(MYIR-S986) in silage rice

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Salinity is one of the major abiotic stress that inhibit growth, yield and productivity of crop plants. Therefore, it is necessary to develop an increased salt tolerance crops for the cultivation in saline soil such as reclaimed land. The objective of this study is to develop a salt-tolerant silage rice lines that grow on reclaimed lands. In order to develop a salt-tolerant silage rice, we carried out to transfer *Saltol*, a major QTL associated with salt tolerance, from IR64-*Saltol*, a salt-tolerant indica variety, into Mogyang, a susceptible elite japonica variety. To determine the effect of salt stress, Mogyang and IR64-*Saltol* cultivars were grown on medium containing various concentrations of NaCl in *in vitro* condition. The shoot length was decrease with increasing salt concentration and roots growth was almost arrested at over 50 mM NaCl concentration in Mogyang cultivar. Based on the preliminary results, we screened salt-tolerant line(MYIR-S986) showing better growth under salt stress conditions. PCR and direct-sequencing results showed that the introgression type of *Saltol* QTL in almost of selected line were derived from IR64-*Saltol* cultivar. Based on the growth and physiological conditions, the new *Saltol* introgression line(MYIR-S986) showed higher salt tolerance compared to the parental cultivar Mogyang. The salt-tolerant lines identified in this study could be used as a genetic resource to improve salt tolerance.

Keywords: salt tolerance, silage rice, QTL, *Saltol*

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PE-0017

A Peanut Variety, 'Da-Ol' with High Oleic Acid and Large Grain

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'Da-Ol' is a new peanut (*Arachis hypogaea* L.) variety which has large-pod and seeds with high-oleic trait. 'Da-Ol' was developed at the Department of Southern Area Crop Science, NICS, RDA, and approved to be released in 2021. It was selected from the pedigree lines crossed between large-grain and early-maturing,'Boreum1' and high-oleic elite line 'YG316'. Through the three years (2019-2021) of regional adaptation trial at four locations, 'Da-Ol' showed 114 g of 100-seed-weight which is highly larger compared to other high-oleic varieties, 'K-Ol' (74g) or 'Hae-Ol' (96g). The seed consists of 29.2% of protein, and 52.5% of crude fat, and its ratio of oleic acid to linoleic acid was 36.5. It exhibited 10.07 MT of fresh-pod yield per ha which was 6% higher than 'Palkwang', a check variety. 'Da-Ol' showed the 4.52g of average fresh pod weight, which is 58% higher than the check variety (2.83g/pod). 'Da-Ol' was also relatively resistant to early leaf spot (*Cercospora arachidicola*) and lodging compared to the check variety.

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PE-0018

논재배 적응 조숙 · 다수성 유채 1대잡종 ‘다보’

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유채(*Brassica napus* L.)는 가을에 파종하여 이듬해에 수확하는 작물로 종실 수량이 많고 종자 안의 조지방 함량도 높아 주로 기름을 생산하기 위해서 재배되고 있다. 우리나라에서 유채는 주로 경관 목적으로 약 5,000ha가 재배되고 있고, 최근에는 식용유 생산을 목적으로 대규모 유채 재배단지가 조성되어 재배면적이 점차 증가하고 있다. 유채유의 생산을 위해서는 파종, 수확 등 재배과정의 생력기계화가 가능한 논 재배가 필수적이다. 따라서 논 재배 적응성이 우수한 내습성 품종뿐만 아니라 후작으로 벼를 재배할 수 있는 조숙 품종의 육성이 필요하다. 농촌진흥청 국립식량과학원은 논에서 생육 및 수량 특성이 우수하고 조숙, 다수성인 1대잡종 품종을 육성하기 위하여 종자친으로 웅성불임계통인 ‘목포CGMS (IT237834)’와 화분친으로 조숙계통인 ‘10007-B-17-3-4 -4’[♂, 내한(IT237768)/탐라(IT237771)]를 인공 교배하여 ‘단교81호’를 양성하였다. ‘단교81호’는 생산력 검정시험(2017~2018)에서 327kg/10a로 수량성이 좋았으며, 전남(무안), 전북(부안) 및 경남(진주)에서 실시한 지역적응시험(2019~2021)에서도 대비품종인 ‘선망’에 비해 숙기가 빠르고, 논 포장에서 생육이 우수하며 수량성이 높은 특성을 보였기에 우수 계통으로 선발하여‘다보’(Da-bo)로 명명하였다. 유채 1대잡종 ‘다보’의 개화기(3월 30일)는 ‘선망’과 같았으나 성숙기(6월1일)는 2일 빨랐고 내병성(균핵병)과 도복저항성은 비슷하였다. 종실수량은 307kg/10a로 ‘선망’에 비해 13%가 많았다. 특히, 논 재배(경남 진주)에서의 수량은 314kg/10a로 ‘선망’에 비해 29%가 많아 논 재배 적응성이 우수하였다. ‘다보’의 종자 내 불포화지방산인 올레산 함량은 65.9%로 ‘선망’의 64.2%에 비해 1.7% 높았으며, 에루스산은 0.3%로 매우 적었다.

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PE-0019

강원 지역 감자 및 배추의 품종별 나비목 해충 섭식 양상 조사

박수형, 강세라, 최장규, 이정태

국립식량과학원 고령지농업연구소

강원 고랭지는 여름철 기온이 서늘하여 병해충의 발생이 국내 타 지역에 비하여 적어 고품질 친환경 농산물의 생산이 가능하였다. 그러나 최근 고랭지 지역도 기온 상승에 따라 기주 범위가 넓고 폭식성인 나비목 해충인 왕담배나방(*Helicoverpa armigera*)과 파밤나방(*Spodoptera exigus*)의 발생이 문제가 되고 있다. 이밖에 진딧물 종류도 과거에 비하여 한 달 이상 일찍 발생하며 작물의 초기 생육과 수량을 감소시키고 있다. 본 조사는 강원 고랭지 지역의 주요 재배 작목인 감자와 여름배추를 중심으로 친환경 재배가 가능한 품종 정보를 제공하고자 강원지역 수집 왕담배나방과 파밤나방 집단을 이용하여 감자와 배추 각각 4품종을 선별하여 품종별 섭식 양상을 조사하였다. 실험용 해충은 고령지 농업연구소에서 인공사료로 2~3회 사육하며 3령에 해당되는 개체를 선발하였다. 왕담배나방(*Helicoverpa armigera*)의 모집단은 횡계 지역에서, 파밤나방(*Spodoptera exigus*)은 강릉 지역에서 수집하였다. 작물은 온실에 파종하여 본엽이 7매 정도 전개되었을 때 지름 1.2cm 크기로 잘라서 페트리디쉬(지름 12cm)안에 품종별로 일정한 간격으로 치상한 후 애벌레를 15마리씩 투여하였다. 왕담배나방의 경우 배추를 먹이로 제공한 경우 t-test 단측검정 결과 5% 유의수준에서 유충의 무게가 증가하였으며 감자는 무게의 변화가 없었다. 감자의 경우 leaf disk 바깥쪽 부분에서 관찰된 개체수가 오히려 많았다. 파밤나방의 경우 배추에서 10% 유의수준으로 유충의 무게가 증가하였으며 감자는 무게 변화가 없었다. 품종별로 살펴보면 배추는 '청*'품종이 왕담배와 파밤나방의 leaf disk에서 섭식중인 유충의 평균 개수가 4.2마리로, 7.7마리로 가장 많았다. 감자는 왕담배 나방의 경우 4품종 간에 큰 차이가 없었으나, 파밤나방의 경우는 '수미' 품종 leaf disk의 유충 개수가 8.5마리로 가장 많았다. 본 조사 결과 나비목 주요 해충인 왕담배와 파밤나방은 고랭지 배추 주요 품종인 '청*'과 '춘*' 품종의 leaf disk를 선호하며 감자의 잎은 품종별로 선호도가 낮았음을 밝혔다. 해당 자료는 고랭지 배추 재배지역의 나비목 해충 대량 발생 억제를 위한 품종 전환의 자료로 활용 가능할 것으로 기대되며 추후 모니터링 품종도 추가할 계획이다.

주제어: 고랭지, 배추, 나비목 해충, 친환경, 방제

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PE-0020

보리누른모자이크병과 도복에 강한 다수성 쌀보리 '소강'

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동계작물인 보리는 국내에서 벼와 이모작 형태로 재배되고 있으며, 주로 혼반용 쌀보리가 가장 많이 재배되고 있다. 하지만 최근 기상변화에 따른 이상기상 발생으로 안정적인 쌀보리 생산이 중요시되고 있어 내병성 및 내재해성이 강화된 품종 개발이 필요한 실정이다. 농촌진흥청 국립식량과학원에서는 재배안정성이 우수한 다수성 쌀보리 신품종 '소강'을 개발하여 육종과정과 특성에 대해 설명하고자 한다. '소강'은 2008년에 '청호'를 모본, '청호/Arta'를 부본으로 교배하여 F_1을 양성하였고, F_2-F_3 세대는 집단으로 F_7 세대까지는 계통으로 선발하였다. 이후 2017~2018년 생산력 검정 시험을 거쳐 전주141호라는 계통명을 부여 받아 2019~2021년 3년간 전주, 나주, 진주, 대구 4개 지역에서 답리작 재배로 지역적응성시험을 수행하였다. 전주141호는 이삭이 6조 밀수형으로 탈망이 양호하였으며, 파성은 Ⅱ로 춘파형이었다. 출수기는 4월 16일로 표준품종인 새쌀과 비슷하였으며, 성숙기는 5월 26일로 새쌀에 비해 1일 정도 늦었다. 간장은 새쌀(80cm)보다 3cm 작았으며, m^2당 수수는 769개로 새쌀(643개)보다 많아 다수의 특성을 보였다. 전주141호의 수량은 답리작 평균 549kg/10a로 새쌀에 비해 9% 증수하였고, 천립중은 25.7g로 새쌀(29.0g)보다 작아 소립종이었다. 또한, 익산 보리누른모자이크병 발병 상습포장에서 내병성을 확인한 결과 이병정도(0: 저항성, 9: 감수성)는 1로 새쌀(8)에 비해 저항성이었다. 내재해성 중 한해는 고휴에서 비슷하였고, 저휴에서 고사주율이 51.0%로 새쌀(66.7%)에 비해 더 좋았으며, 도복(0: 저항성, 9: 감수성)은 2로 새쌀(4)보다 더 강하였다. 전주141호의 원맥 품질특성 결과 아밀로오스 함량이 22.2%로 메성이었으며, 취반특성 중 흡수율과 퍼짐성이 각각 230%, 384%로 새쌀(199%, 356%)보다 우수하였다. 이에 전주141호를 신품종심의위원회에 상정하여 '소강'으로 명명하였고 품종으로 육성되었다. 신품종 '소강'은 보리누른모자이크병 및 도복에 강한 다수성 쌀보리로 재배안정성이 우수한 특성을 가지고 있어 농가 안정생산에 기여할 수 있을 것으로 기대된다.

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PE-0021

보리누른모자이크병과 쓰러짐에 강하고 정립률이 높은 맥주보리 '호단'

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국내 맥주용 보리는 2003년 육성된 '호품'이 수량성과 품질면에서 우수하여 가장 많이 재배되고 있다. 그러나 '호품'은 내도복성, 흰가루병 저항성, 종실의 대립화, 정립률 증진, 베타글루칸 함량 저하 등의 재배적, 품질적 개선이 요구된다. 이에 수량성이 우수하고 종실이 둥글며 도복에 강한 '단원'과 바이러스병에 저항성인 'Myogi nijo'를 교배하여 F_1을 얻고 이를 다시 '단원'으로 2006년도에 인공교배하였다. F_2와 F_3는 bulk로 F_4 이후부터는 1수 1열법으로 계통을 전개하면서 키가 작으면서 도복에 강하고, 농업형질이 우수한 계통을 선발하였다. 2017년부터 전주186호라는 계통명을 부여하여 3개년간 전북, 전남, 경남, 제주 4개 지역에서 출수기, 간장 등 농업적 형질과 수량성을 표준 품종인 '호품'과 비교하였다. 시험결과 전주186호는 간장이 79cm로 '호품'보다 7cm 작고, 도복 저항성 검정(0: 저항성, 9: 감수성)에서 3으로 '호품' 5보다 강한 특성을 보였다. 분자마커를 이용한 (MWG2134) 보리누른모자이크(Barley yellow mosaic virus, BaYMV) 저항성 유전자 확인결과 *rym1* 유전자가 확인되었으며, 바이러스검정에서 저항성 정도가 1로 나타났다(0: 저항성, 9: 감수성). 출수기는 4월 10일로 '호품'보다 2일 빨랐고, 성숙기는 5월 19일로 '호품'과 같았다. L 중은 709g으로 '호품'(693g) 보다 무거웠고, 천립중은 40.9g으로 '호품'(42.9g) 보다 가벼웠다. 수량성은 471kg/10a으로 '호품'보다 3% 증수하였으며, 제주도(전작)에서는 591kg/10a로 '호품'보다 13% 증수하였다. 맥주용 원맥 및 맥아 품질에서 정립률 90.1%(호품 88.0%), 베타글루칸 3.1%(4.0%), 단백질 11.7%(11.3%), Friability 89.7%(86.4%), 효소역가 243WK(244WK) 등으로 우수한 품질 특성을 보였다. 보리누른모자이크병과 쓰러짐에 강하고 맥주용 원맥 및 맥아 품질이 우수한 전주186호는 2019년 신품종으로 선정되어 '호단'으로 명명되었다. '호단'은 1월 최저 평균기온이 -4℃이상 지역에서 안전 재배가 가능하며, 흰가루병이 자주 발생하는 고온다습한 지역은 밀식재배를 피해야 한다.

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PE-0022

쓴맛이 없는 저탄닌이며 소화율과 장 건강 개선 효능이 있는 '노을찰' 수수

한상익*, 최명은, 김지영, 이병원, 추지호, 송석보, 안연주, 정찬식

경남 밀양시 점필재로 20, 국립식량과학원 밭작물개발과

'노을찰' 수수는 2019년 개발되어 등록된 찰수수 품종으로 흰색 찰수수 RTx2907과 대표적인 찰수수 품종인 소담찰을 2015년 인공교배하여 육성된 품종이다. 노을찰은 종피색이 밝은 갈색이며 받침껍질색이 황색을 띄고 있어 기존에 육종된 품종과 차별성을 보였다. 탄닌은 수수의 대표적인 성분으로 아주 떫은맛과 쓴맛을 내는 페놀성 화합물이다. 탄닌은 복잡하게 결합된 폴리페놀로서 항산화 활성 등의 기능성을 보유하고 있지만 다량의 탄닌은 떫고 기분 나쁜 맛을 느끼게 하고 소화를 방해하는 작용을 한다고 알려져 있다. 노을찰의 탄닌 함량은 40ug/g으로 동안메의 75.0mg/g에 비해 극히 적은 양을 함유하고 있고 폴리페놀 함량도 251.6mg/100g으로 아주 적은 양을 함유하고 있으며 플라보노이드와 안토시아닌 색소의 함량도 매우 낮은 특성을 보였다. 반면 노을찰의 전분 특성 검정에서 전분함량은 70.9%로 보통 수준이며 저항전분(8.7%)과 식이섬유(4.0%)도 일반적인 함량 분포를 보이고, 전분의 구조를 결정하는 아밀로펙틴 체인분포나 열흡수 특성에서도 `보통의 특성을 보였다. 전분을 추출하여 도정곡 분말과 소화율 분석 비교에서 전분과 도정곡 분말 모두 소화가 잘되는 특성을 보이고 있음을 확인하였다. 이 결과는 낮은 탄닌 함량에 기인한 것으로 사료되며, 특히 도정곡 분말을 50% 함유한 빵을 이용한 장건강 개선 효능 검정에서 비만과 관련되는 장내 미생물의 비율을 낮추고, 과민성장증후군, 유해 황화물 생성, 장염 발생을 유발하는 세균을 감소시킴을 확인하여 노을찰 수수는 쓴맛과 떫은맛이 없으며 소화도 잘되고 장 건강 개선 효능이 있음을 확인하였다.

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PE-0023

Development of drought tolerant temperate rice varieties utilizing *Pup1* QTL

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The effects of climate change on crops such as rice can result in lower crop yields and nutritional quality due to drought and high temperature. A major issue with climate change in Korea is that drought in the spring leads to the application of huge amounts of fertilizer and water supply. These high-input farming systems increase greenhouse gas emissions and can further contribute to climate change. To reduce high-input farming, it is therefore essential to develop rice varieties that lower the use of chemical fertilizers and are suitable for low greenhouse gas emission-type cultivation. *Pup1* QTL might be effective for good establishment and phosphorous uptake in early growth stage in low water condition. We have developed backcross inbred lines (BILs) harboring *Pup1* QTL by marker-assisted backcrossing (MABC) into temperate rice varieties. Background genotyping of breeding lines was performed by Axiom Oryza 580K genotyping array. Genomic structure of the breeding lines showed more than 67% similarity to the recurrent parent. Under 80% field capacity, the BILs showed advantage in terms of early establishment in that the number of tillers was significantly higher than that of the parents until 40 days after transplanting (DAT). The developed varieties showed better yield and fertility under mild drought condition. The pyramiding of *Pup1* might provide useful breeding materials for the climate-ready rice development.

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PE-0024

습해에 강하고 기계수확이 가능한 동부 '홍원'

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동부는 지방과 단백질 함량이 낮고 비교적 전분 함량이 높아 주로 송편의 소나 떡고물, 죽 등으로 다양하게 이용된다. 전남 영광군을 중심으로 모싯잎송편 소(앙고) 원료 국산화를 위해 종실 생산용 동부가 재배되고 있다. '홍원'은 수량이 많고 기계수확이 가능하고 적갈색 종피인 동부 품종 개발을 목표로 하여 'IT145387'와 IT145373을 2012년 인공교배를 하였으며, 계통육종법으로 'JC1212-B-10-4-2'을 선발하였다. '16~'17년 2년간 실시한 생산력검정시험에서는 적갈색 종피, 다수성 계통으로 유망 시 되어 '전남12호'로 계통명을 부여하고 '18~'20년 3년간 전국 3개소에서 지역적응시험을 실시하였다. '홍원'은 반유한 직립형이고 경장이 43㎝로 표준품종인 '옥당'보다 7㎝ 커 기계수확에 유리하다. 종자 모양은 신장형, 종피색은 붉은색을 띤 갈색, 100립중은 16.4g인 중립종이다. 성숙시는 8월 28일로 '옥당'과 비슷하며, 습해에 강하고 수량성은 지역적응시험 3개소 평균 171㎏/10a로 '옥당(144㎏/10a)' 보다 19% 증수되었다. 적갈색 종피 '홍원'은 유인덕 설치가 필요 없고 콤바인수확이 가능하여 대면적 재배 가능하여 지역 특산 가공품 원료곡 국산화에 기여할 수 있을 것으로 기대된다.

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PE-0025

붉은색, 흑색 점박이 색소찰옥수수 '미현찰' 육성

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찰옥수수는 여름철 대표적인 간식으로 소비되고 있으며 전국 재배면적은 평균 15,000 ~ 16,000ha로 형성되고 있다. 찰옥수수는 주로 풋옥수수로 소비되기 때문에 장기보관이 어려워 여름철에만 판매되므로 시장 규모가 제한적이며 대부분 흰색 또는 검은색의 찰옥수수가 재배되고 있어 시장의 다양성이 부족한 상황이다. 본 연구에서는 기존의 재배되는 찰옥수수의 색과 차별화 된 특징을 가진 색소찰옥수수 품종 육성을 통해 판매자 및 소비자에게 선택의 다양성을 제공하여 찰옥수수 소비 시장 규모를 확대하고자 하였다. 육성경위는 검은색 찰옥수수(수집종)를 8년간 인공교배 하여 육성된 자식계통과 기능성 자색옥수수/HW3//HW3집단에서 분리육종 한 자식계통을 2016년 교배하여 홍교291호로 명명하였다. 홍교291호는 2017년 강원 3개소 생산력 평가 결과 수량성 등 농업형질이 우수하여 2018~2020년 전국 6개 지역에 '강원찰55호'로 공시하여 3년간 평가하였다. 평가 결과 표준품종인 일미찰과 비교하여 출사일수는 3일정도 빠른 중만생종이며 분지 발생이 적으며 병해충 저항성이 강하였으며 이삭수는 6,580개/10a로 일미찰 대비 112%, 이삭중은 1,203kg/10a로 일미찰 대비 96%로 수량성도 우수하였다. '강원찰55호'는 2020년 강원도내 직무육성 신품종 선정위원회에서 우수성이 인정되어 2021년 '미현찰'로 명명하여 품종출원(출원 2021-184)하였다. 신품종 '미현찰'은 시장 테스트와 농가 실증을 거쳐 기존의 찰옥수수와 차별화된 찰옥수수를 원하는 소비자에게 선보일 예정이다.

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PE-0026

Development of Endophyte-Free Tall Fescue (*Festuca arundinacea* Schreb.) Cultivars

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One of the most wide-spread and heavily utilized forages in the world is the cool-season grass, tall fescue (*Festuca arundinacea* Schreb.). 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.

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PE-0027

Evaluation and screening of elite Italian ryegrass (*Lolium multiflorum* L.) germplasm for salinity stress

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The Italian ryegrass (*Lolium multiflorum* L.) is the most popular forage crop among farmers in South Korea. Their excellent palatability and high feed value make them prominent forage crops, harvested in paddy fields and reclaimed lands during the winter. In particular, the Italian ryegrass is grown in large amounts in the reclaimed lands of Korea, which are used as farmlands for large-scale mechanized cultivation. However, the excessively accumulated salt concentration in the soils of reclaimed lands is one of the notable factors that reduces crop productivity and quality. In particular, soil conditions with high salinity are the most important factors that inhibit seed germination, and they are external environmental stimuli closely associated with the growth, development, and productivity of the crops. Therefore, the aim of this study was to investigate the germination rate between varieties and the activity of enzymes related to initial growth and oxidative stress by applying various salt concentrations under *in vitro* conditions to secure the fundamental data required for the development of salt-resistant varieties of Italian ryegrass. In addition, through field demonstration tests on reclaimed land soil, elite salt-resistant lines were bred to develop Italian ryegrass varieties that exhibit exceptional growth and development under salinity stress conditions. The development of new Italian ryegrass varieties suitable for large-scale cultivation in reclaimed lands is expected to contribute significantly to maintaining the foundation for forage production and enhancing the self-sufficiency rate of the forage.

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PE-0028

수량성 높고 탈립에 강한 중소립 녹자엽 검정콩 ‘소만’

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경상남도 밀양시 점필재로 20, 국립식량과학원 남부작물부 밭작물개발과

검정콩은 주로 주식인 쌀과 함께 밥을 지어 먹는 용도로 많이 사용되어 왔으나, 최근 종피에 들어있는 기능성 물질에 대한 연구가 활발해 지면서 두유 등 가공식품의 원료곡으로서도 사용이 확대되고 있다. 이처럼 우리나라에서 검정콩은 앞으로 단순 혼반용에서 가공용으로 사용이 확대될 것으로 전망되어 다양한 종실 특성을 가지면서도 재배하기 쉬운 품종을 만드는 것이 중요한 선발 지표가 되고 있다. 이에 국립식량과학원에서는 수량성이 높고 탈립에 강한 중소립 녹자엽 검정콩 ‘소만’을 개발하였다. ‘소만’은 초형이 우수하고 수량성 높은 소립 녹자엽 검정콩 개발을 위하여 소립인 검정콩 ‘소청2호’와 초형이 우수한 ‘남풍’을 2010년 인공교배하여 계통육종법에 의해 개발된 품종(YS2296-B-B-12-2-2-3)이다. 2017년부터 2018년 2년간 실시한 생산력검정시험에서는 초형이 우수하고 수량성이 높은 중소립 녹자엽 계통으로 유망하여 ‘밀양365호’의 계통명을 부여하고 2019년부터 2021년 3년간 전국 8개소에서 지역적응시험을 실시하였다. ‘소만’은 유한형으로 엽형이 피침형, 꽃색이 흰색, 모용색이 갈색, 종실은 편구형으로 검은색 종피에 자엽색이 녹색인 고유특성을 가지고 있다. 성숙기는 10월 15일로 ‘소청자’와 비슷하였고, 100립중은 17.6g으로 ‘소청자’ 대비 다소 큰 중소립 품종이다. 내도복성은 전국 8개소 시험포장에서 ‘3’으로 평가되어 ‘소청자(5)’ 대비 강하였고, ‘소만’은 내탈립성 유전자(*pdh1*) 유전자를 가지고 있고, 40℃ 건조기에서 48시간 처리하여 조사한 협개열성도 9.2%로 ‘소청자(97.9%)’ 대비 강하였다. ‘소만’의 불마름병 저항성은 전국 8개소에서 시험포장과 인공접종 시 ‘소청자’와 대등하여 강하였고, 콩모자이크바이러스는 인공접종 시 상위엽에서 모자이크 증상이 나타났다. ‘소만’의 수량성은 적응지 평균 303kg/10a로 ‘소청자(267kg/10a)’ 대비 13% 높았다. ‘소만’은 초형이 우수하고 수량성이 높은 검정콩 품종으로 안정생산이 가능하여 앞으로 가공용 검정콩으로서 사용될 수 있을 것으로 기대된다.

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PE-0029

Investigation of Alfalfa Cultivars Forage Performance in Central Region of South Korea

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Alfalfa (*Medicago sativa* L.) is one of the most grown perennial forage crops worldwide, due to its great yield potential, high nutritive value, and wide adaptation. This study was conducted in Cheonan of central region in South Korea to identify alfalfa cultivars with superior adaptability to the local environment. To evaluate the forage performance, and feed value of 26 alfalfa cultivars, field experiments were conducted with a randomized block design for three years. Among the 26 alfalfa cultivars, “Natsuwakaba” showed the highest dry matter yield (DMY), with a significantly higher three-year average than that of other cultivars. Furthermore, the three-year-average DMYs of “Alfalfa short” and “Radar II Brand” were significantly higher than those of other cultivars. In case of feed values “Jin Huang Hou” and “Certified organic” exhibited the highest feed values when cultivated in central region in South Korea, however “Natsuwakaba” outperformed all cultivars in both productivity and feed value. Whereas the acid and neutral detergent fiber (ADF and NDF, respectively) contents of “Jin Huang Hou” were significantly lower than those of other cultivars. In contrast, the ADF and NDF contents of “Burgaltai” implied poor feed value upon cultivation in South Korea. The crude protein (CP) content in the alfalfa cultivars ranged from 14.95% to 19.44% during early flowering, and the highest CP content was observed for “Certified organic”. The in-vitro digestibility of alfalfa was approximately 70% for all cultivars during early flowering, indicating good digestibility of most of the cultivars.

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PE-0030

Evaluation of Maize × Legume Intercropping Systems in a Summer Season Paddy Field

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Intercropping is an important role in the sustainable development of agriculture and food production worldwide. Therefore, this study was conducted to evaluate the forage production, nutritional value, soil chemical properties, and rhizosphere microorganism composition of maize × legume intercropping systems in fallow paddy fields. Before seeding, the fields were sprayed with 210 kg/ha of nitrogen composite fertilizer (NPK: 21-17-17). From 2020 to 2021, maize was intercropped with seven different legume cultivars at the National Institute of Animal Science, Republic of Korea. The forage productivity of the intercropped soybean cultivars, Chookdu 1 and Chookdu 2, lablab, and cowpea, was relatively higher compared with the other legumes. Chookdu 1 and 2 showed higher forage productivity in monoculture than when intercropped. When intercropped with maize, the Daewon and Daepung soybean cultivars showed the lowest neutral detergent fiber and acid detergent fiber contents and the highest crude protein in 2020. However, the forage productivity of Daewon and Daepung was low, indicating unsuitability for intercropping with maize in paddy fields. The microorganism composition in the root rhizosphere showed a higher proportion of Proteobacteria under legume than maize cultivation. Proteobacteria were substantially more abundant in soils intercropped with lablab than in the lablab monoculture. Maize and cowpea appeared to be the best intercropping combination considering forage productivity and feed value. However, the Chookdu 1 and 2 cultivars and lablab also showed potential for intercropping with maize in paddy fields.

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PE-0031

Single Cross Corn Hybrid ‘Jindaok’with Lodging Tolerance and High Yield

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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 ‘Jindaok’ was developed by Maize Research Institute, Gangwon ARES in 2021. The hybrid ‘Jindaok’ was acquired by crossing two inbred lines, ‘HF9’ and ‘DHF3’. Silking date of ‘Jindaok’ was two days earlier than control cultivar‘Kwangpyeongok’. It is resistant to lodging due to the low ratio of upper ear height to plant height of 49%. ‘Jindaok’ is a yellow-orange and dent-like corn, and one hundred seed weight is 32.9g. Resistance to disease and harmful insect of ‘Jindaok’ were similar to those of ‘Kwangpyeongok’. The dry matter yield of ‘Jindaok’ was 23.32 ton/ha which was increased 14% compared with a check hybrid, ‘Kwangpyeongok’ at the regional yield trials from 2019 to 2021. additionally, the TDN (Total Digestible Nutrients) yield (15.66ton/ha) of ‘Jindaok’ was 12% higher than that of ‘Kwangpyeongok’. ‘Jindaok’ can be planted anywhere in Korea. We are also expected to expand farmers choice of field corn varieties.

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PE-0032

QTL mapping for tiller number with Korean *japonica* rice varieties

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Tiller number ia an important agronomic trait related with yield in rice. In addition, it was proposed that low tiller number rice varieties will emit less methane, a potent greenhouse gas, during rice cultivation. To analyze the quantitative trait loci (QTLs) for tiller number in *japonica* rice, tiller number was measured in 160 recombinant inbred lines (RILs) derived from a cross between the temperate *japonica* varieties Odae and Unbong40 at 41 and 47 days after seeding (DAS). A genetic map comprising 239 kompetitive allele-specific PCR (KASP) and 49 cleaved amplified polymorphic sequence (CAPS) markers constructed with the RIL population was used in QTL analysis. A major QTL for tiller number was found at 133.2 cM in chromosome 3 with LOD scores of 38.0 and 32,0 at 41 and 47 DAS, respectively. In order to make a fine-mapping population, we performed backcross between Odae and Unbong40 in opposite directions, and made 15 Odae^{*5}/Unbong40 BC4F1 and 17 Unbong40^{*5}/Odae BC4F1 plants. We genotyped them with 180 (KASP) and 14 (CAPS) markers distributed across whole rice genome and selected two BC4F1 plants with the highest recurrent parent genome recovery rates in the two cross combinations. We grew 198 Odae^{*5}/Unbong40 BC4F2 and 182 Unbong40^{*5}/Odae BC4F2 progeny plants from the selected BC4F1 plants in field and genotyped them wih KASP and CAPS markers on chromosome 3. Tiller number will be measured in their BC4F3 populations. This QTL can be used in breeding temperate *japonica* varieties with optimum tiller number for increased yield and decreased methane gas emission.

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PE-0033

국내외 벼 품종의 SUSIBA2 상동 유전자 주요 haplotype 분석

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벼의 논 재배는 농업부문 온실가스 배출량에서 가장 높은 비율(29.5%)을 차지하고 있고, 최근 탄소 중립 정책에 대한 필요성이 대두되고 있는 상황에서 메탄 발생 감축에 대한 연구는 필수적이다. 기존의 연구에서 보리 유전자 *HvSUSIBA2*가 벼에 도입되었을 때에 지상부-지하부 동화산물 분배 조절을 통해 메탄 발생 감축에 효과적이었다고 보고되었다. 이에 벼에서 *HvSUSIBA2* 유전자 후보를 찾아 국내외 품종으로부터 염기서열 변이를 조사하고 주요 haplotype들을 살펴보았다. *HvSUSIBA2*의 아미노산 서열을 NCBI에서 다운로드한 후 RAP-DB에서 BLASTP를 실시하여 가장 높은 일치율(77.85%)을 보이는 벼의 7번 염색체의 *OsWRKY87*(*Os07g0583700)*을 확인했고, 이를 *HvSUSIBA2*의 상동유전자 후보로 선정했다. *OsWRKY87*의 변이를 탐색하고자 IRRI에서 제공하는 SNP-SEEK을 사용했다. 3024개 품종(3K ALL)에서 탐지된 총 132개의 염기서열 변이 중 아미노산 서열을 변화시키는 nonsynonymous 변이는 39개였다. 그 중 결측치가 100개 이상이거나 소수대립유전자빈도(MAF; minor allele frequency)가 3% 이하인 SNP는 분석에서 제하였다. 이를 통해 선정한 Exon 3의 T/C SNP와 A/G SNP, Exon 6의 3bp 결실과 A/G SNP 총 네 가지 변이에 대하여, 4가지의 Haplotype이 탐색되었다. 해당 haplotype 분포를 국내 벼 169품종에서 살펴보기 위하여 각 변이에 대한 CAPS 마커, dCAPS 마커를 작성하여 유전자형을 검정한 결과 2가지 haplotype으로 분류되었다. 추후 OsWRKY87의 기능연구를 병행함으로써 해당 유전자와 변이의 활용 가능성을 보다 정밀하게 살펴보고자 한다.

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PE-0034

COWPEA BREEDING AND IMPROVEMENT: STRATEGY TO ACHIEVE FOOD SECURITY IN NIGERIA

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Cowpea is a widely grown legume in Northern Nigeria due to its economic and nutritional values. Its production is greatly hampered by its susceptibility to parasitic weeds, pathogens, and insect pests at every stage of development. Cowpea yield per hectare in Nigeria is below the world average yield per hectare. Hence, a need for improvement of cowpea to attain food security in Nigeria. This can be achieved through the breeding of better-performing cowpea cultivars with combined resilience and high-yielding traits. Efforts were initially made in the collection of different cowpea accessions and characterization to utilize beneficial genes for future crop improvement. This has greatly helped in developing cowpea genomic resources and the basis for modern breeding to achieve genetic gain. Breeders have made progress in identifying some wild cowpeas and landraces with inherent resistant traits against biotic stresses. Presently, TVu 483-2, TVu 1583, and TVu 347 are identified Nigerian landraces with such resistant genes useful in the cowpea breeding program. Structured mating was employed in intercrossing eight founder parents in cowpea trait discovery and breeding. However, cross-compatibility between most identified wild relatives and cowpea limits breeding for improved varieties against parasitic weeds and insect pests. The IT89KD-288 remains a promising improved cowpea variety that assures a boost in Nigeria's cowpea production and is currently well adopted by farmers. There is a further need to develop better-performing cowpea varieties to limit losses associated with biotic stress and prevent heavy importation of cowpea.

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PE-0035

병에 강하고 수량성이 높은 중만생 흑미 품종 ‘제이제이603블랙’

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‘제이제이603블랙’은 농촌진흥청 국립식량과학원에서 흑미 품종의 내병성 증진과 수량성을 향상시키고자 개발되었다. 중만생 흑미 품종인 ‘흑향’을 모본으로 하고 벼흰잎마름병 저항성 유전자 *Xa4*+*xa5*+*Xa21*이 집적된 내병성 계통 ‘SR30075-1-12-6-1-1-1’에 단간내도복 중만생 최고품질 ‘호품’을 2회 여교배한 BC_2F_1 개체를 부분으로 하여 육성되었다. 육성과정 중 흑미 종피에 대한 선발, 벼흰잎마름병 K3a균계 저항성 평가, 직립 초형과 수량성 등 농업형질에 대한 선발을 통하여 우량 고정계통을 선발하여 생산력 검정시험과 지역적응성 검정시험을 거쳐 육성되었다. ‘제이제이603블랙’은 보통기 보비재배에서 평균 출수기 8월 19일로 ‘흑남’에 비해 8일 늦은 중만생종 흑미 품종이다. ‘제이제이603블랙’은 간장이 76 cm인 단간 내도복 직립 초형이며 주당수수는 14개로 ‘흑남’에 비해 2개 적고 수당립수는 100개로 ‘흑남’에 비해 9개 많으며, 등숙비율은 85.8%로 ‘흑남’(83.8%)에 비해 높고 현미 천립중이 23.1g으로 ‘흑남’(22.0g)에 비해 무거웠다. ‘제이제이603블랙’은 내병성 저항성 유전자 *Xa3*+*Xa21*+*Stvb-i*가 집적되어 있어 흑미 품종 중 최초로 병원성이 강한 K3a균계를 포함하여 국내 벼흰잎마름병 대표균계 모두에 저항성이며 줄무늬잎마름병에도 강한 복합내병성 품종이다. 지역적응성 검정시험 특수미 보통기 보비재배 평균 현미수량이 602kg/10a로 ‘흑남’에 비해 14%로 증수하였으며, 흑미 품종 중 최초로 600kg/10a 수량을 넘은 다수성 품종이다. ‘제이제이603블랙’은 안토시아닌 함량이 58mg/100g로 ‘흑남’(51mg/100g)에 비해 높았으나 총폴리페놀 함량은 137mg/100g로 ‘흑남’(165mg/100g)에 비해 낮았다. ‘제이제이603블랙’은 흑미품종의 내병성과 수량성을 한 단계 향상한 품종으로 흑미 품종의 재배안정성 증진과 가격경쟁력 제고에 기여할 것으로 기대된다.

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PE-0036

진녹자엽 극대립 검정콩 ‘새바람(경북 5호)’

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콩(*Glycine max* [L.] Merr)은 대표적인 두과 작물로서 주요 식량작물 중 하나로, 특히 검정콩은 대표적인 블랙푸드로 항암작용, 골다공증, 당뇨병, 고혈압, 동맥경화 개선 등에 효과적인 생리활성 성분들이 풍부하게 함유되어 있어 최근 기능성 식품으로 각광받고 있다. 녹색자엽을 가진 검정콩은 속이 푸른색을 띤다하여 ‘속청’이라 부른다. 이러한 검정콩은 약리작용이 우수하다고 알려져 있어 높은 시장가격이 형성되어 있다. 국내 육성된 녹색 자엽을 가진 검정콩들을 보면, 농업적 형질 및 수량성은 많이 개선되었으나, 백립중이 30g 내외 중소립이며 자엽의 색깔이 황색에 가까울 정도로 연한 녹색을 띠는 등 아직까지 종실품질 특성은 재래종에 못 미치는 실정이다. 이에 경상북도 농업기술원에서는 재래종 서리태의 종실 특성인 진한 녹색자엽, 극대립 검정콩을 육성하고자 하였다. 2011년에는 농촌진흥청에서 육성한 ‘선흑’을 모본으로하고, 경상북도농업기술원에서 수집하여 순계분리한 만숙검정콩 유전자원 ‘RCS640’을 부본으로 하여 인공교배를 실시하였고, 계통전개 및 세대고정을 통하여 준유한신육형, 엽형은 뾰족한 난형, 꽃색은 자색, 모용색은 회색, 성숙기 협색은 연갈색, 종피색과 배꼽색은 흑색, 종실모양은 편구형의 극대립(42.8g/100립)이며 도복, 불마름병, 모자이크바이러스 등에 강한 내병성 및 내재해 다수성 품종 ‘새바람(경북 5호)’을 개발하였다.

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PE-0037

콩나물 수율과 업체 선호도가 높은 극소립 나물용 콩 ‘소미’

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[2]전라북도 전주시 완산구 농생명로 370 국립농업과학원 농업생명자원부 유전자공학과

콩나물은 자라면서 다양한 생화학적 변화를 유도해 1차 및 2차 대사물을 축적하면서 유용한 물질들을 제공한다. 이러한 이점으로 인해 한국에서는 예로부터 식단에 이용해 왔으며, 현재에 이르러서도 시장규모가 약 3천억 원으로 추정 될 정도로 중요한 식재료이다. 특히 콩나물의 경우 재배특성 뿐 아니라 가공특성도 중요하다. 그렇기 때문에 국립식량과학원에서는 생산농가와 더불어 가공업체의 수요에 맞춘 품종을 개발하기 위하여 극소립 고수율 나물용 콩 ‘소미’를 육성하고, 그 과정과 특성에 관해 소개하고자 한다.

‘소미’는 2011년 ‘풍원(IT 229420)’을 모본, ‘SS02152-3S-40-2-3-5-1’을 부본으로 인공교배하여 계통육종법으로 선발하였다. 2012년~2013년에 F1 및 F2 집단을 양성하였고, 2014년~2016년에 F3~F5 세대를 전개하여 2017년~2018년에는 생산력검정시험을 수행하였다. 2019년~2021년에는 전국 4개 지역(수원, 나주, 달성, 제주)에서 지역적응시험을 통해 재배 성능, 균일성 및 안정성을 평가하였고, 이후 신품종선정위원회를 거쳐 ‘소미’로 명명해 품종으로 출원하였다. ‘소미’는 백립중이 11.0g인 풍산나물콩보다 3.3g 가벼운 7.7g으로 극소립이며, 꽃색은 자색, 종피색과 배꼽색은 황색이다. 그리고 풍산나물콩 대비 개화기는 8월 7일로 1일 늦었으나, 성숙기는 10월 8일로 3일이 빨랐다. 또한 경장은 60cm, 착협고는 12cm로 풍산나물콩보다 착협고가 높은 편이고, 마디수는 16개, 분지수는 5.7개 그리고 협수는 개체 당 111개로 분지수가 평균적으로 1.1개 많은 편이다. 소미의 내도복성은 ‘1’로 풍산나물콩(‘5’) 보다 개선되었으며, 협개열성의 경우 포장검정은 ‘1’, 실내검정은 51.3%로 풍산나물콩(‘4’, 97.1%)보다 협개열성에 강한 것으로 나타났다. 지역적응시험 결과 수량성은 295kg/10a로 풍산나물콩(289kg/10a) 대비 102% 수준이며, 가공적성 평가에서는 물콩비율, 불완전발아율, 부패율은 풍산나물콩 대비 각각 0.4%p, 5.2%p, 0.6%p 낮고 콩나물 수율은 156%p 높아 품질특성이 우수한 것으로 나타났다. 2020년 가공업체에서 진행한 특성평가에서는 풍산나물콩 대비 수율이 129%p 높았고, 설문평가에서는 외관 9.0, 상품성 9.0 등 종합점수가 7.8점으로 풍산나물콩(6.8)에 비해 높은 것으로 평가되었다. ‘소미’는 수량성이 풍산나물콩과 비슷해 아쉬운 점이 있으나, 착협고가 높아 기계수확 적응성이 좋고 콩나물 수율이 높아 가공업체의 경제성이 향상되어 농가와 가공업체 모두가 선호할 것으로 기대된다.

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PE-0038

진녹자엽 이모작형 검정콩 ‘경흑청(경북 6호)’

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콩(*Glycine max* [L.] Merr)은 영양학적으로 우수성이 알려진 식재료로, 우리나라 음식문화와 밀접한 관련을 맺고 있는 중요한 식량작물 중 하나이다. 특히 검정콩은 건강 기능성이 부각되면서 소비자 수요가 증가하고 있다. 녹색 자엽을 가진 검정콩은 속이 푸른색을 띤다하여 ‘속청’이라 부른다. 숙기가 늦어 11월경 서리를 맞은 뒤에 수확을 한다고 하여 ‘서리태’라고도 부르는데, 약리작용이 우수하다고 알려져 있어 다른 콩들에 비해 높은 시장가격이 형성되어 있다. 국내 육성된 녹색 자엽을 가진 검정콩들을 보면, 농업적 형질 및 수량성은 많이 개선되었으나, 자엽의 색깔이 황색에 가까울 정도로 연한 녹색을 띠는 등 아직까지 종실품질 특성은 재래 서리태에 못 미치는 실정이다. 서리태는 만숙검정콩으로 숙기가 늦어 작부체계에 불리한 단점이 있다. 이에 경상북도 농업기술원에서는 재래 서리태의 종실 특성인 진한 녹색 자엽에, 숙기는 빠른 검정콩을 육성하고자 하였다. 2011년에는 경상북도 농업기술원에 수집하여 순계분리한 만숙검정콩 유전자원 ‘RCS640’을 모본으로 하고, 농촌진흥청에서 육성한 조숙검정콩 ‘검정새올’을 부본으로 하여 인공교배를 실시하였고, 계통전개 및 세대 고정을 통하여 준유한 신육형, 엽형은 뾰족한 난형, 꽃색은 자색, 모용색은 회색, 성숙기 협색은 연갈색, 종피색과 배꼽색은 흑색이며, 자엽색은 매우 진한 녹색, 숙기는 서리태 대비 30일 이상 당겨진 이모작형으로, 불마름병, 모자이크바이러스 등에 강한 내병성 다수성 품종 ‘경흑청경북 6호)’을 개발하였다.

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PE-0039

Identification of QTLs related to leaf blast resistance derived from a Korean weedy rice, Wandoaengmi 6

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Rice blast, caused by *Magnaporthe grisea*, is one of the most serious diseases in rice. These days, blast resistance of many *japonica* varieties has broken down by climate change. To improve the leaf blast resistance of *japonica* variety, Hwayeong, we developed the recombinant inbred lines (RIL) from a cross between Hwayeong and Wandoaengmi6, Korean weedy rice. A total of 155 RILs, and the two parents, were evaluated for blast resistance in two locations, Jeonju and Gyehwa. The average degree of 155 RILs for blast resistance measured in the field was 4.4±1.54 and 4.4±1.42, for Jeonju and Gyewha, respectively. Two quantitative trait loci (QTL) for blast resistance, *qBL4* and *qBL6*, mapped on chromosomes 4 and 6, respectively. *qBL4* was detected in both of the experimental sites, while *qBL6* was only detected in Gyehwa. They explain from 18.8 to 25.5% of total phenotypic variation, this supposes the presence of major QTLs. However, *qBL4* exhibits a significant threshold (LOD >9.8) at both locations, suggesting a high resistance range across environments. Among two test filed, no significant differences were observed by the presence of QTLs. Effect of QTL combination *qBL6, qBL4, qBL6+qBL4* and *none* on leaf blast were 4.9-5.0, 3.0-3.0, 3.7-3.8 and 6.2-6.8, respectively. QTL *qBL4* had significant degree to resist leaf blast, the development of markers using QTL *qBL4* is expected to contribute to improving the breeding efficiency.

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PE-0040

부품성이 개선된 신규 벼 소재 탐색을 위한 남일 돌연변이 계통의 주요 작물학적 특성

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최근 쌀을 활용한 다양한 제과・제빵제품이 개발 및 판매되고 있다. 하지만, 쌀은 밀과 달리 부피를 유지시켜주는 글루텐이 없기 때문에 쌀빵 제조시 활성 클루텐을 일정비율 첨가하여야 한다. 일본에서 벼 저장단백질 단위체 간에서 이황화결합을 형성하는 돌연변이 계통은(*esp2* mutant; Endosperm storage protein2(*esp2*) mutant) 부품성이 개선되어 쌀빵제조에 유리한 보고된 바 있다. 이를 반영하여 국립식량과학원에서는 준조생종 자포니카 초다수 벼 품종 '남일'의 유전적으로 고정되어 있는 돌연변이 집단(6,332계통)에서 부품성 개선 유망소재를 탐색하였다. 일반적으로 쌀의 심복백(흰티)은 품질 외관판정에 열악형질로 판단되지만, 벼 *esp2* mutant의 현미 외관은 심복백 발현이 높다고 알려져 있어 외관평가에 초기 선발지표로 활용할 수 있다. 본 연구에서는 남일 돌연변이 집단에서 심복백이 높고, 단백질 함량에 변화가 있어 부품성 개선 유망 소재로 판단되는 24계통과 원품종('남일')의 주요 작물학적 특성을 보고하는 바이다.

2021년 국립식량과학원 완주포장에서 공시하였고(보통기), 주요 농업형질은 다음과 같다. 원품종인, '남일'의 출수기는 7월 31일인 준조생종이며, 간장은 79cm, 수장은 26cm, 수수는 9개이었다. 부품성 유망 24계통의 출수기는 7월 30일에서 8월 7일 사이였고, 간장 범위는 67~87cm, 수장 범위는 19~26cm, 수수는 6~11개였다. 원품종 '남일'의 단백질 함량은 6.43%였고, 부품성 유망계통의 단백질 함량 범위는 5.79%~10.45%였다. 부품성 유망 24계통 중 저단백(5.79%) 1개, 고단백 4개 계통(8.65%~10.45%)등을 포함하여 유전분석 등 추가적인 연구를 수행할 계획이다. '남일' 유래 단백질 돌연변이 후보 24계통은 벼 형질전환 방법이 아닌 돌연변이 육종방법으로 육성된 고정 계통으로 부품성 개선 벼 품종 소재 개발에 유용하게 활용될 것으로 기대된다.

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PE-0041

김치가공에 적합한 지역맞춤형 배추 신품종 ‘순정아삭이’ 육성

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구의 형태가 우수하고 조직이 치밀하며 아삭한 식감을 보이는 배추 신품종 ‘순정아삭이’가 국립원예특작과학원 및 괴산군 농업기술센터 협력을 통해 육성되었다. 모본으로 사용된 원교20041호는 뿌리혹병 평창균주에 저항성을 보이는 계통이고 부본으로 사용된 원교20048호는 내한성, 내서성이 우수한 계통으로 본 신품종은 2017년도 교배되었다. 2018년~2021년에 생산력 검정시험을 완료하였으며, 전북지역과 괴산지역에서 적응시험을 완료하였다. 새로 육성된 품종은 품종의 특성 및 본 품종이 선발된 괴산지역의 브랜드명 등을 참고하여 ‘순정아삭이(구 괴산1호)’로 최종 명명하였다. ‘순정아삭이’의 전반적인 특징을 살펴보면 구중 무게는 2,085.2g으로 대조품종인 ’불암플러스‘의 2,387.8g보다 다소 가벼웠으며 엽폭은 264.7mm로 대조군과 비교하여 약간 작았다. 엽수는 85.1개로 대조군보다 약간 적었으며, 중륵의 폭은 45.6mm로 대조품종의 54.7mm보다 짧았다. 이 배추는 숙기가 늦어 결구가 늦게 이루어지므로 일반 김장 배추 수확 공백기 시장에 더 유리할 것으로 기대된다. 또한 중륵이 단단하고 쉽게 무르지 않으므로 김치 가공 목적으로 사용하기 적합하며 당도가 높고 고소한 맛을 가져 절임배추로도 활용가치가 높다. ‘순정아삭이’ 품종은 2021년 가을, 완주 및 괴산 포장에서 불암플러스 외 5개 이상의 대조품종과 육안조사(진딧물, 노균병, 무름병 등 주요 병충해 조사)를 진행하였으며 대조품종과 비교하여 피해 정도는 거의 나타나지 않음을 확인하였다. 해당 신품종은 현재 출원 진행 중에 있으며 괴산 지역 맞춤 품종으로 보급할 예정이다.

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PE-0042

Comparative analysis of soybean seeds expressing *Physaria* fatty acid desaturase 3-1 using untargeted metabolite profiling based on LC-MS

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Soybean (*Glycine* max [L.] Merr.) is an important source of human dietary protein and oil. *PfFAD3-1 t*ransgenic soybean lines expressing omega-3 fatty acid desaturase 3-1 gene (*FAD3-1*) increased level of α-linolenic acid in seed. The seed metabolite profiles of three *PfFAD3-1* transgenic soybean lines, their non-transgenic counterpart (Kwangan) and four conventional varieties cultivated at Jeonju in 2021 were compared to investigate the substantial equivalence of *PfFAD3-1*. Obtained 92 MS data were normalized to an internal standard (terfenadine), and then subjected to statistical analyses, and 42 MS were identified out of 92 MS data. The PLS-DA score plot revealed that three *PfFAD3-1* lines were well clustered with Kwangan, but clustered separately from other conventional varieties by component 1. The metabolites with high variable importance of projection values, contributing the separation among varieties, were 5-methylcytidine, phenylalanine, genistein, daidzein, tryptophan, linolenic acid, and linoleic acid. Notably, levels of isoflavones including daidzin, malonyldaidzin, malonylglycitin, and genistin, and some soyasaponins were significantly lower in Kwangan along with *PfFAD3-1* lines in comparison with four conventional varieties. Significantly increased linoleic acid and reduced linoleic acid of *PfFAD3-1* were well associated with targeted engineering pathway. In *PfFAD3-1* #10 and #11, levels of tryptophan, phenylisoxazole, and *p*-methylcinnamonitrile were significantly changed compared to those of Kwangan, and found to be out of the range of conventional varieties' values. It was suggested to include more cultivation environments and commercial varieties to understand the altered changes in these metabolites of *PfFAD3-1* #10 and #11 in the natural metabolic variation.

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PE-0043

콩 역병 국내 수집 균주에 대한 저항성 F2 세대 유전 양상 분석

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경상남도 밀양시 점필재로 20 국립식량과학원 남부작물부 밭작물개발과

최근 국내 논 콩 재배면적이 10,658ha로 전체 재배면적의 19.6%까지 확대되면서('21, 통계청), 배수가 불량하거나 습한 토양에서 발생이 조장되는 콩 역병의 피해 증가가 우려된다. 콩 역병의 선제적 대응을 위해 국내 수집 균주의 병원성을 파악하고, 역병 저항성 유전자(Rps gene, Resistance to *Phytophthora sojae*)의 유전 양상을 분석하였다. 2021년 국립식량과학원 남부작물부 온실에서 역병 균주의 레이스 판별을 진행하였다. 시험재료는 유전자원센터와 미국 ARS에서 분양받은 유전자원 16점을 사용하였고, 균주는 2019년에 김제, 안동, 완주, 대구에서 각각 수집한 3053, 3617, 3624, 3968과 KACC 등록 균주인 40412, 40468을 사용하였다. 유묘의 자엽 아래를 1cm 자른 후 주사기로 균 슬러리를 1ml 주입하여 접종하는 유묘줄기 검정법으로 2반복 진행하였다. 또한 균주 3617에 저항성인 '만풍'을 모본, 균주 3053에 저항성인 '소백나물콩'을 부본으로 인공교배하여 2021년~2022년 온실과 스피드브리딩 시설에서 F1 및 F2 재료를 양성하였다. F2 집단은 유묘줄기 검정법으로 균주 3053과 3617을 접종하였으며, 분리비를 활용하여 R프로그램을 통해 적합도 검정을 진행하였다. 역병 저항성 유전자를 보유한 유전자원의 저항성 검정을 통해 균주의 레이스를 분석한 결과, 대부분 자원에서 감수성을 보였다. 균주 3053은 'vir 1a,1b,1c,1d,1k,2,3a,3c,4,5,6,7,8', 3617은 'vir 1a,1b,1c,1d,3a,3b,3c,4,5,6,7,8'의 병원성을 나타내었다. 균주 3624는 'vir 1a,1b,1d,2,3a,3b,3c,4,5,6,7,8', 3968과 40412는 'vir 1a,1b,1c,1d,1k,2,3a,3b,3c,4,5,6,7,8', 40468은 'vir 1b,1d,2,3a,3b,3c,4,5,6,7,8'의 병원성을 나타내었다. 또한 만풍/소백나물콩 F2 집단의 검정 결과 균주 3053은 접종한 150개체 중 저항성 117개체와 감수성 33개체, 균주 3617은 148개체 중 저항성 113개체와 감수성 35개체로 나타났다. Rps gene은 단일 우성 유전자로 알려져 있으므로 기대분리비를 3:1로 하여 적합도 검정을 진행하였다. 균주 3053과 3617의 검정통계량(x^2) 값은 각각 0.72, 0.14로 모두 $x^2_{0.05(1)}$인 3.84보다 작아 단일 우성 유전하는 것으로 확인되었다. P-value 값은 균주 3053은 0.3961, 3617은 0.7042로 분석되어 기대분리비에 적합하다고 판단되나 균주 3053의 경우 고사하지 않고 잎이 시든 개체가 3617보다 상대적으로 많아 P-value 값이 낮은 것으로 파악된다.

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PE-0044

Growth and phenotypic mutation analysis of M_1 and M_2 population induced by ionizing radiations

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Developing appropriate early-generation populations with appropriate mutation frequency is crucial for screening and selecting mutant individuals with desirable traits. We developed M_1 and M_2 populations from the rice seeds exposed to ionizing radiations and analyzed growth and frequency of phenotypic mutants in M_2 populations. Although the M_1 plants showed reduced survival rate and seedling growth at the transplanting stage, the growth parameters of survived plants were almost restored and the effective tiller numbers were higher compared with those in non-irradiated control plants at the mature stage. A notable difference was observed in fertility that the average fertility rate was reduced in each radiation treatment while from normal fertile to complete sterile panicles coexisted in each M_1 plant. Thus, we harvested seeds from each M_1 plants by classifying panicles based on the visual inspection of fertility, undamaged (UD), half-damaged (HD), and fully-damaged (FD), and separately advanced M_2 populations. Each M_2 population did not show noticeable differences in both survival rate and plant growth in length. However, the tiller number and the numbers of semi-sterile and sterile plants increased and in the order of UD, HD, and FD. Phenotypic mutant screening of M_2 showed different frequency and spectrum of mutation, which were the highest in HD. These suggest that the fertility of M_1 panicles could serve as an indicator of different initial cell lines and harvesting seeds from HD M_1 panicles could be a successful strategy to carry mutants (or mutations) with high frequency and a broad spectrum in M_2 population.

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PE-0045

북방지역 적응 준조생 내수발아 다수성 벼 ‘철원108호’ 특성

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북방지역 적응 벼 품종은 ‘평원’이 유일한데 내병성이 미흡하고 도정수율이 낮은 한계를 가지고 있어 개량이 필요하고, 통일 이후 안정된 주곡생산을 위하여 다양한 북방지역 적응 품종 개발이 필요하다. 본 연구는 ‘평원’에 수량성과 내병성 및 내랭성을 도입하여 북방지역 재배가 가능한 준조생 다수성 ‘철원108호’를 육성하여 그 특성을 밝히고자 수행하였다. ‘철원108호’는 ‘평원’과 ‘운광’을 교배한 SR30271을 모본으로, 태봉과 운봉37호를 교배한 SR30281을 부본으로 복교배하여 내병성, 내수발아성 등 재배안전성을 갖추고 수량성이 높으며 쌀알이 깨끗한 고품질 계통이다. ‘철원108호’의 출수기는 8월 1일로 ‘오대’보다 5일 늦은 준조생이다. 간장은 68㎝로 ‘오대’보다 약 6㎝ 작고, 현미천립중은 23.9g으로 약 1.3g 가볍다. 쌀 수량성은 653kg/10a 로 ‘오대’보다 16% 증수되었다. 쓰러짐에 강하고 도열병 중, 흰잎마름병(K1,K2,K3균계)에 강하며, 수발아는 1.6%로 강한 반응을 보였다. 쌀알 외관이 깨끗하고 윤기치가 71, 완전미율이 95.5%로 높아 유사시 우리나라 북방지역 쌀공급에 중요한 역할을 할 것으로 기대된다.

사사: 본 연구는 농촌진흥청 연구사업(세부과제명: 중북부지역 중간지 적응 수요자 참여형 조숙 고품질 벼 품종개발, 세부과제번호: PJ01315007)의 지원에 의해 이루어진 결과임.

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PE-0046

조생 친환경재배 가능 복합내병성 고품질 벼 '철원110호' 특성

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최근 중북부지역 조생종 벼 재배지역에서도 도열병, 흰잎마름병 및 바이러스병 발생이 증가되고 있다. 전세계적인 기후온난화로 인하여 돌발병해충 및 재해 발생이 증가하여 이에 대응한 다양한 내재해성 고품질 품종 개발이 시급하다. 본 연구는 중북부 중간지 및 중산간지 재배에 적응하고 복합내병성을 갖춘 조생 고품질 '철원110호'를 육성하여 그 특성을 밝히고자 수행하였다. '철원110호'는 중생종 '수원546호'를 모본, 중만생이면서 흰잎마름병 K3a균계에 저항성인 강백과 중생이면서 줄무늬잎마름병에 저항성인 영덕54호를 교배한 F1을 부본으로 삼원교배하여 선발된 조생이면서 복합내병성, 내수발아성 등 재배안전성을 갖추고 밥맛이 우수한 고품질 계통이다. '철원110호'의 출수기는 7월 28일로 '오대'보다 1일 늦다. 간장은 77㎝로 '오대'보다 약 3㎝ 크고, 현미천립중은 20.8g으로 약 4.4g 가볍다. 쌀 수량성은 550㎏/10a 로 '오대' 대비 98% 수준이었다. 키가 크지만 쓰러짐에 강하고 도열병 중, 흰잎마름병(K1,K2,K3,K3a균계), 줄무늬잎마름병에 강하며, 수발아는 1.9%로 강한 반응을 보였다. 쌀알 외관이 깨끗하고 단백질함량이 낮으며 윤기치는 72.6, 완전미율은 93.9%로 높다. '철원110호'는 내병성, 내재해성 및 밥맛이 '오대'보다 우수하여 조생종 재배 지역에서 고품질 쌀 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.

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PE-0047

벼 종자의 폴리코사놀과 스테롤, 토코페롤 함량 자연변이에 미치는 유전 및 환경요인의 영향 평가

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국립농업과학원 생물안전성과

벼는 전 세계적으로 이용되고 있는 주요 작물 중 하나로, 기능성 물질인 폴리코사놀과 스테롤, 토코페롤이 함유되어 있다. 폴리코사놀은 콜레스테롤 수치 저하 및 혈소판 응집 억제, 관상동맥질환을 저해하며, 스테롤, 토코페롤은 심혈관 질환 예방과 항암효과 등이 있다고 알려져 있다. 식물의 기능성 물질 함량은 여러 조건에 의해 변화되는 것으로 알려져 있기에, 본 연구를 통해 벼 종자에 함유된 기능성 물질인 폴리코사놀과 스테롤, 토코페롤의 자연변이를 분석하고자 하였다. 이를 위해, 다양한 벼 품종을 서로 다른 지역에서 재배하고, GC-TOFMS를 활용하여 폴리코사놀과 스테롤, 토코페롤을 동정하고 각 함량을 비교 분석하였다. 그 결과, 2개 지역(전주, 천안)에서 재배한 23개 품종(인디카 4종, 통일 4종, 자포니카 15종)에서 7종의 폴리코사놀과 4종의 스테롤, 5종의 토코페롤을 동정할 수 있었다. 각 성분의 자연변이 분석을 위해, 성분별 함량 데이터를 이용하여 다변량 통계분석을 진행하였다. 주성분분석 결과, 재배지역별(전주, 천안) 자연변이 차이는 보이지 않았지만, 자포니카 품종이 인디카 및 통일 품종과 차이가 있는 것으로 나타났는데, 이를 통해 폴리코사놀과 스테롤, 토코페롤의 함량 변이에는 재배 환경보다는 유전적 특성이 미치는 영향이 더 큼을 알 수 있었다. 또한, 피어슨 상관계수 및 계층적 군집분석을 통해 α-tocopherol, β-tocopherol, heptacosanol, triacontanol이 γ-tocopherol, δ-tocopherol과 음의 상관관계가 있음을 확인하였다.

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PE-0048

꼬투리 달림이 높고 쓰러짐에 강하며 무분지 초형의 기계화 콩 품종 '장풍'

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경상남도 밀양시 점필재로 20 국립식량과학원 남부작물부 밭작물개발과

콩의 초형은 크게 타원형, 장타원형, 원통형, 도원추형, 도삼각형, 단지형 등 크게 6가지로 구분할 수 있으며, 최근 필수적인 기계 수확 적응성과 주당 본수가 표준재배(2본)보다 밀식된 상태로 재배되는 실제 농가 현장의 상황에서는 꼬투리 달림이 높고 분지가 적은 단지형(무분지) 초형의 콩이 개체당 수량 확보 효율이 높아 재배 적응성이 높다고 볼 수 있다. '장풍'은 꼬투리 달림이 높은 '신기'를 모본으로, 무분지 초형인 'SS03102-2B-3S-21-4'를 부본으로 2010년 인공교배하여 계통선발을 거쳐 2017년~2018년 생산력검정시험과 2019년~2021년 지역적응시험을 거쳐 신품종선정심의위원회를 통해 '장풍'으로 명명하고 품종으로 출원하였다. '장풍'은 착협고가 25cm, 분지수가 1.4개로 '대원콩' 대비 착협고가 14cm 높고, 분지수가 2.1개 적은 무분지 고착협 초형을 나타내는 품종이다. 주요 기계화 보급 품종인 '선풍'과 비교시에도 착협고가 5cm 더 높고 분지수가 1.6개 적다. 고유 특성으로는 신육형이 유한형, 엽형은 난형, 꽃색은 자색, 모용색은 회색, 협색은 황색, 종피색과 제색은 황색, 종실 모양은 구형이다. 가변특성은 개화기 8.9, 성숙기 10.22로 만숙종이다. 경장 90cm, 착협고 25cm, 마디수 16개, 분지수 1.4개, 협수 44개, 100립중 28.2g, 립균일도 87.5%로 경장이 크고 분지가 적으며 알멩이가 굵은 특성을 나타낸다. 적응지역(전북, 전남)의 수량성은 317kg/10a로 '대원콩' 대비 3% 향상되었으며, 논 재배 시험에서는 388kg/10a로 25% 증수되었다. 현장실증시험에서도 기계작업이 용이하고 도복에 강하며 콩 외관이 우수해 선호도 '8'로 높은 평가를 받았다. 내병성은 SMV와 불마름병에 강하고, 내재해성은 내도복성 '1'로 쓰러짐에 강하고 분자마커(*qPDH-KS*) 및 협개열성(0.4%) 검정 결과 내탈립성 품종이다. 가공적성은 두부수율이 218%로 '대원콩'과 유사한 특성을 나타내며, 발효적성은 아미노태질소함량이 408mg%로 '대원콩'보다 낮았다. '장풍'은 최근 콩 자급률 향상 정책과 관련되어 증가하고 있는 논 재배 확대에 따라 전북과 전남 지역을 중심으로 '선풍', '대찬'과 함께 논 재배용 콩 품종 선택지를 늘이고 우수한 기계화 및 내재해성 특성을 통해 농가의 논콩 재배 확대와 재배 안정성 향상에 기여 할 수 있을 것으로 기대된다.

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PE-0049

생육일수 100일 수준의 내탈립성 개선 중립 2모작용 콩 품종 '선올'

강범규*, 서정현, 백인열, 김준회, 허수빈, 최만수, 고지연, 황재복, 성정숙, 정찬식

경상남도 밀양시 점필재로 20 국립식량과학원 남부작물부 밭작물개발과

2모작 작부체계를 구성하는 것은 소득을 향상시킬 수 있고 토지 이용 효율을 높여 전체적 관점에서 작물의 생산량 증대와 '콩'의 경우 자급률 향상에도 기여할 수 있다. 동계작물인 난지형 마늘은 9월 중순 ~ 10월 초순에 정식하여 6월 중순 ~ 하순에 수확하는데 하계작물인 콩과 2모작이 가능하나, 콩의 생육기간이 90일 ~ 100일은 되어야 작업 상 어려움 없이 재배할 수 있다. 기존에 개발되어 있는 생육일수 100일 내외의 품종인 '참올', '황금올' 등은 생육일수는 적합하나 탈립에 약한 단점이 있어 이를 개선할 필요가 있었다. '선올'은 생육일수가 짧으면서도 내탈립성을 개선한 품종이다. '선올'은 생육일수가 짧은 '참올'을 모본으로, 내탈립 장경 단기성인 'SS01402-30-4-1-2-1-1'을 부본으로 2010년 인공교배하여 계통육종법으로 선발하여 2017년~2018년 생산력검정시험, 2019년~2021년 지역적응시험을 통해 재배 성능과 균일성과 안정성을 평가하고 신품종선정위원회를 거쳐 '선올'로 명명하고 품종출원하였다. '선올'은 반무한형이며 엽형이 난형, 꽃색이 백색, 모용색이 회색, 협색이 담갈색, 종피색이 황색, 배꼽색이 담갈색이며 종실 모양이 편구형이다. 개화기는 7.27, 성숙기는 9.23일로 생육일수 100일로 표준품종인'새올콩' 대비 5일 빠르다. 경장은 66cm, 착협고는 13cm, 마디수는 12개, 분지수는 1.8개, 협수는 31개, 100립중은 23.2g의 특성을 지니고 있다. 수량성은 226kg/10a로 '새올콩' 대비 3% 증수되었다. '선올'은 불마름병과 SMV, 쓰러짐에 강하며 분자마커(*qPDH-KS*)와 협개열성 검정 결과 내탈립성 특성을 지니고 있다. 가공적성은 두부 수율이 232%로 높은 편이며 경도가 낮아 부드러운 특성이 있고, 발효물 아미노태질소 함량이 461mg%로 발효적성이 우수하다. 최근 콩 자급률 향상이 중요한 정책적 목표로 추진되고 있으며, 2모작은 자급률 향상에 기여할 수 있는 한 가지 대책이 될 수 있다. '선올'은 기존 품종 대비 재배 안정성을 향상시키고 난지형 마늘과 같은 동계작물과 재배에 적합한 품종으로서 활용될 것으로 기대된다.

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PE-0050

Variation of ω-6/ω-3 Ratio by the combinations of Three mutant alleles of *FAD2-1A* with a *hd* gene in Soybean

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Since modern eating habits have generally high level of ω-6, intake of an unbalanced ω-6 and ω-3 causes various health problems. The microsomal delta-12 fatty acid desaturase 2 (*FAD2*) genes is involved in the conversion of oleic acid to linoleic acid (ω-6), and microsomal ω-3 fatty acid desaturase (*FAD3*) catalyzes the conversion of ω-6 to α-linolenic acid (ω-3). In our previous study, we identified a homeodomain transcriptional regulator (*HD*) which may be interacted with *FAD3* gene at the early seed development, resulting in increased ω-3 content in soybean. The objective of this study was to find a proper combination of mutant alleles which reduce the ω-6/ω-3 ratio. The three different F_2 populations were developed from crosses of S08-14719 (*fad2-1a*$_{DEL}$ from M23) x a breeding line (*hd* allele), Hosim (*fad2-1a*$_{S117N}$ from 17D) x a *hd* line and PE529 (*fad2-1a*$_{W294stop}$) x a *hd* line. Each F_2 individual was genotyped for mutant alleles of *FAD2-1A* and *HD* genes and chipped seed were analyzed for fatty acid profile. Seeds with functional allele of *FAD2-1A* and *HD* showed 4.2-5.9 of the ω-6/ω-3 ratio. On the other hand, the ω-6/ω-3 ratio of F_2 seeds having both the mutant allele of *FAD2-1A* and the *HD* gene was slightly different depending on the *FAD2-1A* mutant alleles. When combined with the *hd* allele, *fad2-1a*$_{DEL}$ was 1.9-2.7, *fad2-1a*$_{S117N}$ was 2.9 of ω-6/ω-3 ratio, and *fad2-1a*$_{stop}$ showed 2.6-3.6 of ω-6/ω-3 ratio. The combination of mutant alleles of the *FAD2-1A* and the *HD* genes was able to reduce the ω-6/ω-3 ratio below 4:1 in soybean seed.

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PE-0051

Mapping QTLs controlling reaction of herbicide Bentazone In Soybean

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As a source of high-quality protein and oils, soybeans are a major crop consumed in various ways in Korea and many other countries. The factors to increase crop production are the environmental, biological and technological factors. As weeds is one of the factors to determine soybean yield and cause an averaged reduction of 37% soybean yield, weed control is very important to help reduce yield loss of soybean. Bentazone is an herbicide which selectively kills broadleaf weeds and widespread in soybean cultivating areas in the world. The utilization of herbicide-tolerant crops is an efficient way to maintain crop yields from the competition between weeds and crops. Depend on soybean genotype, soybean genotypes show tolerance to bentazone treatment, and a few bentazone-sensitive soybean genotypes have been reported. With a core collection of Korean cultivated soybean, we identified two accessions to be showed as bentazone tolerant (CMJ416) and sensitive (CMJ169). In this study, we developed a RIL population from a cross of CMJ416 and CMJ169 to identify QTL regions to be associated with the reaction of bentazone treatment in soybean. One hundred seventy nine of RILs will be genotyped with 3K SNPs. Hyperspectral camera (SpecimIQ) will be used for the measurement of the normalized difference vegetation index (NDVI), photochemical reflectance index (PRI), and anthocyanin reflectance index (ARI) as physiological parameters. In addition, visual scoring of leaf necrosis after bentazone treatment will be determined for further analyses. The results can be used as marker assisted selection to improve selection accuracy in breeding program.

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PE-0052

Evaluation of diversity of agronomic traits by collection regions of Korean landrace Sorghum germplasms

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In this study, 139 Korean landrace sorghum germplasms collected in 10 different Korean regions were evaluated agronomic traits including stem length(SL), stem diameter(SD), days required for heading(HD), days required for maturation(MD), number of branches per plant(NB/P), ear length(EL), ear width(EW) and thousand grain weight(TGW). As a result of the ANOVA analysis, there were significant differences of the traits by the collection regions except SL, EW and TWG. As for HD and MD, Gyeongnam germplasms had the shortest average HD and MD with 47.7 and 85.3 days, respectively. Gangwon Yeongseo germplasms had the longest average HD and MD with 57.8 days and 97.9 days, respectively. Two accessions(IT124172 and IT103099) had shortest HD with 40 days, and 3 accessions (IT124172, IT185816 and IT185796) had shortest MD with 77 days. As for EL, Gyeongbuk germplasms had the shortest average EL with 23.1cm, but Chungnam germpalsms had the longest average EL with 31.4cm. IT331878 had the shortest with 16.0cm, but IT124172 had the longest with 59.3cm. The correlation analysis based on each agronomic quantitative traits showed that SL had a positive significant correlation with EL, EW, HD and MD. SD also had a positive significant correlation with HD and MD. The principal component analysis presented that 3 subpopulations were divided. In Group1, Gangwon Yeongseo and Gangwon Yeongdong germplasms were mainly included. In Group2, Jeonnam and Jeonbuk germplasms were mainly included. Group 3 showed a mixed pattern. This results could contribute to expend diversity of NAC's sorghum collections and discover breeding materials.

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PE-0053

Physicochemical characteristics and free amino acid content of high yield Tong-il type red rice Chohong based on germination days

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We analyzed the germination rate, color value, physicochemical properties, antioxidant capacities, and amino acid content of germinated brown rice (Chohong, Nampyeong, and Dasan) and the correlation among parameters. Chohong recorded the highest germination percentage and the total color difference value (3.89) at 24 h. The amylose and crude protein contents were increased on the first day of germination in all varieties but decreased over time ($p<0.05$). In the same way, the paste viscosity values showed a significant decrease pattern over time in all cultivars. The activity of DPPH and ABTS showed an uneven pattern specific to each variety (decrease or increase over time). The total phenolic and flavonoid content showed an increasing pattern in all cultivars. Total phenolic content negatively correlated with L^* value ($r=-0.778$) while showing a strong positive correlation with $\triangle E$ ($r=0.927$). The essential amino acid content was the highest on the third day of germination in Chohong (276.9 mg/100 g) and Dasan (344.1 mg/100 g). Furthermore, total free amino acid and GABA content increased gradually concomitant with the germination days. Therefore, these results suggest that the germinated brown rice of Chohong could be suitable for Functional medical materials such as health supplements and its paste viscosity, high essential amino acid, and GABA content.

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PE-0054

Physicochemical characteristics of high yield Tong-il type glutinous rice Mirchal based on soaking time

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The physicochemical and structural characteristics of high yield, tongil type, Mirchal glutinous rice (Milyang328) were compared with those of other glutinous rice varieties (Baegokchal, Dongjinchal, and Sinseonchal). Mirchal showed the highest crude protein content (8.47%). Mirchal also displayed the highest water binding capacity (209%) and swelling power (55.82 g/g) upon long term soaking. The mean and median particle diameter of Mirchal rice flour after long term soaking was 50.54 and 22.72 μm, respectively. Long term soaking of glutinous rice flour reduced its particle diameter compared with unsoaked or wetted glutinous rice flour. The crystalline fraction of glutinous rice flour presented an A type structure, with no change with increasing soaking time. Mirchal glutinous rice flour displayed the lowest onset temperature (To). Mirchal achieved its lowest To values upon soaking (58.70~60.77℃) and long term soaking (57.15~60.85℃). Mirchal's highest breakdown viscosities were obtained with glutinous rice flour (1,386 cP) and soaked glutinous rice flour (1,416 cP). The chain length distribution of amylopectin A chain in glutinous rice flour decreased in the following order: Baegokchal (30.82%), Mirchal (29.59%), Dongjinchal (20.02%), and Sinseonchal (27.10%). Moreover, B1 chain length decreased in similar order: Dongjinchal (47.85%), Mirchal (47.17%), Baegokchal (45.83%), and Sinseonchal (44.47%). This study revealed the functional properties of Mirchal for food processing obtained by soaking.

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PE-0055

Analysis of Tannin Content from Sorghum by UV Spectrophotometer and HPLC

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Tannins are emerging as health functional ingredients because they contain abundant antioxidants, but they also have a bitter taste when combined with proteins. Thus, tannins of sorghum were recognized as nutritional inhibitors by animals and humans, so study on the development and analysis of sorghum with low tannin content were conducted. In this study, total tannin content and component of tannins were analysed through UV spectrophotometer and HPLC to the 6 varieties of sorghum. After extracting sorghum powder with methanol containing 1% HCl, the total tannin content of sorghum was measured by absorbance at 500nm using the Vanillin method, and quantified using catechin as a standard. In addition, the components of tannins such as gallocatechin and procyanidin were analysed by HPLC and a total of 14 calibration curves were prepared and quantified. When comparing the total tannin content of 6 sorghum varieties, Noeulchal and 93414 showed the lowest contents of tannin, indicating that it was less than limit of quantification. As a result of HPLC analysis, about 8 out of 14 component of tannins were detected, and additional studies such as analysis of condensed tannin will be needed. Continuous research is also needed to improve the palatability of sorghum and its quality characteristics such as antioxidants. Based on these results, it is expected that sorghum can be used for breeding and industrial use.

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PE-0056

Natural variation in total phenol and total flavonoid content of maize varieties cultivated under different environment conditions

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Maize is one of the most important food resources for humans and animals all over the world. The content of functional substances in maize could be different by their own genetic diversity or environmental condition. To confirm this, we obtained 3 types of maize such as sweet maizes, waxy maizes and nornal maizes cultivated 3 regions(Suwon, Daegu, Hongcheon) of Korea in 2021, analyzed total phenol, total flavonoid content and compared the content using statistical analysis. As a result, sweet maizes grown in Daegu showed the highest total phenol, the total phenol content of sweet maizes were in the order of Suwon and Hongcheon, and the difference was clear. But, waxy maizes and normal maizes had similar average content. For total flavonoids, Sweet maizes that cultivated in Suwon and Daegu had the highest content among the three types, and Hongcheon had the highest content of waxy maizes among them. In the same way, normal maizes had the lowest total flavonoid content in all regions. These results suggest that total phenol of sweet maizes are influenced by the environment factor, and genetic effect more than environment effect impacts on the normal maizes that show lower total flavonoids.

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PE-0057

Genetic Diversity and Genome-wide Association Study of Korean Soybean Landraces(*Glycine max*(L.) Merr.)

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Soybean originated in East Asia (including Korea) and used for various purposes. Wide variation has been accumulated in Korean soybean landraces because soybean has been cultivated in Korea for a long time. The National Agrobiodiversity Center (NAC) preserve approximately 15,000 accessions of Korean soybean landraces to prevent genetic erosion and to preserve genetic diversity.

In this study, 542 accessions of Korean soybean landraces from the NAC were evaluated 14 agricultural traits and genotyped using Axiom_Soya SNP array 180K. Correlation between 6 quantitative traits, flowering stage, leaflet number, growth habit, plant height, the maturity and seed number per pod, was analyzed. Population structure analysis results showed determination of 5 subpopulation. Principal component analysis (PCA) showed the differnece in quantative traits of 5 subpopulations.

Axiom_Soya SNP array developed by Rural Development Administration (RDA) includes 180,961 markers for genotyping cultivated and wild varieties of soybean, making it ideal for whole-genome association studies and high-density genetic mapping to identify important adaptive genes in whole soybean germplasms. The results of genome-wide association study (GWAS) of 534 accession using 58,347 SNPs (after quality control) showed that 7 traits (including plant height, maturity, hypocotyl color, flower color, plant growth type, pod color and seed coat color), associated with 9 quantitative trait loci (QTL). This result is one-fifth of six-year project beginning of 2021, we're planning to evaluate agricultural traits and genotype using Axiom_Soya SNP array 180K 2,500 Korean soybean landraces to develop core collection sets for security for genetic diversity until 2026.

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PE-0058

황금알밀의 주요 농업형질 및 품질특성

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전라북도 완주군 이서면 혁신로 181 국립식량과학원 밀연구팀

국내 밀 품종은 1970년 이후 약 40여 품종이 개발되었지만, 국수용 밀 품종이 대부분을 차지하고 있다. 최근 제빵용에 대한 수요가 증가하고 있지만, 재배되고 있는 빵용 품종 중 2004년에 개발된 조경밀은 붉은곰팡이병과 수발아에 약하고 단백질함량이 낮아 제빵적성이 떨어지는 단점이 있다. 이에 농촌진흥청에서는 제빵용에 적합한 새로운 품종 '황금알'을 개발하였기에 주요 농업형질과 품질・제빵적성 특성을 보고하고자 한다. 출수기는 전작에서 4월 22일로 조경보다 3일 빠르고, 답리작에서 4월 19일로 동일하였다. 성숙기는 전작에서 6월 3일로 조경과 동일하였고, 답리작에서 5월 31일로 조경보다 1일 빠르게 나타났다. '황금알'의 간장과 수장은 각각 75㎝와 7.1㎝로 준단간형이며, 이삭은 조경보다 약간 짧게 나타났다. 단위면적당 수수, 1수립수, 리터중과 천립중은 각각 699개, 30립, 798g, 44.2g으로 조경에 비해 수수는 적고, 1수립수는 비슷하고, 리터중과 천립중은 적게 나타났다. 지역별 수량은 전작에서 513㎏/10a으로 조경보다 16%, 답리작에서 442㎏/10a으로 조경보다 13% 적게 나타냈다. '황금알'의 수발아율은 4.9%로 조경(67.6%)보다 매우 낮게 나타나 수발아에 강하게 평가되었으며, 붉은곰팡이병과 흰가루병은 조경밀과 유사한 수준을 나타내었다. 품질 조사결과, 제분율은 71.4%로 조경보다 약간 낮고, 회분함량은 0.45%로 약간 높게 나타났다. 단백질과 글루텐 함량은 14.0%와 10.3%로 조경보다 높게 나타났으며, 식빵의 부피는 994㎖, 속질경도는 1.02N으로 조경보다 크고 부드럽게 나타나 제빵적성이 우수하게 평가되었다. 이와 같이'황금알'은 단백질함량과 질적특성이 기존 품종(조경)보다 우수하여 소비자가 요구하는 고품질 강력분.용 밀가루를 공급하여 국산밀 산업활성화에 크게 기여할 것으로 기대된다.

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PE-0059

백립계 경질밀 다수성 ‘중모2015’의 주요 농업형질 및 품질특성

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전라북도 완주군 이서면 혁신로 181 국립식량과학원 밀연구팀

국내 밀 품종은 1970년 이후 약 40여 품종이 개발되었지만, 국수용 밀 품종이 대부분을 차지하고 있고, 보급종으로는 금강, 조경, 백강, 새금강 등 4품종이 재배되고 있다. 보급종 중 ‘금강’의 품질은 우수하나 단위면적당 생산량이 적고, 국수 식미감이 떨어지는 단점이 있어 생산성과 식미향상이 요구되었다. 이에 국수적성이 우수하면서, 이모작에 적합하고, 추위와 도복저항성이 증진된 ‘중모2015’가 개발되었기에 주요 농업형질과 품질 특성을 보고하고자 한다.‘중모2015’의 종실은 크기가 크고 색은 백색을 나타낸다. 출수기는 전작에서 4월 22일로 금강과 같고, 답리작에서는 4월 19일로 2일 늦게 나타났다. 성숙기는 전작에서 6월 3일로 금강과 동일하였고, 답리작에서 5월 30일로 금강보다 1일 빠르게 나타났다. ‘중모2015’의 간장과 수장은 각각 80㎝와 7.8㎝로 준단간형으로 금강과 비슷하게 나타났다. 단위면적당 수수, 1수립수, 리터중과 천립중은 각각 804개, 32립, 831g, 43.0g으로 금강에 비해 수수는 같고, 1수립수는 5립 많고, 리터중은 많고, 천립중은 적게 나타났다. 지역별 수량은 전작에서 575kg/10a으로 금강보다 16%, 답리작에서 527kg/10a으로 금강보다 18% 많게 나타났다.‘중모2015’의 겨울철 동사주율은 고휴에서 6.3%로 금강밀(17.3%)보다 낮게 나타나 동해에 강하게 평가되었으며, 붉은곰팡이병과 흰가루병은 금강밀과 유사한 수준을 나타내었다. 밀 품질 조사결과, 제분율은 72.32%로 금강보다 약간 낮고, 회분함량은 0.46%로 약간 높게 나타났다. 단백질과 글루텐 함량은 11.65%와 9.03%로 금강보다 낮게 나타났으며, 최고점도는 109BU로 금강보다 높게 나타났다. 국수면대 밝기는 83.10으로 금강보다 약간 밝고, 경도, 점성과 탄성은 금강보다 약간 높아 건면에 적합하게 평가되었다.

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PE-0060

밥맛이 우수한 고품질 조생종 벼 '금송미'

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강원도는 중북부내륙지, 북부평야지, 중산간지, 동해안 북부 해안지 및 중북부 고랭지 등 벼 재배지대별 구분이 매우 다양하여 지대별 적합 벼 육종의 중요성이 매우 높다. 또한, 타지역 대비 상대적으로 낮은 평균기온으로 인해 벼 재배가능 기간이 짧아 오대벼 등 조생종 벼의 재배면적이 2021년 기준 강원도 벼 재배면적의 59%를 차지하고 있다. 조생종 벼는 중생종, 중만생종 대비 짧은 등숙기간과 등숙기 고온 등으로 인해 상대적으로 품질이 떨어지는 측면이 있어 쌀 품질이 우수한 조생종 품종 개발이 필요하다. 강원도의 다양한 재배지대에 적합하고 밥맛과 품질이 우수한 조생종 품종 개발을 목적으로 '금송미'는 운광과 오대를 각각 모부본으로 하여 2007년에 교배되었다. 초형과 쌀품질이 우수하고 도열병과 줄무늬잎마름병 저항성을 보인 GR7034-24-3-3-2-1을 선발하여 강원24호의 계통명을 부여하였다. 2년간의 생산력검정시험과 3년간의 지역적응시험 결과 수량 및 품질에서 우수성이 인정되어 2020년 농작물 직무육성 신품종 선정 심의회를 거쳐 2021년 품종출원 하였다. '금송미'는 조생종(출수기 8월 4일)으로 밥맛과 품질이 우수하여 생산자와 소비자 모두 만족할 수 있고, 확실한 추천품종이 없는 강원도 동해안 지역에 적응할 수 있는 품종으로의 역할이 기대된다.

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PE-0061

Advancement potato breeding for French fries from 2019 to 2021

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The potato processing industry is growing steadily globally. Import of processed potato products such as frozen French fries are increasing steadily in Korea. Processing of potatoes into French fires requires oblong to long oval tubers basically. The most potato varieties made in Korea are not suitable to process French fries because tuber shape of them is round or short oval. 'Sepung(Shepody)' that was introduced in 1988 are not cultivated now because this cultivar is susceptibility of disease. The purpose of this study was to make excellent potato breeding lines with oblong tubers, shallow eyes, processing quality of French fries. We had been crossing potato resource with oblong tubers and good processing quality in Daegwallyeong from 2019 to 2021. We had acquired 68 cross 68,554 seed in 3 years. We selected 13 potato breeding lines with oblong tubers and low incidence of physiological disorders from clonal generations. 12 lines of them have long dormancy are suitable for single-cropping, the other have short dormancy is suitable for double-cropping. We are performing preliminary yield test of 13 breeding lines in two regions in 2022. We will select good potato breeding lines through the evaluation of the yield and processing quality of French fry.

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PE-0062

Profiling of volatile compounds related to the eating quality of *japonica* rice

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Eating quality of rice is most significantly considered amongst all quality traits, hence achieving high eating quality has been a major goal of many breeding programs worldwide. With the limitations of sensory panel test due to its time-consuming and labor-intensive procedure, assessment of eating quality has been relying on analysis of physicochemical properties excluding aroma and flavor attributes. In this study, the eating quality of 14 non-aromatic *japonica* rice cultivars was evaluated using the sensory panel test, Toyo taste-meter, and volatile compound profiling. A number of volatile compounds were identified for the first time in cooked non-aromatic *japonica* rice, and these compounds showed a strong correlation with the eating quality of rice. PLS-DA demonstrated an outstanding classification effect of the identified volatile compounds on eating-quality discrimination. Several volatile compounds related to lipid oxidation and fatty acid degradation were identified to affect the eating quality in *japonica* rice. Of them, 1-octen-3-ol, 1-ethyl-3,5-dimethylbenzene, 2,6,11-trimethyldodecane, 3-ethyloctane, 2,7,10-trimethyldodecane, methyl salicylate, 2-octanone, and heptanal were selected as important compounds. To take into account the aroma and flavor characteristics of cooked rice in evaluating its eating quality, a highly accurate discriminant model was generated. The contents of listed significant volatile compounds could be suggested for the new eating quality standard. The results could serve as a foundation for future research on integrated rice eating quality, and could facilitate the development of high-quality rice varieties.

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PE-0063

Development of Effective Screening Method and Evaluation of Sweetpotato Cultivars for Resistance to Fusarium Root Rot

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Fusarium root rot is a devastating disease to sweetpotato cultivars, especially infecting tubers during storage periods. It has become important to develop resistant varieties against Fusarium root rot. Therefore, the purpose of this study is to develop reliable screening methods for evaluating resistance from genetic populations. We investigated the development of Fusarium root rot with three sweetpotato cultivars, previously known about response to the disease, such as 'Jinyulmi' (resistant), 'Juhwangmi' (moderate), and 'Beniharuka' (susceptible), according to incubation periods (7-, 14-, 21-, 28-days) and inoculum concentrations (10^4-, 10^5-, 10^6-, 10^7-conidia/mL). As a result, there was a difference in disease development between resistance and susceptibility from 14 days after inoculation. Also, disease severity of Fusarium root rot on sweetpotato tubers represented a significant difference after 1×10^7 conidia/mL inoculation. Using the screening method established from the results, the 112 cultivars from genetic resources were evaluated for disease severity and degree of resistance to Fusarium root rot. Among them, 19 cultivars were resistant, 60 cultivars were moderately resistant, 26 cultivars were moderately susceptible, and 6 cultivars were susceptible to Fusarium root rot. Therefore, the screening method established in this study is efficient for phenotyping resistance to Fusarium root rot and the results of the screening were used for Genome-Wide Association Study (GWAS).

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PE-0064

배가반수체 기술을 이용한 국내 육성 찰옥수수 계통의 유전적 다양성 분석

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옥수수 품종 육성을 위해서는 자식계통의 유전적 다양성을 이용하고 1대교잡종의 잡종강세를 높이는 것이 중요하다. 우수 계통 육성을 위해 많은 노력과 시간이 필요하지만 강원도농업기술원 옥수수연구소에서는 2014년부터 배가반수체(Doubled Haploid)를 이용한 계통육종을 진행하여 효율성을 높이고 육종 연한을 단축하고 있다. 또한 유전체 분석기술이 발달하여 SNP를 이용한 유전적 다양성 및 집단 구조분석 결과를 육종 프로그램에 활용할 수 있게 되었다. 옥수수연구소에서 육성된 흰찰옥수수 32계통, 검정찰옥수수 9계통, 노란찰옥수수 2계통, 색소찰옥수수 1계통 등 44계통과 2016년부터 배가반수체 기술을 이용해 육성된 찰옥수수 계통 중 농업형질이 우수한 111계통을 포함하여 총 155계통을 분석에 사용하였다. 고밀도의 Illumina MaizeSNP50 beadchip을 사용하여 49,574개의 SNP 중 Minor Allele Frequency(MAF) 5%, Call Rate 95% 이하는 제외하였다. 계통의 평균 이형접합율은 2%이며 배가반수체 계통에서도 잔존 이형접합율이 0.2%에서 1.6% 범위로 나타났다. 유전적 거리를 기반으로 하여 neighbor-joining tree 계통수 분석한 결과 4개의 그룹으로 분류되었다. 첫번째 그룹에는 미백2호의 모・부본인 HW3, HW9을 포함한 38개 계통이 포함되었다. 두번째 그룹은 HW11을 포함한 21개, 세번째 그룹은 검정찰옥수수 8개를 포함한 56개, 네번째 그룹은 40개 계통이 포함되었다. 향후 정밀한 표현형 데이터 수집을 통해 전장 유전체 연관분석(GWAS)을 활용하여 정밀한 디지털육종이 가능할 것이라 기대된다.

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PE-0065

RGB 컬러 이미지를 이용한 국산밀 품종 내한성 간이 평가

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국내 밀 품종은 주로 겨울에 파종하여 다음해 6월 경에 수확하기 때문에, 월동기 동안 저온에 의한 손상은 밀의 성장에 영향을 미치는 주요 자연환경 문제 중 하나이다. 국내 밀 육종 프로그램에서는 월동 시 저온으로 인한 밀 잎의 고엽 피해 정도를 분석하여 저항성 계통을 선발하는 데 참고한다. 일반적으로 밀의 저온으로 인한 피해 정도는 육안관찰(달관조사)에 의해 이루어진다. 그러나 육안관찰의 경우 관측하는 사람의 기준에 따라 크게 달라질 수 있으며, 고엽율의 경우는 분석하고자 하는 잎의 차이에 따라 크게 달라진다. 따라서 정밀하고 효율적인 내한성 특성평가 기술이 요구되고 있다. 본 연구에서는 RGB 영상분석 방법이 기존의 육안평가 및 엽록소 함량분석 방법과 비교하여 밀의 내한성 평가에 효율성 여부를 확인하였다. 먼저 저온에 의해 고엽된 정도가 다른 잎 수준에서 조사하였을 때 RGB 이미지 분석에 의한 녹색지수는 고엽율 및 엽록소 함량과 유사한 양상을 보였다. 다음으로 식물체 수준에서 RGB 이미지 분석의 정확성을 비교하였다. RGB 영상분석에 의한 녹색지수는 육안평가에 의한 고엽율과 높은 상관관계를 보였다. 마지막으로 총 40여종의 국내 밀 품종을 전라북도 남원시 운봉시험지(해발 400 m)에서 전개하여 월동 후 생육재생기인 2월 말에 캐노피 이미지를 수집하여 RGB 영상분석에 의한 녹색지수와 육안평가, 고엽율을 비교하였다. RGB 영상분석 방법에 따른 녹색지수와 육안평가 간에는 높은 상관관계를 보였다. 그러나 고엽율과 육안평가 또는 RGB 영상분석에 의한 녹지지수 사이에는 상관관계가 없었다. 이러한 결과는 시각적 평가 대신 RGB 이미지 분석을 사용하여 월동 시 동결에 의한 밀 피해를 식별하는데 유용하게 사용할 수 있으며, RGB 이미지 분석을 통해 누구나 동일한 내한성 평가 값을 구현하는 디지털 육종에 이바지할 수 있을 것으로 판단된다.

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PE-0066

Evaluation of Growth Characteristics to Expand Breeding Resource in Faba bean(*Vicia faba*) and Pea(*Pisum sativum*)

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Faba bean and Pea are suitable for cropping systems because these crops can be cultivated in winter due to their strong cold resistance. Although these crops are rarely cultivated in Jeju Island and the southern part of Korea, they are attracting attention as new income crops due to their higher price than wheat and barley. Also, Faba bean and Pea can be sustainable agricultural solutions. Because they have the ability to fix nitrogen, which can reduce the use of additional chemical fertilizers. Currently, Faba bean and pea are being studied as they are known to have positive effects on crop growth and the soil environment by influencing the activity of the soil rhizosphere microbial community. To expand the cultivation area of Faba bean and pea, early harvesting, high productivity, and cold-tolerant cultivars are needed. We evaluated of growth characteristics of 13 Faba bean accessions and 37 Pea accessions obtained from the gene bank of the National Agrobiodiversity Center, Jeonju, Korea. As a result, two accessions of Faba bean and three accessions of pea with early flowering characteristic and high productivity were selected. We will develop polymorphic SSR markers for cold-tolerant cultivars. The developed SSR markers will be able to be used as breeding materials, genetic resource analysis, and identification of cultivars for Faba bean and Pea.

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PE-0067

Identification of QTLs related Japonica rice pre-harvest sprouting by QTL-seq

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Climate change has been threatening the sustainability of agricultural production. High temperature and frequent rainfalls accelerate the pre-harvest sprouting(PHS) during the rice ripening period in Korea. Especially, most japonica cultivars of Korea are highly vulnerable to PHS which affect grain quality such as milling recovery and head rice ratio as well as rice yield. PHS occurred at 15,000 hectares mainly in south Jeola province in 2016 and 1,300 hectares in east Gangwon province in 2021, which caused serious economic damages.

To develop molecular marker for PHS tolerance, 200 recombinant inbred lines were derived from the cross between sensitive late-maturing cultivar, 'Gopum' and tolerant early-maturing cultivar, 'Joun'. Three panicles were collected from each plant at 40 days after heading and incubated at 25℃ with 100% humidity. After 7 days of treatment, each panicle was checked out for PHS. Among the PHS-investigated 200 lines, the yearly stable resistant and susceptible lines were grouped. Genomic DNA from the two groups were extracted and mixed to analysis the QTL-seq, which finds the QTL region associated with the trait using the NGS analysis in the BSA method that has been traditionally used. As a result, we identified significant QTLs located in chromosome 11 and 12. These QTLs would provide the basic marker to select PHS-tolerant lines in the breeding population.

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PE-0068

중북부 고랭지 적응 복합내병성 고품질 조생 벼 '진부75호'의 특성

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중북부 고랭지 적응 벼 품종은 최근'진평', '진한', '진옥' 등이 개발되었으나 내병성과 품질이 우수한 품종이 다양하게 필요하고, 특히 통일 대비 안정된 주곡생산을 위해서도 북한지역에 적응하는 고랭지 적응 품종 개발이 필요하다. 본 연구는 '진한'에 수량성과 내병성을 도입하여 중북부 고랭지 재배가 가능한 조생 '진부75호'를 육성하여 그 특성을 밝히고자 수행하였다. '진부75호'는 내랭성이 양호하고 밥맛이 우수한 '진부56호(진한)'를 모본으로, 복합내병성인 조평을 부본으로 교배하여 내병성, 내수발아성 등 재배안전성을 갖추고 수량성이 높으며 쌀알이 깨끗한 고품질 계통이다. '진부75호'의 출수기는 8월 4일로 '진부'와 같은 조생이다. 간장은 64㎝로 '진부'보다 약 11㎝ 작고, 현미천립중은 21.6g으로 약 1.4g 가볍다. 쌀 수량성은 571kg/10a로 '진부'보다 3% 증수되었다. 쓰러짐에 강하고 도열병, 흰잎마름병(K1균계)에 강하며, 수발아는 11.7%로 강한 반응을 보였다. 쌀알 외관이 깨끗하고 윤기치가 79.8로 높아 통일 대비 북한지역 쌀공급에 중요한 역할을 할 것으로 기대된다.

사사: 본 연구는 농촌진흥청 연구사업(세부과제명: 이상기후 대비 벼 육성계통 내냉성 강화 및 검정기술 개선, 세부과제번호: PJ01315006)의 지원에 의해 이루어진 결과임.

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PE-0069

DNA메틸화 억제제 제부라린 처리에 따른 보리의 생육 관찰 및 돌연변이 유도

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이 연구는 DNA메틸화 억제제인 제부라린을 처리하여 DNA메틸화가 종자의 발아, 식물의 생육, 및 종자성분에 미치는 영향을 확인하기 위해 수행되었다. 국내 보리 품종인 흰찰쌀보리를 이용하여 침종처리구(1,000 μM, 4°C, 암조건, 72시간)와 재침종처리구로 구분하여 간장, 수장, 분얼수, 엽록소 함량, 및 기공특성을 조사하였다. 재침종처리구는 1차 처리(1차, 400 μM, 4°C, 암조건, 72시간) 후 채종한 종자를 2차 침종처리(1,000 μM, 4°C, 암조건, 72시간)하였으며, 1차 처리 후 채종된 종자를 종실성분분석에 이용하였다. 침종된 종자의 뿌리(43.36 ± 19.57 mm)와 초엽(17.90 ± 4.25 cm)의 신장은 무처리구에 뿌리(87.24 ± 8.75 mm)와 초엽(24.22 ± 3.06 cm)의 신장에 비하여 억제되었다. 침종한 종자 중(M_0와 재처리M_0)에서 발아세가 좋은 100개 개체를 선발하여 하우스에 점파하였으며, 제부라린 처리에 의한 생육 변화를 관찰하기 위하여 고사하지 않은 26개 개체의 간장, 수장, 분얼수, 엽록소 함량, 및 기공특성(내기공 및 외기공의 길이와 너비)을 조사(n=3)하였다. 간장은 무처리(57.5 ± 2.5 cm)에 비하여 26개체 모두 유의미하게 줄어들었으며, 가장 짧은 간장은 20.5 ± 0.4 cm로 측정되었다. 수장은 변화의 폭이 간장에 비하여 작았으며 가장 짧은 수장은 4.6 ± 0.4 cm로 무처리구(5.8 ± 0.6 cm)에 비하여 다소 짧았다. 분얼수는 처리구에서 최대 34개, 최소 4개의 유효분얼수로 무처리구에 비하여 개체간 변이의 폭이 컸다. 엽록소함량은 무처리구(61.1 ± 0.2)에 비하여 처리구에서 다소 높은 개체들이 확인되었으며, 가장 높은 엽록소 함량은 69.7 ± 0.9로 확인되었다. 지엽의 향축면의 내기공 너비와 배축면의 외기공과 내기공의 차이는 유의미하였으며, 엽록소 함량과 상관이 있는 것으로 설명할 수 있다. 재침종처리구의 무작위로 선발된 2개체에서 채종된 종실의 성분분석(P_2O_5,g/kg; K_2O,%; CaO,%; MgO,%; Na_2O,%; C,%; 및 N,%) 결과, P_2O_5, K_2O, CaO, 및 Na_2O는 무처리구(P_2O_5, 1.67; K_2O, 0.43; CaO, 0.06 및 Na_2O, -0.01)에 비하여 P_2O_5는 2.39와 2.22로 K_2O는 0.79와 0.77로, CaO는 0.09와 0.07로, Na_2O는 0.02와 0.01로 유의미한 차이를 보였다.

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PE-0070

국내 최초 초다수성 일대교잡종 찰수수 ‘하이찰 ’육성

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경남 밀양시 점필재로 20, 국립식량과학원 남부작물부 밭작물개발과

수수(*Sorghum bicolor* L.)는 쌀, 밀, 옥수수, 보리와 함께 세계 5대 곡식으로 기능성이 우수하고 환경적응성이 우수한 작물이다. 일대교잡종 수수는 잡종강세로 인해 수량성이 높고 형질이 균일하며 병해충 및 재해 저항성이 우수하여 전 세계적으로 수수의 일대교잡종에 대한 연구와 재배가 활발히 이루어지고 있다. 일대교잡 육종방법을 통해 수수 품종을 개발하면 수량성을 30-40% 향상시킬 수 있다. 이에 따라 일대교잡 육종방법을 이용해 국내 최초 일대교잡종 찰수수 품종인‘하이찰’을 육성하였다.‘하이찰’은 웅성불임성을 이용한 일대교잡 육종을 통해 2021년 육성된 신품종으로 고유특성은 이삭 측면 모양이 도란형으로 산수형의 형태를 가지며, 이삭밀도는 성긴편이다, 종실의 받침껍질색은 짙은 갈색이고 종실색은 적갈색이며, 배유특성은 찰성이다. `19~`21년도 5개소에서 실시한 지역적응시험 결과, 출수일수는 62일로 소담찰 보다 4일 빠른 편이었으며, 간장은 101cm로 소담찰에 비해 23cm 크지만 기계 수확은 가능하며, 이삭길이는 30cm로 소담찰보다 5cm정도 길다. 이삭목 길이는 14cm로 소담찰보다 이삭추출이 양호하여 기계수확에 적합하다. 이삭당 종실중(g/이삭)은 61g, 천립중은 23.2g으로 소담찰보다 천립중은 작지만 이삭당 종실중이 무거운 특성을 가지고 있다.‘하이찰’의 수량은 10a당 481kg으로 소담찰 보다 수량이 57% 증수된 기계수확이 가능한 초다수성 품종이다.

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PE-0071

내도복 단간형 황차조 ‘아리찰’

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조는 생육 후반 도복에 의한 수량피해가 잘 발생하기 때문에 간장이 짧은 단간형 품종 개발이 필요하다. 기존에 국립식량과학원에서 개발한 단간형 조 품종은 모두 메조로 국내에 주로 소비되고 있는 차조는 단간형 품종이 없는 상황이다. 이에 국립식량과학원은 2021년 단간형 차조 품종인 ‘아리찰’을 개발했다. 아리찰은 단간형 메조 품종인 단아메와 일본에서 수집한 유전자원을 교배하여 육성한 품종이다.

국립식량과학원에서 육성중인 차조 계통 중 생육일수가 짧고 간장이 짧아 ‘밀양21호’로 계통명을 부여하고 지역적응성시험계통으로 상정하였다. 2019~2021년에 3년 동안 4개소(경남 밀양, 경기 평택, 충북 청원, 대구 등)에서 지역적응성시험을 수행한 결과, 도복에 강하고 수량이 우수해 2021년 농작물직무육성 신품종선정위원회에서 신규등록품종으로 결정되었다.

‘아리찰’은 출수일수가 64일로 삼다찰보다 짧고 생육일수는 119일로 삼다찰보다 8일 더 빠르다. 간장은 108cm로 기존에 육성된 차조 품종보다 30cm가량 더 짧은 단간형 품종이다. 주당 이삭수는 1.9개, 이삭당 종실중은 10.0g으로 삼다찰과 비슷하고 천립중은 2.4g인 소립 황차조이다. 3년 동안 수행한 지역적응성 시험결과 수량은 2.54t/ha로 삼다찰과 비슷하였다.

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PE-0072

조기재배 가능한 다수성 흰색 찰기장 '탐나찰'

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국내 월동채소의 주요 생산지인 제주지역에서는 월동채소의 후작으로 생육일수가 짧은 단기성 기장을 많이 재배하고 있다. 월동채소 후작으로는 4월에서 7월사이의 조기에 재배가 가능한 단기성 기장 품종이 필요하다. 이에 '탐나찰'은 국립식량과학원에서 2017년 개발한 한라찰을 모본으로, 2016년 개발한 올레찰을 부본으로 교배하여 육성한 품종이다.

육성 중 생육일수가 짧으며 수량이 높아 '밀양19호'로 계통명을 부여하여 지역적응성시험계통으로 상정하였다. 2019~2021년에 3년 동안 경남 밀양, 제주시 애월읍 등 2개소에서 지역적응성시험을 수행한 결과, 수량이 우수하고 도복에 강해 2021년 농작물직무육성 신품종선정위원회에 상정결과 선정되었고, 2022년 품종출원하였다.

'탐나찰'은 출수일수가 49일로 올레찰보다 3일 느리지만, 모본인 한라찰보다 제주지역 기준 10일 더 빠르다. 간장은 83.4cm로 단간이며, 주당 분얼수는 4.1개로 올레찰보다 적은 편이다. 천립중은 6.3g인 중대립이며 종피는 흰색을 띤 찰기장이다. 3년 동안 수행한 지역적응성 시험결과 수량은 2.02t/ha로 올레찰 대비 25% 증수한 다수성 품종이다. 도정수율은 84%로 올레찰보다 높아 우수하다. 포장에서 도복정도는 올레찰과 비슷하였고 세균성줄무늬병 피해 정도도 올레찰과 비슷한 정도였다.

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PE-0073

Growth condition for speed breeding in soybean [*Glycine max* (L.) Merr] using various light condition

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The conventional soybean breeding program by single seed descent (SSD) method required around 8 to 9 years to develop cultivar. Through advancement of breeding techniques using marker-assisted selection, required resources could be significantly saved, but genetic stage advancement step still slow down the entire soybean breeding program time course. In this study, 28 soybean cultivars were tested with different light condition (LED and sodium lamp), LED intensity (80%. 40% of total LED intensity were observed 506 and 257.4 μmol/(m^2 · s) at 50cm from the light source), and planting density (5 x 5 cm and 10 x 11 cm) in LED growth room system (Wooreebio, Korea) and glass house. Plant were kept under short-day condition (9-h light/15-h dark). Comparison of LED and sodium lamp, most of soybean cultivars showed consistent flowering date under LED light condition, but wide range of it under sodium lamp condition. Even though the flowering date difference under two LED intensity was only 3 days, few soybean germplasm under 40% LED intensity showed lodging due to insufficient light supply. The proposed breeding condition, 506 μmol/(m^2 · s) at 50cm from the light source, 5 x 5 cm of density, irradiation for 9 hours, temperature of 25℃ ± 1℃, and humidity of 50% ± 10%, could be progressed to get more than 3 pods of next generation breeding line in just 73 days with minimum labor input. It means when we plant a soybean breeding line to field and LED chamber, we can breed at least 4 cycles in year.

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PE-0074

품종 및 재배지역에 따른 옥수수의 지방산 조성 자연변이 분석

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옥수수는 벼과에 속하는 1년생 식물로 원산지는 중남미이며, 쌀, 밀과 함께 세계 3대 작물 중의 하나이다. 알곡은 주로 사료 및 전분, 식용유 제조 원료로 쓰이며, 찰옥수수 및 단옥수수는 간식용으로 널리 사용된다. 옥수수에 함유된 성분은 전분이 가장 많고, 단백질, 지방, 섬유소 등으로 구성되어 있으며, 이들의 함량은 품종 및 재배지역, 성숙시기 등에 따라 상당한 차이가 나타나는 것으로 알려져 있다. 그러나 국내에서 생산되는 옥수수의 품종 및 재배지역에 따른 지방산 조성의 자연변이에 대해 보고된 바가 없어, 본 연구를 통해 옥수수 지방산 조성의 자연변이에 미치는 유전요인 및 환경요인을 비교 분석하였다. 옥수수는 단옥수수 2개 품종, 찰옥수수 3개 품종, 사료용 3개 품종을 선정하고 국내 3개 지역(대구, 수원, 홍천)에서 재배한 후 시험 재료로 사용하였다. 총 8개 품종 옥수수의 지방산 조성을 분석한 결과, 리놀레산(C18:2) 이 35~63%를 차지하고 다음으로 올레산(C18:1)이 21~46%, 팔미트산(C16:0)이 10~17%의 분포를 보였다. 이러한 조성비는 모든 재배지역에서 품종별로 유사하였으나, 수원과 홍천에서 재배한 고당옥(단옥수수) 품종은 리놀레산 보다 올레산이 더 높은 조성비를 나타냈다. 이러한 결과를 통해, 옥수수의 지방산 조성은 재배환경 보다는 유전요인에 의해 자연변이 영향을 더 크게 받으며, 일부 품종에서는 재배환경에 따른 영향을 더 크게 받음을 알 수 있었다.

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PE-0075

항산화 강화 유색 밀 품종 '아리진흑'의 주요 농업형질 및 품질특성

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최근 건강 기능성 식품에 대한 관심이 증가하면서, 기능 성분이 풍부한 재료를 활용한 식품 개발이 활발히 진행되고 있다. 기능성 소재 중에서 색을 지니고 있는 유색밀은 일반 밀 품종과 달리 종자의 외피에 자색 또는 흑색이 착색되어 있는 밀로서, 최근 농촌진흥청 국립식량과학원에서는 기능성 색소를 함유한 '아리진흑'밀 품종을 개발하였다. 2010년도에 흑립소맥76과 재래종 흑2을 교배한 것을 모본으로 신미찰을 부본으로 추가 교배하였고, F_1 세대에서 F_{10} 세대까지 계통 육성단계 중에서 2016년과 2017년에 걸쳐 생산력 검정 시험을 거쳤으며, 2018년부터 2020년까지 지역적응 시험을 하였다. 그 중 '밀양48호'를 선발하였고, 신품종 선정심의회를 거쳐 대국민 공모 품종 이름짓기를 통해서 '아리진흑'으로 명명하였다.

'아리진흑'의 농업적 특성으로는 수량이 ㏊당 5.4톤으로 일반 밀(금강밀) 대비 많은 편이고, 식물체의 키는 76㎝ 정도로 작아 기존 유색밀 '아리흑'의 키가 커서 쓰러질 수 있는 단점을 보완하여 일반 밀과 유사하게 키를 작게 개량하였다. 출수기는 논에서 재배시 4월 16일 정도, 성숙기는 5월 30일 정도이며, 일반 밀과 이삭이 익어가는 정도가 유사하였다. 이삭당 종자립수는 33립 정도였고, 리터중은 809g, 천립중은 34.3g으로 일반 밀보다 가벼운 소립종이다. '아리진흑'의 재배적인 특성으로는 밀 수확 전에 다량의 강우로 인해 발생할 수 있는 수발아에 강하지만, 병에는 일반 밀과 유사하게 다소 약하다.

'아리진흑'의 종피가 가진 색소에는 항산화 효과가 있는 폴리페놀, 안토시아닌 등의 성분이 함유되어 있다. 품질을 분석한 결과, 밀가루 부분은 단백질 10.9%, 회분 0.41%로 측정되었으며, 종피 부분인 밀기울에는 기능성 성분인 폴리페놀 137.07mg/100g, 플라보노이드 20.32mg/100g, 안토시아닌 10.12mg/100g이 함유되어 있다. 이러한 성분들로 인하여 항산화 능력을 나타내는 DPPH 라디칼 소거능은 100.94 TEAC mg/100g으로 기존 일반 밀보다 높은 수준을 나타냈다. 이러한 유색밀 '아리진흑'은 폴리페놀, 안토시아닌을 함유하여 항산화능이 강화된 기능성 식품의 재료로서 활용 가능성이 매우 높을 것으로 생각된다.

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PE-0076

십리향, 전북 대표 브랜드쌀 육성 모델

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십리향은 2010년부터 2019년까지 호품벼(모본)와 도화향2호(부본)을 교잡하여 육성한 품종이다. 2019년 이름짓기 소비자 공모를 거쳐 '쌀밥의 향이 십리까지 난다'라는 의미로 붙여졌으며, 쌀알이 맑고 신동진보다 늘씬하고 찰기가 있어 식감이 부드럽다.

2021년 재배면적 기준, 전북 벼 재배면적의 64.1%는 신동진이며, 동진찰벼는 10.3%, 새누리 등 다른 품종이 25%로 신동진 의존도가 높았다. 2021년 가을장마로 신동진의 이삭 도열병 다발생에 따른 생산량 감소 등 문제가 발생하여 이를 대체할 수 있는 신품종이 필요할 상황이었다. 전북쌀에 대한 새로운 인식을 확장시키는데 십리향이 그 역할을 할 수 있을 것으로 판단하였다.

이에 2019년부터 전라북도농업기술원, 전북도청(농축산식품국), 전북농협(본부, 군산 등)과 연계하여 재배단지 조성(25ha), 시제품 생산, 소비자 및 업체 반응 조사를 실시하는 등 대표 브랜드쌀(예담채 십리향)로 육성하기 시작했다. 향(2-AP)이 풍부하고 미질이 우수한 장점을 내세워 일본품종(고시히까리 등) 보다 판매가격이 높게 설정하고 가격 유지를 위해 판매실적을 고려하여 3년 동안 생산단지 면적 확대를 제한하는 등 생산단계부터 유통까지 고가 브랜드로 자리잡힐 수 있도록 체계적으로 관리하였다. ㈜노블젠의 참여로 '벼꽃향미'의 새로운 브랜드가 개발되었으며, 잼, 식혜, 누룽지 등 가공식품 중심으로 시장 확장에 힘쓰고 있다. 특히, 농업기술원에서는 재배단지(22년 283ha)에 안정적인 우량종자 보급을 위해 2021년부터 종자사업소에서 본격적인 십리향 재배를 시작하였고 향 성분과 수량성을 고려한 적정 이앙시기 결정(5월28일~6월5일), 종자소독(62℃ 7분 온탕처리, 약제소독 24시간) 및 육묘기술, 드문모심기 기술 연구 등 고품질 생산기술 개발을 지속적으로 추진하고 있다. 2022년 현재, 매년 6회 이상 정례회의에서 종자생산, 십리향 안정생산, 가공시설 보완, 시장 변화에 따른 가격 변동, 가공식품 등 신상품 개발, 새로운 시장 개척(제주), 참여 업체 확대(김제 농협) 등을 검토하고 합리적인 해결책을 모색하고 있다.

향후 십리향 소비 시장 확대를 위해 수확 전 품질 검사(단백질 6.5%이하)로 생산단계 품질관리 강화, 기후변화 등에 대비한 고품질 안정생산 기술 지속 개발, 소비 습관 변화에 적합한 가공상품 개발 등을 통해 전라북도 대표 육성품종으로 자리매김할 것으로 기대한다.

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PE-0077

전북지역 적응 단간 다수성 찰벼 '다복찰'

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전북지역 적응 찰벼계통을 육성하기 위하여 2012년 하계에 단간이면서 초형이 우수하고 수량성이 높은 신명흑찰을 모본으로 하고 단간이면서 수량성이 높은 익산488호를 부본으로 인공교배하여 계통육종법으로 품질이 우수하고 쌀알이 큰 다수성 찰벼 '다복찰'을 개발하였다. '다복찰'은 출수기가 호남평야 보통기 보비재배에서 8월 13일로 대비품종인 '신선찰벼'보다 8일 정도 늦은 중만생종이며, 간장은 70cm로 '신선찰벼' 보다 16cm 작고 이삭은 22cm로 '신선찰벼'와 비슷하며, 주당수수는 16개로 '신선찰벼'와 같다. '다복찰'은 수당립수가 92개로 '신선찰벼' 보다 많고 등숙비율은 84.9%로 낮으며 현미 천립중은 24.9g으로 '신선찰벼' 보다 무겁다. 제현율은 83.8%로 '신선찰벼' 81.8%보다 높았고 단백질함량은 6.5%로 '신선찰벼' 와 차이가 없다. 2017년과 2018년 실시한 생산력검정에서 '다복찰'의 쌀수량은 보통기 보비재배 시 평균 551kg/10a 이었으며, 2018~2020년 실시한 지역적응시험에서 '다복찰'의 쌀수량은 보통기 보비재배 4개소에서 평균 591kg/10a로 '신선찰벼'보다 22% 높았다. '다복찰'의 적응지역으로는 전북지역 표고 360m이하 지역이 적합하다.

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PE-0078

Study of Genome-wide association for fatty acid composition in Korean rice accessions

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Although rice grain is not a kind of lipid-enriched seed, brown rice contains about 2.5 to 3.0% of lipids and relatively high composition of unsaturated fatty acids have been reported. Fatty acid composition in rice grain is known to be strongly associated with palatability and eating quality, especially high composition of unsaturated FAs is preferred by Korean customers. In recent, the analysis method of multiple- traits GWAS was developed and applied to multiple traits. Complex traits controlled by many genes are interconnected in networks of traits and genes and each gene may contribute incrementally to the variation in complex traits. In addition, principal component analysis (PCA) is a method of extracting few key information from phenotypically complex traits that are highly correlated while retaining the original information.

To integrate and focus the overlapped loci among the analyses, we divided these results into two category including saturated fatty acid and unsaturated fatty acid. For the unsaturated fatty acid, the results of linoleic acid and Oleic acid from UV-GWAS, PC1 and PC 2 from PC-GWAS, and the phenotypic set of unsaturated fatty acid from MV-GWAS were compared. For saturated fatty acid, the results of mystric, palmitic, stearic, arachidic, behenic acid from UV-GWAS, the results of PC1 and PC2 from PC-GWAS, and the result of the phenotypic set of saturated fatty acids form MV-GWAS were compared. Collectively 27 loci were detected for unsaturated fatty acid. Among them 6 of loci were overlapped in the results of linoleic acid from UV-GWAS and the result of set of unsaturated fatty acid from MV-GWAS. Total of 26 loci were detected for saturated fatty acid. Among them 8 of loci were overlapped in two analyses where were overlapped in both analysis of UV-GWAS of palmitic acid and MV-GWAS of saturated fatty acid, 4 loci were overlapped in both UV-GWAS of mystric acid and V-GWAS of saturated fatty acid, 1 locus was overlapped in both UV-GWAS of stearic and PC-GWAS of PC1, and 1 locus was overlapped in both PC-GWAS of PC2 and MV-GWAS of saturated fatty acid.

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PE-0079

Multi-trait GWAS of grain shape study with advanced breed lines of Korean rice

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Grain shape is an important factor affecting the grain yield potential and physical or appearance quality, where slender grains with grain length-to width ratio by rice consumer's preference. Grain shape is specified by grain length, grain width, the ratio of length-to-width, grain thickness. The grain weight is positively correlated with these four traits. Total 952 of advanced breed lines were used for the mutit-trait GWAS with the traits of grain length, grain width, grain thickness, and the ratio of length-to-width. In addition, single trait GWAS with each trait were also conducted. the genotype for 952 of Korean advanced breed lines were obtained from the DNA chip analysis with the SNP chip of KNU Axiom Oryza 580K Genotyping Array. The significant threshold was set -log10(P)>5.17. From the result of muti-trait GWAS, 58 significance SNP were detected. Considering the LD block of 250kbp, the significant SNP inside the 500kbp of the lead SNP were considered a same QTL. In the results, we detected 5 lead SNPs as a QTLs associated with grain shape. The 5 QTLs were located at Chr 2, 4, 5, 7, and 8. In this poster, we compared among the QTLs for the multi-trait of grain shape and the QTLs detected from single-trait GWAS of each grain shape.

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PE-0080

Genetic diversity of wheat (*Triticum aestivum* L.) cultivars and differential selection during domestication

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In the background of climatic changes and a food crisis mainly on wheat, ensuring the safety of wheat cultivars is a top priority. The purpose of this study was to obtain information on the genetic diversity of wheat cultivars, and to evaluate the rationality of germplasm selection based on the genetic distances of the germplasms in each cultivation area and combined with climatic conditions. To elucidate the gene functions of the genomic selection differential interval between subpopulations, it can be used to explain the domestication goals of wheat germplasm in each subpopulation and identify security loopholes. Genetic diversity analysis and population structure analysis were performed on 384 germplasms using 19,718 quality-controlled SNPs. The population originating in China had the highest genetic diversity (Shannon's Information Index = 0.512). The genetic distance matrix and genetic differentiation index marked the distribution of wheat cultivars with similar genetic distance. Mantel test showed that geographic distance could explain 26.8% of the variation in genetic distance. In the genome-wide sliding-window Tajima's D results of the three subpopulations, it was found that regions with large differences in the degree of selection were found on chromosome 1 of A, B, and D. To understand the function of these selection difference intervals, Genome-Wide Association Studies (GWAS) were performed on 20 traits. In the selection degree difference interval, the marker-trait association (MTA) related to seed roundness, stem length, and thousand-kernel weight exceeded the threshold. In this study, the gene encoding E3 ubiquitin ligase related to seed roundness was analyzed.

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PE-0081

종실의 생산성과 안토시아닌 함량이 높은 옥수수 신품종 '색소6호'

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소비자들의 기능성 식품에 대한 관심 및 상품의 요구도가 높아짐에 따라 다양한 작물에서 안토시아닌이 함유된 품종이 개발되고 있다. 강원도농업기술원 옥수수연구소에서 지속적으로 알곡, 속대, 포엽, 줄기에 자색이 함유되어 있는 옥수수 품종을 개발하고 있으며, 색소 1, 5호는 포엽, 속대부분에 자색이 발현되며, 색소 2호는 포엽, 속대, 종실에 자색이 발현되는 품종이다. 자색옥수수 추출물의 간보호, 항비만 및 항콜레스테롤 효능이 동물실험을 통해 입증되었으며 항산화, 항당뇨 등 다양한 효능이 보고되어있다. 현재 자색옥수수 종실 추출물은 액상차, 빵류 등에 첨가되어 다양한 기능성 가공품이 생산・판매되고 있으며, 업체의 개발요구도가 높아지고 있는 실정이다. 따라서 본 연구는 옥수수 안토시아닌 색소가 많이 발현되는 종실의 생산성과 안토시아닌함량이 높은 품종을 개발하기 위해 수행하였다. "색소6호"는 색소용 모집단에서 분리된 HA11를 모본, HA12을 부본으로 하여 2017년에 인공교배 하였으며, "색소2호" 대비 종실 수량성은 26% 증수한 576kg/10a, 안토시아닌 함량은 8% 증가한 0.28g/100g이었으며, 도복지수는 1로 낮아 내재해성도 강하며, 100립중은 24.1g이었다. 출사일수는 "색소2호"와 비슷한 86일이며, 착수고율은 53.6% 이다. "색소6호"는 "색소2호"에 비해 종실의 생산성이 높고 안토시아닌 함량이 높아 천연색소 추출 등을 위한 가공용 옥수수로 적합한 특성을 가지고 있다. 앞으로 다양한 기능성 가공품에 첨가되는 추출물로 활용되면 자색옥수수 재배면적 확대 및 산업화에 기여할 것으로 기대된다.

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PE-0082

잎 및 잎자루 채소용 고구마 품종 '통채루'

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고구마의 잎과 잎자루에는 식이섬유, 루테인, 베타카로틴, 폴리페놀, 플라보노이드 등 기능성 성분이 다량 함유되어 있으며 항산화, 항알레르기, 항염증, 항균, 항고혈압, 간 보호 및 대장암 예방에 효과가 있는 것으로 알려져 있다. 국내에서는 잎자루용으로 잎자루색이 자색인 '하얀미', 녹색인 '신미' 품종이 재배되고 있다. 기존 잎자루 채소용 고구마 품종들은 잎자루 껍질이 질겨 껍질을 벗기기 위한 비용이 발생하고, 껍질에 함유되어 있는 기능성 성분을 이용하지 못하는 단점이 있었다. '통채루' 품종은 잎과 잎자루에 안토시아닌 등 기능성 성분이 풍부하고 잎자루 껍질째 섭취가 가능한 다수성 채소용 고구마 품종을 육성하기 위해 잎자루색이 자색이고 껍질이 부드러운 'Red Top Leaf'(IT232314)를 모본, 잎자루 수량이 많은 'MI2011-31-09'(IT334865)를 부본으로 하여 육성되었다. '통채루'는 잎자루와 줄기가 자색이다. '통채루'는 생잎자루 저작시 섬유질의 남는 정도(-3~3)가 -1.6으로 '하얀미'(0)보다 적고 생으로 섭취가 가능하다. '통채루' 잎자루의 감미도(sweetness)는 13.3으로 '하얀미'(6.6)보다 높아 단맛이 강하고 생잎의 식미(-3~3)가 1.0으로'하얀미'(0)보다 우수하다. '통채루' 품종의 잎자루에는 루테인 6.9 mg/100g dw (dry weight basis), 베타카로틴 8.3 mg/100g dw, 비타민C 15.9 mg/100g dw, 안토시아닌 180.2 mg/100g dw이 함유되어 있으며 비타민C와 안토시아닌 함량은'하얀미'보다 각각 51.4%, 24.3% 높아 기능성이 우수하다. 잎자루 수량은 하우스 재배시 10,320 kg/10a, 노지 재배시 6,908 kg/10a으로 '하얀미'보다 각각 4.1배, 3.0배 많다. '통채루'는 고구마뿌리혹선충에 약하므로 뿌리혹선충 상습발생지에서는 재배에 유의하여야 한다. '통채루' 품종은 2021년에 품종등록(제8788호) 되었으며 광주광역시, 경남 통영시 등 잎자루 재배단지를 중심으로 보급을 확대할 계획이다.

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PE-0083

세대단축을 이용한 밀 붉은곰팡이병 저항성 육종체계 구축

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경상남도 밀양시 점필재로 20 국립식량과학원 남부작물부 논이용작물과

붉은곰팡이병(Fusarium head blight, FHB, scab)은 밀(*Triticum aestivum* L.), 보리(*Hordeum vulgare* L.) 등 화본과 작물에 주로 발병하는 곰팡이병으로 우세종인 *Fusarium graminearum* Schwabe를 비롯하여 *F. culmorum*, *F. poae* 등에 의해 발생한다. 붉은곰팡이병에 감염되면 종실이 오그라들고 변색되는 등 정상적으로 등숙하지 못하여 작물의 수량과 품질이 하락하고, 데옥시니발레놀(DON), 니발레놀(NIV), 제랄레논(ZEA)와 같은 독소(mycotoxin)을 생성하여 인축에 구토, 설사, 암 등을 유발하는 강한 독성을 나타내기도 한다. 붉은곰팡이병은 잎녹병에 이어 밀 수량감소에 가장 치명적인 병으로, 이에 의한 경제적 손실은 미국에서만 10억 달러에 이르고, 중국에서는 밀 재배면적 중 7백만 ha에서 붉은곰팡이병이 발생하여 250만 톤의 수량이 감소한 바 있다. 밀 붉은곰팡이병은 경종적, 유전적 방법을 통해 경감할 수 있지만 가장 효과적인 수단은 저항성 품종을 재배하는 것이다. 붉은곰팡이병 저항성 품종 중 가장 잘 알려진 것은 아시아 지역의 재래종인 Sumai-3, Wangshuibai 등으로 이들 품종에서 다양한 QTL이 밝혀져 있어 교배모본으로 활용되고 있다.

한편 겨울밀은 정상적인 출수를 위해 최대 12주간의 춘화처리(vernalization)가 필요하여 하작물에 비하여 생육기간이 길다. 따라서 새로운 품종개발을 위한 계통의 고정이나 출수기 병해충 검정 시 오랜 기간이 소요된다는 단점이 있다. 이를 보완하기 위해 장일식물인 밀의 특성을 이용하여 저온처리를 통한 종자 휴면 타파 및 장일처리를 통한 출수기 단축으로 1년에 6세대를 진전할 수 있는 스피드육종법이 개발된 바 있다. 스피드육종법을 활용하면 여교배를 통한 저항성유전자 도입 후 빠르게 고세대로 진전이 가능하고, 병 저항성에 대한 신속한 검정 및 반복 실험이 가능하다.

본 연구에서는 KASP마커 PFT_KASP(Singh *et al*., 2019)를 이용하여 국내외 164품종을 대상으로 붉은곰팡이병 저항성 유전자원을 선발하고 세대단축을 이용하여 여교배 및 세대를 진전하고자 한다. 또한 세대단축시설 내 붉은곰팡이병 저항성 검정법을 구축하기 위하여 이들 품종을 상온에서 48시간 침종한 후 72구 육묘상자에 각 1립씩 파종하였다. 일장은 22시간 명조건/2시간 암조건(차 등, 2020)으로 처리하였으며 최저온도 25℃로 유지하였다. 병원균은 국내 우점균주로 알려진 *Fusarium asiaticum* #73를 이용하였으며 밀 이삭이 50% 이상 개화하였을 때 1×10^5/ml 농도로 하여 분사하였다. 접종 후 온실 내 검정상에서 온도 22℃, 습도 90% 이상으로 36시간 유지하였으며 접종 2주 후 이병영화수를 조사하였다.

유전자형 검정 결과, 국내 품종 63품종 중 늘찬, 중모2008 등 19품종이, 해외 유전자원 101품종 중 Ning Mai 50, Sumai-3 등 8품종이 붉은곰팡이병 저항성인 것으로 나타났다. 붉은곰팡이병 저항성 품종개발을 위해 Sumai-3, 금강, 백강, 황금알을 세대단축시설 내 재배하였으며 이때 출수일수 차이가 3~5일로 균일하여 여교배가 용이하였다. 또한 생육일수가 85일로 노지에 비해 단축되어 신속한 세대진전이 가능하였다. 세대단축시설 내 밀 붉은곰팡이병 검정법 구축을 위한 *F. asiaticum* 처리 결과, 곰팡이균 분사 후 약 24시간 이후부터 병징이 나타나기 시작하였으며 기존 보고된 조사시기인 접종 72시간 이후에는 과습에 의한 기타 균의 발생으로 정확한 평가가 어려웠다. 이병영화비율은 Sumai-3, 금강, 백강이 각각 20.8, 12.8, 46.5%였으며 황금알은 접종 후 식물체가 고사하여 이병율을 조사할 수 없었다. 접종 3주 후에는 대부분 식물체가 성숙하여 이병된 영화를 조사하기 어려우므로 접종 1~2주 내 평가를 실시할 필요가 있다. 본 시험결과를 활용하여 국내 품종에 붉은곰팡이병 저항성유전자를 도입하고 이를 평가하기 위한 검정법을 확립할 예정이다.

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PE-0084

Exploring SNP related wheat's heading date in Korean wheat core collection accessions by GWAS analysis

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Wheat is one of major crops for mankind in the world and a huge genome size 17G. Despite the draft sequence information was released in 2018, it is still difficult to apply to Korea cultivar genetic diversity and domestic environment. In order to overcome the hurdle, Korean wheat core collection was built based on accessions collected from various countries. And there is a tendency to prefer precocious breeding programs and pre-harvest resistance in Korea. Investigation of the heading date in the core collection accessions for we would like to select an excellent growth accessions suitable for the domestic cultivation environment.

In this study, we are evaluating heading date in Korean wheat core collection at 2018-2019. Korean wheat core collection for phenotyping. For genotyping, a total of 566 accessions of the 614 core collection selected after consideration of DNA QC to SNP chip. Process to GWAS in R on GAPIT method's FarmCPU. Korean wheat core collection for phenotyping.

The early heading accessions were selected #55, #98, #162, #676, and #829 in mid-April, but the late heading accessions were selected #700, #1360, #1770, #1797, and #1632 in mid-May. Various SNPs were searched through GWAS and among them, SNPs that can be used as markers were selected. Exploring useful SNPs AX-95222044(4B, Log to p.value:13.169), AX-94795073(1D, Log to p.value: 7.598) were performed HRM(High Resolution Melting) to confirm heading date difference for top5, bottom5. With the bioinformatics tool, 250Kbp was searched around the SNP to secure a useful gene candidate group. The AX-94795073 is not known for the transcription but, AX-95222044, it belongs to the transcription of the protein Thymidine kinase protein. In the future, developing that excellent accessions crossbreeding and cultivating suitable for the environment will have been proving gene expression test.

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PE-0085

Identification and characterization of wheat salt tolerance-related genes through GWAS

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Salt stress is considered to be one of a major abiotic stress that negatively affects the growth, development, productivity and the quality of crop species. Wheat (*Triticum aestivum*) is one of the most important grains, with the second largest production worldwide. However, it is a crop sensitive to salt stress, and salt stress in the early growth stage can have a more serious effect on the final yield. This study compared the phenotypes of treated and control groups when 200mM salt was treated at the seedling stage using 614 core collection. Based on this, GWAS was performed by applying MLM, MLMM, Farm CPU, and blink models, and significant SNPs were searched for in all models. As a result, BA00735388 was selected and it was confirmed through HRM that the alleles of the Top 5 and Bottom 5 lines were G/A in 614 core collection. Gene candidates within ±250 kbp of the corresponding SNP were investigated. Of the total 14 transcripts within the range, 11 transcripts had no elucidated function in wheat. As a result of examining the similarity of the 11 transcripts with those of *Hordeum vulgare* and *Aegilops tauschii*, it is estimated that 5 of them are BTB/POZ and MATH domain-containing protein1(BPM1). BPM1 is known to be involved in cellular responses to iontophoretic stress. The gene expression patterns of BPM1 were compared with the RNF and UGT genes, which were studied for salt resistance, in 5 Top and 5 Bottom lines in the core collection. The results of study are expected to contribute to the development of salt-tolerant in wheat.

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PE-0086

Identification of Transcriptome and Proteome related metabolite mechanisms under pre-harvest sprout (PHS) of Korean wheat (*Triticum aestivum*)

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Wheat (*Triticum aestivum*) is one of the world's most commonly consumed food crops. Wheat is rarely used immediately after harvest and usually requires a secondary process (milling). Global warming and abnormal climate are the cause of various biotic and abiotic stress damage and affect wheat growth and harvest worldwide. Especially, Pre-Harvest Sprouting (PHS) is considered to be one of the main factors that weaken wheat end-use quality. In this study, transcriptome analysis was performed on PHS-induced Keumgang, Woori, and Jeonju 377, a Keumgang mutation line by the Rural Development Administration (RDA) using RNA-seq. Mapping was performed based on wheat reference genome information. And DEGs were analyzed by setting a comparison group based on the mapping. Protein analysis was performed using Ingenuity Pathway Analysis (IPA) on the same sample, and the wheat reference genome used in RNA-seq was translated into proteins and controlled. At the same time, functional analysis was performed using the Ingenuity Pathway Analysis (IPA), and protein analysis was performed by translating and contrasting the wheat reference genome used in RNA-seq. Keumagng PHS0 vs Jeonju 377 PHS0 and Keumgang PHS0 vs Woori PHS0 were set to focus on expression under dormancy. And functional annotations were simultaneously explored based on the overlapped DEGs. Phytohormones (abscisic acid, GO:0009737), glucose (gluconeogenesis, GO:0006094), starch (starch biosynthesis process, GO:0019252) and amyloplast metabolism (GO:0009501) were identified as overlapping functions, and it was predicted as a function related to dormancy. It is expected that it will be possible to investigate the function of seed germination and dormancy and further analyze the related seed dormancy relate metabolism and pathway. Furthermore, it is expected to provide detailed research information on the occurrence and dormancy of PHS in wheat.

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PE-0087

대립, 기계수확에 유리한 장류용 콩 '대왕2호'

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건강기능식품, 웰빙추구의 소비트렌드 변화는 기능성 잡곡의 소비수요도 증가시켰다. 하지만 잡곡시장은 생산기반 취약, 높은 가격 등으로 가격경쟁력이 낮아 오히려 위축되고 있다. 이를 해결하고 농가소득에 기여하고자 다수성, 기계화적응성이 우수한 콩 '대왕2호'를 육성하였다. '대왕2호'는 대립이면서 쓰러짐과 탈립에 강하여 기계수확에 유리한 품종으로 '강일콩'과 '강원105호(강원91호×석량풋콩)'를 '06년 인공교배하여 계통육성법으로 'GSL06035-2B-1-2-2-2'를 선발하였다. '14~'15년도 실시한 생산력검정시험에서 생육특성이 우수하고 대립・다수성이며 탈립에 강한 계통으로 유망하여 '강원140호'의 계통명을 부여한 후 3년간 강원 3개소에서 지역적응시험을 실시하였다. '대왕2호'는 유한신육형, 엽형은 난형, 꽃색은 자색, 모용색은 회색이며 종실은 황색의 구형인 고유특성을 가지고 있다. 성숙기는 10월 25일로 주 재배품종인 '대원'보다 2일 빠른 만생종이며 100립중은 33.5g으로 대립종이고 기능성 물질인 이소플라본 함량이 높은 품종이다.
'대왕2호'는 기존 대립・다수성 품종인 '대왕'에서 꼬투리 터짐과 쓰러짐에 강하게 개량한 품종으로 기계수확이 용이하여 강원지역(고랭지 제외)의 두부 및 장류용 콩으로 재배가 확대될 것으로 기대된다.

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PE-0088

출수기에 기반한 벼(*Oryza sativa* L. cv. Donjin 1) 선발계통의 특성 비교

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조기출수 벼 육종소재를 개발할 목적으로 벼 건조종자에 300 Gy의 감마선(^{60}Co)을 조사하여 M_2 세대에서 출수기 관련 개체를 선발한 후 계통재배하여 M_{18} 세대까지 진전시킨 9 계통의 동진 1호 벼 유래의 선발계통을 대상으로 출수기 등 농업형질 특성과 미질 특성을 조사하고, 출수기 및 초장 관련 유전자의 동태를 파악하고자 하였다. 순천지역에서 M_{18} 세대 공시계통의 출수기를 조사한 결과 모품종(8월 8일)보다 11일 빠른 계통(γ-3)부터 16일 느린 계통(γ-7)까지 다양하게 출수기가 관찰되었다. 초장의 경우, 조기출수 계통 중 왜성인 계통(γ-1, γ-2, γ-3)은 모품종(90.2 ㎝)에 비해 약 8 ㎝ 작았으며, 키가 큰 계통(γ-4, γ-5)은 모품종보다 약 3 ㎝ 크게 나타났다. 만기출수 계통(γ-6, γ-7)의 초장은 모품종보다 각각 08 ㎝, 17 ㎝ 크게 나타났다. 수당립수와 등숙율은 모품종에 비해 모든 공시계통에서 낮게 나타났으며, 천립중은 모품종(23.9 g)에 비해 γ-8 (26.6 g), γ-9 (25.4 g), γ-7 (25.1 g) 계통이 높게 나타났으며, 다른 공시계통에서는 모품종과 유의적인 차가 인정되지 않았다. 미질특성을 분석한 결과, 아밀로스의 함량이 모품종(17.5%)에 비해 높거나(γ-7, γ-8, γ-6 계통) 낮게(γ-9, γ-3, γ-1, γ-5, γ-2, γ-4 계통) 나타났으며, γ-9 계통이 16.3%로 가장 낮게 나타났다. 단백질 함량은 γ-8 계통(6.15%)을 제외한 공시계통에서 모품종(6.14%)보다 모두 낮게 나타났으며, γ-7 계통이 5.66%로 가장 낮게 나타났다. 백도는 모품종을 포함한 모든 공시계통에서 40 이상으로 나타났고, Toyo 식미값은 γ-4 계통(75.8)을 제외한 공시계통에서 모품종(76.2)보다 모두 높게 나타났다. 출수기와 초장 관련 유전자의 동태를 파악하고자 조기출수 및 왜성 관련 유전자를 분석한 결과 모품종 처리구 2개와 9개의 공시계통에서 조기출수 유전자 6개(*OsEhd1*, *OsEhd2*, *OsEhd3*, *OsHd1*, *OsHd3a*, *OsMADS50*), 왜성 관련 유전자 5개(*D1*, *D18*, *SD1*, *EUI*, *D11*)의 존재를 확인할 수 있었다. 향후 위 유전자의 기능해석을 위하여 조기출수 및 왜성 관련 유전자의 발현과 기능에 대한 추가연구가 필요할 것으로 사료된다.

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PE-0089

Study the genetic interaction among rice yield components and traits related to yield potential under low nitrogen paddy field conditions

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Nitrogen is a major essential macronutrient to achieve optimum growth and development for plant. Once nitrogen is deficient, it causes many negative problems to the synthesis of numerous critical biological compounds such as amino acids, proteins, nucleic acids, chlorophyll, and some plant hormones. Therefore, crop productivity highly depends on nitrogen fertilizer, and nitrogen is a major limiting factor in most agricultural practices. Rice cultivation requires intensive use of nitrogenous fertilizers. However, excessive use of nitrogen fertilizers, even in normal use, can cause crucial concerns with nitrate leakage in the field. It is especially ecological pollution or emission of greenhouse gas connected to climate change. In this study, our goal is to reveal the main factor associated with yield decrease in rice under low nitrogen conditions. Japonica-MAGIC and 232 core set of rice, consisting of temperate *japonica*, tropical *japonica*, *indica*, Korean rice landraces, and Tongil type rice, were transplanted spaced at 30 x 15 cm with three replications under two nitrogen(N) conditions: low-N (4.5 kg/10a) and normal-N (9 kg/10a). The yield related traits and yield per plant for each of the lines in two nitrogen conditions will be evaluated at the mature stage. We will figure out the main factors for decreased yield under low-N by analysis of relationships between evaluated traits.

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PE-0090

Correlation analysis between agronomical traits and functional of barley (*Hordeum vulgare*) genetic resources

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One of the objectives of crop breeding focuses on the enhancement of functional components. Barley is also receiving attention for its functional ingredients, mainly due to its high beta-glucan (β-glucan) content compared with other grains. β-glucan is known for improving immunity and lowering blood cholesterol content. However, it is not always easy to develop a variety with enhanced functionality using breeding materials. Studies that investigate the association between agronomical properties and metabolite contents are of great importance in this regard. In this study, the correlations between selected agronomical traits and functional components such as β-glucan content, total phenolic content, 2,2'-azino-bis (3-ethylbenzthiazoline-6-sulphonic acid) (ABTS) scavenging activity, and 1,1-diphenyl-2-picrylhydrazyl (DPPH) radical scavenging activity were analyzed in 215 Korean barley genetic resources. The results revealed some important associations between the functional components and agronomical traits. β-glucan contents and thousand-grains weight showed a positive and significant correlation ($r = 0.340$, $p < 0.001$) with each other. Unlike this, β-glucan contents showed a negative and significant correlation with heading date after sowing($r = -0.458$; $p < 0.001$). On the other hand, the two antioxidant activities including ABTS and DPPH-radical scavenging activities showed a strong and positive correlation with each other ($r = 0.659$; $p < 0.001$). In general, this study indicated the wide-ranging associations between functional components and agronomical traits in barely genetic materials. The results of the study could be applied during the selection of barely genetic resources for breeding.

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PE-0091

Mapping of quantitative trait loci associated with mineral element contents in brown rice using an *Oryza sativa* x *O. rufipogon* introgression line population

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'Minerals play a vital role in human health. Globally, rice is one of the most essential consumed cereal crops. However, rice grain has comparatively small amount of some essential nutrients like zinc, iron, and calcium compared to other staple crops like wheat and corn. Insufficient intake of nutrients could lead to malnutrition. Thus, increasing the nutrient contents of rice has presently become a target by some breeding programs to address malnutrition. Wild rice establishes an extended gene pool that can be used for rice cultivar improvement. In our study, 96 introgression lines (ILs) derived from a cross between the Korean elite O. sativa japonica cultivar 'Hwaseong' and *O. rufipogon* (IRGC 105491) was generated to identify quantitative trait loci (QTLs) associated with rice grain mineral elements. The mineral contents (iron, zinc, manganese, and calcium) in brown rice of ILs were evaluated in two locations: Chungnam National University (two-year data) and Chungcheongnam-do Agricultural Research and Extension Services (CNARES) (one-year data). In this study, six QTLs for mineral elements were identified by single marker analysis. The trait enhancing alleles of identified QTLs were derived from *O. rufipogon.* The identified QTL for iron and zinc on chromosome 10 was characterized and further defined the location using additional markers. The results suggested that the 0.78-Mbp *O. rufipogon* segment between RM1873 and RM25633 is associated with an increase in iron and zinc content in brown rice. The favorable *O. rufipogon*-derived QTLs identified in our study will be useful in improving the nutritional quality of rice.

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PE-0092

소비재배 시 벼 품종별 작물학적 특성 및 수량구성요소 변화 분석

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우리나라에서 벼 재배는 농업분야 온실가스 배출량의 29.5%를 차지하고 있다. 반면 지속가능한 쌀산업을 위해 온실가스 저감 기술 개발이 요구된다. 논농업 분야 온실가스 감축을 위한 고투입・다수확 재배법에서 화학비료 및 합성농약의 사용을 최소화하는 정책을 추진 중이다. 김 등. 2019 에 의하면 화학비료를 50% 감축했을 때 온실가스가 약 11% 감소되었다. 따라서 본 연구에서 화학비료 감축 시 품종별 작물학적 특성과 수량 및 수량구성요소의 변화를 분석하였다.

시험구별 시비량은 무비구 0kg/10a, 소비구 4.5kg/10a, 보비구는 9kg/10a로 설정하였다. 인디카 품종은 한아름4호, 금강1호, 밀양392호, IR72, 93-11을, 자포니카 품종은 새일미, 소비, 남평을 공시하였다. 시비량별로 작물학적특성인 경수, 초장을 이앙 후 20일부터 2주 간격으로 조사하였고, 수확 전・후 수량구성요소인 간장, 수수와 천립중, 수당립수를 조사하였다.

전체 품종의 보비 대비 소비와 무비의 수량 감소율은 각각 20%, 50%였으며, 수당립수는 보비 대비 각각 6%, 23% 감소하였고, 수수는 각각 25%, 42%로 수량구성요소 중 감소율이 가장 컸다. 비료 감축에 따른 수량과 수량구성요소의 감소율은 아종간 차이는 없었다.

본 연구에서는 화학비료의 시비량을 감축했을 때의 벼 품종별 작물학적 특성 및 수량과 수량구성요소를 비교분석하여 수량감소 요인을 파악하였으며, 추후 온실가스 저감을 위한 소비재배 적응 벼 육종에 방향을 제시할 수 있을 것이다.

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PE-0093

통일형 초다수성 기능성 적미 ‘초홍’

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경상남도 밀양시 점필재로 20 국립식량과학원 남부작물부

“초홍”은 내염성 및 벼멸구 저항성이며 현미 종피색이 적색인 Pokkali에 수량성이 높고 복합내병성인 한아름2호(밀양240호)를 두 번 여교배하여 육성하였다. 2010년 하계에 교배하여 2010/2011년 동계에 양성한 F_1(YR29222)에 한아름2호(밀양240호)를 여교배하여 2011년 하계에 F_1을 양성하였다. 2012년 F_2집단에서 개체별로 1립씩 채종하여 2013년 하계 F_3을 집단육성하여 가을에 16계통을 선발하였고, 이 후 계통육종법에 따라 계통을 전개하였고, 2017년부터 2년간의 생산력검정시험을 거쳐 2018년 “밀양356호”의 계통명이 부여되었다. 2019년부터 2021년까지 3년간의 지역적응시험 결과, 수량성이 높고 벼 주요 병해 및 벼멸구에 강하며, 기능성 적미로서 우수성이 인정되어 2021년 농작물 직무육성 신품종선정위원회에서 “초홍”으로 명명되었다. “초홍”은 출수기가 8월 13일인 중만생종이며, 간장은 85㎝로 “다산”보다 크고, 주당수수가 15개로 “다산”보다 2개 많다. “초홍”은 현미수량이 766kg/10a으로 “다산”보다 4% 많으며, “초홍”은 종자의 길이가 “다산”보다 짧고 너비는 넓어 장폭비가 낮다. 현미 종피색은 적색으로 항산화활성이 적진주 등 일반계 적미 품종보다 높았으며, 총폴리페놀과 총플라보노이드 함량도 일반계 적미 품종보다 1.3배~2.4배가량 높은 품종이다.

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PE-0094

Growth Characteristics and Productivity of an Italian Ryegrass (Lolium multiflorum Lam.) New Variety, 'IR605'

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Italian ryegrass (*Lolium multiflorum* Lam) is the most popular winter annual grass in Korea, and it is cultivated for hay, haylage, or silage. It offers rapid establishment, starts growing early in the following spring, and has fast regrowth after defoliation. This study compared the growth characteristics of the new variety of Italian ryegrass, 'IR605', and ‘Kowinearly’. IR605 is a diploid with green leaves and has a semi-erect growth habit before wintering and an erect growth habit in the spring. It is a medium-maturing variety with a heading date of ca. May 15. It was observed that IR605 had a flag leaf width of 9.9 mm, flag leaf length of 26.7 cm, and plant length of 100 cm on the heading date, which is approximately 5 cm longer than that of Kowinearly. The stem thickness and ear length of IR605 were 0.08 mm thicker and 0.5 cm longer than those of Kowinearly, respectively. 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%, slightly higher than that of Kowinearly. The total digestible nutrient value was 58.5%, slightly lower than that of Kowinearly. Overall, the feed quality characteristics of IR605 were similar to those of Kowinearly.

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PE-0095

강화지역 조생품종 대체를 위한 고품질 벼 '수원657호'

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2024년까지 벼 외래품종 재배면적을 1만 헥타르까지 줄인다는 정책 목표를 지원하기 위해 '수요자 참여형 벼 품종 개발 연구(SPP)'를 확대하고 있다. 국내에서 재배되는 주요 외래 벼 조생품종은 '고시히카리', '히토메보레' 등으로 병해충에 약하고 잘 쓰러지는 등의 문제가 있다. 본 연구는 강화지역에서 많이 재배되고 있는 '고시히카리'를 대체할 수 있는 조생품종을 육성하기 위해 수행되었다. 강화지역 조생품종 대체를 위해 하점면과 화도면에서 13개 계통 및 품종을 시험하였으며, 중간 평가 결과 1차로 선발된 3계통에 대해 식미검정을 실시하였다. 그 결과 '수원657호'가 53% 선호도의 높은 점수로 가장 밥맛이 좋다고 평가받았다. '수원657호'는 중북부지역에 적응하며 내병성이 강화된 조생품종 육성을 목적으로 진부54호와 익산556호를 교배한 F_1을 부본, 밥맛이 우수하고 도정특성 및 완전미율이 양호한 고품질 품종 '화왕'을 모본으로 2013년에 삼원교배하였다. '수원657호'의 출수기는 7월 28일로 '조평'보다 약 1주일 늦다. 간장 76cm, 수장 19cm, 현미천립중 20.4g으로 '조평'과 비슷하다. 쌀 수량성은 559kg/10a로 '조평'대비 114% 수준이었다. 도열병에 강하고 흰잎마름병에는 중도 저항성을 보였다. 등숙률 92.5%로 높았으며 쌀알 외관이 깨끗하고 단백질 함량이 낮으며 윤기치는 74.2, 완전미율은 95.0%로 높다. '수원657호'는 강화지역에서 많이 재배되는 고시히카리를 대체할 수 있는 조생품종이 될 것으로 기대된다.

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PF-0001

Evaluation of Chinese cabbage, cabbage and radish genetic resources for resistance against soft rot caused by *Pectobacterium carotovorum* subsp. *Carotovorum*

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Soft rot caused by *Pectobacterium*, a bacterial phytopathogen is highly detrimental to the production of several crops including cabbage, Chinese cabbage and radish in East Asia where they are largely grown. In the current work, accessions of Chinese cabbage, cabbage and radish plants collected at the National Agrobiodiversity Center, RDA, South Korea were screened for their innate resistance against *Pectobacterium carotovorum* subsp. *Carotovorum* KACC10421 and KACC21701. Control groups consisted of at least two sensitive varieties in all the three studied crops and one moderately resistant variety Grandmart in case of cabbage. Pathogen infection was carried out at 4-leaf stage for radish and Chinese cabbage whereas for cabbage plants infection with pathogen at 2-leaf stage. A total of 25 individual plants were drainage inoculated for each accession and stored at 30℃ in the dark (RH 90%) for the first day followed by 12h/12h light/dark conditions (RH 80%) for four more days. Disease Index (DI) values were manually recorded at the end of the infection period at a range of 0-4 where perfectly heathy plants were recorded as zero (0) and completely dead plants were marked 4. Overall, 5 accessions out of 593 in cabbage; 22 out of 561 radish accession and 23 out of 238 Chinese cabbage accessions showed resistance at DI values 0-1. These accessions belonged to Korea, Hong Kong, India & UK respectively for Cabbage, Radish and Chinese cabbage. Establishment of such accumulative information on available germplasms can serve as potential resource for breeders and researchers in the future.

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PF-0002

A new NLR mediates RipY recognition from *Ralstonia solanacearum* phylotype I in *Nicotiana benthamiana*

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Bacterial wilt disease caused by *Ralstonia solanacearum* (Rso) is one of the most destructive disease in Solanaceae crops. Due to genetic diversity within Rso strains, they are classified into four phylotypes correlating with geographical regions. Rso uses a large repertoire of effector proteins injected into host cells via type III secretion system to promote infection. In turn, plants have evolved intracellular receptors (Nucleotide-binding Leucine-rich Repeat receptors, NLRs) that monitor effector presence and activate immune responses including hypersensitive response (HR), a type of programmed cell death, and restriction of pathogen proliferation. However, identification of NLR genes remains a hard task in complex crop genome. The solanaceous model *Nicotiana benthamiana* (Nb) is well suited to identify NLR genes due to accessibility of genome-wide annotated NLR genes and amenability for genetic tools. Here, we found that RipY from Rso phylotype I not only induced strong HR but also could restrict the pathogen growth when delivered into host cell by type III secretion system. We applied a reverse genetic screen to identify RipY matching NLR in Nb. Using a genetic complementation assay, we confirmed that the identified NbNLR-A was sufficient to induce cell death in the presence of RipY in null mutant plants. To investigate the range of recognition of NbNLR-A, we tested whether RipY alleles from other Rso phylotypes could trigger HR in Nb. This revealed that the polymorphic amino acid sequences in the C-terminal region of RipY constitute a key region for the recognition by NbNLR-A in Nb.

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PF-0003

GAs promote secondary growth and ginsenoside biosynthesis in *Panax ginseng* roots

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Gibberellins (GAs) are an important group of phytohormones associated with diverse growth and developmental processes, including cell elongation, seed germination, and secondary growth. Recent genomic and genetic analyses have advanced our knowledge of GA signaling pathways and related genes in model plant species. However, functional genomics analyses of GA signaling pathways in *Panax ginseng*, a perennial herb, have rarely been carried out, despite its well-known economical and medicinal importance. Here, we conducted functional characterization of GA receptors and investigated their physiological roles in the secondary growth of *P. ginseng* storage roots. We found that the physiological and genetic functions of *P. ginseng* GIBBERELLIN INSENSITIVE DWARF1s (PgGID1s) have been evolutionarily conserved. Also, the essential domains and residues in the primary protein structure for interaction with active GAs and DELLA proteins are well conserved. Overexpression of *PgGID1s* in *Arabidopsis* completely restored the GA deficient phenotype of the *Arabidopsis gid1a gid1c* (*atgid1a/c*) double mutant. Exogenous GA treatment greatly enhanced the secondary growth of tap roots; however, paclobutrazol (PCZ), a GA biosynthetic inhibitor, reduced root growth in *P. ginseng*. Transcriptome profiling of *P. ginseng* roots revealed that GA-induced root secondary growth is closely associated with cell wall biogenesis, the cell cycle, the jasmonic acid (JA) response, and nitrate assimilation, suggesting that a transcriptional network regulates root secondary growth in *P. ginseng*. Furthermore, exogenous GAs treatment critically influenced to saponin biosynthetic related gene expression and contents. This critical information of GAs has potential to be used in the future genetic engineering and breeding of *P. ginseng* and to understand perennial plant developments.

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PF-0004

Identification and molecular characterization of novel genes in response to abiotic stress in *Lactuca sativa* L.

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Lettuce (*Lactuca Sativa* L.) is one of the most important leaf vegetables and is consumed widely worldwide. It is a cool season vegetable that is very sensitive to high temperature and water supply. Due to the unexpected climate change, the limitation of crop productivity by abiotic stresses has become a major problem in agriculture. Late embryogenesis abundant (LEA) proteins which have been reported as molelar chaperones to bind enzymes, membranes and reactive oxygen species (ROS), plays a role in stabilizing proteins or membranes and maintaining cellular homeostasis under abiotic stress. LEA proteins were identified in major crop species such as tomato, tobacco, maize and rice. In this study, we identified a novel LEA gene in lettuce using bioinformatic tools from lettuce genome database (Lactuca Sativa v7, EnsemblPlants). Phylogenetic analysis and sequence alignment compare with other crops were performed. Expression analysis was performed using qRT-PCR in response to abiotic stresses and hormone treatments. Subcellular localization was performed in lettuce protoplast. Forthermore, LEA protein exhibited transcriptional activity in yeast. These results will be helpful for functional characterization to understand abiotic stress response mechanism in plants.

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PF-0005

강원 주요 산채 곰취, 고려엉겅퀴의 육종 기초기술 확보

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강원도농업기술원 산채연구소는 30년 동안 산나물의 임야 직접 채취 방식을 시설 또는 노지에서 안정적으로 재배가 가능하도록 연구하여 약 40작목에 대한 발아, 재배, 번식, 수확 기술을 정립하였고, 곰취, 두릅 등 4작목에서 6품종을 개발하는 성과를 거두었다. 하지만 최근 곰취는 병해충, 내서성, 품질 등의 문제로 재배가 불안하고, 다수의 산채가 기능성 효과가 탁월하여 재배확대 요구가 많음에도 균일성과 재배안정성 부족으로 안정생산이 이루어지지 못하고 있어 효과적이고 효율적인 작목별 육종체계 수립이 절실한 실정이다. 그동안 곰취는 수집과 자식분리에만 의존하여 의도하는 계통간 교잡을 정확히 구현하지 못하여 변이창출이 제한적인 문제를 가지고 있었으나, 설상화에서 수술은 없고 암술머리만 있는 특성에 착안하여 하나의 꽃에서 나머지 통상화는 모두 제거하고 설상화에만 교배함으로서 정확한 인공교배가 가능하게 되었다. 2021년 인공교배 49조합을 구성하면서 4,783개의 설상화에서 교배종자 1,058립을 획득하여 임실율은 22.1%였으며, 특히 통상화를 제거하고 설상화만 남기게 되어 일반 종자보다 더 충실한 교배 종자를 획득하여 발아율은 96.2%로 우수하여 효과적인 곰취 인공교배 방법으로 활용 가능함을 확인하였다. 또한 고려엉겅퀴(곤드레)는 농가에서 재배되고 있는 재래종의 집단에서 2021년 완전웅성불임성 5개체, 반 웅성불임성 12개체를 확보하는 성과를 올렸는데, 이는 약 0.21% 빈도로 완전 웅성불임개체가 존재함을 확인할 수 있었다. 향후 이것을 활용한 웅성불임의 종류 확인, 우량 웅성불임계통 육성, 회복계통 또는 유지계통 확보, 동시에 잡종강세를 보이는 자식계통 육성을 통하여 곤드레 F_1 교잡종 육종을 추진할 수 있을 것으로 판단한다.

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PF-0006

Morphological characterization of mustard (*Brassica juncea*) germplasm from Korea

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Mustard (Brassica juncea) is a representative crop used as an ingredient in kimchi along with Chinese cabbage in Korea. The National Agrobiodiversity Center (NAC) gene bank has conserved 1,859 the mustard accessions from 43 countries including Korea, Pakistan and India. Twenty quantitative agronomic traits of mustard were characterized. Moreover, resistance to powdery mildew and downy mildew fungal diseases were also studied on low vitality 87 germplasms. The length of cotyledon ranged from 1.3 to 2.6 cm, while length and width of leaf ranged from 22.3 to 44.2 cm and 12.2 to 28.8 cm, respectively. The number of leaf per plant ranged between 3 and 22. Principal component analysis was performed using the agronomic traits to study the distribution patterns of the genetic resources. Six germplasm with strong resistance to both fungal diseases were selected for further study in breeding program.

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PF-0007

Morphological and glucosinolate characterization of leaves of landrace mustard (*Brassica juncea*) germplasm from Korea

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Mustard (*Brassica juncea*) is among the most important species in genus *Brassica* and widely grown as an oilseed crop. Intact glucosinolates (GSLs) and morphological characters of 355 *Brassica juncea* accessions were investigated to select potentials genetic resources for breeding to produce improved lines with respect to glucosinolates levels of the leaves. All the accessions were characterized for 25 morphological traits and seven glucosinolates. A huge variation in plant weight, length of petiole, width of petiole, no. of leaves per plant and glucosinolate content was observed among the accession. The total glucosinolate level ranged between 320.4 and 8055.3 μmole/kg DW. Aliphatic glucosinolates were predominant, contributing from 23.3 to 98.4 % of the total glucosinolates. Singrin (SIN) was the most dominant glucosinolate that ranged between 13.0 and 4184.6 μmole/kg DW, accounting as high as 75% of the total GSLs, followed by gluconapin (GNA) and gluconastrutiin (GNS) which were ranged from 44.1 to 7708.7 μmole/kg DW and 27.2 to 3393.5 μmole/kg DW, respectively. Glucobrassicin (GBS) was the other glucosinolate which was detected in appreciable level ranging between 17.3 and 351.9 μmole/kg DW. Glucobrassicanapin (GBN), Glucoiberin (GIB) and glucobarbarin (GBB) were found in very low amount. The accessions with relatively high contents of SIN, GNA, GNS and GBS could warrant detailed studies for future breeding programs to produce nutrient dense and stress resistant *Brassica* lines.

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PF-0008

Genetic diversity and genome-wide association study in pumpkins (*Cucurbita moschata*) originated from East Asia

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Pumpkin (*Cucurbita moschata*) is an economically important crop all over the world. It is used for food and the rootstock of other cucurbits. Until now, a few studies on genetic diversity for various accessions and identification of single nucleotide polymorphism (SNP) loci associated with horticultural traits have been reported in *C. moschata*. In this study, we assessed the genetic relationship of 167 *C. moschata* accessions and conducted the genome-wide association study (GWAS) for four traits including fruit shape, fruit rind color, leaf lobe, and leaf silver patch in mostly East Asia. A total of 10,528 SNPs were generated from genotyping-by-sequencing (GBS) for a pumpkin collection. Phylogenetic tree, principal component analysis (PCA), and population structure indicated the accessions could be classified into three subpopulations according to geographical location and their uses (subpopulation 1 for Southeast type, 2 for Northeast edible type, and 3 for Northeast rootstock type). Genetic differentiation based on F_{ST} values revealed the most distant relationship was between subpopulations 1 and 3 (0.161), while subpopulations 2 and 3 (0.024) were the highest similarity. AMOVA showed 13.5% variation among the subpopulations and 86.5% within subpopulations. This result suggested that high gene flow and genetic exchange between the subpopulations occurred due to breeding between limited genetic resources in East Asia. Moreover, GWAS revealed 25 significant association signals related to four traits in generalized linear model (GLM) and mixed linear model (MLM). These SNP loci explained 4.4-23.0% of total phenotypic variation. Among them, 23 associations were identified as novel SNP loci, and only two signals were overlapped with previously reported genomic regions. Especially, the strongest signal (Chr03_8099023) was detected near the ortholog gene (*CmoCh03G011750*) of *CpDll*, which is associated with deeply lobed leaf in *C. pepo*. Our work provides a foundation for genetic diversity and associations with horticultural traits in pumpkins originated from East Asia.

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PF-0009

고온기 잎상추 생산이 우수한 토종상추 '청하랑' 육성

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우리나라의 상추는 국내 쌈문화와 결부되어 잎상추가 주류를 이루고 있으며 꾸준히 생산 소비되는 신선 채소류의 대명사라 할 수 있다. 최근 식생활의 변화로 상추 시장은 다양한 기능성 및 샐러드 수요가 증가하면서 재배 품종도 쌈 채소에서 샐러드용으로 다양해지고 있으며 이런 시장 수요 변화에 따라 재배시설도 토경재배 비가림하우스에서 수경재배 스마트팜, 식물공장까지 연중생산이 가능하도록 다양한 형태로 확대되고 있다. 또한 최근 팬데믹 시대에 직접 재배하여 먹을 수 있는 수경재배를 이용한 가정용 식물재배기 시장도 크게 성장하고 있다. 본 연구는 이런 기능성 채소와 스마트가드닝 시장 성장에 발맞춰 다양한 품종 육성을 위해 수행하였다. 2012년에 재래종자를 30년이상 재배하면서 생태적으로 적응하여 보존해 온 농가를 대상으로 상추 토종종자를 수집하였다. 2012년부터 2015년까지 수집된 종자를 자식하고 특성 검정을 통해 표현형이 다르고 추대가 늦은 개체를 선발하였고 집단교배, 이형주 도태 등을 반복하는 세대진전을 하면서 순계분리를 실시하였다. 2021년 기술원 포장에서 가을재배로 3반복 실험을 통해 균일성 검정을 하여 고정도와 안정성을 확인하였다. 청하랑 상추는 '장흥수집종'에서 순계분리하여 엽색과 형태가 재래종에 가까운 신품종이다. 수량(kg/10a)은 1,380으로 시중품종인 청치마와 유사하게 나타났으며 비교적 시중품종에 비해 추대가 빠른 토종자원보다 추대성이 낮아 고온기에 잎생산이 안정적인 것으로 나타났다. 신품종 '청하랑' 은 종자색은 회색, 잎은 긴 타원모양으로 끝이 뾰족한 거꿀창끝형이며 엽색은 연한 녹색으로 광택이 좋고 쌉쌀한 맛과 단맛이 나며 아삭한 식감으로 샐러드로도 이용 가능하다. 기능성분으로는 쓴맛 성분인 락투신(latucin+ 8-deoxylactucin+lactucopicrin)이 268.7㎍/g 일반 청치마(100.0)보다 2.7배 높았으며 또한 카페익산은 1,185㎍/g(대조품종 649.5)으로 청치마 대비 2배 이상 많았으며, 토코페롤은 32.3ug/kg(대조품종 27.3)로 청치마 대비 1.2배 높은 것으로 나타났다. 결과적으로 신품종 '청하랑' 상추는 봄, 가을뿐만 아니라 여름에 적합한 토종 개량품종으로 일반 농가 뿐만 아니라 식물재배기내에서도 잎상추 생산이 안정적인 기능성 품종으로 추천할 수 있다.

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PF-0010

Early Defense Mechanisms of Brassica oleracea in Response to Attack by *Xanthomonas campestris* pv. *campestris*

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Black rot disease, caused by *Xanthomonas campestris* pv. *campestris* (*Xcc*), results in significant yield losses in *Brassica oleracea* crops worldwide. To find black rot disease-resistant cabbage lines, we carried out pathogenicity assays using the scissor-clipping method in 94 different *B. oleracea* lines. By comparing the lesion areas, we selected a relatively resistant line, Black rot Resistance 155 (BR155), and a highly susceptible line, SC31. We compared the two cabbage lines for the *Xcc*-induced expression pattern of 13 defense-related genes. Among them, the *Xcc*-induced expression level of *PR1* and antioxidant-related genes (*SOD, POD, APX, Trx H*, and *CHI*) were more than two times higher in BR155 than SC31. Nitroblue tetrazolium (NBT) and diaminobenzidine tetrahydrochloride (DAB) staining analysis showed that BR155 accumulated less *Xcc*-induced reactive oxygen species (ROS) than did SC31. In addition, 2,2-diphenyl-1-picrylhydrazyl (DPPH) radical scavenging assays showed that BR155 had higher antioxidant activity than SC31. This study, focused on the defense responses of cabbage during the early biotrophic stage of infection, indicated that *Xcc*-induced ROS might play a role in black rot disease development. We suggest that non-enzymatic antioxidants are important, particularly in the early defense mechanisms of cabbage against *Xcc*.

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PF-0011

Identification of freesia infecting viruses based on next-generation sequencing technique in Korea

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Freesia is an herbaceous perennial flowering plant. It is widely used and distributed in the world as a cut flower. It has been explored that freesia can be infected by freesia mosaic virus (FreMV), cucumber mosaic virus (CMV), tobacco rattle virus (TRV), and bean yellow mosaic virus (BYMV). In 2021, we collected freesia leaves showing striking virus-like symptoms cultivated in chungcheong nam do agricultural research & extension. We carried out next-generation sequencing (NGS) followed by bioinformatics analysis using four total RNA samples. We identified a total of 761 virus-associated contigs assigned to two different viruses such as FreMV and BYMV. Among four freesia samples, two freesia samples (library 15 and library 45) were infected by FreMV, while two freesia samples (library 43 and library 44) were infected by FreMV and BYMV, simultaneously. FreMV of all libraries exhibited 98% and 99% of sequence similarity to FreMV isolate FreMV-Sol (GenBank LC647195.1) isolated from freesia hybrid cultivar Soleil cultivated in Korea. BYMV identified from library 43 and 45 showed high sequence similarity (99%) with BYMV isolate Fr (GenBank FJ492961.1). Our results showed that two viruses, FreMV and BYMV are common viral pathogens in cultivated freesia in korea. Furthermore, FreMV is a dorminant viral pathogen to freesia in Korea.

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PF-0012

Classification of various cucumber (*Cucumis sativus* L.) genotypes based on cucurbitacin and volatile compound profiles

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Cucumber (*Cucumis sativus*L.) is an economical horticultural crop cultivated and consumed worldwide. Bitterness and flavor are important quality attributes of cucumber fruit, so it is necessary to provide qualitative an quantitative information responsible for them using various cucumber genotypes. In this study, we used 69 cucumber genotypes with different fruit shape, color, and origin and provide profiles of cucurbitacins conferring the bitterness and volatile compounds. Among the six types of cucurbitacins (CuA-E, I), only CuC was identified in six inbreds. Most cucumbers didn't contain the cucurbitacins, meaning that most modern cucumbers loss the bitterness in fruit during cultivation. The genotypes were divided into four clusters based on the profiles of cucurbitacins and volatile compounds. Cluster 2 and 3 showed the largest difference with the highest and lowest volatile contents, respectively. Cluster 1 and 4 accumulated different types of compounds, especially for the minor compounds. Furthermore, they showed different fruit phenotypes in length and color, suggesting the relationship between volatile composition and fruit phenotypes. To investigate the hybridization effect, 15 F1 hybrids from selected lines were analyzed. Total volatile compounds content was lower in the hybrids compared the mid-parent values, especially for alcohol content. This profiling will contribute to a cucumber breeding program to produce cucumber fruit with no bitterness and improved flavor. This work is supported by the Korea Institute of Planning and Evaluation for Technology in Food, Agriculture and Forestry (IPET; Grant No. 821009-03-1-HD020) and the Ministry of Agricultural, Food and Rural Affairs (MAFRA) of the Republic of Korea.

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PF-0013

Genetic Diversity of Pumpkins (*Cucurbita* Spp.) Germplasm Based on Morphological Traits and SNP Markers from cpDNA Sequence

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The genus *Cucurbita* comprises five (*C. pepo, C. maxima, C. moschata, C. ficifolia,* and *C. argyrosperma*) domesticated species. *Cucurbita* has a large genetic diversity with various growth forms, size, shape, color, composition, taste and resistance to biotic and abiotic factors. Maintaining the biological diversity of genetic resources and managing the right historical information are an important first step in the development of new varieties with desirable traits. This study presented the genetic diversity of *Cucurbita* germplasms collected from around the world based on morphological characters and single nucleotide polymorphisms (SNPs) markers. A total of 51 resources containing four *Cucurbita species* (*C. pepo, C. maxima, C. moschata*, and *C. ficifolia*) were planted to characterize the morphological traits. The chloroplast DNA (cpDNA) of 51 germplasms along with 3 additional *C. argyrosperma* germplasms was extracted and three universal barcoding regions (matK, rbcL, and psbA-trnH) were sequenced. Neighbor-Joining (NJ) trees were constructed using the nucleotide sequence of the cpDNA barcodes. The rbcL and psbA-trnH barcodes failed to differentiate between *C. moschata* and *C. argyrosperma*, whereas the matK region efficiently differentiates with 87% bootstrap support. Moreover, the matK region showed a species identification rate of 100%, which is considered an efficient marker to identify five domesticated *Cucurbita* species. Multiplex SNaPshot (mini sequencing) analysis was performed with four SNPs of the matK region and revealed the four SNPs that conveniently classify the *Cucurbita* species into five groups. Therefore, these SNPs markers can be used for efficient management of *Cucurbita* genetic resources in genebanks around the world.

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PF-0014

신규 수박 육종소재 발굴을 위한 국내외 수집자원 특성평가

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우리나라의 수박 재배면적은 11,580ha, 생산량은 467천 톤으로 대형과 위주의 생산이 이루어지고 있으나 1인 가구 비율 증가, 절단 및 섭취 후 잔여부분의 품질 저하, 음식물 쓰레기 처리 부담 등으로 인해 대형 수박의 소비는 감소하고 중소형 수박에 대한 소비자의 관심과 요구가 증가하고 있다. 또한 건강 기능성에 대한 관심이 증가함에 따라 기능성분 함량이 높은 채소 품종개발이 요구되고 있다. 그러나 높은 가격, 낮은 당도, 균일하지 못한 품질 등으로 인해 중소형 수박의 재구매 의향은 75% 정도에 그쳐 수박 시장 확대를 위해서는 고품질 중소형 수박 품종 및 고기능성 품종 개발이 요구된다. 따라서 본 연구에서는 국내외에서 수집한 수박 자원의 원예적 특성을 평가하고 기능성분 함량을 조사하여 유용형질을 보유한 신규 육종소재를 발굴하고자 하였다. 이전의 연구과제를 통해 수집하고 선발한 자원 43점에 대해 과중, 과피두께, 과육경도, 당도 등을 조사하였으며 과육에 함유된 라이코핀 및 베타카로틴 함량을 HPLC로 분석하였다. 대상 자원은 Fluidigm 시스템을 이용하여 192개의 유전자좌에 대한 유전형을 분석하고 고정도를 평가한 후 이를 기반으로 계통 혹은 개체선발을 수행하였다. 고정도 분석 결과 8개의 자원에서 95% 이상으로 나타나 육종소재로 활용가능한 정도의 고정계통인 것으로 판단되었으며 이 중 과피가 얇고 당도가 높은 계통 1점, 라이코핀 및 베타카로틴 함량이 높은 계통 1점을 선발하였다. 이 외에 고정도가 다소 낮은 35점 중에서는 과육 경도가 높은 개체 16점, 당도가 높은 개체 13점, 라이코핀 함량이 높은 개체 5점을 선발하였다. 선발한 개체는 자식교배를 통한 세대진전을 수행하였으며 다음 세대의 고정도를 검정하고 유용형질을 평가하여 새로운 육종소재 발굴에 활용할 예정이다.

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PF-0015

A Study on the Genetic Pattern of polyembryony in the F1 Population of citrus (‘Citrus kiyomi’ x ‘Citrus sunki’)

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Polyembryony, multiple embryos in an individual seed, is found in many of citrus and one of the barriers as well as long-juvenile in citrus breeding. Citrus of polyembryony are composed of zygotic embryo, fertilized male and female cells, and nucellar embryos developed from nucellar cells in ovule, same genotype as the female parent, so it is not easy to distinguish between zygotic seedlings and nucellar seedlings. This study was conducted to determine genetic pattern of the genes controlling polyembryony in citrus. F1 progeny between ‘Citrus kiyomi’, monoembryonic and ‘Citrus sunki’, polyembryonic. In this study, seeds of the 75 F1 progenies as well as ‘Citrus sunki’ were germinated in vitro and number of germinated plants and ungerminated embryos were counted 4 weeks later. As a result, 33 out of 75 progenies were determined as monoembryonic while 42 were as polyembryonic. In polyembryony, eight were only polyembryo type and 34 were poly-embryo mixed types. These results will be used as basic data for the development of molecular markers to improve the efficiency of citrus breeding.

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PF-0016

Development of a Speed Breeding System in Pepper (*Capsicum annuum*) by Extending Photoperiod and Supplementing Far-red Light

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Pepper (*Capsicum* spp.) is a vegetable and spice crop in the Solanaceae family with nutritional benefits for human health. For several decades, horticultural traits including disease resistance, yield, and fruit quality have been improved through conventional breeding, nevertheless, cultivar development is time-consuming because of the long generation time of pepper. Recently, speed breeding has been introduced as a solution for shortening the breeding cycle in long-day or day-neutral field crops, but there have been only a few studies on speed breeding in vegetable crops. In this study, a speed breeding protocol for pepper was developed, which is based on controlling the photoperiod and light quality. Under the condition of low red (R): far-red (FR) ratio (0.3) with an extended photoperiod to 20 h (95±0 DAT), the time to first harvest was shortened by 75 days after transplant (DAT) compared to that (170±2 DAT) of control, suggesting that FR with an extended light period is an important factor for flowering in pepper. By gene expression analysis, it appeared that extended photoperiod and FR induced flowering, by up-regulating the flowering-promoting gene *GIGANTEA* (*GI*) and down-regulating the *FLOWERING LOCUS T* (*FT*) in pepper. This is a primary study of the pepper-specific speed breeding system and genetic analysis of flowering genes. The results demonstrate the effect of a combination of extended photoperiod and FR light by genetic analysis of flowering gene expression. Overall, this study demonstrated that speed breeding could shorten the breeding cycle and accelerate genetic research in pepper through reduced generation time.

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PF-0017

적포도주 양조용 포도 신품종 ‘아그데’

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전라북도 완주군 이서면 농생명로 100 국립원예특작과학원

국내 와인 시장 성장과 함께 국내 와인 생산자로부터 적포도주 양조용 포도 품종에 대한 수요가 있어왔으며 이에 대응하고자 농촌진흥청 국립원예특작과학원은 재배가 편이하며 가공적성이 우수한 양조용 포도 신품종 ‘아그데’를 개발하였다. 국내에서 안정적으로 재배되고 있는 주요 포도 품종인‘Campbell Early’와 ‘Muscat Bailey A’를 교배하여 교배 실생 중 과실특성이 양조에 적합한 것으로 판단한 99-09-11을 2013년 1차 선발하였다. 생육 및 추가적인 과실특성 검토 후 2017년 2차 선발하여 ‘원교라-50호’로 명명하여 2017년부터 2020년까지 8개 지역에서 지역적응시험을 수행하였다. 재배적응지역 검토 후 2020년 최종 선발하였고 2021년 3월 8일 국립종자원에 품종 출원하였다. ‘아그데’ 품종의 만개기는 5월 말로 대조품종인 ‘캠벨얼리’와 유사하나 숙기는 9월 초로 대조품종에 비해 10일 가량 늦다. ‘아그데’는 단초전정이 가능하며 생리장해가 적어 재배적응성이 우수한 품종이다. 포도 알 무게가 2.2g으로 작은 편이라 과육대비 껍질의 비중이 높아 포도주의 색도가 1.12로 대조품종인 캠벨얼리(0.75)에 비해 색이 진한 포도주를 만들 수 있다. 당도는 19.9°Bx로 높고 산 함량 또한 0.91%로 높아 장기 숙성 가능한 와인을 생산할 수 있다. ‘아그데’는 포도 알이 작고 밀착되지 않아 따로 알을 솎아주지 않아도 되고 꽃떨이 현상 등 생리장해도 적으며 비가림 시설에서 봉지를 씌우지 않고 재배가능하다. ‘아그데’품종으로 시험 양조한 포도주는 전문가 및 소믈리에 평가회에서 대조품종으로 만든 와인에 비해 우수한 평가를 받았으며 적포도주 양조용 포도 품종으로 보급될 예정이다.

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PF-0018

Analysis of major components of unripe and ripe fruits of radiation mutant micro-tomato population and evaluation of their cytotoxicity in FaDu cells

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Tomatoes, fruits of *Solanum lycopersicum* L. have been widely eaten fresh and used in cooking for their ripe fruit. Ripe red tomatoes have been steadily attractive due to the high content of lycopene, but other constituents such as steroidal glycoalkaloids have been also found: tomatine (1) from the unripe green fruit and esculeoside A (2) from the ripe red fruit. Tomatine has been reported to have anticancer, anti-inflammatory, and antibiotic effects. Esculeoside A has been demonstrated its various pharmacological effects such as anti-atherosclerosis, anti-allergic, and anti-arthritis effects. As part of our research project for the development of new varieties with improved quality, we developed mutant lines of micro-tomatoes through radiation breeding, to produce mutants with the improved yield of phytochemicals. In this study, a comparative study for the contents of tomatine and esculeoside A at two different ripening stages of micro-tomato original cultivar and its mutant lines was conducted using ultra-performance liquid chromatography coupled with electron spray detector. Compared with the original cultivar, potential candidates with high contents of eculeoside A were found among ripe fruits of mutant lines, and these lines also had a high content of tomatine even in unripe fruits. Mutant lines with a low content of tomatine in the unripe stage, which can be consumed as a green tomato, were also discovered. In addition, the methanol extract of unripe and ripe fruits of micro-tomato original cultivar and its mutant lines, tomatine, and esculeoside A were examined for cytotoxicity against FaDu human hypopharynx squamous carcinoma cells. Only tomatine exhibited cytotoxicity with an IC_{50} 5.589 μM, and the other samples did not show cytotoxicity.

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PF-0019

탄저병 저항성 육성소재 개발을 위한 수박 유전자원 평가

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수박 탄저병은 잎, 줄기, 과실 등 지상부의 거의 모든 부위를 침입할 수 있으며, 조직 괴사, 썩음, 가지 마름 등의 증상을 일으킨다. 탄저병은 따뜻하고 습기가 많은 곳에서 발생이 쉬우며 특히 장마철에 많이 발생을 하며, 방제를 위해서는 무병 종자 재배와 합성농약을 이용한 화학적 방제에 의존하고 있다. 탄저병 저항성 품종 이용은 탄저병 방제의 근본적인 해결책이 될 수 있으나 수박 탄저병 저항성 품종 개발은 미비한 실정이다. 수박 탄저병 저항성 품종 육성을 위하여 육종소재 발굴을 위해 국립원예특작과학원의 수박 114계통 및 3교배조합에 대해 수박 탄저병 저항성 평가를 실시하였다. 본엽 3~4엽이 전개되었을 때 수박 탄저병 균 *Colletotrichum orbiculare* KACC40809를 $5x10^5$ conidia/ml 농도로 분무접종 하였다. 접종 후 25℃ 습실상에서 암상태로 48시간 동안 배양 후 25℃ 항온실에서 재배하며 탄저병 발생을 유도하였으며, 접종 8-11일 후 탄저병 병반면적율에 따라 탄저병 발병정도를 조사하였다. ANA 13 등 5계통이 발병도 2.5 이하로 중도저항성을 나타내었으며, 109계통과 3교배조합이 감수성으로 판별되었다. ANA 13등 5계통은 기존에 저항성으로 알려진 Charleston gray, Fairfax wilt Resistant 등의 품종보다 높은 저항성을 나타내었다. 저항성으로 선발된 계통들은 우량계통과 조합하여 탄저병 저항성 품종육성에 활용할 계획이다.

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PF-0020

군자란(*Clivia miniata*) 육종을 위한 도입 유전자원 특성평가

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남아프리카 원산의 군자란은 수선화과로 6가지 원종(*Clivia. miniata, C. caulescens, C. gardenii, C. robusta, C. nobilis C. mirabilis*)이 있다. 군자란은 꽃이 없어도 사철 푸른잎을 관상할 수 있으며 건조와 낮은 광도 조건에 대한 내성이 있어 훌륭한 실내 식물이다. 6종 중 *C. miniata*는 산형화서에서 나오는 크고 직립하는 매력적인 꽃들 때문에 관상용으로 가장 인기가 있다. 나머지 5종들은 늘어진 작은 꽃들이 핀다. 군자란 신품종 육성을 위해 도입한 군자란 중 실제로 국내에서 재배되며 관상가치가 높은 *C. miniata*를 대상으로 특성평가를 진행하였다. 먼저 기부(basal stem)의 색소(pigment) 유무를 기준으로 2가지 그룹으로 나누었다. 그 다음 군자란 신품종 심사를 위한 특성조사요령 중 화피편 내측 색의 비율에 따라 분류했고 화색은 color chart를 참조하였다. 그 결과 기부에 색소가 있는 유색소(pigmented) 그룹에는 국내에서 주로 재배되고 있는 색상인 Orange-Red, Apricot-Light Orange, Yellow(blushed), Peach-Pink 그리고 화피편 내측의 색상이 녹색인 Bronze 등 5개의 그룹으로 나뉘었다. 기부에 색소가 없는 무색소(unpigmented) 그룹에는 Yellow, 화피 내외부 색상이 다른 Yellow(versi color), Green 등 3개의 그룹으로 나뉘었다. 기존에 국내에서 재배되는 주황색 군자란과 화색이 확실히 구별되는 새로운 *C. miniata*의 유전자원을 도입하고 분류함으로써 향후 국내 신품종 군자란 육종 연구에 활용하고자 한다.

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PF-0021

만생종 완전단감 계통 '단연10-13-6'의 주요 특성 분석

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국내 감 재배 규모는 약 27,203ha('20년, FAO)로 중국에 이어 세계 2위이며, 단감은 8,404ha, 1위로써 국내 주요 6대 과일에 속한다. 단감 품종별 재배면적 비중은 '부유'가 전체의 80%를 차지하고 있어 재배편중이 심한 실정이다('20년, 통계청). '부유'는 만생종 중과 완전단감으로써 숙기가 11월 상순으로 남부지방의 서리시기와 겹쳐 완숙과 수확에 어려움이 있고, 응애에 취약한 품종이다. 경상남도농업기술원 단감연구소에서는 '부유'의 단점을 개선한 우량 만생종 단감 품종을 육성하기 위하여, 2010년 떫은감 대과 '갑주백목'과 고당도 단감 '태추'를 교배하여 47주의 교배실생을 획득하였고, 이 중 당도가 높은 극대과 완전단감 계통 '단연10-13-6'을 2015년에 1차 선발하였다. 이후 3년간 수체 생육과 과실 특성을 조사한 결과, 연차간 변이가 적고 수세가 건전하여 2차 선발하였다. 숙기는 서리시기보다 10일 빠른 10월 25일(김해)이며, 과중 368g(부유 247g)의 극대과종이다. 당도는 16.2°Bx로 '부유'(15.6°Bx)보다 높고, 단감 생육초기 주요 해충인 응애에 대한 저항성이 '부유'에 비해 월등히 강하다. '단연10-13-6' 계통은 향후 국립종자원에 품종보호출원을 진행할 예정이다.

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PF-0022

수박 유전자원의 원예적 형질 평가 및 증식

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수박자원은 표현형 형질고정을 위한 세대진전(5~8세대)이 필수적이며 연구와 육종소재 분양을 위하여 품질고도화와 대량증식을 통한 종자확보가 필요하다. 전라북도농업기술원 수박시험장에서는 우수자원을 파악하고 수요자와 연계하여 육종소재를 제공하고자 농업유전자원센터에서 분양받은 수박 100자원을 대상으로 원예적 형질을 평가하였다. 형질 평가는 질적형질 13항목(잎 결각 깊이, 씨방솜털, 암꽃 개화기, 과실형태, 과피의 바탕색, 과피의 바탕색 강도, 과실 줄무늬, 과실 줄무늬색 강도, 과실 골 분포, 과육의 주요색, 잎몸 대리석 무늬, 꽃자리 부위 모양, 종피의 바탕색)과 양적형질 10항목(꽃자리 크기, 과실 줄무늬 너비, 과실 무게, 과실 길이, 과실 너비, 과피의 두께, 종자의 수, 종자 길이, 종자 너비, 당도)에 대하여 실시하였고, 라이코펜(Lycopene) 성분분석과 이미지 정보 3종(수확기 잎, 수확 후 과일, 수확 후 종자)을 구축하였다. 조사된 자원들중 라이코펜 함유량이 55㎍/g이상으로 높은 4계통(IT199774, IT271031, IT294372, IT394382), 11 ° Brix이상의 고당도 5계통(IT110847, IT191195, IT251854, IT271030, IT271049) 등은 신품종 개발에 유용할 것으로 판단된다.

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PF-0023

Morphological characterization of cucumber (*Cucumis sativa* L.) germplasms

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Cucumber has a long history of being cultivated and remains one of the most important vegetable crop consumed all over the world. We investigated the morphological characteristics of 313 cucumber germplasms conserved at the National Agrobiodiversity Center, RDA. A majority of the germplasms were of indeterminate growth type containing medium to dark green colored leaves. Though the number of female flowers per node ranged from 1 to 3, and 92% of the accessions produced only one female flower per node. The skin color of fresh fruits was mostly green (97%), with few accessions displaying white (2%) and yellow (1%) colored fruits. At the ripening stage, most of the fruits turned yellow (79%), followed by continuing to remain green (11%) or turning white (10%). The quantitative characteristics however, showed a huge variation among accessions. The length of the fruits ranged from 5.6 cm to 57.9 cm, with an average of 23.1 cm and the number of seeds per fruit varied between 4.1 and 971, with an average of 257.2. The seed length ranged at 0.56 to 1.44 cm, while the seed width ranged between 0.1 and 0.6 cm. The laricyresinol content in nine cucumbers was investigated by HPLC which ranged between 1.57 and 6.66 mg/g (dry weight). Pearson's correlation analysis indicated no correlation between laricyresinol content and seed size or seed number but a weak correlation was observed between laricyresinol content and seed length. This study provides potential breeding baseline data for future breeding of nutrient-dense cucumber varieties.

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PF-0024

반밀폐형 온실에서 포그 사용시간에 따른 냉방효과 연구

배효준, 정유석, 전문석, 황정수, 이시영, 최인찬*

전라북도 완주군 이서면 농생명로 310 국립농업과학원 농업공학부

고온기 시설하우스의 내부온도는 과채류의 착과불량 및 생육 저하의 원인이 된다. 내부온도는 피복재 차광제, 차광망, 포그시스템, 히트펌프와 축열조를 이용한 냉난방 시스템 등으로 조절하고 있으며 최근 반밀폐형 온실의 수요가 증가하고 있다. 반밀폐형 온실은 기존의 온실과 다르게 외부공기 유입으로 강제환기가 가능할 뿐만아니라 축열조와 팬코일유닛(FCU)를 사용한 냉・난방이 가능하며 포깅을 이용한 온・습도를 적절하게 관리할 수 있다. 본 연구는 토마토가 생장하고 있는 농촌진흥청 첨단디지털온실(동고 8.3m 측고 7m) 2개동(24m*40m)에서 일주일 동안 온실의 온・습도 변화를 비교 분석하였다. 자연환기형 온실은 외부공조창 0%, 내부공조창 100%를 개방한 상태에서 환기온도에 따라 천창을 제어하였고, 반밀폐형 온실은 환기온도에 따라 외부공조창이 작동되도록 설정했으며 외부공조창이 열린만큼 내부공조창은 닫히도록 제어하고 내외부 공조창의 열림 정도 합이 100이 되도록 설정하였다. 포그시스템은 온실 습도가 65% 이하일 경우에 작동되었다. 천창 및 공조창이 작동하는 7:30부터 19:00까지 데이터를 분석한 결과 자연환기형와 반밀폐형 온실의 내부온도는 24.6℃, 상대습도는 각각 68.4%, 69.4%, 포그 가동시간은 각각 2,362.5분, 1,773분 이였다. 자연환기형과 반밀폐형 조건에서 내부온도와 상대습도는 제어범위 내로 큰 차이가 없었으나 반밀폐형 온실의 포그시스템이 33% 적게 사용되었다. 이는 자연환기형은 온실 온도제어를 위해 포깅을 한 것으로 생각되며 반밀폐형 온실이 에너지 및 원수사용량 절감에 도움이 될 것으로 기대한다.

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PF-0025

고추 풋마름병 저항성 대목용 품종 '원강 5호' 육성

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국립기상과학원에서 발간한 한국 기후변화 평가보고서 2020에 따르면 우리나라 연평균 기온 변화량은 지난 10년간 0.18℃ 상승하였다. 기온상승에 따른 고온과 관련된 극한 기후 지수는 증가하였고 여름은 98일에서 117일로 19일 길어진 것으로 보고된 바 있다. 고추 풋마름병은 고온에서 발생이 증가하는 대표적인 세균병으로 1~3개의 편모를 가지는 고온성 세균인 *Ralstonia solanacearum*이 병을 일으킨다. 고추 풋마름병 방제에 사용할 수 있는 농약은 재배 전 토양에 처리하여 토양 내 세균밀도를 낮춰주는 토양소독제에 국한되어 있다. 또한 국내 시판품종 중 풋마름병 저항성으로 유통되는 품종은 거의 없어 대목을 포함한 고추 풋마름병 저항성 품종 개발에 대한 요구가 높은 실정이다.

국립원예특작과학원에서는 2021년 풋마름병 저항성 대목 및 중간모본으로 활용이 가능한 '원강 5호'를 육성하였다. '원강 5호'는 세계채소센터(World Vegetable Center)에서 도입한 고온 착과성이 우수한 자원을 활용, 2014년부터 2018년까지 매 세대마다 풋마름병 저항성 및 원예적 특성이 우수한 개체를 선발하고 세대 진전하였다. 2019년부터 2021년까지는 풋마름병 저항성을 재확인하고 수량성 및 품질 등을 확인하여 최종적으로 풋마름병 대목 및 중간모본 '원강 5호'를 육성하였다. 유묘기 풋마름병 인공 접종시 병저항성 지수가 3년 평균 0.43으로 대조품종 2.1에 비해 저항성이 안정적으로 높았다. 일반 건고추 품종을 접수로 하여 접목시 모든 개체가 활착되어 접목 친화성에는 문제가 없는 것을 확인하였으며, 접목묘에 풋마름병을 인공접종한 결과 대조품종에 비해 높은 저항성을 보였다. '원강 5호'는 일반 건고추 품종보다는 다소 낮은 수량을 보이나 고춧가루 색소를 나타내는 ASTA는 140.3으로 대조 품종들 평균(ASTA 100)보다 높은 것으로 확인되었다. '원강 5호'는 현재 품종보호출원 중으로 향후 대목용 품종 및 풋마름병 저항성 육종소재로 활용 가능하도록 적극적으로 보급할 계획이다.

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PF-0026

Zebularine, DNA methylation inhibitor treatment in wheat and observation of growth characteristics and mutated chromosomes

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Zebularine is known as DNA methylation inhibitor and tumorigenesis inhibitor. DNA methylation inhibitor leads chromosome breakage through DNA breakage and DNA repair becomes chromosome rearrangement in plant cell. Zebularine treated in two different ways to Keumkang, Korean wheat cultivar by absorption through roots and by seed imbibition. First, seed imbibition treatment in 1,000 μM of zebularine solution for 72 hours in dark condition. Second treatment to seedlings of Keumkang also treated in 1,000 μM of zebularine solution for 72 hours after germination. Root and shoot showed different elongation in each treatment. Mitotic index and chromosome structure were observed by microscope. Root absorption treatment showed shorter elongation than control and seed imbibition treatment. Root and shoot of control elongated 8.16±0.61 cm and 4.03±0.48 cm. But seed soaking treatment was 4.33±0.80 cm and 2.48±0.36 cm, root absorption treatment was 3.01±0.47 cm and 2.00±0.26 cm. It is considered because of zebularine damaged on DNA in mitosis. Mitotic index of root absorption treatment showed fewer living cells than others. Observation of chromosome showed some short chromosomes and loosen chromosomes affected by zebularine. We observed “gap by chromosome breakage” in chromosomes that has loosen part between centromere and telomere. It seems demethylation of zebularine occur chromosome breakage.

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PF-0027

Construction of a High Density Genetic Linkage Map and Identification of QTLs Associated with Fruit Quality Traits in an Interspecific Pear hybrid (*Pyrus* spp.)

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Pear (*Pyrus* spp.) is an economically important fruit tree grown extensively worldwide. To identify QTL related to agronomically important fruit traits, QTL mapping was performed using 187 F_1 populations derived from a cross between 'Manpungbae' and 'Ooharabeni'. Single nucleotide polymorphisms (SNPs) detected by genotyping-by-sequencing (GBS) and simple sequence repeats (SSRs) developed from pear were analyzed for construction of integrated genetic linkage map. Phenotyping data consisting of fruit weight, fruit length and diameter, fruit shape index (FSI), fruit firmness, titratable acidity, and soluble sugar contents were investigated from 2016 to 2018. Total of 1,807 GBS-SNPs and 41 SSRs were successfully anchored to 17 linkage groups (LGs) spanning a total 1,519.4 cM with an average marker density of 0.87 cM. Based on this integrated linkage map and fruit phenotyping data for three years, a total of fourteen significant QTLs linked to the control fruit weight, fruit length and diameter, FSI, fruit firmness, and titratable acidity were mapped to five LGs (LGs 3, 10, 11, 12, and 13). These results will improve our understanding for genetic control of fruit traits and provide new information for genetic and genomic research.

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PF-0028

Identification of QTLs Controlling Fruit Skin Color Using a High-Density Genetic Map in Pear

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Red skin color, which can make pear fruit more attractive to potential customers, is considered an important trait to target in breeding program around the world. We used interspecific hybrids of pear to develop red skin color cultivar and improve efficiency of red skin color breeding program via maker-assisted selection. In this study, the genetic control of red skin color in pear was investigated in an interspecific population derived from a cross between the Korean bred pear cultivar 'Manpungbae' (*Pyrus pyrifolia*) and the red-blushed skin Japanese pear cultivar 'Oharabeni' (*P. pyrifolia* × *P. communis*). We constructed a genetic map with 187 F_1 populations using SSR and SNP markers. The map consisted of 17 linkage groups (LGs) with included 1,848 genetic markers and covered 1,519.4 cM. The individual of the population was phenotyped for the presence or absence of red and red skin coverage percent. As a result of QTL analysis, genomic regions on LGs 4 and 5 were found to be associated with red skin color. These markers identified in the QTL regions in this study will help screening of young seedlings for selection of red skin color and enhance the efficiency of pear breeding program.

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PF-0029

Expression Analysis of Carotenogenesis Network Genes During Citrus Fruit Development by the Real-Time PCR Approach

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Carotenoids, a family of isoprenoid molecules, are natural pigments essential for the coloration of various organs, and also stabilize cellular membranes in many plant species. Moreover, they are beneficial to human health, acting as health-promoting phytonutrients that have been related to the prevention of degenerative processes, certain cancers and cardiovascular illness. Citrus fruit is an important reservoir of diverse carotenoids. Because of their important functional roles, many efforts have been made to identify genes involved in carotenogenesis and factors regulating 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, we mined carotenoid biosynthesis-related genes from two citrus reference genomes (*Citrus clementina* v1.0 and *Citrus sinensis* v1.1) and identified a total of 60 isoforms for 16 enzymes and 26 putative transcription factors (TFs). We established real-time PCR primer sets for the mined 42 genes (16 biosynthetic genes and 26 TF genes) and their PCR conditions including PCR efficiency and primer specificity. Finally, during the fruit maturation, their temporal expression patterns were analyzed in fruit peel/flesh of two representative citrus cultivars and distinct characteristics of gene expression profiles between two cultivars will be discussed.

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PF-0030

중생종 당도높고 단단한 완전단감 ‘단연09-11-6’ 육성

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단감 국내 총 생산량(’21년) 72천톤 중 만생종 비율이 81%로 편중되어 있어, 홍수출하에 의한 가격하락, 인력 수급난, 소비자 품종선택권 축소 등 많은 문제점을 야기시킨다. 본 연구는 숙기가 빠른 단감 품종을 육성하여 만생종 편중 문제해결을 위해 수행되었다. 2009년도에 중생종 완전단감 ‘전천차랑’를 모본으로 하고 ‘태추’를 부본으로 하여 인공교배하였다. 교배실생 22계통 중에서 수확기가 빠르고 씨가 적고 경도가 높은 계통을 선발하였다. 농림축산식품부 국립종자원 특성조사요령에 준하여, 2019년부터 2021년까지 수체 생육과 과실 특성을 조사하여, 수확시기가 빠르고 경도가 높은 ‘단연09-11-6’을 최종선발하였다. 중생종 완전단감인 ‘단연09-11-6’의 수세는 중간이고 개장성이다. 암꽃만 착생하는 특성이 있으며, 개화기는 5월 22일경(상서조생 5월 15일)이고, 과실 성숙기는 10월 8일(상서조생 10월 17일)이다. 과중은 238g(상서조생 195g)으로 중과이며, 당도 16.1°Bx(상서조생 15.6°Bx)이다. 과피색은 노란색 띤 오렌지색이며 특히 단연09-11-6의 경도가 31.8N5mm∅(상서조생 26.2N)으로 매우 높아, 유통과정에서 오손과 발생이 적고, 기존 중생종에 비해 당도가 높은 점을 미루어 봤을 때 견고한 중생종 단감 시장형성에 기여할 것이라고 기대된다.

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PF-0031

단감 육종소재의 다양화를 위한 부본용 단감 '단연12-2-73' 육성

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우수한 단감 품종을 육성하려면 우수한 모본과 부본이 필요하다. 대부분 단감은 암꽃만 피는 품종으로 다양한 교배모본은 존재하나 수꽃이 피는 교배부본은 소수이다. 우리나라 단감 연구기관(경상남도농업기술원, 농촌진흥청)에서 육성한 단감 신품종 29품종을 조사한 결과 부본으로 사용된 품종은 태추 65%, 서촌조생 18%, 그 외 3품종 17%등 5품종으로 제한적이다. 따라서 본 연구는 교배부본의 다양화를 위해 우수한 부본용 단감을 육성하고자 수행되었다. 2012년도에 단감 '부유'를 모본으로 '태추'를 부본으로 교배하였다. 교배실생 102계통 중에서 수꽃 개화시기가 암꽃 개화시기와 일치하며 수꽃이 충실한 계통을 1차 선발하였다. 이후 공대에 접목 증식하여 묘목을 양성하였고 2019년부터 2021년까지 3년간 수체 생육과 과실 특성을 조사한 결과, 연차간 변이가 적고 과실품질이 우수한 '단연12-2-73'을 최종 선발하였다. '단연12-2-73'는 반직립성으로 수세는 중간정도이며 잎 길이는 11.6cm(태추 10.2cm)이다. 발아기는 3월18일(태추 3월23일)이며, 수꽃 개화시기는 5월13일(태추 5월11일), 암꽃 개화시기는 5월15일(태추 5월16일), 수확기는 10월10일(태추 10월10일)이며 과중은 155g(태추 280g), 당도는 18.0°Bx(태추 17.0°Bx), 경도는 25.2N(태추22.4N, 5mm∅), 종자수는 0.2개(태추 1.4개)의 특징을 갖고 있다. '단연12-2-73'는 품질이 우수한 수꽃이 피는 품종으로 단감 신품종 육성을 위해 교배할 때 우수 부본이 될 것으로 기대된다.

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PF-0032

Identification of the *CaAN3* Gene that Regulates Fruit-specific Anthocyanin Biosynthesis in Pepper (*Capsicum annuum*)

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The key regulatory gene *CaAN2* encodes an R2R3 MYB transcription factor that regulates anthocyanin biosynthesis in various tissues in pepper (*Capsicum annuum*). However, *CaAN2* is not expressed in certain pepper accessions showing fruit-specific anthocyanin accumulation. In this study, we identified the novel locus *CaAN3* as a regulator of fruit-specific anthocyanin biosynthesis, using an F_2 population derived from a hybrid cultivar with purple immature fruits and segregating for *CaAN3*. We extracted total RNA, assembled two RNA pools according to fruit color, and carried out bulked segregant RNA sequencing. We aligned the raw reads to the pepper reference genome Dempsey and identified 6,672 significant single nucleotide polymorphisms (SNPs) by calculating the Δ(SNP-index) between the two pools. We then conducted molecular mapping to delimit the target region of *CaAN3* to the interval 184.6-186.4 Mbp on chromosome 10. We focused on Dem.v1.00043895, encoding an R2R3 MYB transcription factor, as the strongest candidate gene. Sequence analysis revealed four insertion/deletion polymorphisms in the promoter region of the green *CaAN3* allele. We employed virus-induced gene silencing and transient overexpression assays to characterize the function of the candidate gene. When Dem.v1.00043895 was silenced in pepper, anthocyanin accumulation decreased in the pericarp, while the transient overexpression of *Dem.v1.00043895* in *Nicotiana benthamiana* leaves resulted in the accumulation of anthocyanins around the infiltration sites. These results showed that Dem.v1.00043895 is *CaAN3*, an activator of anthocyanin biosynthesis in pepper fruits.

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PF-0033

Comparison of Gene Expression Related to Chlorophyll Metabolism Pathway in Green- and Yellow-fleshed Kiwifruits

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The flesh color of yellow-fleshed kiwifruit is converted green to yellow by chlorophyll degradation and carotenoids accumulation during fruit maturation and ripening. The present study was conducted to identify genes affecting flesh coloration in kiwifruits through transcriptome analysis. Two kiwifruit cultivars, 'Hayward' (*Actinidia deliciosa*) and 'Hort16A' (*A. chinensis*), were collected at 120, 160 days after full bloom (DAFB), and after ripening. Flesh samples of the two cultivars were used to investigate chlorophyll and carotenoid contents and extract RNA for transcriptome analysis. Total chlorophyll content decreased in 'Hort16A' at 160 DAFB and ripening stage. Lutein content increased, but zeaxanthin content decreased from 160 DAFB to ripening stage in 'Hort16A'. In addition, total carotenoid content was higher in 'Hayward' than 'Hort16A'. The expression levels of chlorophyll biosynthetic genes showed positive correlation with chlorophyll contents in 'Hayward'. However, the expression levels of chlorophyll degradation genes displayed negative correlation with chlorophyll content in 'Hort16A'. Up-regulation of *stay green-like* and *NAC* transcription factor could affect chlorophyll degradation in 'Hort16A'. These results suggest that chlorophyll degradation during ripening affects flesh coloration in green and yellow-fleshed kiwifruits.

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PF-0034

An InDel Marker for Distinguishing Sex in *Actinidia arguta*

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Actinidia arguta, Korea native kiwifruit, has cold resistance and high vitamin C. *A. arguta* is dioecious species and cannot distinguish the sex in juvenile period. In the present study, Insertion/Deletion (InDel) markers was developed to distinguish the sex by comparing the female and male genomes. The re-sequencing was performed on the Illumina Hiseq X platform in female (K5-10-5) and male (K5-3-7) of *A. arguta*. The 23 InDels, which were heterozygous in female and homozygous in male, were identified as candidate markers for discriminating the sex. Candidate InDel markers were designed using identified 23 InDels and PCR was performed. The polymorphism of InDel markers was observed with 2% agarose gel electrophoresis. Among 23 InDel markers, one InDel marker (CBk25id01) can distinguish the sex in *A. arguta*. The expected DNA amplicons of female and male were generated with 133 bp and 113/133 bp, respectively. Females and males of *A. arguta* accessions were separated with expected DNA fragments. The CBk25id01 could distinguish the sex in juvenile period. Therefore, this marker will be used for improving efficiency of the kiwifruit breeding program.

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PF-0035

Identification of Genes Regulating Stone Cell Development in Pear through Transcriptome Analysis

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Pear is one of the most important fruit trees in the world, and has been widely grown in temperate regions. Stone cell distributed in the fleshes of pear negatively contributes to the fruit quality. Transcriptome analysis is a tool for identification of differentially expressed genes (DEGs). Therefore, transcriptome analysis was performed to identify stone cell related genes. Fruits of 'Minibae' were collected at 30, 55, and 100 days after full bloom (DAFB). Stone cell contents were calculated as the numbers of pixels using MATLAB. RNA-sequencing was performed. Stone cell clusters rapidly formed at 30 to 55 DAFB (30 vs. 55), and their distribution became gradually decreased. After DEG filtering, genes significantly up- and down-regulated were detected. Gene ontology was conducted to annotate functions of genes. Fifteen and twenty-five up- and down-regulated genes were annotated in peroxidase activity catalyzing lignin biosynthesis. Among them, three genes were up-regulated only at 30 vs. 55 DAFB and could regulate stone cell content. As a results of correlation analysis, *L-ascorbate peroxidase 2* showed high correlation coefficient at $p < 0.05$. Therefore, *L-ascorbate peroxidase 2* could be candidate gene regulating stone cell formation.

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PF-0036

수경재배에 있어서 완숙토마토 생육과 수량 측정을 통한 대목 선발

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토마토 수경재배는 작물 생육에 필요한 양수분과 온도 등의 환경 제어가 가능하며 장기재배 작형을 통해 생산량을 증가시킬 수 있는 반면, 경영비 소요가 많아 적은 투자 비용 대비 생산성을 극대화할 수 있는 재배기술이 요구된다. 장기재배 토마토의 생산량을 증대시키기 위한 방법으로 생육 후반기까지 세력을 유지할 수 있는 접목묘를 이용하는 방법이 있지만 국내에서 주로 통용되는 대목은 외국 품종으로 비용이 높은 단점이 있다. 육묘과정에 투입되는 종자값 등의 초기 투자 비용을 줄이기 위해서는 저렴한 가격으로 우수한 성능을 가진 국산 대목 품종의 개발이 필요하다. 본 연구는 수경재배 시 대목 종류에 따른 완숙토마토의 생육과 수량을 측정하여 국내 개발 대목의 성능을 검정하고자 수행하였다. 실험재료는 국내 개발 대목 3종류와 상업용 대목 1종류를 접목한 완숙토마토와 접목하지 않은 완숙토마토 1종류를 사용하여 생육과 수량을 측정하였다. 식물 생육조사는 생장강도, 개화위치, 화방 간 거리, 엽장 및 엽폭 등을 조사하였다. 생육후기인 정식 후 221일에 국내 개발 대목의 생장강도는 비접목 처리구보다 높았다. 국내 개발 대목의 총 수량은 상업용 대목보다 많았으며 모든 처리구의 화방 내 꽃을 같은 개수로 적화하였기 때문에 수량의 차이는 과중의 차이인 것으로 판단된다. 국내 개발 대목의 근활력이 생육 후기까지 지속되어 양수분 흡수율과 수분 이용 효율이 높아 잎 등의 영양기관의 생장이 발달하여 광합성능이 높아짐에 따라 수량이 증가한 것으로 판단된다. 이상의 결과를 볼 때 실험에 사용한 상업용 대목보다 세력이 오래가는 국내 개발 대목 품종 2종류가 선발될 가능성이 높은 것으로 판단된다.

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PF-0037

Evaluation of cucumber germplasm resistance to fusarium wilt by *Fusarium oxysporum* f. sp. *cucumerium*

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Fusarium wilt is a serious disease causing of damping-off, serious wilt symptom or wither to death in cucumber. The aim of this study was to evaluate resistance of melon germplasm to Fusarium wilt and select promising disease resistant accessions for further applications. Resistance to Fusarium wilt was examined in 123 cucumber germplasm by root-dipping inoculation method with *Fusarium oxysporum* f. sp. *cucumerinum*. Roots of 1~2 leaf stage cucumber seedlings were dipped in spore suspension of 1×10^6 conidia · mL^{-1} for 20 minutes. And inoculated seedlings were incubated for 4 weeks and evaluated disease index 1 (no symptom) to 5 (plant wither) based on discoloration of underground parts and severity of stunting every 7 days. There is no accession has shown disease index 1 (no symptom) 4 weeks after inoculation, but 3 accessions had shown disease index 2.0 (discoloration in underground parts but not wilted). These accessions could be expected to help to breeding commercial varieties with fusarium wilt resistance.

Keyword: cucumber, germplasm, resistance, fusarium wilt

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PF-0038

Identification of a Novel Self-compatible Phenotype and its Mutant *SRK* Allele Harboring an LTR-retrotransposon in Radish (*Raphanus sativus* L.)

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Self-incompatibility (SI) responses of radish (*Raphanus sativus* L.) are determined by two tightly linked genes encoding an *S* receptor kinase (SRK) and an *S*-locus cysteine-rich protein/*S* locus protein 11 (*SCR/SP11*), respectively. A radish showing an almost self-compatible (SC) phenotype was identified in this study. Inheritance patterns showed that this SC phenotype was dominant over an SI phenotype. In addition, the SC phenotype co-segregated with an *S* haplotype in an F_2 population. This SC radish contained an *RsS-26* haplotype in which duplicate *SRK*-like genes were previously identified. Full-length sequences of two *SRK*-like genes of 18,133-bp and 6,200-bp in length were obtained, and they were designated as *RsSRK-26-1* and *RsSRK-26-2*, respectively. No critical mutation was found in the coding region of *SRK*-like genes. However, a 4,146-bp intact LTR-retrotransposon was identified in the third intron of *RsSRK-26-1* of the SC radish. Interestingly, this LTR-retrotransposon was not detected in three other breeding lines containing the same *RsS-26* haplotype. While normal transcription of *RsSRK-26-1* and SI phenotypes were observed in these three breeding lines, no transcript of *RsSRK-26-1* was detected in the SC radish, suggesting that recent transposition of an LTR-retrotransposon in the *RsSRK-26-1* gene might be responsible for the SC phenotype of radish.

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PF-0039

양파 F1 종자생산용 중만생계 웅성불임계통 '원예30016' 육성

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일대잡종(F_1) 품종의 생산은 전세계 종자 시장의 흐름이며 양파 품종 또한 극조생계를 제외하고 대부분은 F1 품종이 보급되고 있다. 양파의 웅성불임계통(A-line)은 종자 생산에 필수적이며 우수한 특성의 웅성불임계통의 선발을 통해 고품질의 F_1 품종을 생산할 수 있다.'원예30016'은 중만생 계통으로 웅성불임개체'LMS1757-3'과 'MSC1758'을 교배하여 유지계통(B-line)'MMS57'을 선발하였다. 웅성불임계통 육성을 위해 2009년부터 2011년까지 2회 자식과 여교배를 하여 모구를 선발하였으며, 2013년부터 2019년까지 4세대 동안 집단선발과 여교배로 형질을 고정하였다. 2018~2019년에는 화분친 계통들(C-line)과 교배하여 F_1 종자를 채종 하고 그 계통들의 조합능력을 검정한 결과 우수한 원예적인 특성과 수량성이 확인되어 2019년 직무육성신품종 선정심의회를 통해'원예30016'로 명명되었으며 2020년에 품종보호출원 하였다.'원예30016'의 도복기는 5월 23일로 대비품종보다 늦으며 초형은 잎 자세가 곧추선 직립형이다. 웅성불임 계통과 유지계통의 구형지수는 각각 0.93, 0.85로 원형에 가까우며 구중과 당도는 각각 230.2g, 8.2°Brix로 대비품종(265.0g)에 비해 구중은 낮았으나 당도는 대비품종(7.1 °Brix)보다 높았다.'원예30016'과 화분친 3계통을 교배하여 F_1 조합능력을 검정한 결과 대비품종과 수량이 비슷하였다.'원예30016'은 중만생계 웅성불임 계통으로 중만생계 또는 중생계통의 당도가 높은 F_1 품종육성에 유용한 중간 모본으로 활용할 수 있을 것으로 기대된다.

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PF-0040

Identification of QTL Linked to Stone Cell Content in 'Whangkeumbae' (*Pyrus pyrifolia*) × 'Minibae' ((*P. pyrifolia* × *P. ussuriensis*) × *P. pyrifolia*)

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Stone cells are peculiar cells in pear flesh formed by the deposition of lignin. The stone cells are agriculturally important traits in pear (*Pyrus* spp.). Previous studies have been reported that stone cells were controlled by polygenes. In the present study, the quantitative trait loci (QTL) regions associated with stone cell content were detected in the linkage map of 'Whangkeumbae' (*P. pyrifolia*) × 'Minibae' (*P.* hybrid). Stone cell content was evaluated using image processing. The interval mapping was used to confirm QTL associated with stone cell content in the constructed linkage map of 'Whangkeumbae' × 'Minibae' in previous study. QTLs controlling stone cell content were identified on the linkage group (LG) 3 and 6 of the 'Whangkeumbae' × 'Minibae' map. Fifteen single-nucleotide polymorphisms (SNPs) were obtained within QTL regions related to stone cells. These results could be used to development of molecular markers, which would be applied in marker-assisted selection for pear breeding.

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PF-0041

Pathotyping of Korean *Ralstonia solanacearum* strains in tomato

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Ralstonia solanacearum is one of the major biotic threats to tomato and other solanaceous plants worldwide. *R. solanacearum* is known to affect more than 200 plant species. The pathogenic characteristics of five bacterial strains collected in Korea were studied by inoculating with bacterial wilt susceptible tomato cultivar Seokwang. Of the five strains inoculated, KACC18644 is found to be pathogenic as it is produced typical bacterial wilt symptoms while four strains, namely, KACC10698, KACC10707, KACC10715, and KACC10717 did not develop disease symptoms in the host. We also found only biotype 3 is causing disease but not biotype 4. The cellulose enzyme assays showed that strain KACC18644 produces the highest amount of cellulose among others. After inoculating seedlings, we compared the pathogenicity of each strain by measuring the CFU from the leaf, stem, hypocotyl, and root of the plants. The strain of biotype 3 showed a high CFU value in all sites. And we confirmed the biotype 4 strains had high CFU values in the hypocotyl, but the CFU values differed depending on the bacterial strains. We measured the severity of each strain on the 12th day after inoculation. The result shows that KACC18644 is highly pathogenic in tomato and produces symptoms s. We also confirmed differences in CFU value were higher in the leaves as the motility increased. The EPS and cellulase amounts were more with stronger virulence. This study will be useful for searching for other factors affecting the virulence of *R. solanacearum* and pathological characteristics among strains.

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PF-0042

국내 국화 핵심자원의 주요 농업 형질에 대한 유전력 검정 및 유용자원 선발

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본 연구는 국내 국화 핵심자원의 농업 형질에 대해 분석하여 국화 계획 육종의 효율성과 정확성을 높일 수 있는 기초자료를 제공하고자 수행하였다. 국립원예특작과학원, 충남화훼연구소, 경남화훼연구소에서 각 32점씩 총 96종의 핵심자원을 분양받아 초장, 줄기직경, 측지수, 착화수, 꽃목길이, 꽃목직경, 꽃직경, 통상화직경, 꽃풍성함, 설상화길이, 설상화너비, 병충해, 개화일의 농업 형질을 조사했다. 생육 조사를 통해 얻은 평균값을 대표치로 Tukey-Kramer HSD를 실시하였고, 형질 간 연관성을 확인하기 위해 상관분석과 주성분분석을 수행했다. 유전변이계수, 표현변이계수, 광의의 유전력, 유전적 진전, 유전적 진전율 등에 대한 통계적 분석이 이뤄졌으며, 이를 바탕으로 유용자원을 선발하였다. 초장과 줄기직경은 모든 형태에서 상관관계가 보였으며, 초장은 스프레이의 겹꽃과 폼폰형, 화단국과 분화국에서 초장이 크면 개화기가 빠른 것으로 나타났다. 착화수와 병충해를 제외하고는 형질의 유전변이계수와 표현변이계수의 차이가 크지 않아 환경적 영향이 적은 것을 보여주었다. 병충해를 제외한 모든 형질의 유전력과 유전적 진전율이 비교적 높은 편이었지만, 형태별로 평균이 유의미하게 낮거나 높은 형태도 있었다. 유전력의 경우, 줄기직경은 스프레이의 홑꽃이 상대적으로 높았고, 착화수는 스프레이 홑꽃, 꽃목길이는 스프레이 겹꽃, 개화기는 스프레이 폼폰형이 상대적으로 컸다. 상관관계와 유전력 등을 고려하여 시장에서의 품질 요소와 관련된 형질을 중심으로 유용자원을 선발했다. 스탠다드 중 큰 초장과 줄기직경, 짧은 꽃목길이, 빠른 개화기를 지닌 자원은 총 세 자원이었고, 스프레이 겹꽃 중 큰 초장과 줄기직경, 짧은 꽃목길이, 큰 꽃, 빠른 개화기를 보이는 자원은 한 자원이 선발되었다. 또한 스프레이 홑꽃에서 큰 초장과 줄기직경, 많은 착화수, 빠른 개화기를 가진 자원은 세 자원이, 분화국에서는 초장과 줄기직경, 꽃직경이 크고 개화기가 빠른 자원으로 한 자원이 각각 선발됐다. 본 연구로 국내 국화 핵심자원의 형태별 주요 형질의 관계와 특성이 나타났고, 이는 국화 계획 육종의 기초자료로 활용할 수 있을 것으로 기대한다.

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PF-0043

Radio-Sensitivity Analysis and Selection of Useful Mutants of Sunflower (*Helianthus annuus* L.) by Gamma-ray

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Sunflower (*Helianthus annuus* L.) is one of the important oilseed crop in the world. Ionizing radiation induced mutation has been used for development of new cultivars in diverse crops. The effects of ionizing radiation on mutation induction have been analyzed on several oil crops, including sunflower. Limited information is available on the comparison of mutation frequency and spectrum based on phenotypes in sunflower plant. In this study, we analyzed the radiation sensitivity, mutation frequency and spectrum of mutants induced by gamma-ray irradiations, and selected mutants at M_2 generation in the two sunflower cultivars from Korea and China. The median lethal doses (LD_{50}) were Korea and China cultivar of 490 and 182 Gy, respectively. In M_2 generation variants showing early or late flowering, dwarf plant, abnormal seed and flower size, chlorophyll deficiencies in leaf and large leaf mutant were selected as potentially useful lines for mutation breeding. The optimal dose of gamma-ray of each cultivar differed as follows: Korea, mutation frequency of 6.7% (600 Gy); China, 2.6% (100 Gy) based on phenotypes at M_2 generation. Information on the mutation frequency will be useful for mutation breeding of sunflower plant.

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PF-0044

Characteristic of trait-associated F_2 population derived from the cross octoploid strawberry inbred lines

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Strawberry is an octoploid heterogeneity, genomic and phenotypic data for genome breeding are insufficient. Therefore, in this study, for genetic analysis of octoploid strawberries, F_2 populations were derived by crossing the octoploid inbred lines and the fruit characteristics were investigated. The inbred lines were generated S_8 to S_9 by repeatedly performing self-pollinations from octoploid cultivars and crossed them to bred three F_2 populations, BS, BC and JB. The F_2 populations were cultivated with RDA standard method and investigated fruit quality such as firmness and sugar content. As a result, BS, BC, and JB groups confirmed the phenotype separation in each firmness, fruit color, and sugar content. The results are expected to provide basic information to help understand the genetic analysis of fruit characteristics and also to provide useful information for breeding studies to assist the development of varieties of strawberry.

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PF-0045

Ploidy assay and microscopic examination of colchicine-treated seedlings and female parent cultivars in Rose of Sharon (*Hibiscus syriacus* L.)

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To develop new varieties of Rose of Sharon (*Hibiscus syriacus* L.) through polyploidy induction, freshly germinated seeds from eight cultivars had been treated with colchicine in 2011. After growing and asexual propagation, ploidy assay and microscopic observation were conducted by flow cytometry and scanning electron microscope for 21 colchicine-treated seedlings and female parent cultivars. While all eight parental cultivars were diploid, seedlings were tetraploid (17 seedlings) or diploid (4 seedlings). The size of both guard cells and pollen grain varied according to the ploidy level, and these were generally larger in the tetraploid than the diploid. For example, length and width of the guard cells in 'Gyewolhyang' were 25.1±3.6 and 16.2±2.3 μm each. From the same female parent, those of tetraploid seedling (no.16) and diploid seedling (no.28) were 28.1±4.0/18.7±3.2 μm and 24.6±4.2/15.3±3.3 μm respectively. The size of the pollen grain was also bigger in tetraploid than diploid. Pollen grain diameter of tetraploid seedlings (no.205 and no.207) from 'Hwahong' was 130.7±8.9 and 137.5±9.7 μm, each. In contrast, that of diploid seedling (no.202) from the same cultivar was 115.1±7.7 μm. In summary, the size of the guard cells and pollen grain increased in the tetraploid seedlings induced by colchicine treatment. From this study, it can be suggested that ploidy level of *H. syriacus* can be determined through microscopic analysis of guard cells and pollen grain size.

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PF-0046

'*suppressor of dwarf*' enhance fruit harvest and yield traits in Micro-Tom

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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 limited 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. RNA seq reads provided evidence of a large deletion in chromosome 2. The interval contained genes such as *XTH8, GA2ox7* and *HSPs. GA2ox7* was chosen 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.

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PF-0047

Genomic Selection with Fixed-effect Markers Improves the Prediction Accuracy for Capsaicinoid Contents in *Capsicum annuum*

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Capsaicinoids provide chili peppers (*Capsicum* spp.) with their characteristic pungency. Several structural and transcription factor genes are known to control capsaicinoid contents in pepper. However, many other genes also regulating capsaicinoid contents remain unknown, making it difficult to develop pepper cultivars with different levels of capsaicinoids. Genomic selection (GS) uses genome-wide random markers (including many in undiscovered genes) for a trait to improve selection efficiency. In this study, we predicted the capsaicinoid contents of pepper breeding lines using several GS models trained with genotypic and phenotypic data from a training population. We used a core collection of 351 *Capsicum* accessions and 96 breeding lines as training and testing populations, respectively. To obtain the optimal number of single nucleotide polymorphism (SNP) markers for GS, we tested various numbers of genome-wide SNP markers based on linkage disequilibrium. We obtained the highest mean prediction accuracy (0.550) for different models using 3,294 SNP markers. Using this marker set, we conducted GWAS and selected 25 markers that were associated with capsaicinoid biosynthesis genes and quantitative trait loci for capsaicinoid contents. Finally, to develop more accurate prediction models, we obtained SNP markers from GWAS as fixed-effect markers for GS, where 3,294 genome-wide SNPs were employed. When four to five fixed-effect markers from GWAS were used as fixed effects, the RKHS and RR-BLUP models showed accuracies of 0.696 and 0.689, respectively. Our results lay the foundation for developing pepper cultivars with various capsaicinoid levels using GS for capsaicinoid contents.

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PF-0048

Broad bean wilt virus 2 Resistance Source Screening and Gene Mapping in Hot Pepper

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Broad bean wilt virus (BBWV) belongs to the *Fabavirus* genus and contains two single-strand RNAs. BBWV is a threatening virus with a wide host range including bean, spinach, grape, and pepper. Previous studies reported two BBWV1 isolates and six BBWV2 isolates, and their host range is steadily expanding. In this study, we screened 1050 pepper genetic resource accessions provided by the Korean gene bank using BBWV2-PAP1 strain. As a result, we were able to obtain 21 candidates of BBWV2-PAP1 resistant accessions. The candidates were cross-checked using symptom index scoring and enzyme-linked immunosorbent assay (ELISA) method. Screening the F_1 generation of resistant and susceptible accession resulted in susceptible phenotypes, which indicates that the resistance gene is a recessive allele. We also used recombinant inbred line (RIL) of BBWV2-PAP1 resistant and susceptible accession for further analysis. 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. Using these GBS markers and BBWV2 screening data, we were able to find the approximate location of the BBWV2 resistance gene on chromosome 9 and 10. We also used pools of RILs for bulked segregant RNA sequencing analyis. By calculating the SNP-index, we were able to locate SNPs that have significant relevance on rendering resistance to BBWV2. These results will serve as a resistance gene source for breeding BBWV resistant cultivars in pepper.

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PG-0001

Growth performance among the provincial Teak (*Tectona grandis* Linn.f,) in Myanmar

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Teak (*Tectona grandis* Linn.f,) is one of the most important and valuable tree species in Myanmar. This study was conducted in the teak provenance trial site located in compartment number (9), Ngalaik Reserved Forest, Tatkone Township, Naypyitaw. It was established with 8 provenances in 2007. The experimental design was the randomized complete block design with 5 blocks and each block comprised of 8 plots. One plot included 25 trees (5 x 5) with a spacing of 2.7 m by 2.7 m. The purposes of this study were to measure the growth characteristics such as height, diameter at breast height (DBH) and estimate the volume of 8 provenances at age 15 years, test for the significant differences in growth characteristics and select superior provenances among them. We measured height and DBH of 745 trees in January 2022. The tree volume was estimated based on the tree height and DBH growth, then calculated by using the breast height form factor method (Perez and Kanninen, 2005, Hlaing and Kyi, 2009). Two-way ANOVA, Duncan's multiple range test and Pearson's correlation analysis were applied. All statistical analyses were conducted using R version 4.0.4 (R Core Team, 2021) to determine the significant of any growth differences among the provenances. There was a highly significant difference of height (ranged from 6.10 m to 22.86 m) and DBH (ranged from 22.86 cm to 127.00 cm) growth among the provenances. According to analyses, three out of eight provenances (Nattalin, Bago, and Phyu) were showed the superior results. The provenance, Thabeikkyin was separated as the poorest one. The results would contribute for selecting mother trees (plus trees) and utilizing seed sources in the future tree breeding program in Myanmar.

Keywords: teak, provenance trial, growth performance, growth characteristics, plus trees

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PG-0002

홉(*Humulus lupulus* L.) 우량묘 대량증식을 위한 조직배양 및 삽목 실험

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최근에 수제 맥주 붐에 따라 외국의 홉을 도입하여 국내 생산을 도모하고 있으나, 적합 품종과 전문 기술의 부족으로 재배 확대에 많은 어려움을 겪고 있다. 국내 홉 생산 확대를 위해서는 국내 적합 품종의 육성과 우량묘 대량증식 및 재배관리 기술체계 확립이 필요하다. 본 연구에서는 홉 6개 품종(Saaz, Cluster, Cascade, Calypso, German magnum, El Dorado)을 이용하여 조직배양 및 삽목증식연구를 수행하였다. 조직배양에 사용된 배지는 MS 배지에 sucrose 20%, Agar 8%로 하였고 pH는 5.8로 조성하였으며, IAA는 0.1mg/L, BAP와 TDZ는 1mg/L 사용하였다. 실험 결과 IAA를 0.1mg/L와 BAP 1mg/L를 사용한 배지에서는 신초가 품종별로 절편체 당 1~3개 정도 발생하였다. IAA를 0.1mg/L와 TDZ 1mg/L를 사용한 배지에서 절편체 당 6~9개의 신초가 발생하여 BAP에 비해 높은 신초 발생률을 보였다. 특히, Calypso의 경우 절편체 당 신초가 8~13개 발생하였다. 또한 삽목기술 개발을 위해 봄에 신초가 50~100cm 정도 생육한 녹지를 5~7cm 길이로(1마디) 채취하여 삽목용 그로우폼에 삽목하여 발근력을 조사하였다. 실험방법으로는 수돗물을 그로우폼에 관주한 것(W)과 수돗물에 아토닉 2,000배 희석하여 관주한 것(A2000), 삽수의 절단면을 아토닉에 담갔다 뺀 다음 삽목한 것(A)으로 진행하였다. 녹지삽의 경우 3가지 처리구에서 15일 이후 개체의 50%가 발근하였다, 특히 German magnum은 W에서 90%, A와 A2000에서 100% 발근 되었다. 뿌리의 개수가 가장 많은 것은 Saaz W로 17.6±1.9개이며 가장 적은 것은 Saaz A로 4.4±0.7개이다. 뿌리의 길이는 German magnum A에서 3.0±1.5cm로 가장 길었고 Saaz A2000에서 0.4±0.1cm로 가장 짧았다.

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PG-0003

Phytochemical compounds and antioxidant activates of Hop (*Humulus lupulus* L.) cultivars

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Hop (*Humulus lupulus* L.) is a dioecious, perennial plant belonging to the Cannabaceae family, became a widely grown agricultural plant because of its use to give bitterness and aroma to beer. The present study investigated the phenolic compounds of strobile extracts from 9 different Hop accessions and evaluated their antioxidant property by using DPPH and ABTS assay. The total phenolic content (TPC) and total flavonoid content (TFC) were extracted by two different methods, which exhibited changing levels dependent on the extract methods in the nine hop accessions. The most abundant prenylflavonoid compound in hop was humulones (α-acid) with levels ranging from 50.44 to 193.25 μg/g. The El Dorado accession showed higher antioxidant activity (DPPH: IC_{50} 124.3 μg/㎖, ABTS: IC_{50} 95.4 μg/㎖) when compared with the other accessions. Correlations between DPPH (IC_{50}) scavenging and TFC extracted by ethanol (TFC_E) (-0.94), TPC_E (-0.90), and between ABTS (IC_{50}) scavenging and TFC_E (-0.93), TPC_E (-0.90), were found statistically significant at $p < 0.05$ level while complete lack of antioxidant activities correlation with TPC and TFC extracted by hot water was observed. These results indicate that the phenolic compound extract method mainly influence to antioxidant activity. This study is the first to report the changes in the phenolic levels and antioxidant activity in various solvent extracts and collected regions, which could provide additional evidence of antioxidant properties in hop cultivars.

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PG-0004

CRISPR/Cas9 system을 활용한 현사시나무 *Myeloblastosis viral oncogene homolog 15* (*MYB15*) 유전자 교정체 제조 및 특성 구명

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CRISPR/Cas9 system을 활용한 유전자 교정 기술은 유용 형질을 갖는 작물 및 임목의 육성에 널리 사용되고 있다. MYB 전사인자는 여러 식물 내에 보존되어 있고 family가 많은 전사인자의 하나로, 다양한 조직에서 식물의 생장, 발달 및 스트레스 반응 조절에 관여하는 것으로 알려져 있다. 본 연구에서는 현사시나무(*Populus alba*×*Populus glandulosa*)에서 MYB15 유전자를 표적으로 하는 guide RNA를 설계하여 *MYB15* 유전자 교정체를 제작, 선별하여 유전자의 특성을 조사하였다. 현사시나무 *MYB15* 유전자는 3개의 exon과 2개의 intron으로 구성되어 있고, 단백질 암호화 부위는 801 bp 길이의 염기쌍으로 이루어져 있으며, 267개의 아미노산으로 구성된 단백질을 암호화하고 있다. 또한 *MYB15* 유전자는 염, 건조 스트레스 조건에서 발현이 증가하였다. 서열분석을 통해 표적부위에 변이가 일어나 단백질 합성이 조기에 종결되거나, 다른 아미노산으로 치환된 교정체를 선발하였다. 선발된 교정체를 대상으로 스트레스 내성과 관련이 있는지 확인하기 위해 염과 건조 스트레스를 처리하였다. 처리 결과, *MYB15* 교정체가 야생형 대비 염 스트레스에 민감한 표현형을 보였고, 건조 스트레스 처리에서는 표현형에 차이가 없었다. 본 연구결과는 유전자 교정 기술을 통해 스트레스 반응에 관여하는 유전자의 동정 및 유용 형질을 갖는 임목의 개발에 활용할 수 있을 것으로 기대된다.

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PG-0005

CSE-knockout reduces lignin deposition by modulating secondary xylem formation in hybrid poplar

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Lignin is essential for the growth and development of terrestrial plants as it contributes to the creation of a very strong secondary cell wall. However, lignin also makes it difficult to process plant biomass into fermentable sugars. Caffeoyl Shikimate Esterase (*CSE*) have been shown to play an important role in lignin biosynthesis in plants. Here, we present transgenic hybrid poplars (*Populus alba* x *P. glandulosa,* clone BH) with knockouts of two *PagCSE* genes achieved by CRISPR/Cas9. We designed four single guide RNAs (sgRNAs); sgRNA1 simultaneously targeted the first exon of *CSE1* and *CSE2*, sgRNA2 targeted the second exon of *CSE1*, and sgRNA3 and sgRNA4 targeted the second exon of *CSE2* gene, respectively. As a result, *PagCSE1*-sg2 and *PagCSE2*-sg3 poplars had up to 29.1% reduced lignin deposition. It has been shown that xylem vessel cells are disrupted and S-lignin is significantly reduced by Maule staining. Above all, we detected no significant differences in growth among *PagCSE1*-sg2 and *PagCSE2*-sg3 poplars and BH poplars in a living modified organism (LMO) field test conducted over a year covering all four seasons. Therefore, it is expected that the CSE-knockout mutants will reduce lignin to improve saccharification efficiency. Our results could contribute to promote of woody biomass for sustainable biofuels through *CSE* gene editing by CRISPR/Cas9.

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PG-0006

Specific regulation of the hormone response-related genes during cell growth kinetics of poplar

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To obtain information on changes in gene expression that could explain morphological and biochemical changes occurring during the developmental course of a batch plant cell culture, we have examined the global growth phase-dependent gene expression of poplar cells by cDNA microarray analysis. Our results reveal that significant changes occur in the expression of genes with functions related to protein synthesis, cell cycling, hormonal responses and cell wall biosynthesis, as cultures progress from initiation to senescence, that are highly correlated with observed developmental and physiological changes in the cells. We also detected a marked up-regulation of genes encoding proteins involved in responses to hormones including auxin, ethylene and gibberellin during both the early-exponential and stationary phases. The results imply that integrated hormonal regulatory mechanisms are involved in the complex cellular changes.

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PG-0007

Identification and Determination of Phenolic compounds in Rapeseed (*Brassica napus* L.) Mutant Lines Derived from Gamma-ray

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Rapeseed (*Brassica napus* L.) seeds are much higher in phenolic compounds compared to other oil crops. Phenolic compounds are generally considered as antinutrients because they may contribute to the bitter taste in rapeseed. While, phenolic compounds to be natural antioxidants with good antioxidant activities for rapeseed. Since natural variation for phenolic compounds are limited in rapeseed, radiation-induced mutation is one of the most effective methods to modify phenolic compound contents. Forty-nine mutants were developed by treatment with 600 Gy of ^{60}Co gamma irradiation of commercial cultivar ('Youngsan'). Mutants that varied in phenolic compound contents that exhibited stable inheritance of the mutated characteristics from M_5 to M_7 generations were selected. Quantitative analysis of phenolic compounds in the seeds of the 49 mutant genotypes and their original cultivar was performed using high performance liquid chromatography mass spectrometry (HPLC-MS). Seven compounds were identified as dihexose, progoitrin, *trans*-sinapine 1, *trans*-sinapine 2, sinapine(4-*O*-8')guaiacyl, sinapoyl malate, methyl sinapate. The *trans*-sinapine 1 and *trans*-sinapine 2 compounds were major (90.2~96.9%) phenolic compound in all rapeseed lines. The total phenolic content of original cultivar was 66.04 mg · g^{-1}. The total phenolic content of the mutant lines ranged from 15.86 to 78.31 mg · $g^{-1.}$ Eight mutant lines had lower (<30 mg · g^{-1}) total phenolic contents. While, two mutants showed significant higher (>70 mg · g^{-1}) total phenolic content than the original cultivar. These results may be useful for identifying the optimal genotypes for breeding new rapeseed cultivar with enhanced qualities and potential as a functional source of food and feed.

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PG-0008

Selection of Valuable Kenaf Genotype with High Stem-Production and Cellulose Content

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Kenaf is known as a jack-of-all-trades crop due to being used in many different fields. The breeding of kenaf with high stem-production and industrial value is important strategy. The elite mutant with superior performances was selected through mutation. Seeds of the original resource named Hongma 300 (Control) were irradiated with 250 Gy gamma-ray. The agronomic performances, cellulose and lignin content of the elite mutant line (JBK-1) were investigated at M8 generation in comparison with the Control. The leaf shape of the Control and the JBK-1 mutant was palmate. Significant differences at leaf color were observed comparing JBK-1 mutant and the Control. The JBK-1 was blooming on August 5, which is 97 days after sowing, being comparable to the Control flowering on September 30. Dry weight of the JBK-1 was 5.7 kg/m^2, which was the statistical same with 6kg/m^2 of Hongma 300. Both genotypes, the Control and JBK-1, had significant difference for seed yield. The latter's amount was 212 g/m^2, however, the former didn't set seeds due to a low temperature below 15℃. In the fuel characteristics analysis, the heating value of the mutant ranged from 4,080 in lower heating value to 4,643 kcal/kg in higher heating value, which was similar to the Control. Based on the cellulose content analysis, JBK-1 showed a significantly difference compared to the two Control. Plus, the lignin content analysis indicated a low value at 19.4% for the JBK-1, which was lower than 19.7% of the Control, JD. Taken together, the genotype would be useful resource for high stem-production and industrial utilization such as bioplastic and activated carbon development.

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PG-0009

Antioxidant activities and phytochemical contents of diverse representative tea germplasm

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Tea(*Camellia sinensis* (L.) Kuntze) is a one of the worldwide consumed non-alcoholic beverages and contains functional phytochemicals such as polyphenols, caffeine and so on. Previously we surveyed genetic and phytochemical diversities conserved in tea collection. In this study, we characterized antioxidant activities of DPPH (2,2-diphenyl-1-picrylhydrazyl) and ABTS (2,2′ -azino-bis-(3-ethylbenzothiazoline-6-sulfonic acid) in representative 86 tea accessions and analyzed its correlation with polyphenols and caffeine. Wide variation of phytochemicals and antioxidant activities were detected in representative tea germplasm. DPPH(1/IC50) was ranged from 0.011 to 0.018(mean=0.015) and ABTS(mgAAE/g) was ranged from 15.988 to 31.765(mean=23.637). The phytochemicals were positively correlated with antioxidant activities. In principal component analysis, there was no distinctive separation according to the origin and four cluster were detected based on the hierarchical clustering analysis. Based on this variation, now we try to find genetically associated factors with phytochemical properties. These could provide information of diversities for the selection and breeding of tea.

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PG-0010

근적외선 분광분석법을 이용한 붉가시나무 종자의 활력 검정

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붉가시나무는 지구온난화 심화에 대비한 탄소중립용 조림수종으로 각광받는 난대상록활엽수종이다. 차후 한반도 기후 변화에 따른 조림수요를 위해 효율적으로 종자를 생산하기 위해서는 저비용, 비파괴적인 분광분석법을 연구하여 적용가능성을 파악할 필요가 있다. 따라서 근적외선 분광분석법을 이용하여 400-1,000nm 구간대에서 붉가시나무 종자의 종자 품질을 판단하고자 본 연구를 실시하였다. 제주도 서귀포시에 조성된 붉가시나무 채종원에서 550립의 종자를 채집하였다. 채집한 종자의 품질을 시각적인 방법으로 온전종자 368립, 충해종자 182립으로 구분하였다. 이후, Calibartion/Validation을 위해 각각 366립(온전 246/충해 120), 184립(온전 122/충해 62)으로 구성된 seed lot들을 랜덤으로 구분하였다. 근적외선 영역 파장데이터를 얻기 위하여 Oceanoptics사의 Flame-S-Vis-Nir 분광분석기와 적분구(ISP-REF)로 종자의 각 방위를 10번씩 측정한 값을 평균하여 총 550개의 파장을 획득하였다. 이후 분광분석 데이터의 오류를 줄이기 위하여, 1/2차 미분, MSC, 표준정규화, SG필터 등의 데이터 전처리를 적용하고, PLS-DA, OPLS-DA 다변량분석법을 적용하였다. 그리고 파장사용구간, 전처리, 다변량분석법에 따른 모델성능을 비교하였다. 근적외선 파장측정 결과, 붉가시나무 종자의 근적외선 파장은 660nm에서 강한 peak를 보여주었고, 900-1,000nm에 걸쳐 미약하게 아래로 향하는 peak를 보여주었다. 다변량분석 결과, 가장 우수하게 충해여부를 분간하는 모델은 400-1,000nm, 780nm-1,000nm 구간대에 1차 미분처리를 하여 OPLS-DA를 적용한 모델들로, 각각 R2cum이 0.43, 0.41, Q2cum이 0.32, 0.35, RMSEE가 0.358, 0.363, 그리고 RMSEcv가 0.384, 0.377($p<0.01$)이었다. 이상의 결과를 토대로 할 때, 400-1,000nm 파장대에서의 근적외선 분광분석은 붉가시나무 종자의 충해여부를 어느 정도 분간하는 경향을 보였다. 특히 780-1,000nm의 근적외선 영역대에 분류가 더 잘되는 경향을 보였다. 그러나, 충해립 분류 시 충해가 겉표면으로 나타나지 않아 시각적으로 분류가 되지 않는 경우가 존재하였다. 벌레 가해 여부 이외에도 종자 내부 미생물들로 인한 부패가 충해와 비슷한 효과를 만들어 내기 때문에, 종자품질 분류 여부 및 모델의 예측력을 높이기 위해서는 x-ray 등의 장비를 이용하여 정확한 사전분류를 할 필요가 있다고 판단하였다.

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PG-0011

A Sesame variety 'Haniall' with non-shattering capsule and early maturity

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Sesame(*Sesamum indicum* L.) is cultivated worldwide for its seeds and oil. Sesame seeds fall out upon maturity in nature. So normally sesame is harvested manually. Non-dehiscent capsule is the most important trait for reducing yield loss during harvesting sesame by machinery combine. A sesame variety 'Haniall'(*Sesamum indicum* L.) with non-dehiscent capsule and early maturity was developed in 2021. It was crossed between 'Suwon 195' and 'IT030100' in 2014. It has many branch and mono capsule per node and pure white seed coat color. And maturing date of it is 13 August. Its height is 149cm and capsule number of it is 102. Especially it showed non-shattering capsule trait. And the yield of it was about 1.04ton per hectare, 20% higher than 'Ansan'. It showed crude fat content with 54% and crude protein content with 26% and lignan content with 6.4mg/g. Thus it would be suitable for mechanized sesame harvesting.

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PG-0012

EMS 처리로 유기된 아마란스 유전자원의 주요 농업형질

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아마란스(*Amaranthus*)는 비름과 작물에 속하는 한해살이풀로 다른 곡물에 비해서 영양학적으로 우수한 '슈퍼 곡물' 중 하나이다. 그러나, 국내에서 육성된 아마란스 품종이 없어 재배가 어려운 실정이다. 본 연구에서는 도복에 강하면서 재배 안정성이 우수한 아마란스 품종을 육성하기 위해서 수집종(ASA, AJB, AWJ, AJS)에 0.5% ethyl methane sulfonate (EMS)를 처리하여 돌연변이 집단을 창출하였다. 이 중 고령지농업연구소 온실에서 수색, 종피 색, 수량 등으로 고 정도를 평가하여 계통화하였다. 선발된 계통의 재배 안정성을 평가하기 위해서 고랭지(대관령), 평난지(강릉)에 설치된 노지 포장에서 농업형질을 조사하였다. 수집종인 ASA, AJB, AJS의 이삭이 노란색이나 EMS에 의해 유기된 ASA-1(적색), AJB-1(자주), AJB-3(자주), AJS-2(자주)의 경우 수집종과 뚜렷한 차이를 보였다. 종피 색에 있어 수집종과 EMS에 의해 유기된 계통의 대부분이 노란색을 띠고 있었으나 AJB-1의 경우 갈색의 종피 색을 보였다. 이처럼 0.5% EMS로 유기된 개체 중 이삭 색 및 종피 색에 있어 수집종과 뚜렷한 차이를 보이는 10개체를 선발하여 계통화하였으며 대관령, 강릉 지역에서 주요 농업형질을 조사하였다. 30일 육묘 후 강릉에 정식하였을 때 수확기는 67일에서 100일이, 대관령에서는 정식 후 수확까지 93일에서 94일이 소요되었다. 강릉에서 초장은 77 cm (AJB-3)~152 cm (AJS-1), 경태는 15 mm (AJB-3)~21 mm (AJS-1), 분지수는 5개(AJB-3)~12개(AJS-1)를 보였다. 대관령의 경우 초장은 80 cm (AJB-3)~120 cm (ASA-1), 경태는 13 mm (AJS-2)~16 mm (AJB-1)로 강릉과 비교해서 유의적으로 감소하였다. 이상의 결과에서 초장, 경태, 분지수 등은 계통 간 유의차가 인정되었다. 초장의 경우 변이계수는 낮았으며 유전율은 높게 나타나 EMS에 의해서 단간형 자원의 창출 효과가 있는 것으로 판단되었다. 특히, EMS에 의해 유기된 AJB-3의 경우 수집종 및 다른 계통에 비해서 단간종으로 내도복성 및 재배 안정성이 우수하였다. 향후 우리나라에서 재배 안정성이 우수한 아마란스 품종을 개발하는 데 EMS에 의해 창출된 자원을 이용할 수 있을 것으로 기대된다.

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PG-0013

드론 항공 영상에서 인공지능을 사용한 등검은말벌집 검출

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유엔 식량농업기구(UN FAO)에서 인간이 먹기 위해 기르는 작물 종의 75%가 꿀벌이나 나비와 같은 화분 매개 동물의 수분에 의존한다고 발표했다. 그에 따라 매개 동물인 꿀벌의 개체수가 중요하다. 2003년 중국 상하이를 통해 부산으로 유입된 등검은말벌은 말벌과 곤충으로 국내 말벌들과는 다르게 꿀벌에 대한 사냥 성공률이 높고 사냥에 걸리는 시간도 짧아 많은 위협을 주고 있으며 2019년 생태계 교란 야생 생물로 지정되었다. 등검은말벌은 고도 10m 이상의 높은 나무 위에 위치하기 때문에 사람의 육안으로 찾기 힘들며 확산성이 좋아 매년 피해가 늘고 있는 실정이다. 본 연구에서는 항공에서 드론을 사용하여 높은 위치에서 쉽게 데이터를 취득하고 인공지능을 사용하여 등검은말벌집 탐색로 연구를 진행했다. 인공지능 YOLOv5에서 YOLOv5x 신경망을 사용하여 등검은말벌집 학습을 진행하였고 등검은말벌집이 있는 항공사진 11,838장을 학습 데이터로 사용했다. 해발고도 65~110m 사이의 비행 기준 촬영 영상들이 활용되고 영상 3,840*2,160 해상도에서 32*32~72*72 크기의 등검은말벌집을 검출할 수 있었다. 정밀도 (Precision)는 90.6%, 재현율(Recall)은 11.6%, 정확도(Accuracy)는 76.0% 결과를 얻을 수 있었다. 모든 촬영 영상 프레임에서 등검은말벌집을 검출하진 못하였으나 일정 장면마다 검출하였기 때문에 특정 위치에 등검은말벌집이 존재한다는 정보는 얻을 수 있었다. 추후 검출률을 높이기 위해 영상 전처리, 인공지능 모델 수치(parameter) 조정 등을 통한 연구를 진행할 것이다.

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PG-0014

Evaluation of early growth and environmental characteristics of *Quercus rubra* plantations in six regions in South Korea

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Quercus rubra, the northern red oak, is a promising introduced tree species with excellent growth characteristics in South Korea. Here, early growth characteristics of *Q. rubra* planted in six regions(Hwaseong, Yangpyeong, Pyeongchang, Samcheok, Chungju, and Gimje) in South Korea were investigated using seeds introduced from Michigan, USA. Saplings of *Q. rubra* (1-0) were planted at a density of 3,000 trees/ha. The average height, root collar diameter (RCD), and volume of 8-year-old *Q. rubra* planted in 2014 were 3.52 m, 3.84 cm, and 0.0023 m^3, respectively. Among the six regions, the growth of *Q. rubra* planted in Hwaseong was significantly higher than those in the other sites, but those of Pyeongchang region were the lowest. In correlation analysis, growth characteristics such as height, RCD and volume represented a positive correlation with average temperature from March to October and daily maximum temperature. However, altitude, topology, and number of rainy days from March to October showed a negative correlation with the growth characteristics. Principal component analysis was represented 84.7% accumulated explanation from third principal component. Hwaseong regions showed strong relationship with growth factors. In addition, the correlation between growth and the meteorological factors was more important rather than the physicochemical properties of the planted soil for the early growth of *Q. rubra*. This study will provide the information to determine the suitable site for *Q. rubra* afforestation.

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PG-0015

Comparative transcriptomic analysis of *Pinus densiflora* and *Pinus strobus* to find resistance candidate genes to Pine wood nematode (*Bursaphelenchus xylophilus*)

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Pine wood nematodes (*Bursaphelenchus xylophilus*) are nematodes that infect pine trees and cause pine wilt disease. *Pinus densiflora*, a native pine tree species in Korea, is susceptible to pine wood nematode and easily killed by pine wilt disease. In contrast, *Pinus strobus* is an introduced pine species from North America and has resistance to pine wood nematode. *P. strobus* ias expected to have resistance genes to pine wood nematode, but the identity of the resistance genes are still unknown. In this study, we compared transcriptome of *P. densiflora* and *P. strobus* to detect resistance candidate genes to pine wood nematode. Three biological replicates of *P. densiflora* and *P. strobus* were inoculated by 10,000 pine wood nematodes per tree. Cambium samples of trees were collected on 0, 2, 4 weeks after inoculation. RNA samples were extracted from the cambium and sequenced by Novaseq 6000 (Illumina, USA). Using Trinity (v.2.13.2), *de novo* transcriptome assembly for both species was conducted from the clean reads of sequenced RNA. We selected the differentially expressed genes (DEGs) showing P-value $\leq$ 0.05 and fold change $\geq$ 2. Total 1,041 million reads of RNA were assembled to 37,533 genes of *P. densiflora* transcriptome and 36,550 genes of *P. strobus* transcriptome. Among 163 upregulated DEGs (0 vs 2 weeks) of *P. strobus*, 13 DEGs which had no homology genes in *P. densiflora* were selected as resistance candidate genes. Further study for the transcriptome of both species would give us a hint about the resistance genes to pine wood nematode.

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PG-0016

건조 온도별 귀리의 발아력 조사 및 항산화 분석

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귀리는 단백질 함량이 높고 반추가축의 기호성이 우수하여 양질의 조사료 작물로 재배되고 있다. 종자는 수확 후 건조 방식에 따라 발아율, 섬유소, 단백질 함량에 영향을 미치는 것으로 조사되었다. 귀리 종자가 수확되는 시기는 장마철이라 천일건조 보다는 주로 기계식 건조가 선호되고 있으나 안전 건조온도 기준이 정해지지 않아 개별농가 채종시 빠른 건조를 위해 고온 건조에 따른 종자 발아불량이 초래되는 경우가 많이 발생한다. 본 연구에서는 영농에서 활용할 수 있는 건조 조건을 제공하기 위해 숙기별로 종자를 수확한 후 온도별로 건조하여 종자내 발아력 조사와 항산화를 분석하였다.

귀리 품종 '하이스피드'의 종자를 숙기별(고숙기, 완숙기)로 수확 후 무가온 송풍, 가온(40, 45, 50℃) 송풍으로 건조하였다. 발아력은 온도 20℃, 상대습도 80%로 유지되는 항온기에서 조사하였다. 항산화 Total phenol, 2,2-diphenyl-1-picrylhydrazyl(DPPH)와 2,2'-azino-bis-3-ethylbenzothiazoline-6-sulphonicacid(ABTS), 조단백 함량은 질소/단백질 분석기(FP628 nitrogen determinator, LECO)를 이용하여 전질소함량을 구한 다음 질소계수 5.83을 곱하여 산출하였다.

귀리 종자는 무가온 송풍 건조에서 숙기와 상관없이 90% 이상의 발아력을 보였고, 고숙기 수확 종자를 40, 45℃ 건조하였을 때 85-84%의 발아력을 나타냈으며, 50℃에서 81%으로 가장 낮았다. 또한 완숙기 종자는 무가온+송풍조건일 경우 40, 45℃ 발아력이 97-95%로 가장 높았지만 송풍+50℃에서는 93-94%으로 낮아졌으며 고숙기, 황숙기 종자도 유사한 경향을 보였다. 단백질의 경우 완숙기 종자는 건조 온도와 관계없이 16%의 함량을 보였다. 반면에 고숙기 종자는 무가온 송풍 조건에서는 16%, 45, 45℃ 15%였으며, 가장 높은 50℃ 건조 온도에서 14%로 낮았다. 항산화력 평가방법중 하나인 DPPH 검사에서 고숙기(무가온 송풍_40.3%, 40℃_39.7%, 45℃_41.2%, 50℃_42.2%), 완숙기(42.7, 43.0, 42.6, 45.4%) 가온온도가 증가함에 따라 항산화력이 증가함을 보였으며, ABTS 검사에서도 고숙기(27.6, 29.8, 32.3, 35.1%), 완숙기(30.2, 36.1, 38.8, 39%) 건조 온도가 증가함에 따라 항산화력이 증가하는 특징을 보여주었다. 가열을 하면 페놀의 화합물의 함량이 증가 하는데 Total phenol 실험에서도 온도별 고숙기(23.3, 24.1, 24.4, 25.4 mg GAE/ml), 완숙기(23.6, 25.9, 25.4, 28.5 mg GAE/ml)의 경향으로 건조 온도가 증가함에 따라 페놀과 항산화 모두 증가하는 것을 확인하였다. 고숙기, 완숙기 모두 50℃에서는 발아력이 감소하는 것을 보아 90% 이상의 발아력과 항산화가 증가하는 시점인 40-45℃의 온도가 귀리 종자의 건조에 적합하다고 판단된다.

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PG-0017

Genetic evaluation of tree growth using pedigree reconstruction and phenotypic spatial structure in a *Larix kaempferi* plantation

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Larix kaempferi is one of the major timber species in Northeast Asia for its fast growth and stem straightness. Forest area of *L. kaempferi* recorded as the second largest in Korea after its first introduction in early 20th century. Recently, the demand for *L. kaempferi* reforestation has risen and remains high according to increased production of large diameter timber from the species. However the progeny trial, which is the essential stage of tree improvement program, has not been established in this species in Korea. In this study, the genetic testing was attempted in a *L. kaempferi* plantation for the purpose of substituting progeny trial. To compensate the absence of experimental design in general progeny trial, the genetic and environmental factors were required to be identified for each individual tree in the plantation. Pedigree reconstruction was carried out using genotype of each tree to obtain the maternal information as genetic factor. Spatial distribution of diameter was used to investigate the environmental factor at individual scale. Genetic testing was performed by animal model and a model considering the spatial structure of bidimensional first-order autoregressive structure (AR1⊗AR1). The fitness of analysis was improved by the latter model resulting estimated heritability of 0.224. The approach in this study was expected to be useful as an alternative to the traditional progeny trial.

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PG-0018

Genetic effect changes and age-age correlation in open-pollinated family growth of *Pinus koraiensis* from forty years of progeny testing

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The long life span of forest tree is one of the major obstacles of advancing tree improvement program. Age-age correlation has been main research topic in tree improvement as it can provide an useful information for deciding the adequate selection age. The objectives of this study were to investigate the genetic parameter changes with tree age, and to find age-age correlation of tree volume growth from progeny trials of *P. koraiensis* for forty years. The study was carried out with the growth data for eleven times from age 5 to 40 in two sites. Height growth continued to increase until Age40 while the DBH growth showed a tendency to slow from Age30. The heritability was estimated to be differed by age and by site at the same age as well. The estimated heritability at Age40 was 0.406 and 0.490 at GP and CJ site, respectively. The heritability estimates were higher in CJ than in GP in all assessed age. The phenotypic and genetic correlation by age was investigated in the two sites. The phenotypic correlation with Age40 was gradually diminished with decreasing age. The genetic correlation with Age40 was 0.988 and 0.998 in the sites at Age30 which is the forest cutting age of *P. koraiensis*. The estimate was decreased to 0.508 and 0.756 at Age15.

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PG-0019

Genetic Diversity and Relationship of Rapeseed (*Brassica napus* L.) Mutant Genotypes Based on Genotyping-by-Sequencing (GBS)

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Rapeseed (*Brassica napus* L.) is one of the most important oil crop in the world, and its economic value is determined by its oil quality. Thus, increasing seed oil and improve the fatty acid profile in rapeseed is important objective in breeding. Radiation-induced mutation is one of the most effective methods to modify oil traits for commercialization. Ninety-five mutant lines were generated by treating seeds of the 'Tamra' cultivar with 700 Gy of ^{60}Co gamma irradiation. These mutant lines that varied in seed yields, disease resistance, crude fat contents, and fatty acid compositions that exhibited stable inheritance of the mutated characteristics from M_5 to M_7 generations were selected and single-nucleotide polymorphisms (SNPs) were identified by genotyping-by-sequencing (GBS). A total of 748,146,194 clean data reads were generated with an average of 6.8 million reads. A set of 108,907 filtered SNPs was used to perform phylogenetic analysis. Hierarchical cluster analysis of the rapeseed mutant lines gave nine related groups and one independent group based on agronomic characteristics and oil traits. The hierarchical cluster analysis was coincided with the pattern of oleic acid content. Comparison of the phylogenetic analysis based on agronomic characteristics and oil traits with those based on GBS data resulted in an unclear pattern of division among the accessions. These results may help identify optimal genotypes for breeding new cultivars.

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PG-0020

Prediction of breeding value of unrelated population using genomic selection in Korean red pine (*Pinus densiflora*)

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Genomic selection (GS) is to select excellent individuals based on genomic estimated breeding value (GEBV) by applying the trained model to a target population. GS could be used even in the absence of linkage disequilibrium because it concerned with identity-by-state between individuals, whereas the prediction using pedigree between unrelated populations is difficult. The purpose of this study is to predict the GEBV of full-sib population using model trained in the half-sib population and to evaluate the predictive accuracy in Korean red pine. A control-pollinated progeny trial planted in Hwaseong was used as the test population and open-pollinated progeny trial planted in six regions was used as the training population. A total of 6,464 markers that has minor allele frequency of more than 0.05 in half-sib population were used for GBLUP model. As the result, the prediction of the GEBV of full-sib population was effective when combined sites of half-sib population were trained, showing the genomic selection accuracy of 0.657 in DBH, 0.501 in height, and 0.896 in volume. The prediction accuracy of GS was improved when markers showed polymorphism in the test population as well as in the training population. It was investigated that 10% of individuals selected based on GEBV for volume belonged to 18 full-sib families, ensuring higher genetic diversity rather than family selection. This study showed the possibility that GS of Korean red pine could be predictable in unrelated population and further study to validate it should be conducted.

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PG-0021

수분 환경에 따른 도라지(*Platycodon grandiflorus*) 생육 및 성분 함량

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도라지(*Platycodon grandiflorus*)는 국내 산간지방에 널리 자생하는 초롱꽃과 식물로 뿌리는 약용 및 나물용으로 많이 이용되고 있다. 본 연구는 특용작물육종을 위한 기반연구의 일환으로 노지 토양의 수분환경을 부여할 수 있는 시설을 구축하여 노지경작지의 환경변화를 계측하고, 이 환경조건에 따른 작물의 생육을 파악하기 위하여 공시작물로 도라지를 식재하여 생육 및 성분함량을 조사하였다. 지중점적자동관개 토양수분측정 제어시스템(주, 아크로TNS)을 사용하여 센서상의 수분농도를 20%, 30%, 40%, 50%로 세팅하여 자동으로 공급되도록 하였다. 노지에서 토양수분조절이 가능한 환경구축은 2020년 12월, 밭토양(333 ㎡ 면적)의 하부를 약 45 ㎝ 정도 깊이로 굴착하여 하단에 수분점적관을 배관하고, 배수장치로는 80 ㎝ 깊이로 굴착하여 상층 30 ㎝ 두께로 왕겨를 투입한 뒤 흙으로 충진하여 자동지중점적시설을 설치하였다. 상기와 같이 구축한 노지 포장의 약 45 ㎝ 위에 작물이 식재되었으며, 2021년 4월 28일(수)에 2년차 도라지 유묘를 식재하여 토양 작토층으로부터 10 ㎝ 하단(6~11.5 ㎝)에 토양센서 〔WT1000B, ㈜미래센서, 대한민국〕 를 설치하여 지온, EC(염류농도), 토양수분을 측정하였다. 생육조사로는 주근장, 주근직경, 엽장폭, 주당착과수, 생체중 및 건물중을 조사하였다. 토양수분에 따른 무기성분, 아미노산류, 진세노사이드 함량을 비교한 결과, 무기성분은 수분함량이 높을수록 증가하였으며, 관행구보다 높게(Na, Ca) 나타나거나 낮게(K, P) 나타났다. 아미노산류(16종)는 프롤린, 티로신, 알기닌을 제외하고는 수분함량이 높을수록 증가하였으나 16종 모두 관행구보다 낮게 나타났다. 한편 사포닌류(진세노사이드 12성분) 함량은 Rf를 제외한 나머지 항목에서는 기준치 이하로 나타났다.

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PG-0022

Development of indel and SNP markers for *Quercus acutissima* 'Gumsura 1ho'

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Quercus acutissima is an economically and ecologically important forest tree species in the family Fagaceae with a wide distribution in world. In Korea, *Q. acutissima* 'Gumsura 1ho' was selected for large acorn size and high yield in candidate *Q. acutissima* clones collected from 9 regions. To develop discriminable molecular markers of 'Gumsura 1ho' in four *Quercus* (*Q. acutissima, Q. serrata, Q. mongolica, and Q. variabilis*), the chloroplast (cp) genome of 'Gumsura 1ho' was assembled and then the 'Gumsura 1ho' cp genome was compared with reference genome. The cp genome size exhibited 161,151bp and reveled 134 genes including 86 protein-coding genes, 40 tRNA genes, and eight rRNA genes. We also found the length and sequence differences between 'Gumsura 1ho' and reference genomes. When three insertion/deletions (indels) and four cleaved amplified polymorphic sequences (CAPS) markers were developed to confirm sequence variants of 'Gumsura 1ho' cp genome using individual collected from four *Quercus* in seed orchard, PCR product size of 'Gumsura 1ho' was differed with individual of four *Quercus*. Subsequently, SNP markers were designed for high-throughput selection of 'Gumsura 1ho' in the confirmed two SNP regions, and then 'Gumsura 1ho' was discriminated among four *Quercus*. Therefore, our results suggested that developed molecular markers could be used for discrimination of 'Gumsura 1ho' among four *Quercus*.

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PG-0023

재배지별 산양삼 판별을 위한 인델(InDel)마커 개발 및 유전다양성 분석

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산양삼의 학명은 *Panax ginseng* C.A. Meyer 로 인삼과 동일한 학명을 사용하지만 인공시설을 하지 않는 곳에서 자연상태로 재배되는 삼이다. 본 연구에서는 공개된 인삼유전체정보를 이용하여 인델마커 10종을 개발하였고 이를 이용하여 산양삼 재배지 9개소에서 수집된 95개 산양삼의 gDNA를 분석하였다. 개발된 인델마커는 10종은 엽록체DNA 3개, 미토콘드리아DNA 1개, 핵DNA 6개로 구성되어 있었다. 95종의 산양삼 DNA 다양성 분석을 위해 형광탐침이 부착된 마커를 제작하여 DNA fragment 분석기법을 활용하였다. PCR 증폭된 산물을 DNA Fragment Analyzer Automated CE System으로 분석하였다. 분석결과는 GeneMarker software를 이용하여 정리하였다. 유연관계 분석은 NTSYS-pc2.10 프로그램을 이용하여 수행하였다. 프로그램 내 옵션을 SIMQUAL로 설정하여 수행하였고 UPGMA 알고리즘을 통해 도출된 데이터를 바탕으로 SHAN 클러스터링을 거쳐 dendrogram을 작성하여 유전적 유연관계를 분석하였다. 각 마커별 가장 많이 증폭되는 allele의 빈도수(MAF)를 분석한 결과 0.40 - 0.97으로 평균 0.67를 나타냈다. 그리고 각 마커에서 나타나는 allele의 수(NA)를 분석한 결과 평균 3.2개의 allele이 있는 것으로 나타났다. 예상이형접합도(HE) 0.01에서 0.99으로 평균 0.44를 나타냈다. 다양성 요소(PIC)의 평균값은 0.34 값을 나타냈다. 따라서 본 연구에서 개발된 마커를 이용하여 향후 산양삼 품종개발 및 원산지 판별 등 유전형 분석에 활용이 가능할 것이라고 사료된다.

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PG-0024

국내 수집 땅비싸리(*Indigofera kirilowii*) 자원의 뿌리 함유 생리활성물질 함량 특성 평가

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땅비싸리(*Indigofera kirilowii*)는 한반도 전 지역에서 분포하고 있는 콩과 식물로, 그 뿌리는 토두근, 산암황기, 화목람, 산두근 등의 생약명으로 불리우고 있다. 땅비싸리의 항염증, 진통 억제, 해독 및 항암 등 생리활성 효과는 보고되고 있으나, 자생지의 생태 환경에 대한 연구나 재배와 번식 등 산업적 활용에 대한 연구는 미흡한 실정이다. 본 연구는 땅비싸리에 함유된 생리활성물질 특성을 평가하고자 국내에서 수집된 9점의 땅비싸리 자원(KJ-01 ~ KJ-09)의 뿌리로부터 항암 효능이 보고된 lupeol, oleanolic acid, ursolic acid를 비롯하여 squalene, α-tocopherol, phytosterol류 등 기능성 성분의 함량과 지방산 조성비율 등을 분석하였다. 땅비싸리 자원 9점의 뿌리 함유 lupeol 함량은 평균 50.94 μg žg^{-1}이었으며, KJ-03 자원이 가장 높은 함량(100.39 μg žg^{-1})을 나타내었다. Oleanolic acid의 경우 13.48 μg žg^{-1}(KJ-002)에서 129.67 μg žg^{-1}(KJ-05) 범위의, 그리고 평균 61.04 μg žg^{-1}의 함량 특성을 나타내었다. Ursolic acid의 경우 9점의 수집 자원 중 KJ-08(17.25 μg žg^{-1})을 포함한 3점에서는 정량분석이 가능하였으나(평균 11.38 μg žg^{-1}), 4점의 자원은 검출한계(LOD: 0.98 μg žg^{-1}) 미만, 2점은 정량한계(LOQ: 2.95 μg žg^{-1}) 미만으로 그 함량이 낮았다. Squalene, α-tocopherol, campesterol, stigmasterol, sitosterol은 9점의 자원 모두에서 관찰되었으며 각각 41.1, 28.0, 123.5, 171.5, 1258.4 μg žg^{-1}의 평균 함량을 보였다. 땅비싸리 뿌리에서는 9종의 지방산이 관찰되었으며 linoleic(58.5%), palmitic(12.8%), oleic(9.2%), linolenic(7.1%) 및 heneicosanoic(5.9%) acid의 조성비율이 상대적으로 높게 나타났다. 이상의 결과를 종합해볼 때, lupeol, oleanolic acid 및 ursolic acid의 함량이 높았던 KJ-03, KJ-05, KJ-08 자원이 식의약품 소재로의 활용 가능성이 높을 것으로 판단되었다.

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PG-0025

산양삼의 재배유형에 따른 생육특성 평가

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경상북도 영주시 풍기읍 소백로 2009 국립산림과학원 산림약용자원연구소

산양삼(*Panax ginseng* C.A. Meyer)이란 차광막 등의 인공시설을 설치하지 아니하며 화학비료와 농약을 사용하지 않고 생산하는 삼을 말하며, 2011년 시행된 [임업 및 산촌진흥촉진에 관한 법률]에 의거하여 특별관리 임산물로 관리되고 있다. 산양삼은 같은 장소에서 오랜 시간 동안 재배해야 하기 때문에 재배지의 입지환경과 산양삼 종자 파종 및 종묘 이식에 대한 방법이 중요하게 여겨지고 있다. 본 연구는 산양삼의 최적재배환경을 구명하고자 산양삼 종자 파종 및 종묘유형에 따른 산양삼의 생육특성을 조사하였다. 종자크기, 줄간격, 파종량, 종묘크기, 식재간격, 뇌두방향의 6가지 유형별로 생육특성을 조사 및 비교하였을 때, 종자크기에 따라 줄기길이와 전체중량에서 유의적인 차이가 나타났으며, 종묘크기에 따른 뿌리중량과 전체건중량에서 유의적인 차이를 보였다. 그러나, 이외의 생육특성 항목에선 유의적인 차이를 보이지 않았으며, 직파와 이식유형에 따른 산양삼의 발아율과 활착률 또한 유의적인 차이가 나타나지 않았다. 이는 입지조건에 따른 생육특성에서 줄기길이 및 뇌두길이, 주근직경, 전체중량에서 유의적인 차이를 나타낸 결과와 다르게 나타났다. 위의 결과를 바탕으로, 산양삼의 생육은 종자와 종묘의 크기를 제외한 직파와 이식의 유형에 관해서는 차이가 미미하지만, 이러한 결과는 해당연도의 기온 및 토양온도, 상대습도 등의 기후요소에 따라 달라질 수 있다. 결과적으로, 파종과 식재할 입지환경의 선정이 생육특성에 영향을 더욱 미치는 것으로 예상되므로, 산양삼 재배의 최적 조건에 부합하는 입지를 구하는 것이 중요할 것으로 사료된다.

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PG-0026

Induction of Mutant Lines from Gamma-Rays Irradiated *Gastrodia elata* Seeds

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Gastrodia elata is a significant orchid species with therapeutic value of the herbal medicine industry in the Korea and China. Plant mutant breeding has been used to increase yield and improved commercially important morphological and biochemical properties. In mutagenesis methods, gamma-rays have been successfully used for direct and indirect mutagenesis in plants. The aim of this study was to investigate the morphological mutagenesis effect of *G. elata* germinated plants by gamma-ray irradiation. The seed capsules of *G. elata* were treated with doses of 50 and 100 gamma-rays (Gy) at Korea Atomic Energy Research Institute. The symbiotic seed germination and subsequent protocorm development was performed with common method of *G. elata* at *In vitro*. Only 50 Gy irradiation seedling were used to morphological characteristics. This is because the seedlings irradiated with 100Gy didn't grow well in protocorm development. The mutant types were selected by measuring the fresh weight (g), number of branches, length of branches (cm), and width of protocorms. Two type A (R50Gy01, R50Gy07) and two type B (R50Gy09, R50Gy10) were selected according to increase in the number and length of protocorm branches, respectively. The mutant type A had an increased fresh weight and the number of protocorm branches and fresh weight compared to untreated control. On the other hand, the mutant type B had rapidly elongated the length of protocorm compared with untreated control. And then it was shown that the fresh weight was more related to the number of branches than the length of the branches. In this study, we were able to obtain the protocorms with improved growth characteristics from gamma-irradiated *G. elata* seeds. This result means that mutagenesis using gamma rays can be usefully used to improve the growth of *G. elata*.

Keywords: *Gastrodia elata*, Gamma-ray irradiation, Mutation breeding, *In* vitro

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PG-0027

Flower characteristics of the selected individuals of Korean dogwood (*Cornus kousa* Bürger ex Hance) for the development of a new ornamental cultivar

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Korean dogwood (*Cornus kousa* Bürger ex Hance) is an indigenous tree species in Korea with the high potential to develop as a landscape tree due to its beautiful flower and elegant tree shape. In order to develop a new cultivar of Korean dogwood, seeds from a total of 30 selected individuals in six regions were collected and propagated in 2005-2006. After the primary screening in 2021, flower characteristics of a total of 44 progenies were examined in May 2022. The shape and color of bracts were mainly ovate-lance and pale green, however, various variations appeared. Especially, bracts with pale yellowish white, yellowish green with the red tip and red-dotted white were showed. The average size of each bract ranged from 14.68 to 56.03 mm in length and from 8.78 to 39.46 mm in width, respectively. Although overall flower size within the same tree was similar, significant variation was showed in two individuals (no.41-5 and no.8-A3). As well, peduncle length and the number of flowers appeared to have a significant variation among selected individuals. In addition to tree shape and leaf characteristics, these flower traits can be used as fundamental data for the development of a new ornamental cultivars.

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PG-0028

대추나무 유전자원의 종자 특성에 관한 연구

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대추나무(*Ziziphus jujuba*. Mill)는 내과피가 경화되어 핵을 형성하는 핵과류로, 핵 안에 종자를 가진다. 대추에 종자가 없는 것은 단위결과에 의한 것으로 알려져 있는데, 품종에 따라 수정 방법이 다르며, 자가불임성을 가진다. 생과, 건과로 이용되는 일반대추와 왕대추는 핵만 있고 종자가 거의 생성되지 않지만 한방에 주로 사용되는 묏대추는 대부분 종자가 형성된다. 한의학에서 '산조'품종의 종자는 Spinosin을 함유하고 있어 심신안정, 수면장애 개선 등의 약재로 사용된다. 연구소가 보유하고 있는 대추 자원의 종자 특성 및 인(仁) 형성여부를 조사하여 산업 소재화 및 교배육종의 기초자료로 활용하고자 본 연구를 수행하였다. 대추호두연구소가 보유하고 있는 대추 유전자원 중 CBJ0002(Jc-28a), CBJ0072(천황) 등 50자원에 대한 종자 특성을 조사하였다. 2018년부터 2021년까지 결실한 과실을 대상으로 연차별(2~4년)로 조사하였다. 종자 형성률이 높은(70%↑) 자원은 CBJ0079(마반조), CBJ0006(Jd-10) 등 25자원이며, 종자 형성률이 낮은(30%↓) 자원은 CBJ0038(천상), CBJ0166(광암) 등 20자원으로 조사되었다. 함인율의 연차별 비교 시 차이를 보이는데 이는 종자 형성에 있어 기상 등 환경적 요인의 영향을 많이 받는 것으로 보인다. 대추에는 saponin의 일종인 jujuboside B를 함유하고 있어 피부 미백효과 등 화장품 소재로 활용가치가 높으나 종자에 대한 기초 연구조사가 많지 않다. 종자 형성률이 높은 자원을 대상으로 성분함량 분석 등을 통하여 산업 소재화 및 교배육종에 기초자료로 활용 가능할 것으로 기대된다.

사사: 본 연구는 농촌진흥청 지역특화작목 기술개발(연구과제명: 대추 안정생산 관리모델 및 소비확대를 위한 산업화 기술개발, 과제번호: PJ016147)의 지원으로 수행되었음

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PH-0001

Identification of *TaF-box2*, a wheat floret development related F-box encoding gene, confers positive regulation of *Arabidopsis* flowering

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The floret development stage in wheat (*Triticum aestivum* L.) is a key process in determining grain production per spike. In this study, we identified the involvement of TaF-box2, a member of the SCF (Skp1-Cul1-Rbx1-TaF-box2) ubiquitin ligase complex, which is involved in reproductive stages of floret development (Waddington scale W2.5 to 10). In addition, *in vitro* ubiquitination assays demonstrated that the $SCF^{TaF\text{-}box2}$ complex possessed a F-box domain that confers ligase functionality. Transgenic *Arabidopsis* plants that constitutively expressed the *TaF-box2* gene had markedly greater hypocotyls and roots length, and grew more rapidly than the WT, leading to an early flowering phenotype. Moreover, the nucleus expressed protein TaCYCL1 (CYCLIN-L1) physically interacted with TaF-box2 in nucleus. We further verified that $SCF^{TaF\text{-}box2}$ ubiquitinated TaCYCL1, causing protein degradation *via* Ub/26S proteasome pathway. Our study will help to improve physiological process of floret development and flowering time in wheat. (Published: *Physiologia Plantarum* **174**)

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PH-0002

Mutation of light signal transduction machinery affects pericarp pigmentation and embryo development in rice grain

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Light is a crucial signaling component that controls a variety of physiological and developmental processes in morphogenesis, germination, metabolic alterations, and flowering in plants. Here, we identified four *yellowish-pericarp embryo lethal* (*yel*) mutants from four different *japonica* cultivars of rice (*Oryza sativa* L). Mutant seeds had yellowish pericarps and exhibited embryonic lethality, with significantly reduced grain size and weight. Genetic analysis and mapping revealed that the phenotype of the *yel* mutants was controlled by an ortholog of *Arabidopsis thaliana CONSTITUTIVE PHOTOMORPHOGENIC 1* (*COP1*) or *DE-ETIOLATED 1* (*DET1*). Seeds of the rice *cop1* and *det1* knockout mutant, generated via CRISPR/Cas9-based gene editing, displayed the *yel* mutant phenotype. Moreover, the knockout seeds of CONSTITUTIVE PHOTOMORPHOGENIC 10 (OsCOP10) and UV-DAMAGED DNA BINDING PROTEIN 1 (OsDDB1) which form the COP10-DET1-DDB1 (CDD) complex together with OsDET1 also showed the yel phenotype. Comparative transcriptome analysis revealed that genes involved in the *C*-glycosyl flavone biosynthesis pathway, including transcription factor, *OsP1*, were activated, whereas anthocyanin biosynthesis genes showed no significant change in expression. Consistent with these results, the level of *C*-glysocyl flavones such as isoorientin and isovitexin was dramatically increased in the *yel* grain. In addition, transcript levels of embryo development-related genes, especially homeobox and auxin regulation genes, as well as somatic embryogenesis-related genes, were significantly downregulated in the developing seed of *yel* mutant. Taken together, these results indicate that *OsCOP1* and *OsDET1* play a crucial role in regulation of flavonoid biosynthesis and embryo development, and the alteration in the light signal transduction could have a significant effect on pericarp pigmentation and embryogenesis in rice seed.

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PH-0003

Novel Sucrose Transporter Genes Identification and Functional Characterization in *Triticum aestivum*. L.

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The primary distinguishing feature of autotrophs from other organisms is its ability to synthesize its own food hence, placing them at the primary levels of food chain. A particularly vital component between the production and utilization of energy is the transportation of the made sugars to the required cell destination in the form of sucrose. This function is actively performed by the plant's sucrose transporters. The purpose of this study is to identify the unidentified sucrose transporters in *Triticum aestivum L.*, understand its working model and to also to attempt to fill in some blanks in regard to the continued work on wheat. *TaSUT1* and *TaSUT2* are two previously recognized and published *TaSUT* genes, while *TaSUT3, TaSUT4, TaSUT6*, and *TaSUT7* were discovered in this study. *TaSUT5* was shown to be a pseudogene due to mutation. RNA sequencing data was also analyzed to see the expression levels of the *TaSUT*s. Moreover, in order to verify interactions between and within the *TaSUT* genes, Yeast II Hybridization assay was performed. Subcellular localization studies were also conducted. Energy production, distribution, and utilization mechanisms can be determined from this research, and future research on modifying these mechanisms for the development of a better wheat cultivar with higher yields can be conducted.

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PH-0004

Wheat (*Triticum aestivum*. L) U-box E3 Ubiquitin Ligases positively regulates drought stress in *Arabidopsis*

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The Plant U-box E3 ligase (PUB) is an important regulator that controls the number of stimuli that trigger an abiotic stress response. However, the cellular mechanism of U-box protein against abiotic stress in wheat has not been well investigated. In our research, we isolated two genes, *TaPUB2* and *TaPUB3*, which were highly induced to drought stress responses in wheat. Moreover, molecular analysis confers that TaPUB2 and TaPUB3 was co-localized in the Golgi apparatus of wheat protoplasts cells and possessed E3 ligase activities functionally. The heterodimeric complex formed by TaPUB2 and TaPUB3 was confirmed by yeast two-hybrid and bimolecular fluorescence complementation assays. Furthermore, the *Arabidopsis* plants overexpressing *TaPUB2* and *TaPUB3* exhibited to drought stress tolerance and an increase in their germination rates and root lengths compared to the wild type plants, respectively. According to our findings, wheat U-box E3 ligases encodes genes, *TaPUB2* and *TaPUB3*, would respond positively to abiotic stress, particularly drought. [Published: *International Journal of Molecular Sciences*, **22**(24)].

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PH-0005

Effects of CO_2 supply on growth and antioxidant activity of fennel (*Foeniculum vulgare* Mill.)

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The *Foeniculum vulgare* Mill. known as fennel is a perennial herb in the family Apiaceae and was used for plant extract with functional materials. This study was conducted to investigate the growth effect of fennel by supplying CO_2 with 400ppm and 800ppm. We identified the increased growth regarding plant length and stem diameter in fennel under 800ppm by compared to 400ppm-treated plants. Also, we observed the various changes of environment and nutrient solution for hydroponics by CO_2 supply. The mRNA levels of genes associated with photosynthesis, lipid metabolism, and flavonoid biosynthesis were deferentially expressed in 800ppm-treated plants. In particular, the several genes involved in flavonoid biosynthesis were upregulated by 800ppm treatment. To observe the distinct effects of secondary metabolites by CO_2, we analyzed the antioxidant activity regarding phenol, flavonoid, DPPH, nitrite scavenging activity, reducing power, and FRAP in fennel extracts. Interestingly the total flavonoid content was increased in the 800ppm-treated plants, while others were decreased. We have confirmed the reliable anti-inflammatory effects of fennel extracts by MTT assay. This study may provide a better understanding of CO_2 effects regarding antioxidant activity in fennel.

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PH-0006

Effects of organic liquid fertilizers from livestock manure on plant growth, antioxidants, and soil microbial population for Chinese cabbage (*Brassica rapa* subsp. *Pekinensis*)

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Livestock excretion is one of the leading causes of environmental pollution all over the world. Therefore, the proper use of manure by recycling waste brings advantages in economic and environmental aspects. This study aims to evaluate the diverse effects (plant growth, antioxidant activity, and soil microbial population) of organic liquid fertilizers in Chinese cabbage (*Brassica rapa* subsp. *Pekinensis*). We used three types of liquid fertilizer such as chemical liquid fertilizer (CLF), fermented liquid manure (FLM) made from pig dropping, and liquid Bio-fertilizer (LBF) made from the Chlorella culture medium for experiments. We observed the highest plant growth regarding plant length, chlorophyll contents (SPAD), the width and length of leaves, and the fresh and dry weight in CLF-treated plants. The LBF led to improve the plant development compared to FLM. Especially, we found the increased photosynthetic efficiency in the chlorophyll contents and color measurements of plants by the addition product of Chlorella. Interestingly, the LBF affects to substance increases regarding the sugar, Vitamin C, and antioxidants in Chinese cabbage compared to other fertilizers. For example, we observed the highest values of the total content of polyphenol and flavonoid, antioxidant activity, nitrite-scavenging capacities, and reducing power in LBF-treated plants. To survey the soil microbial changes by liquid fertilizers, we conducted 16S rRNA sequencing. In the amplicon sequence variants (ASVs) analysis, we have identified the increased formation of bacteria by supplying liquid fertilizers. The LBF had the highest bacterial diversity compared to others. Finally, we found significant changes in the bacterial population, for example, the presence of phylum *Verrucomicrobia* was increased in soils after FLM and LBF treatments. The LBF-treated soils had a high formation of phylum *Proteobacteria* compared to FLM. These results will provide useful information to understand the diverse effects of organic liquid fertilizer on plant growth and soil microbial formation.

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PH-0007

Soybean Cultivar 'Saedanbaek' possesses a resistance allele to *Phytophthora sojae*, distinct from that of the cultivar 'Daewon'

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Phytophthora root and stem rot is an important soybean disease that causes economic losses worldwide. Disease management has been based on using soybean cultivars with *Rps* (Resistance to *Phytophthora sojae*) genes. The present study aimed to identify a major gene locus conferring resistance to *P. sojae* isolate 2858 in the recombinant inbred line (RIL) population of Daepung (susceptible) × Saedanbaek (resistant). Seventy-three RILs of the population were evaluated for the resistance against *P. sojae* isolate 2858. Via single-marker analysis with 26,130 polymorphic single nucleotide polymorphisms (SNPs), adjacent 28 SNPs on chromosome 3 were highly significant, indicating association with the resistance (R^2=~82%). Linkage mapping identified a 921-Kbp region (3.3–4.2 Mbp) on chromosome 3, explaining 93% of phenotypic variance (LOD=38.7). Based on soybean Williams 82 reference genome (Glyma2), there are seven leucine-rich repeat coding genes and one serine/threonine protein kinase-coding gene annotated in the identified region, which are well-known types of genes for conferring disease resistance in crops. Although this interval is adjacent to the known *Rps* locus in the cultivar Daewon against *P. sojae* isolate 2457. Additional phenotypic assays showed that Saedanbaek was susceptible to isolate 2457 and Daewon was susceptible to isolate 2858. Consequently, Saedanbaek should possess a different resistance gene to the *P. sojae*, distinct from that of Daewon. For further studies, qRT-PCR will be conducted to investigate differential expression of annotated genes in this region.

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PH-0008

가축분뇨를 이용한 친환경 바이오액비의 토마토 생육 및 생리적 효과

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한정적인 자원으로 인해 지속가능한 농업이 필요한 현재 가축 농가에서 발생하는 축분으로 인한 환경오염은 큰 문제로 대두되고 있으며, 이를 자원으로써 활용한 경축순환 농업은 유기농업의 지속가능성을 실현한다는 점에서 매우 의미가 있다. 본 연구는 토마토의 수경재배에 있어 연구를 위하여 개발한 돈분 정제액비, 클로렐라 바이오액비의 작물 생육에 대한 효과를 곁순제거, 간격, 계분, 무처리 등의 다양한 재배 방법에서 평가하였다. 엽장과 엽폭, 경경, 과실수의 경우 화학양액에서 높은 평균 수치를 보였고 이후 바이오액비, 정제액비 순으로 나타났다. 초장의 경우 바이오액비 처리구간이 높은 평균 수치를 보였고 화학양액, 정제액비 순으로 나타났다. 엽록소 함량의 경우도 위와 마찬가지로 시판용 화학양액에서 가장 높은 수치를 보였으나 바이오액비와 정제액비에서 유의미한 차이는 보이지 않았다. 수경재배 시 배지의 계분퇴비 시용이 토마토의 생육변화에 영향을 미치는지 조사한 결과, 계분비료 처리구와 무처리구 사이의 유의미한 차이는 관찰되지 않았다. 광합성과 과실 및 잎의 발달에서는 시판용 화학양액이 높은 생육효과를 나타냈다. 바이오액비의 경우 토마토의 신장에 관해서 생육 증진의 효과를 보였다. 그러나, 잎의 발달에서는 정제액비와 유의미한 차이를 보이지 않았다. 다양한 재배방법에서 곁순제거를 한 토마토에서 과실의 높은 수량성을 나타내었다. 항산화활성 실험에서 바이오액비의 상대적으로 높은 수치를 확인하였다. 이러한 결과는 가축분뇨의 자원화를 통한 경축순환 농업에서 토마토 재배에 대한 적용가능성과 재배 방법에 대한 유용한 정보를 제공할 것이다.

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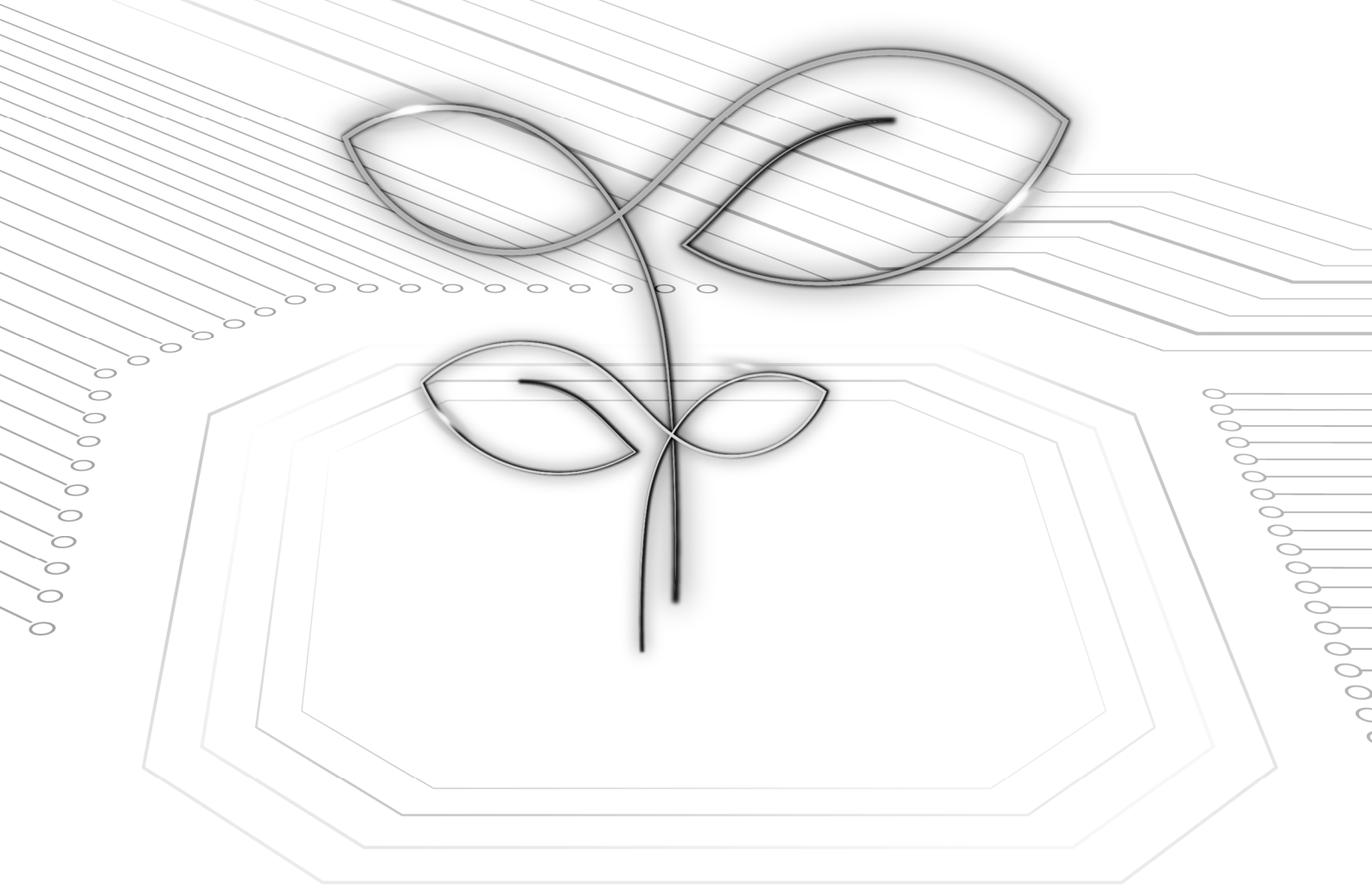
Special A.
국립농업과학원 발표
「디지털 육종 추진전략」



SA-0001

디지털육종 추진전략

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[4]전라북도 완주군 이서면 농생명로 100 국립원예특작과학원
[5]전라북도 완주군 이서면 콩쥐팥쥐로 1500 국립축산과학원

최근 육종은 생명공학 뿐 아니라 빅데이터, 인공지능 등 디지털 기술이 함께 활용되는 융복합 기술로 고도화가 가속되고 있다. 글로벌 종자기업은 생명공학과 첨단 융복합기술 접목을 통한 디지털 육종시스템의 선제적 구축으로 글로벌 종자 시장을 지속 선점하고 있다. 국내의 경우 생명공학 기술을 활용한 품종개발은 기술력 확보에도 불구하고 아직 상업화 단계에는 이르지 못한 상태이며, 디지털육종의 경우는 아직 연구개발 초기 단계라고 분석되고 있다. 농진청과 대학 그리고 일부 종자회사의 경우 「차세대바이오그린21사업」과 「다부처유전체사업」 등을 통해 농생명체 오믹스 데이터 생산, 유전체와 표현체 연관분석 등 유전체육종 기반 구축 및 디지털육종 전환에 노력 중이나, 일부 종목을 제외하고는 육종현장에 적용하기엔 기술의 완성도나 실효성이 아직 미흡한 상태이다. 이와 같이 디지털 육종기술이 現 육종현장에 전면 적용까지는 시간이 필요하지만, 기존 육종기술의 한계를 극복하고 향후 종자산업의 혁신과 미래형 산업으로의 발전 도모에는 절대적으로 필요한 기술이라는 것에 대부분의 전문가들이 동의하고 있다. 이런 관점에서, 글로벌기업 중심의 선진국과의 디지털육종 기술격차 해소를 넘어 향후 차세대 선도기술 확보를 위해서는, 디지털육종 과정별 핵심기술과 인프라 확보 및 실시간 기술지원 가능한 통합 디지털육종 기술지원 플랫폼 구축이 필요하다. 이를 위해서는 산학관연이 함께 참여하는 국가 디지털육종 종합계획 수립과 함께 이를 효율적으로 추진할 전략 공유가 매우 중요할 것이다. 이에 현재 진행 중인 국가 디지털육종 연구개발 계획에 대해 학계와 종자산업 전문가들의 검토와 함께 향후 주진 계획에 대한 다각적 논의를 통해, 디지털육종 시대를 대비할 국가 차원의 보다 실효성 있는 종합전략 수립 마련에 대한 논의를 하고자 한다.

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Special B.
강원대학교 농업생명과학연구원 발표

SB-0001

첨단 디지털 기술을 적용한 작물 육종 연구 현황

황현승*

제주특별자치도 제주시 한라대학로 38 제주 한라대학교 생명 자원학부

2022년 현재 지구의 인구는 80억까지 증가하여 식량의 안정적 생산이 중요하지만, 농경지의 지속적인 감소, 농업인구의 감소 및 고령화, 작물 생산에 필요한 물과 에너지는 충분하지 않은 상황이다. 지속 가능하며 안정적으로 농업 생산성을 높이기 위해 첨단 과학 기술의 농업 적용은 이제는 필요가 아닌 필수가 되었다. 인공지능과 빅데이터 분석 기술, 자율 주행 모빌리티, 각종 로봇 기술의 발전을 이용하여 경험적 노하우에 기반을 둔 농업이 아니라 과학적인 디지털 데이터에 기반을 둔 농업으로의 전환이 이뤄지고 있으며, 재배 기술을 포함하여 토양관리, 물관리, 온실의 제어 등 농업 전 분야에 다양한 첨단 디지털 기술이 적용되고 있다. 작물의 육종 연구 또한 피노믹스 데이터를 활용한 디지털 육종 기술 개발 및 실용화 등 경쟁력 있는 품종 개발을 위해 첨단 디지털 기술을 접목하고 있다. 본 발표에는 현재 국내외 첨단 디지털 기술의 연구 사례와 환경 변화, 기술 개발 방향 및 향후 전략을 포함하였다.

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SB-0002

옥수수 육종의 현재, 그리고 디지털육종으로의 전환

류시환*, 왕승현, 남궁민, 김문종, 한정헌, 최재근, 김희연, 김기선

강원도 홍천군 두촌면 장남길 26, 강원도농업기술원 옥수수연구소

국내 옥수수 육종이 본격적으로 시작된 1960년대 이후 204개의 품종 및 계통이 국립종자원에 품종보호 출원 및 등록되었다. 많은 품종이 육성되었으나 실용화 및 다양성 차원에서는 부족한 상황이다. 또한 거의 모든 품종이 전통적인 육종방법에 의해 육성되었으므로 신기술을 바탕으로 육종한 품종은 전무하다고 할 수 있다. 단, 강원도농업기술원 옥수수연구소에서 배가반수체 기술을 이용하여 육종한 계통인 DHF1, DHW1과 단교잡종 황금옥 등 3개 정도만이 신기술과 연관되어 있다. 국내에서 전통적인 육종방법으로 집단육종, 계통육종, 교배육종, 여교잡육종, 돌연변이육종 등이 활용되었으며, 국외 선진국을 중심으로 새로운 육종방법인 sequencing, genotyping, transformation, 배가반수체, 유전체정보 활용 등이 실용적으로 이용되고 있다. 현대의 품종육성은 상품성이 우수한 품종을 단기간에 육종하는 방법에 중점을 두고 있다. 동계기간 열대지방에서 세대촉진은 전통적인 육종기간 단축의 좋은 예이다. 최근 배가반수체 기술 도입으로 계통의 육종기간이 획기적으로 단축되었다. 배가반수체 기술은 육종기간의 단축과 더불어 대량의 계통을 육종할 수 있는 방법이다. 따라서 육성한 계통 중에서 활용성이 높은 우수한 계통을 조기에 선발하는 것이 필수적이며 이는 전통적인 방법으로 해결하기 어려운 분야이므로 디지털육종이 절실히 필요한 상황이다. 디지털육종은 생물정보를 수집하고 big data 분석을 통하여 양적형질 유전자를 탐색하고 육종예측 모델을 개발하여 실용화하는 과정으로 요약할 수 있다. 국내에서 옥수수를 이용한 디지털육종은 시작되지 않은 상황이므로 이제 걸음마 단계라고 할 수 있다. 따라서 디지털육종을 위한 핵심집단 구축, 핵심집단을 기반으로 하는 표현형 및 유전형 데이터 수집, 축적된 big data를 활용한 데이터 분석 및 선발모델 개발 등이 순차적으로 진행되어야 한다. 옥수수는 시작단계라서 디지털육종의 데이터 축적, 시스템 확립, 선발에 적용 및 실용화 등에 타 작물보다 더 많은 시간과 노력이 소요될 전망이다. 그러나 고기능성, 기후변화 대응 내재해성, 내병성, 색의 다양성, 식량안보 대응 등 향후 육종목표의 달성과 전통육종의 한계 극복을 위해 반드시 개척해야할 분야임은 분명하다.

사사: 본 연구는 기관고유사업(배가반수체 기술을 이용한 계통육성, LP0034302022)의 지원에 의해 이루어진 것임

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SB-0003

A case study of invasive pest, fall armyworm *Spodoptera frugiperda*, in corn field

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The fall armyworm, *Spodoptera frugiperda*, originated in America. In addition, this pest was first detected in Africa in early 2016 and has been become one of the most invasive lepidopteran pests in worldwide. In Korea, *S. frugiperda* was first observed in cornfields at Jeju in early June 2019, end of May 2020, and mid-May in 2021 and 2022. The migration of this pest has been fastened, but there are limitations to simple and accurate diagnostic methods for the identification of this species in the field. Diagnostic tools to identify *S. frugiperda* are urgently needed because farmers and agricultural managers have no prior experience with this pest. Species-diagnostic primers were designed and applied in a loop-mediated isothermal amplification (LAMP) assay to identify field-collected samples of *S. frugiperda*. The optimal incubation conditions for the LAMP assay were 61°C for 90 min with four LAMP primers. We used with a DNA-releasing technique for larval and adult samples, without a DNA extraction step, by incubating the tissue sample at 95°C for 5 min. Based on the field collection of *S. frugiperda*, a appearance of this pest was different among the corn varieties. Therefore, we compared the fitness difference (survival rate, S_{xj}) from six different corn varieties (미백2호, 흑점2호, 오륜2호, 오륜팝콘, 미흑찰, 드림옥) which are the most universal in Kangwondo. Results show that there was the difference in fitness among the six corn varieties, which 미백2호 and 드림옥 were revealed as the most nutritive and preferred host plants. These studies will be a resource for future ecological studies and intensive field monitoring of *S. frugiperda*.

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SB-0004

Genome-wide and physiological assays of a rice *drought-insensitive TILLING line 1* (*ditl1*) mutant

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

Climate change is having a critical impact on agriculture production in many countries. Drought, a consequence of climate changes, is the most severe abiotic stress reducing rice yield, especially in Korea. We previously developed 150 rice M_{10} mutant lines using gamma-ray irradiation, and a drought-insensitive rice mutant (*ditl1*) was selected. The *ditl1* mutant showed significantly decreased water loss, leaf curling, and H_2O_2 accumulation. Toluidine blue staining and chlorophyll leaching assay demonstrate that the *ditl1* mutant has a drought insensitive phenotype by the low cuticle permeability against water loss. The higher cuticular wax accumulation on the epidermal surface in *ditl1* mutant than in wild-type plants was detected by transmission electron microscopy. Whole-genome resequencing analysis suggests that the deletion of a single nucleotide on *LOC_Os05g48260* gene, which is a putative ortholog of *WSD1* (wax ester synthase/diacylglycerol O-acyltransferase in Arabidopsis), maybe be the key candidate gene increased the drought insensitive phenotype of the *ditl1* mutant. The developed *ditl1* mutant will be a valuable genetic source for enhancing drought stress tolerance in rice breeding programs.

Acknowledgement: This work was supported by a grant from “Cooperative Research Program for Agriculture Science and Technology Development (Project No. PJ0159002022)’’ Rural Development Administration, Republic of Korea and by Basic Science Research Program through the National Research foundation of Korea (NRF) founded by the Ministry of Education (2021R1A 6A1A0304424211).

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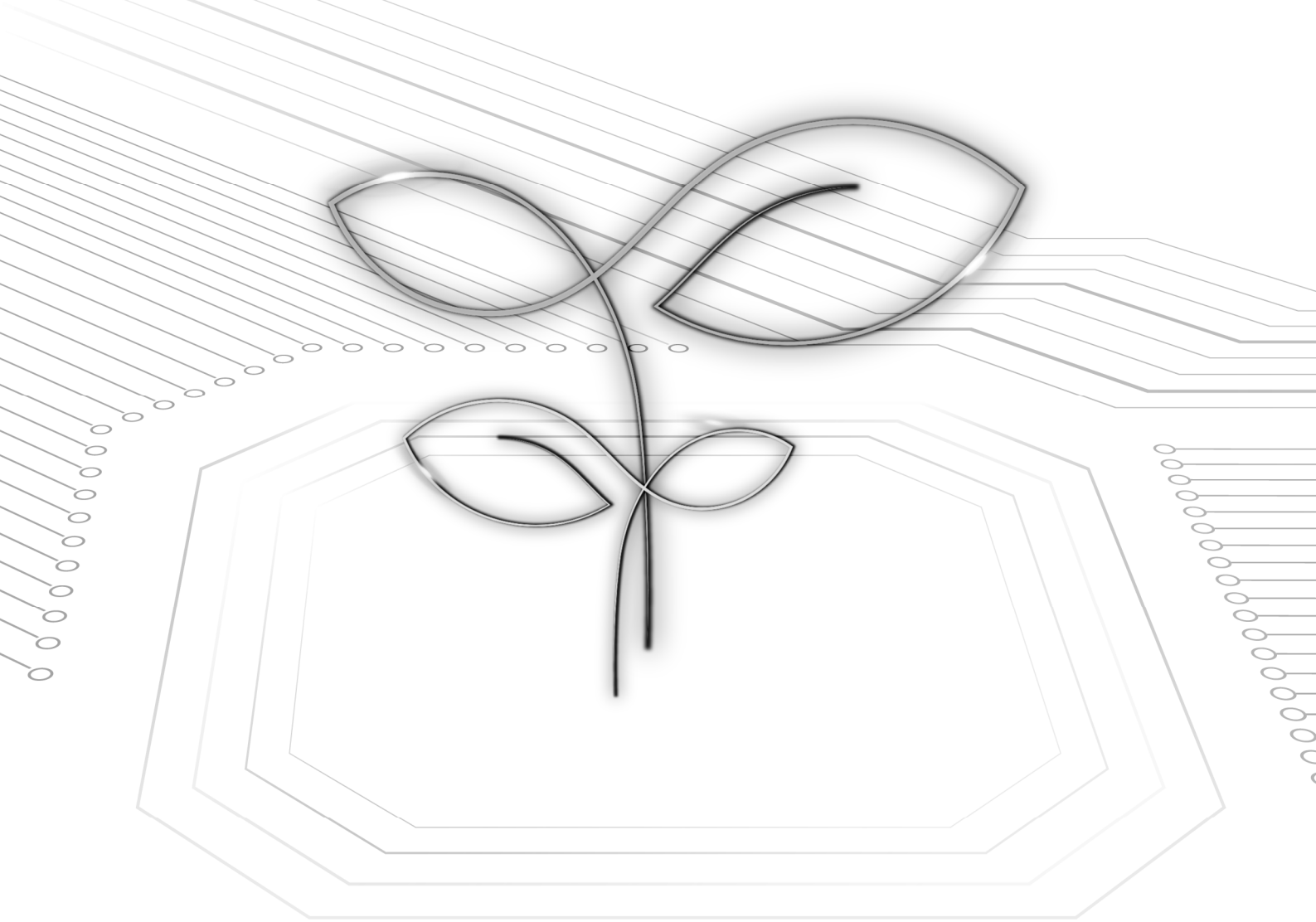
2022년 한국육종학회 학회상 시상

The Korean Society of Breeding Science's Award



2022년 한국육종학회 학회상 시상
The Korean Society of Breeding Science's Award

ㅇ 시상일 : 2022년 6월 30일(목)

ㅇ 장　소 : 라마다프라자 제주호텔, 9시 30분~

ㅇ 시상내용

1. 한국육종학회상 연구상 (36호)

수상자	이준대(전북대학교 농업생명과학대학)
수상내용	Identification of Interspecific and Intraspecific Single Nucleotide Polymorphisms in *Papaver* spp. (Plant Breed. Biotech. 2021;9:55-64)
포상내용	상장 및 부상 100만원 (한국육종학회)

2. 한국육종학회상 품종상 (32호)

수상자	이지윤(농촌진흥청 국립식량과학원)
품종명	금강1호(벼), 품종등록번호 제 7686호
논문제목	자식계 벼 품종 중 생산성이 세계 최고인 "금강1호"를 개발하여 쌀 수량성 증대와 육종기술 발전에 크게 기여함
포상내용	상장 및 부상 200만원 (한국육종학회)

3. 우수논문상 다피인용부문

- 한국육종학회지 -

수상자	박수철(농촌진흥청 국립농업과학원)
논문제목	유전자교정 농작물의 실용화 현황 및 전망 (Korean J Breed Sci 2019;51(3):175-183)
포상내용	상장 및 부상 50만원 (한국육종학회)

- Plant Breeding & Biotechnology -

수상자	지현소(농촌진흥청 국립농업과학원)
논문제목	Kompetitive Allele-Specific PCR Marker Development and Quantitative Trait Locus Mapping for Bakanae Disease Resistance in Korean *Japonica* Rice Varieties (Plant Breed. Biotech. 2019;7:208-219)
포상내용	상장 및 부상 50만원 (한국육종학회)

4. 우수논문상 다수논문게재부문

- 한국육종학회지 -

수상자	안억근(농촌진흥청 국립식량과학원)
포상내용	상장 및 부상 50만원 (한국육종학회)

- Plant Breeding & Biotechnology -

수상자 진중현(세종대학교 스마트생명산업융합학과)

포상내용 상장 및 부상 50만원 (한국육종학회)

5. 농우육종학회상 (12호)

수상자 박기진(강원도농업기술원)

수상내용 다수의 고품질 찰옥수수 품종을 개발하여 국내 찰옥수수 생산, 보급에 크게 기여함으로써, 육종 분야 학문과 종자산업 발전을 위해 크게 공헌함

포상내용 상장 및 부상 500만원 (농우바이오)

6. 코레곤품종상 (7호)

수상자 신서호(전라남도농업기술원)

품종명 새청무(벼), 품종등록번호 제 7276호

수상내용 고품질 밥쌀용 품종 "새청무"를 육성하여 전남지역 대표 품종으로 정착시켜, 재배면적 확대와 쌀소비에 기여함

포상내용 상장 및 부상 200만원 (코레곤)

7. 월드그린시드피아 육종상 (3호)

수상자 박용진(공주대학교 산업과학대학)

수상내용 벼 핵심집단 구축 및 유전체 연구를 통해 벼 유전체 육종 기반 확립과 민간 육종기업과 협력하여 프리미엄 향미품종 개발을 통하여 육종기반 구축과 농산업 발전에 크게 공헌함

포상내용 상장 및 부상 1,500만원 (월드그린, 시드피아)

8. 월드그린시드피아 젊은육종가상 (5호)

수상자 한고은(농촌진흥청 국립원예특작과학원)

수상내용 주요 원예작물의 유용형질 조절 유전인자 탐색 및 대량 마커 개발 등 종자 산업의 발전을 위해 우수한 성과를 이루었으며 미래 한국육종 발전을 견인할 젊은 과학자로 인정함

포상내용 상장 및 부상 500만원 (월드그린, 시드피아)

9. 월드그린시드피아 젊은육종가상 (6호)

수상자 김백기(서울대학교 식물유전체육종연구소)

논문제목 고식미 및 유색미 품종육성을 통한 쌀 산업 고부가가치화에 기여하였고, 벼 품종육성을 위한 다양한 연구에 우수한 성과를 이루어 미래 한국 육종분야 발전을 견인할 젊은 과학자로 인정함

포상내용 상장 및 부상 500만원 (월드그린, 시드피아)

10. 한국육종학회 공로상

양태진(서울대학교), 34대 한국육종학회장

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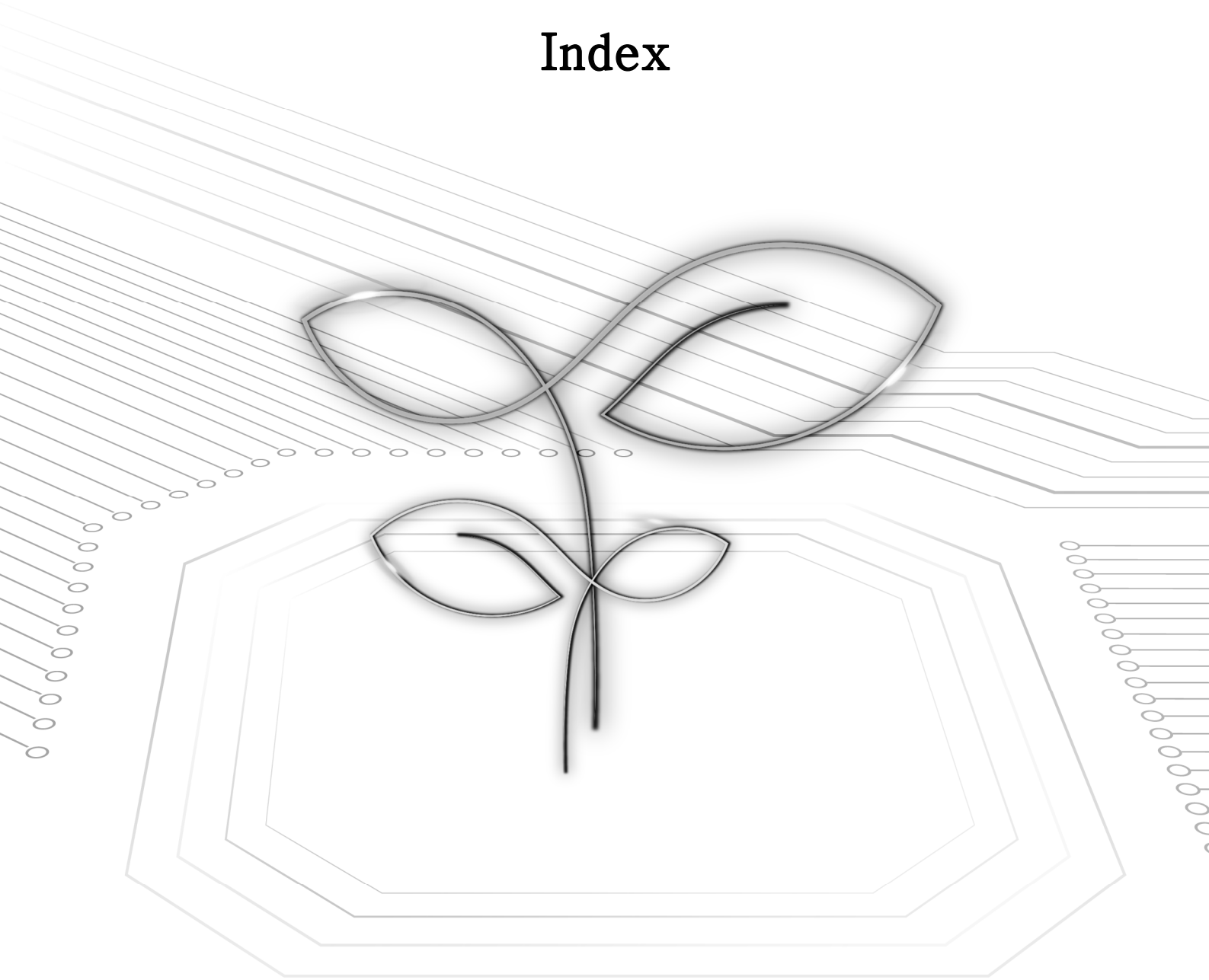

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