2023 KSBS International Conference on

Plant Breeding Strategy for Seed Industry Growth

June 28 (Wed) - 30 (Fri), 2023 / Ramada Plaza Jeju Hotel

종자산업 발전을 위한 작물육종 전략

Co-organized by
The Korean Society of Breeding Science
New Breeding Technology Center
Plant Genomics and Breeding Institute
Vegetable Breeding Research Center

Sponsors by
The Korean Association of Societies for Agriculture, Food, and Life Sciences
The Korean Federation of Science and Technology Societies

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

사단법인 한국육종학회 The Korean Society of Breeding Science

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Editorial Committee

Soonwook Kwon	Pusan National University	Joohyun Lee	Konkuk University

Office Address

(16429) 126, Suin-ro, Gwonseon-gu, Suwon-si, Gyeonggi-do, Republic of Korea
TEL +82-31-296-6898 EE-mail koreabreed@hotmail.com Web http://www.breeding.or.kr

"본 사업은 기획재정부의 복권기금 및 과학기술정보통신부의 과학기술진흥기금으로 추진되어 사회적 가치 실현과 국가 과학기술 발전에 기여합니다."
This work was supported by the Korean Federation of Science and Technology Societies(KOFST) Grant funded by the Korean Government.

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2023년 한국육종학회 조직위원회

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경기도 수원시 권선구 수인로 126 국립식량과학원 중부작물부 내 (16429)
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[Opening Address]

The Korean Society of breeding science will hold the 2023 regular academic conference from June 28th to 30th at the Jeju Ramada Plaza Hotel in Jeju City. This conference is jointly held with New Breeding Technology Center, Plant Genomics and Breeding Institute in Seoul National University, and The Korean Association of Socienties for Agriculture Food and Life Science and The Korean Federation of Science and Technology Societies were sponsored.

The main topic of this conference is “Plant Breeding Strategy for Seed Industry Growth”. Compared to the past few years of academic conferences that focused on breeding methods for developing excellent varieties, this conference focused on the industrialization of developed varieties. Therefore, at this conference, we would like to provide a forum for discussion on technology development, breeding targets, and seed distribution programs to activate variety industrialization. To this end, 5 domestic and foreign speakers were invited to the Plenary Session, and 42 speakers were invited to 10 concurrent sessions to hear and discuss the latest research results. In addition, academic exchanges will be made through a large number of poster presentations. In particular, this year, a Breeding Commercialization (breeding industrialization) concurrent was newly established and the Forestry Division became independent to prepare a more substantial and in-depth discussion.

I am very pleased to be able to hold a face-to-face academic conference this year again, and I hope that the academic conference will be successful with active participation and heated discussions from members.

I would like to express my sincere gratitude to the many people who helped make this conference a success.

Organizing Committee Chairman
Sungtaeg Kang

[Welcoming Address]

Korean Society of Plant Breeding has made significant contributions to the academic development of plant breeding and the advancement of the seed industry over the past 50 years since its establishment in 1969. Currently, it has evolved into one of the foremost agricultural societies in Korea, with a membership of over 1,000 professionals consisting of breeders and individuals engaged in related tasks from universities, national research institutes, and seed companies.

The Korean Society of Plant Breeding has been actively involved in disseminating genetic and breeding knowledge, which forms the fundamental basis for crop improvement and breeding, thereby promoting the progress of plant breeding in our nation. By extending this knowledge to the field of seed industry, it has contributed significantly to the development of plant breeding in Korea.

Advanced countries are allocating substantial budgets to the development of cutting-edge breeding technologies such as biotechnology, genomics-based breeding, and gene editing, resulting in a growing academic and technological gap between them and our country. However, we face challenges in securing budgets for large-scale government initiatives such as the Next-Generation Bio-Green Business and the Golden Seed Project. Moreover, while countries like Japan are commercializing genetically edited varieties without categorizing them as genetically modified organisms (GMOs), the seed industry in Korea is facing difficulties due to pending legislation in the National Assembly that classifies genetically edited varieties as GMOs. In order to overcome these challenging circumstances and ensure continuous progress in academia and industry, it is imperative for us to pool our collective wisdom.

Since its inception, the Korean Society of Plant Breeding has been actively organizing annual regular academic conferences, serving as a platform for fruitful collaboration and information exchange between crop breeding research teams. This year, we are hosting an academic conference under the theme "Plant Breeding Strategy for Seed Industry Growth." The objective is to gain insights into the contributions of developed varieties to the advancement of the seed industry.

I extend our sincere gratitude to President-elect Sungtaek Kang, Professor Sim Sung-Chur, and the members of the academic divisions for their dedicated efforts in preparing for the conference. Although the schedule spans just one night and two days, we hope that it will serve as a vibrant arena for academic discourse, exchange of ideas, and productive discussions. Thank you.

President of Korean Society of Breeding Science
Byoung-Cheorl Kang

2023 KSBS International Conference

Plant Breeding Strategy for Seed Industry Growth [종자산업 발전을 위한 작물육종 전략]

June 28~30, 2023, Jeju Ramada Plaza Hotel

June 28, 2023		
17:00~18:00	KSBS Committee Meeting	(Ramada Ballroom)

June 29, 2023		
09:00~09:30	Registration, Poster 'odd number' attachment	(Lobby)
09:00~10:30	**KSBS General Meeting & Award**	(Ramada Ballroom)
10:30~10:40	**Opening Ceremony**	
	Chair: Jong-Wook Chung (Secretary General)	
	Opening Address: Sungtaeg Kang (Chairman of the Organizing Committee)	
	Welcoming Address: Byoung-Cheorl Kang (President of the The KSBS)	
10:40~12:40	**Plenary Session 1**	(Ramada Ballroom)
	Chair: Tae-Jin Yang (Seoul National University)	
(10:40~11:20)	PS-01 Peter van Dijk (Keygene, Netherlands) Apomixis: Plant Breeding Technology of the 2020s	
(11:20~12:00)	PS-02 Ji Won Jung (CJ CheilJedang Food R&D Institute, Korea) Breeding for Globalization of Processed Foods	
(12:00~12:40)	PS-03 Kenneth L. McNally (International Rice Research Institute, Philippines) Digitizing Rice: Tools and Resources to Accelerate Breeding	
12:40~14:00	Lunch	
14:00~15:00	**Poster presentation Part 1_Odd Number**	(Lobby)
	Special Session	
14:00~14:40	SS-A. Digital Breeding Based on Supercomputing	(Ramada Ballroom 1)
17:20~18:50	SS-B. Monitoring Strategy of GM Variety	(Ramada Ballroom 2)
15:00~18:00	**Concurrent Session Part 1**	
	CS-A. Breeding Commercialization	(Ramada Ballroom 1)
	CS-B. Breeding for Major Crops	(Ramada Ballroom 2)
	CS-C. Breeding for Horticultural Crops	(Ramada Ballroom 3)
	CS-D. Breeding for Forest Trees	(Ramada Ballroom 4)
	CS-E. Molecular Breeding	(Ora Hall)

June 30, 2023		
09:00~10:00	Registration, Poster 'even number' attachment	(Lobby)
10:00~11:20	**Plenary Session 2**	(Ramada Ballroom)
	Chair: Gang-Seob Lee (National Institute of Agricultural Sciences)	
(10:00~10:40)	PS-04 Seonghee Lee (University of Florida, U.S.A) Genomics Informed Octoploid Strawberry Breeding: Reflecting on the Past 10 Years and Current Progress	
(10:40~11:20)	PS-05 Ju-Kyung Yu (Chungbuk National University, Korea) Interdisciplinary Breeding Strategies to Reinforce the Competitiveness of the Seed Industry	
11:20~13:00	Lunch	
13:00~14:00	**Poster presentation Part 2_even number**	(Lobby)
14:00~17:00	**Concurrent Session Part 2**	
	CS-F. Breeding for Special Crops	(Ramada Ballroom 1)
	CS-G. Phenomics	(Ramada Ballroom 2)
	CS-H. New Breeding Technology	(Ramada Ballroom 3)
	CS-I. Young Breeding Scientist	(Ramada Ballroom 4)
	CS-J. Genome Sequence & Genomics	(Ora Hall)
17:00~	**Closing Ceremony**	(Ramada Ballroom 1)

July 3, 2023		
Online	**Announcement of Presentation Award**	Homepage

2023 KSBS International Conference [Concurrent Session]

Plant Breeding Strategy for Seed Industry Growth [종자산업 발전을 위한 작물육종 전략]

June 28~30, 2023, Jeju Ramada Plaza Hotel

June 29, 2023	
	CS-A. Breeding Commercialization (Ramada Ballroom 1)
	Chair: Jung-Kyung Moon (National Institute of Crop Science) Younghoon Park (Pusan National University)
15:00~15:25	OA-01 Hyeokgeun Lee (Nongwoobio Co., Breeding Institute) Development of molecular markers for breeding and Club root resistant cabbage
15:25~15:50	OA-02 Jeong-Dong Lee (Kyungpook National University) Start-up through the development of soybean varieties with improved fatty acid composition
15:50~16:15	OA-03 Yoon-Sup So (Chungbuk National University) Case review on corn hybrid commercialization in South Korea
16:15~16:40	OA-04 Jin-Kyung Kwon (Seoul National University) Development and Commercialization of Pepper Varieties with High Capsiate Content
16:40~17:05	OA-05 Sungtaeg Kang (Dankook University) Development and commercialization of black seed coat and green cotyledon soybean variety "Noksim"
	CS-B. Breeding for Major Crops (Ramada Ballroom 2)
	Chair: Youngjun Mo (Jeonbuk National University) Jaeyoon Kim (Kongju National University)
15:00~15:30	OB-01 Dae Yeon Kim (Kongju National University) Genome-wide association study in wheat identifies genomic regions associated with seed color
15:30~16:00	OB-02 Dong-Soo Park (National Institute of Crop Science) Progress and Prospects in Breeding Bakanae Disease-Resistant Rice Varieties
16:00~16:30	OB-03 Chan Seop Ko (Korea Atomic Energy Research Institute (KAERI)) Analysis of wheat genes to respond under heat stress during grain filling stage
16:30~17:00	OB-04 Young-Mi Yoon (National Institute of Crop Science) Special features of newly developed barley varieties in Korea
17:00~17:10	break time
17:10~17:30	OB-05 Sovetgul Asekova (Sultan Qaboos University, Sultanate of Oman) Development of drought-tolerant bread wheat genotypes that can be grown in Oman under severe drought conditions

	CS-C. Breeding for Horticultural Crops (Ramada Ballroom 3)
	Chair: Jundae Lee (Jeonbuk National University) Wonbyoung Chae (Dankook University)
15:00~15:30	OC-01 Soon Ju Park (Gyeongsang National University) Newly Discovered Alleles of *SELF PRUNING* Provide a Range of Plant Compactness and Yield
15:30~16:00	OC-02 Junkyoung Choe (BioTo Co., LTD) Development of Identification Markers for Ginseng Variaties Using Improved GBS
16:00~16:30	OC-03 Suhyun Yun (National Institute of Horticultural and Herbal Science) Citrus breeding in rural development administration
16:30~17:00	OC-04 Myongkyoon Yang (Jeonbuk National University) Artificial Intelligence for Data-driven Horticultural Crop Breeding
17:00~17:30	OC-05 Wonbyoung Chae (Dankook University) Indirect selection for heat-tolerance using impedance flow cytometry in tomato
	CS-D. Breeding for Forest Trees (Ramada Ballroom 4)
	Chair: Donghwan Shim (Chungnam National University) Insik Kim (National Institute of Forest Science)
15:00~15:30	OD-01 Kyu-Suk Kang (Seoul National University) Phenotypic characteristics and comparative transcriptome analysis of six pine species inoculated with pine wood nematodes (*Bursaphelenchus xylophilus*)
15:30~16:00	OD-02 Youn-Il Park (Chungnam National University) Spectral Unmixing of Hyperspectral Images of Coniferous Trees for Monitoring Needle Color
16:00~16:30	OD-03 Hyunmo Choi (National Institute of Forest Science) Improvement of poplar trees to mitigate global climate change using gene editing technology
16:30~17:00	OD-04 Il Hwan Lee (National Institute of Forest Science) Research on development of fast-growing trees for reducing particulate matters formation
17:00~17:10	break time
17:10~17:30	OD-05 Hanna Seo (National Institute of Forest Science) Development of DNA Markers to Distinguish between *Salix caprea*, *Salix gracilistyla*, and their Interspecific Hybrids

	CS-E. Molecular Breeding Ora Hall
	Chair: Yeongdeuk Jo (Chungnam National University) Bokeun Ha (Chonnam National University)
15:00~15:30	OE-01 Hyeonso Ji (National Institute of Agricultural Sciences) Development of high-throughput SNP genotyping system for Korean rice varieties based on genome sequence analysis
15:30~16:00	OE-02 Kyung Do Kim (Myongji University) Genome-wide association study of resistance to new cyst nematode species in soybean
16:00~16:30	OE-03 Sun-Hyung Lim (Hankyong National University) Transcription Factor-Mediated Control of Anthocyanin Biosynthesis in Rice Pericarp
16:30~17:00	OE-04 Dong-Hwan Kim (Chung-Ang University) Transcriptomic and epigenomic analyses revealed that polycomb repressive complex 2 (PRC2) regulates not only the developmental program but also stress-responsive metabolism in *Brassica rapa*
17:00~17:10	break time
17:10~17:30	OE-05 Seo-Young Lee (Seoul National University) Leaky mutations in the zeaxanthin epoxidase in Capsicum annuum result in bright red fruit containing a high amount of zeaxanthin
17:30~17:50	OE-06 David Charles Simiyu (Chonnam National University) The patatin-related *phospholipase-AIIIδ* gene regulates lignification and leaf senescence in *Arabidopsis*

June 30, 2023	
	CS-F. Breeding for Special Crops (Ramada Ballroom 1)
	Chair: Ickhyun Jo (Dankook University) Yujin Kim (Pusan National University)
14:00~14:30	OF-01 Eunsoo Lee (National Institute of Crop Science) Unveiling the Genetic and Functional Insights of Sesame Lignans for High-Lignan Variety Development and Industrial Utilization
14:30~15:00	OF-02 Jeonghoon Lee (National Institute of Horticultural and Herbal Science) *Glycyrrhiza* interspecific hybrid cultivar development and Korea Pharmacopoeia (KP) registration for domestically producing licorice
15:00~15:30	OF-03 Jung-Woo Lee (National Institute of Horticultural and Herbal Science) Large-scale micropropagation of *Panax ginseng* Meyer
15:30~16:00	OF-04 Hyun-Seung Park (Sejong University) Utilizing Genomic Insights for the Breeding of Special Crops: A Study on Chimeric Ornamental Plants
16:00~16:10	break time
16:10~16:30	OF-05 Hyun Uk Kim (Sejong University) Molecular analysis of high-linoleic acid perilla mutants and the functional characterization of *PfrFAD3a* and *PfrFAD3b* genes

	CS-G. Phenomics (Ramada Ballroom 2)
	Chair: Yongsuk Jung (Jeju National University) Kyunghwan Kim (National Institute of Agricultural Sciences)
14:00~14:30	OG-01 Sungyul Chang (National Institute of Crop Science) Comparison of rice growth patterns with field phenotyping data in rice paddy field
14:30~15:00	OG-02 Song Lim Kim (National Institute of Agricultural Sciences) Current status and applications of crop phenomics in the National Institute of Agricultural Sciences in Korea
15:00~15:30	OG-03 Yun-Hee Shin (Korea Institute of Science and Technology) The current status of plant phenotyping technologies being developed at the KIST Phenomics Research Group
15:30~16:00	OG-04 Younghae Do (Kyungpook National University) Crop phenomics to genomics in the mathematical point of view
	CS-H. New Breeding Technology (Ramada Ballroom 3)
	Chair: Hyeran Kim (Kangwon National University) Kihong Jung (Kyung Hee University)
14:00~14:30	OH-01 Young Geun Mok (GreenGene Inc) Development of targeted base editing of cellular organelle DNA in plants
14:30~15:00	OH-02 Keunsub Lee (Iowa State University, U.S.A.) A new ternary vector system for efficient maize transformation and targeted mutagenesis
15:00~15:30	OH-03 Woo-Jong Hong (Kyung Hee University) Beyond genome sequencing: Data-driven crop research toward digital breeding
15:30~16:00	OH-04 Jinmi Yoon (Inha University) Study on nucleic acid metabolic pathways during early seed development to improve rice grain quality
16:00~16:10	break time
16:10~16:30	OH-05 Jin Hoon Jang (Chonnam National University) Loss-of-function of gynoecium-expressed phospholipase pPLAIIγ triggers maternal haploid induction in *Arabidopsis* and its application in *japonica* rice

	CS-I. Young Breeding Scientist (Ramada Ballroom 4)
	Chair: Taesung Kim (Korea National Open University) Soocheul Yoo (Hankyong National University)
14:00~14:30	OI-01 Girim Park (National Institute of Horticultural and Herbal Science) Genetic inheritance and candidate gene-based markers for fruit flesh color in watermelon (*Citrullus lanatus* L.)
14:30~15:00	OI-02 Yoon Kyung Lee (Seoul National University) Genes associated with the eating quality traits of japonica rice
15:00~15:30	OI-03 Jung Min Kim (Korea Atomic Energy Research Institute) GWAS and QTL mapping for identification of key factors underlying isoflavone contents in soybean mutants
15:30~16:00	OI-04 Bongju Kim (Onist Co., Ltd.) Identification of the genes associated with cytoplasmic male sterility and development of the molecular markers for improvement of breeding efficiency in onion (*Allium cepa* L.)
16:00~16:10	break time
	CS-J. Genome Sequence & Genomics Ora Hall
	Chair: Changsoo Kim (Chungnam National University) Taehwan Jun (Pusan National University)
14:00~14:30	OJ-01 Seungill Kim (University of Seoul) Haplotype-resolved assembly highlights crucial components of pine genome evolution and allelic imbalance in *Pinus densiflora*
14:30~15:00	OJ-02 Jin-Hyun Kim (National Institute of Agricultural Sciences) Dissecting seed pigmentation-associated genomic loci and genes in soybean: A dual approaches of reference-based and k-mer-based GWAS
15:00~15:30	OJ-03 Yeisoo Yu (Department of R&D, DNACARE Co. Ltd.) Development of an integrated breeding platform for data-driven crop improvement
15:30~16:00	OJ-04 Jungmin Ha (Gangneung-Wonju National University) Metabolic profiling and gene expression analysis in the biosynthetic pathways of antioxidants in mungbean sprout

2023 KSBS International Conference [Special Session]

June 29, 2023, Jeju Ramada Plaza Hotel

June 29, 2023	
	SA. Digital Breeding Based on Supercomputing (슈퍼컴퓨터 기반 디지털 육종)
	(Ramada Ballroom 1)
	Chair: Byeongok Ahn (National Institute of Agricultural Sciences)
14:00~14:20	SS-01 Donghwan Shim (Chungnam National University) Analysis of digital breeding big-data based on supercomputing
14:20~14:40	SS-02 Tae-Ho Lee (National Institute of Agricultural Sciences) Establishment and support of a supercomputing infrastructure for digital breeding era
	SB. Monitoring Strategy of GM Variety (GM 품종의 관리방안)
	(Ramada Ballroom 2)
	Chair: Dongheon Kim (Future Food Resources Forum)
17:40~18:00	SB-01 Dongsun Kim (Korea Seed & Variety Service) Safty Management Measures for Non-approved LMO Seed for Seeds
18:00~18:20	SB-02 Hyo-Yeon Lee (Jeju National University) Trends in commercialization of GM crops and the current status of practical application of herbicide-resistant GM zoysiagrass
18:20~18:50	Discussion

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(B) Breeding for Major Crops

(C) Breeding for Horticultural Crops

(D) Breeding for Forest Trees

(E) Molecular Breeding

(F) Breeding for Special Crops

(G) Phenomics

(H) New Breeding Technology

(I) Young Breeding Scientist

(J) Genome Sequence & Genomics

Poster Session

(A) Breeding Commercialization

(B) Breeding for Major Crops

(C) Breeding for Horticultural Crops

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Plenary Session

Plenary Session

Peter van Dijk

Position: Distinguished Scientist
Institution: KeyGene
Address: KeyGene, Agro Business Park 90, 6708 PW Wageningen, The Netherlands
Phone: +31317466866
E-mail: peter.van-dijk@keygene.com

<Research Interests>

1. Plant genetics
2. Plant breeding systems, especially apomixis

<Education>

1. Master in Biology, Groningen University, The Netherlands
2. Ph.D. in Population Genetics, Groningen University, The Netherlands

<Professional Experience>

1. Senior scientist at the Netherlands Institute of Ecology, Royal Netherlands Academy of Sciences (NIOO-KNAW)
2. Distinguished Scientist at Keygene N.V., Wageningen, The Netherlands

<Selected Publications>

1. Cornaro, L., Banfi, C., Cucinotta, M., Colombo, L. and P.J. van Dijk 2023. Asexual reproduction through seeds: the complex case of diplosporous apomixis. Journal of Experimental Botany. https://doi.org/10.1093/jxb/erad054
2. Underwood, C.J.·········.and P.J. van Dijk. 2022 A PARTHENOGENESIS allele from apomictic dandelion can induce egg cell division without fertilization in lettuce. Nature Genetics, 54: 84-93.
3. Van Dijk, P.J., R. Op den Camp and S.E. Schauer 2020. Genetic dissection of apomixis in dandelions identifies a dominant parthenogenesis locus and highlights the complexity of autonomous endosperm formation. Genes, 11, 961. https://doi.org/10.3390/genes11090961
4. Van Dijk P.J., D. Rigola and S.E. Schauer 2015. Plant Breeding: Surprisingly less sex is better. Current Biology 26: 122-124.
5. Ozias-Akins P. and van Dijk P.J. 2007. Mendelian genetics of apomixis in plants. Ann. Rev. Genet. 41: 509-37

PS-0001

Apomixis: Plant Breeding Technology of the 2020s

Peter van Dijk*

KeyGene, Agro Business Park 90, 6708 PW Wageningen, The Netherlands

Apomixis is clonal reproduction through seeds, producing offspring genetically identical to the mother plant. This reproductive system occurs in some 300 wild plant species but not in major crops. Introducing apomixis in crops can yield significant benefits for plant breeding and seed production. The most obvious is the perpetual fixation of heterosis, but in principle, any genetically determined trait can be fixed, regardless of its complexity. In order to introduce apomixis into sexual crops, genes that skip meiosis and fertilization must be identified and brought together. There are two main approaches to making apomictic crops. The first is the knock-out mutations in known meiotic genes combined with genes causing parthenogenesis (synthetic apomixis). The second is cloning naturally dominant apomixis genes and modifying the sexual orthologs (copy-nature apomixis).

Recently, remarkable progress in apomixis research has been made. Synthetic apomictic rice with high apomixis penetrance has been produced, suggesting that this application may be close to the market. In addition, the first naturally dominant parthenogenesis genes have been isolated (*BabyBooMLike* in *Pennisetum* and *PARthenogenesis* in *Taraxacum*). Apomixis genes are not completely new but modifications of sexual genes. In the presentation, I will discuss the identification of the PAR gene in Taraxacum and the possible future application of apomixis in plant breeding programs. Concerning the application in breeding, the dominance of apomixis genes and the female specificity of apomeiosis is essential. The recent breakthroughs in apomixis research justify the expectation that apomictic crops will be a reality before the end of this decade.

***Corresponding Author:** Tel. +31-317-466-866, E-mail: peter.van-dijk@keygene.com

Ji Won Jung

Position: Principal researcher
Institution: CJ Cheiljedang Food R&D Institute
Address: Agro Business Park 90, 6708 PW Wageningen, The Netherlands
Phone: +82-31-8099-1290
E-mail: jwjung@cj.net

<Research Interests>

1. Development of agricultural materials for food production
2. Standardization of raw material quality
3. Pretreatment for the enhancement of processing suitability

<Education>

1. Mar. 1998 - Feb. 2004 PhD of Department of Plant Science, Seoul National University
2. Mar. 1992 - Feb. 1994 MS of Department of Plant Science, Seoul National University
3. Mar. 1988 - Feb. 1992 BS of Department of Plant Science, Seoul National University

<Professional Experience>

1. Jan. 2008 - Present Food R&D Master CJ Cheiljedang Food R&D Institute
2. Apr. 2004 - Mar. 2007 Post Doctor National Horticultural Research Institute, RDA

PS-0002

Breeding for Globalization of Processed Foods

Ji Won Jung*

Food R&D Institute, CJ Cheiljedang CJ Blossom Park, 55, Gwanggyo-ro 42beon-gil Yeongtong-gu, Suwon 16495, Republic of Korea

Dramatic climate change has fueled more active discussions on securing stable agricultural products than ever. Topics like climate change-resistant seeds, smart farming, and diversification of global production locations are predominantly discussed in agricultural production. A common factor necessary for optimizing these elements is the development of suitable cultivars. From a food industry perspective, better cultivars can contribute to a stable supply of raw materials, enhance product consistency, improve the competitiveness of raw material prices, and ultimately meet consumer needs. In 2021, 31.7% of raw materials used in food manufacturing were domestically produced. Imported materials were primarily utilized due to the higher costs of domestic products affecting price competitiveness. In the case of food, consumers tend to be quite sensitive to price fluctuations rather than sticking to specific products. Thus food companies, therefore, welcome new cultivars improving agricultural price competitiveness. On the other hand, the 'Chungwang' variety of kimchi cabbage, initially used as the standard ingredient for mass-produced kimchi, still remains one of the favored cultivars among food companies even after over 20 years since its development. The food industry is the largest buyer of agricultural products, and Korean food's export and overseas production is more vibrant and growing than ever before. It is now suggested to closely integrate the development of new cultivars with the food industry and to cooperate with institutions possessing the necessary technologies for more planned and successful breeding.

***Corresponding Author:** Tel. 031-8099-1290, E-mail: jwjung@cj.net

Kenneth L. McNally

Position: Head of Bioinformatics & Genomics
Institution: International Rice Research Institute, Philippines
Address: Bioinformatics and Breeding Innovations, Rice Breeding Innovations Department, International Rice Research Institute, Pili Dr., Los Baños, Laguna 4031, Philippines
Phone: +63-917-552-6120
E-mail: K.McNally@irri.org

<Research Interests>

1. Genomics
2. Bioinformatics
3. Genetic Diversity

<Education>

1. 1982 - B.S. in Mathematics and Biology (and minor in Chemistry) with honors from Northwestern Oklahoma State University
2. 1990 - Ph.D. Biochemistry from Oklahoma State University

<Professional Experience>

1. 1988-1990: University of Colorado Health Sciences Center
2. 1990-1993: University of California at Santa Barbara
3. 1994-1996: Cornell University

<Selected Publications>

1. W Wang, R Mauleon, Z Hu, D Chebotarov, S Tai, Z Wu, M Li, T Zheng, ... Kenneth L. McNally, Zhikang Li & Hei Leung. 2018. Genomic variation in 3,010 diverse accessions of Asian cultivated rice. *Nature vol 557, 43-49.*
2. Kenneth L. McNally, Kevin L. Childs, Regina Bohnert, and Jan E. Leach. 2009. Genomewide SNP variation reveals relationships among landraces and modern varieties of rice. *PNAS vol 106, 12273-12278.*
3. SR McCouch, MH Wright, CW Tung, LG Maron, KL McNally, M Fitzgerald, ...2016. Open access resources for genome-wide association mapping in rice. *Nature Communications vol 7, 10532.*
4. L. Shen, B. Courtois, K. L. McNally, S. Robin & Z. Li. 2001. Evaluation of near-isogenic lines of rice introgressed with QTLs for root depth through marker-aided selection. *Theoretical and Applied Genetics vol 103, 75-83.*
5. Amelia Henry, Veeresh R.P. Gowda, Rolando O. Torres, Kenneth L. McNally, Rachid Serraj. 2011. Amelia Henry, Veeresh R.P. Gowda, Rolando O. Torres, Kenneth L. McNally, Rachid Serraj. *Field Crops Research Vol 120, 205-214.*

PS-0003

Digitizing Rice: Tools and Resources to Accelerate Breeding

Kenneth L. McNally*

Bioinformatics and Breeding Innovations, Rice Breeding Innovations Department, International Rice Research Institute, Pili Dr., Los Baños, Laguna 4031, Philippines

The release of the Nipponbare reference genome in 2005 was a game-changer for rice science serving as the foundation for numerous discoveries. One such effort was the discovery of genomic variants from sequencing 3000 accessions in the 3000 Rice Genomes (3K RG) Project, a collaboration between IRRI, the Chinese Academy of Agricultural Sciences and BGI. To make use of the vast dataset, we created the SNP-Seek database (https://snp-seek.irri.org) to curate genomic diversity. Our data, tools, and genetic stocks have been used extensively to discover genes and donors associated with many traits. We are moving beyond the 3K RG by producing new reference genomes across rice diversity and resequencing further accessions with the goal to create the *Digital Rice Genebank* for the global community. Concurrent to these efforts, the International Rice Informatics Consortium (IRIC) was established to secure and curate data for rice improvement, create resources, and to promote and foster broader community collaborations. IRIC supports SNP-Seek API development and curation of datasets for the public to access, analyze, and use for discovery. Additional tools supporting various aspects of digital breeding have been created: 1)Haplotool for extended haplotype analysis; 2) Crop Galaxy (http://cropgalaxy.excellenceinbreeding.org) with GS, ML, GWAS, among others; Rice ImageBreed for UAV data curation and analysis; a Streamlit G2P prediction engine for LM and ML methods from UAV data; Rice-pilaf for post-GWAS analyses to provide supporting evidence for candidate genes. Together, the new genomics resources and bioinformatics tools will allow *in silico* modeling of rice, and accelerate rice improvement through allele mining and digital breeding.

***Corresponding Author:** Tel. +63-917-552-6120, E-mail: k.mcnally@irri.org

Seonghee Lee

Position: Associated Professor
Institution: University of Florida
Address: Horticultural Science Department, Gulf Coast Research and Education Center, Institute of Food and Agriculture Science, University of Florida, Wimauma, Florida, U.S.A
Phone: +82-10-6843-2938
E-mail: seonghee105@ufl.edu

<Research Interests>

1. Strawberry molecular genetics and genomics
2. Strawberry trait discovery for disease resistance and fruit quality

<Education>

1. Ph.D. North Dakota State University
2. M.S. Chungbuk National University

<Professional Experience>

1. Senior Research Associate. The Samuel Roberts Noble Foundation
2. Postdoc. USDA National Rice Research Center

<Selected Publications>

1. Fan, Z, Tieman, D. M., Knapp, S. J., Zerbe, P., Famula, R., Barbey, C. R, Folta, K. M., Rampazo, R. A., Lee, M. B., Oh, Y., Lee, S. and Whitaker, V. Mc. 2022. A multi-omics framework reveals strawberry flavor genes and their regulatory elements. New Phytologist
2. Lee, S. Vemanna, R. S., Oh, S., Rojas, C. M., Oh, Y., Kaundal, A., Kwon, T., Lee, H., Muthappa, S. and Mysore, K. S. 2022. Functional role of formate dehydrogenase (FDH1) for host and nonhost disease resistance against bacterial pathogens. PLoS One
3. Tapia, R., Abd-Elrahman, A., Osorio, L., Whitaker, V. M. and Lee, S. 2022. Combining canopy reflectance spectrometry and genome-wide prediction to increase response to selection for powdery mildew resistance in cultivated strawberry. Journal of Experimental Botany
4. Barbey, C. R., Hogshead, M. H., Harrison, B., Schwartz, A. E., Verma, S., Oh, Y., Lee, S., Folta, K. M. and Whitaker, V. M. 2021. Genetic analysis of methyl anthranilate, mesifurane, linalool and other flavor compounds in cultivated strawberry (Fragaria ×ananassa). Frontiers in Plant Science 12: 615749
5. Oh, Y., Barbey, C. R., Chandra, S. Fan, Z., Bai, J., Plotto, A., Folta, K. M., Whitaker, V. M. and Lee, S. 2021. Genomic characterization of the fruity aroma gene, FaFAD1, reveals a gene dosage effect on γ-decalactone production in strawberry (Fragaria ×ananassa). Frontiers in Plant Science 12:639345

PS-0004

Genomics Informed Octoploid Strawberry Breeding: Reflecting on the Past 10 Years and Current Progress

Seonghee Lee*, Hyeondae Han, Youngjae Oh, Natalia Salinas, Yoon Jeong Jang, Fan Zhen, Cheolmin Yoo, Mark Porter, Ronald Tapia, Jinhee Kim, Sujeet Verma, Vance M. Whitaker

Horticultural Science Department, Gulf Coast Research and Education Center, Institute of Food and Agriculture Science, University of Florida, Wimauma, Florida, U.S.A

Strawberry is one of the most important horticultural crops grown in Florida. The University of Florida strawberry breeding program is extensively implementing advanced molecular breeding and genomics tools to develop new and improved varieties. In this presentation, we will highlight the recent achievements accomplished in UF strawberry breeding program through the application of genomics-enabled breeding approaches for improving flavor and disease resistance. Furthermore, the recent completion of high-quality, chromosome-scale phased genomes of UF elite breeding lines, including the major commercial cultivar ‘Florida Brilliance’, will be underlined to discuss their use for discovering genetic components and genes for important breeding characteristics. Furthermore, we will provide the latest updates on our gene discovery for disease resistance and fruit quality improvement, and its application to CRISPR gene editing research in cultivated octoploid strawberry. In conclusion, an enlightening discussion will be presented for outlining future perspectives and notable milestones in strawberry breeding research.

***Corresponding Author:** Email: seonghee105@ufl.edu

Ju-Kyung Yu

Position: Assistant Professor
Institution: Chungbuk National University, Department of Crop Scienc
Address: College of Agriculture and Life Sciences, Chungbuk National University Chungdae-ro 1, Seowon-Gu, Cheongju, Chungbuk 28644
Phone: +82-43-261-2513
E-mail: yujk0830@chungbuk.ac.kr

<Research Interests>

1. Crop science and breeding
2. Genomics
3. Seed business

<Education>

1. Ph.D. in Crop Science, Oregon State University, USA (2001)
2. B.S. in Agricultural Science, Kyungpook National University, Korea (1994)

<Professional Experience>

1. 2023-present: Assistant Professor at Chungbuk University
2. Syngenta Inc.: Global Leader in Molecular Analysis
3. Syngenta Inc.: Global Head of Soybean R&D Project

<Selected Publications>

1. Ju-Kyung Yu, Sungyul Chang, Gyung Deok Han, Seong-Hoon Kim, Jinhyun Ahn, Jieun Park, Jaeyoung Kim, Yong Suk Chung. 2023. Implication of high variance in germplasm characteristics. Scientific Reports. 13:515.
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4. Ju-Kyung Yu. 2020. Advanced breeding technologies for accelerating genetic gain. Plant Breed. Biotech. 8: 203-210.
5. Jaeyoung Kim, Ju-Kyung Yu (co-first author), Renato Rodrogues, Yoonha Kim, Jieun Park, Ji-Hyeon Jung, Sung Taeg Kang, Kyung-Hwan Kim, JeongHo Baek, Eungyung Lee and Yong Suk Chung. 2022. Case study: cost-effective image analysis method to study drought stress of soybean in early vegetative stage. J. Crop Sci. Biotechnol. 25: 33-37

PS-0005

Interdisciplinary Breeding Strategies to Reinforce the Competitiveness of the Seed Industry

Ju-Kyung Yu*

College of Agriculture and Life Sciences, Chungbuk National University Chungdae-ro 1, Seowon-Gu, Cheongju, Chungbuk 28644, Republic of Korea

As the world population grows, global demand for food will double in the next 50 years. In addition, the reduction in farmland due to increased urbanization has led to an upsurge in the use of advanced agricultural technology and innovations to meet and sustain the demand. In fact, the AgTech market is booming, with no signs of slowing (Forbes, February 2023), and AgTech is going to play a vital role in the future of food production.

In order to maintain agricultural technology at its current high level and innovate it even further in the 21st century, public-private partnerships are essential to advance research, bring science to market faster, and prompt economic growth. Only through constructive collaboration will we be able to accomplish them.

This presentation will discuss the mutual benefits of public-private collaborations. It will demonstrate how the seed industry can contribute to advancing public research (and vice versa) and how the exchange of innovative ideas will accelerate the development of seed science. We will consider which science and technology areas are beneficial for both industry and academia to maximize public-private partnerships.

***Corresponding Author:** Tel. 043-261-2513, E-mail: yujk0830@chungbuk.ac.kr

Oral Session

OA-0001

Development of molecular markers for breeding and Club root resistant cabbage

Hyeokgeun Lee[1], Yong Pyo Lim[2*]

[1]Department of Horticultural Science, Graduate School Chungnam National University Daejon, Korea
[2]Nongwoobio Co., Breeding Institute, Yeoju, Korea

Clubroot are widespread and devastating diseases in *Brassica oleracea* crops. In order to detect quantitative trait loci (QTL) for resistance to clubroot diseases, we constructed Bulked segregant analysis (BSA) using F2 populations, molecular markers derived from whole genome sequencing (WGS). Clubroot resistance in the populations against race 4 (CR-YC) were evaluated using F2 progenies, and one major QTL (BoCR4-1) and one minor QTL (BoCR4-2) for CR-YC isolate were identified. The QTLs show similar locations to the previously reported CR loci for Race 4 in *B. oleracea*. In exploring the overall disease incidence, it was apparent that a single involvement of major QTL (BoCR4-1) is not enough to confer sufficient resistance. one major QTL (BoCR4-1) plus one minor QTL (BoCR4-2) conferred moderate resistance. Accumulation of several CR genes by MAS is necessary to conduct CR breeding. These QTLs identified in this study will be useful for cabbage breeding.

***Corresponding Author:** Tel. 031-887-6533, E-mail: gurrmsdl@nongwoobio.co.kr

OA-0002

지방산 조성이 개선된 콩 품종 개발을 통한 산업화

이정동*

대구광역시 북구 대학로 80 경북대학교 응용생명과학과

콩은 종자의 약 20%가 지방으로 되어있고 지방은 일반적으로 12%의 palmitic acid(16:0) 4%의 stearic acid(18:0) 23%의 oleic acid(18:1), 53%의 linoleic acid(18:2), 8%의 linolenic acid(18:3)로 구성되어 있다. 각각의 지방산 마다 기능이 있어 지방산의 조성에 따라 기름의 품질이 달라진다. 포화지방산인 16:0과 18:0은 함량을 낮추어야 하고, 불포화 지방산들의 함량은 높이는 것이 건강에 이롭다. 특히, 불포화지방산중 18:1은 오메가-9 지방산으로 함량이 높아지면 기름의 안정성이 향상되고, 기름중 70% 이상 함유 되었을때는 심혈관 질환을 예방하는 기능이 있는 것으로 보고되고 있다. 오메가-3 지방산인 18:3은 기름의 산화안정성을 위해서는 함량을 낮추어야 하지만 식물성 오메가-3를 섭취하기 위하여는 높여야 한다. 특히, 섭취하는 지방의 오메가-6(18:2)와 오메가-3의 비율이 매우 중요하다. 두 지방산 비율이 4:1 이하일 때 건강에 매우 좋다고 연구되고 있다. 교육기관인 대학교에서 연구를 하는 동안 18:1의 함량이 약 80%인 콩 품종을 육성하였고, 오메가-3 함량을 높일 수 있는 유전자원을 개발하여 오메가-3 함량이 높은 콩을 개발하고 있으며, 또한 오메가-6와 오메가-3 함량 비율이 낮은 콩을 개발하여 산업화 하고 있는 과정에 대하여 발표하고 고찰하고자 한다.

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

OA-0003

Case review on corn hybrid commercialization in South Korea

Yoon-Sup So*

Department of Crop Science, Chungbuk National University, Cheongju, South Korea

Plant breeding, traditionally, was said to be art and science. Art means the breeder's eye indicating selection involves the subjectivity while science indicates data-driven decision makting process, the objectivity. In addition to these two, breeders emphasizes business part of plant breeding. The emphasis not only focuses on all post-release activities such as marketing and sales but also business-minded setup of plant breeding goals at the beginning of cultivar development and throughout breeding process. Plant breeding programs can be devided into public and commercial programs, which may differ from the way cultivars are commercialized or supplied. It, however, may have the same final goal as the development of cultivar that is chosen by farmers. The presenter will go over the various cases of successful and failed corn hybrids in Korean market and discuss the strategy for successful commercialization. Current breeding and commercialization activities and experience of the presenter as maize breeder will also be shared.

***Corresponding Author:** Tel. 043-261-2517, E-mail: yoonsupso@chungbuk.ac.kr

OA-0004

Development and Commercialization of Pepper Varieties with High Capsiate Content

Jin-Kyung Kwon[1], Siyoung Jang[1], Seo-Young Lee[1], Hye Jeong Choi[2], Dong-Am Kim[3], Yong-Jik Lee[3], ChanSung Park[4], Byoung-Cheorl Kang[1,2*]

[1]Department of Agriculture, Forestry and Bioresources, Research Institute of Agriculture and Life Sciences, Plant Genomics and Breeding Institute, College of Agriculture and Life Sciences, Seoul National University, Seoul 08826, Republic of Korea
[2]FarmyirehSe Co., Ltd., #200-3115, College of Agriculture and Life Sciences, Seoul National University, 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Republic of Korea
[3]R&D Center, Hana Seed Co., Ltd., 331 Shindumangok-ro, Miyang-myeon, Anseong-si, Gyeonggi-do 17601, Republic of Korea
[4]Naturalendo Tech Co., Ltd., 301, Bldg A, C's Tower 58, Pankyo-ro 255, Bundang-gu, Seongnam-si, Gyeonggi-do, Republic of Korea

Pepper (*Capsicum* spp.) is esteemed high-value crops widely utilized as fresh fruit and versatile food ingredients. Their distinctive characteristic of pungency, conferred by the presence of capsaicinoids, distinguishes them as a desirable vegetable in culinary preparations. The pungent taste of capsaicinoids not only enhanced the taste of food but also imparts various physiological effects, including modulation of energy balance, metabolic rate, and satiety.

Capsiate, a capsaicinoid analog with a similar molecular structure, is a non-pungent compound primarily derived from the mutant *pAMT* gene in the capsaicin biosynthetic pathway. Studies have shown that capsiate can mimic the thermogenic and metabolic effects of capsaicin, promoting energy expenditure and elevating core body temperature. Additionally, capsiate exhibits multiple bioactive properties, such as antioxidant, anti-inflammatory, and anticancer activities, contributing to its potential health benefits. These attributes have led to the commercialization of capsiate as a weight management supplement.

In this research we strategically selected a *pAMT* mutant line and successfully developed pepper varieties enriched with capsiate content through inter/intra specific crossing, marker-assisted selection (MAS), and marker-assisted backcrossing (MABC). We selected the high content capsiate variety *Capsicum chinense* "SNU11-001" and crossed with highly pungent variety *C. chinense* 'Habanero' to construct the population. Subsequently, two distinctive lines, including the "SNUWonder HO" (orange line) and the "SNUWonder HR" (red line), both characterized by elevated capsiate content, were developed. Non-pungent pepper variety was developed using MABC that crossed the desirable sweetness of *C. annuum* 'Shinhong' peppers with "SNU11-001". For the plant factory, we developed various capsiate-enriched dwarf-type pepper varieties using *C. annuum* cv. "MicroPep Long" and the capsiate line *C. annuum* cv. "Maeunhyang,". Notably, the 'SNUWonder HO' was thoughtfully formulated and successfully introduced as a dietary supplement to assist with weight management.

The successful development and subsequent industrialization of these novel high content capsiate varieties hold great promise not only in terms of providing fresh and healthy produce but also as a means to efficiently produce functional health compounds. The anticipated positive impact on public health and well-being underscores the significance of this research endeavor.

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

OA-0005

녹자엽 검정콩 품종 '녹심'의 개발과 기술이전을 통한 상업화

강성택[1*], 김지민[1], 문중경[2], 황지혜[3]

[1]충청남도 천안시 동남구 단대로 119 단국대학교 생명자원학부 식량생명공학전공
[2]전라북도 완주군 이서면 혁신로 181 국립식량과학원
[3]대전광역시 유성구 유성대로 1689 (주)윕스

검정콩은 우리나라에서 주로 밥에 넣어 먹는 용도로 이용되고 소비자들은 종실 크기, 자엽이 자엽의 녹색정도, 안토시아닌 함량, 취반 후 종실의 당도 등에 따라 선호도가 달리한다. 또한, 농민들은 생산의 편리성을 위해 수량성이 높고, 내도복 및 내탈립성이며 숙기가 빨라 일반콩처럼 수확할 수 있는 품종을 요구하고 있다. 이에 부응하고자 단국대학교 작물분자 육종실험실에서는 품질이 우수하여 소비자 선호도가 높고 농가에서 안정적으로 재배가 가능한 진한 녹색자엽 검정콩 품종 개발을 위해 기존 검정콩 품종 중 품질이 우수한 '일품검정'과 핵유전 녹색자엽 유전자(*d1d2*)를 보유하는 콩 유전자원 'PI547426'을 인공교배하고, 계통육종법을 통해 우수계통을 선발 후 성숙기, 내탈립성 및 종실 클로로필 함량, 취반 후 당도를 포함한 식미를 평가하여 '녹심' 품종을 개발하였고, 2019년 품종보호권을 확보하였다.(품종보호 : 제7734호). 우리나라는 국가가 개발한 주요 식량작물 품종을 국가종자생산체계를 통해 보급하는 특수한 상황에 있어 대학이나 기업이 개발한 고품질 기능성 품종을 공급하는 데는 한계가 있다. 특히 자식성 작물인 콩의 경우 종자로서의 판매는 상업적인 측면에서 불리한 점이 많아 개발한 "녹심"을 종자회사를 통한 보급은 불가능한 상황을 인식하고, 개발자들이 스스로 판로를 개척하여 상업화하는 방법을 모색하였다. 이를 위해 개발된 고품질 품종을 중계연구를 통해 제품화 특성과 생산성을 충분히 검정하였고, 이울러 기업대상 품종설명회를 개최하여 홍보를 강화하였으며, 기술이전 전문기관을 통한 지속적인 마케팅을 실시하여 기업에 기술이전 하였다. 특히 차별화된 접근방법은 기술이전기업이 종자회사나 농산물을 활용하여 제품을 생산하는 기업이 아닌 농산물 유통하는 기업에 기술이전을 실시하였다는 점이다. 따라서 기술이전 후에도 개발자와 기술이전기업간 지속적인 협업체제를 구축하여 종자를 생산하였고, 기술이전기업은 원료콩 대량생산을 위해 기업주도로 농민과 계약재배를 통해 원료콩을 생산하였으며. 이후 생산된 원료콩은 콩을 원료로 제품을 생산하는 기업이나 대형유통판매처에 생산된 원료콩을 공급하거나 인터넷을 통한 온라인 판매를 실시함으로서 궁극적으로는 유통기업이 중심이 된 생산・유통 선순환 체계를 구축하여 개발종자의 상업화를 실시하고 있다. 현재 추진되고 있는 콩 품종 "녹심"의 상업화 모델은 앞으로 민간 주도의 고부가가치 기능성 품종개발 활성화와 산업화 가능성을 보여주는 선례로 평가되어 이와 관련한 세부 과정을 소개하고자 한다.

***교신저자:** Tel. 041-550-3621, E-mail: kangst@dankook.ac.kr

OB-0001

Genome-wide association study in wheat identifies genomic regions associated with seed color

Min Jeong Hong[1], Yong Weon Seo[2], Dae Yeon Kim[3*]

[1]Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, 29 Geumgu, Jeongeup, 56212, Korea
[2]Department of Plant Biotechnology, Korea University, Seoul 02841, Republic of Korea
[3]Department of Plant Resources, College of Industrial Sciences, Kongju National University, 54, Daehak-ro,Yesan-eup, Yesan-gun, Chungnam 32439, Republic of Korea

Hexaploid wheat is one of the most important cereal crops for human nutrition, and colored-grain wheat that contains high phenolic compound and a large number of flavonoid is useful material for the advancement of quality trait. In this study, a total of 155 lines were included, which comprised 153 F_3 populations derived from the Yellow (Ye) and Deep Purple (DP) wheat accessions, along with the parental lines (Ye and DP), were genotyped using the iSelect 90K wheat SNP arrays. Anthocyanin, chlorophyll a/b, carotenoid contents in seedlings, and CIELAB value were evaluated for genome-wide association studies (GWAS). A total of 105 significant marker-trait associations (MTAs) were identified across 21 chromosomes [-log10(P) ≥ 3]. Notably, four MTAs on Chromosome 1A and 7A exhibited high -log10(P) values (≥ 8), and four superior alleles were found to have positive effects on *L**, *a**, chlorophyll b, and carotenoid contents. In addtion, transcriptome analysis was performed on three different grain developmental stages of Ye and DP, enabling the identification of high-confidence wheat genes within ±250 kb of representative SNPs for the respective genomic regions, along with their expression patterns. These findings provide valuable insights into the genetic basis of seed color traits in wheat. The associated SNP markers and predicted candidate genes will facilitate marker-assisted selection in wheat breeding.

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***Corresponding Author:** Tel. 041-330-1205, E-mail: dykim@kongju.ac.kr

OB-0002

벼 키다리병 저항성 연구현황

이샛별[1], 강주원[1], 이지윤[1], 성기운[1], 권영호[1], 이소명[1], 조준현[2], 오성환[1], 신동진[1], 이종희[1], 오기원[1], 박동수[1*]

[1]국립식량과학원 남부작물부 논이용작물과
[2]국립식량과학원 상주출장소

키다리병은 벼 키가 비정상적으로 자라거나 말라죽는 병으로, 2007년도 이후 급격히 발생이 증가하여 매년 벼 농가에 피해를 입히고 있어 키다리병 방제를 위해 많은 비용과 노동력이 소모되고 있는 병이다. 키다리병에 대한 가장 확실하고 경제적인 방제 대책은 저항성 품종을 재배하는 것이나 현재까지 국내 벼 품종 중에는 키다리병에 견디는 힘이 강한 품종은 많지 않은 실정이다. 따라서 본 연구는 키다리병 저항성 대량검정법 개발, 유전자원의 키다리병 저항성 평가, QTL탐색 및 이를 활용한 저항성 품종 개발을 통해 국내 벼 품종의 키다리병 피해와 방제 비용을 줄이고자 수행하였다.

***교신저자:** Tel. 055-350-1165, E-mail: parkds9709@korea.kr

OB-0003

Analysis of wheat genes to respond under heat stress during grain filling stage

Chan Seop Ko[1], Jin-Baek Kim[1], Min Jeong Hong[1], Dae Yeon Kim[2], Joo Sun Lee[3], Yong Weon Seo[4,5*]

[1]Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute (KAERI), Jeongeup, Republic of Korea
[2]Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan-gun, Republic of Korea
[3]Smart Farm Research Center, Korea Institute of Science and Technology (KIST), Gangneung, Republic of Korea
[4]Department of Plant Biotechnology, Korea University, Seoul, Republic of Korea
[5]Ojeong Plant Breeding Research Center, Korea University, Seoul, Republic of Korea

Hexaploid wheat (*Triticum aestivum* L.) accounts for over 30% of the world's cereal production. However, high-temperatures during the grain filling stage can have detrimental effects on grain yield and quality, making heat stress a serious global concern. Heat stress accelerates plant growth, resulting in premature initiation of phenological stages, accelerated maturation, and poor grain development from anthesis through early spike maturity. In addition, the position of grains on a spike can greatly influence their end-use quality and rate of filling. The high-molecular glutenin gene *TaHMW1D*, which has four different transcript variants, has been shown to decrease in its full form and undergo specific deletion sites between repetitive regions. Heat stress led to a significant increase in the expression of the transcript variants, especially in the spike's distal parts. This suggests that stressed plants might choose shorter polypeptides while retaining glutenin function. TaLSD, which plays a role in stress resistance and grain mature dehydration during grain filling period, was found to be highly expressed in grains located at the basal positions of the spike under high-temperature stress. TaUHS interacts with TaLSD, mediating ubiquitination and proteasomal degradation. Proteolysis of TaLSD in conjugation with E3 ligase may occur to maintain cellular homeostasis and stability in response to unfavorable environmental conditions. Overall, this study will be helpful to elucidate heat tolerance mechanism in wheat, and could aid in the breeding of heat stress tolerant wheats.

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

OB-0004

Special features of newly developed barley varieties in Korea

Young-Mi Yoon*, Jin-Cheon Park, Chang-Hyun Lee, Seul-Gi Park, On-Sook Hur, Kyong-Ho Kim

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

Barley is divided into hulled barley and hull-less barley, and is also divided into two-row and six-row barley according to the number of grains arranged. In Korea, Barley is used for food as barley tea, barley sprout, long malt(for making Sikhye), malt(for making beer), and cooked barley, so we have developed barley varieties suitable for each processing purpose. The six-row hull-less barley "Baeksoojeonchal", which was developed in 2019, is barley with low proanthocyanidine content and low browning of cooked barley. The content of proanthocyanidine in "Baeksoojeonchal" was 0.011 mg/g, and "Saechal" was 0.152 mg/g. Twenty-four hours after cooking, there was little change in whiteness of "Baeksoojeonchal" from 35.1 to 32.1, but "Saechal" changed significantly from 30.0 to 19.9. The six-row hulled barley "Ssagirang" and "Ssagnuri", which was developed n 2022, showed high sprout yield and high content of polycosanol, which was a functional ingredient of sprouts. The amount of sprouts of "Ssagirang", "Ssagnuri" and "Olbory" were 157 mg/m^2(dry weight), 144 mg/m^2, and 133 mg/m^2, respectively, and the polycosanol contents of those were 448 mg/100g, 397 mg/100g, and 245 mg/100g, respectively. "Hyemalgeun", developed in 2021, is a six-row hulled barley suitable for producing bright Sikhye due to its low proanthocyanidin content and high enzyme activity. The proantocyadinidin contents of "Hyemalgeun" and "Hyeyang" were 0.010 mg/g and 0.140 mg/g, respectively, and the enzyme activities of those were 460 WK and 397 WK, respectively. The color difference (L, bright) of Sikhye, which was manufactured using the long malt of "Hyemalgeun" and "Hyeyang" were 78 and 66, respectively. In Korea, malting barley varieties has been developed two-row covered barley with large kernel and low protein content, and has shown weak about barley yellow mosaic virus (BaYMV) and powdery mildew disease. "Gangmaeg", developed in 2021, possessed BaYMV resistance genes, *rym1* and *rym5*, and showed resistance to BaYMV and powdery mildew disease. Beta-glucan, a major functional component of barley, is a component of endosperm cell walls and is known to lower cholesterol and stabilize blood sugar. Barley contains an average of 4-7% beta-glucan. The six-row hulled barley "Betahealth," which was developed in 2022, had a beta-glucan content of 14.4%, two to three times higher than that of conventional barley. The *in vitro* digestion rates of "Betahealth" raw barley and cooked barley were 3.99 and 5.84 glucose mg/g, respectively, lower than "Hyeyang" 5.38 and 7.52 glucose mg/g. Barley breeding is being developed for high-quality, high-functionality varieties for each processing purpose and disease-resistant varieties such as BaYMV and powdery mildew. Furthermore we try to develop moecular markers with these specific traits for effective selection of low-generation lines.

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***Corresponding Author:** Tel. 063-238-5227, E-mail: mi3710@korea.kr

OB-0005

Development of drought-tolerant bread wheat genotypes that can be grown in Oman under severe drought conditions

Sovetgul Asekova*, Muhammad Farooq, Abdullah Al-Sadi, Mahmoud Yaish, Ali Al-Subhi

College of Agricultural and Marine Sciences, Sultan Qaboos University 123 Muscat, P.O. Box 38, Sultanate of Oman

Bread wheat's (*Triticum aestivum* L.) high yield and wide adaptation make it one of the leading grains in the world and the basic diet for billions of people around the world, including the Sultanate of Oman, where it is considered one of the most important food crops consumed daily. Oman still faces a number of challenges, the most important of which are the lack of water, soil and water salinity, high temperature and drought, as well as biotic diseases that significantly affect wheat production in the country. The low yield of bread wheat grown in the Sultanate of Oman is mostly due to biotic and abiotic stresses and it does not give proper responses to inputs such as irrigation and fertilizer. Wild relatives of wheat are being regarded as a valuable source of genetic variation for many biotic and abiotic traits that can be utilized for further wheat improvement. A promising and seamless way of introducing these exotic alleles from diploid and tetraploid *Triticum* species into modern common wheat is generation of synthetic hexaploid wheat (SHW). Phenotypic evaluation was conducted on two hexaploid (SHW) wheat populations consisting of a total of 228 genotypes each. Plant height (PH) and spikelet length (SL) as well as physiological parameters such as water use efficiency (WUE), net photosynthetic rate (A), and other traits were measured during the grain-filling stage in 2022/23 season. Under drought and rescued conditions, 62 genotypes were evaluated for PH, SL, WUE and A. Drought tolerance is quantitative in nature, controlled by a number of genes/QTL (quantitative trait loci). With the help of QTL mapping, researchers are able to break down complex characteristics such as drought tolerance into their constituent parts. Each constituent part is governed by QTL. If QTL with large impacts on crop output in stress situations can be found, marker-assisted breeding might dramatically accelerate efforts in increasing agricultural drought resistance. In order to further characterize the quantitative trait loci underpinning these traits, mapping populations from current observations are being under process.

***Corresponding Author:** Tel. 968-9964-3642, E-mail: a.sovetgul@squ.edu.om

OC-0001

Newly Discovered Alleles of *SELF PRUNING* Provide a Range of Plant Compactness and Yield

Jung Heo, Soon Ju Park*

Division of Applied Life Science, and Plant Molecular Biology and Biotechnology Research Center (PMBBRC), Gyeongsang National University, Jinju 52828, Republic of Korea

In tomato cultivation, a rare natural mutation in the flowering repressor antiflorigen gene *SELF-PRUNING* (*sp-classic*) induces precocious shoot termination and is the foundation in determinate tomato breeding for open field production. Heterozygous *single flower truss* (*sft*) mutants in the florigen *SFT* gene in the background of *sp-classic* provide a heterosis-like effect by delaying shoot termination, suggesting the subtle suppression of determinacy by genetic modification of the florigen-antiflorigen balance could improve yield. Here, we isolated three new *sp* alleles from the tomato germplasm that show modified determinate growth compared to *sp-classic*, including one allele that mimics the effect of *sft* heterozygosity. Two deletion alleles eliminated functional transcripts and showed similar shoot termination, determinate growth, and yields as *sp-classic*. In contrast, amino acid substitution allele *sp-5732* showed semi-determinate growth with more leaves and sympodial shoots on all shoots. This translated to greater yield compared to the other stronger alleles by up to 42%. Transcriptome profiling of axillary (sympodial) shoot meristems (SYM) from *sp-classic* and wild-type plants revealed six misregulated genes related to the floral transition, which were used as biomarkers to show that the maturation of SYMs in the weaker *sp-5732* genotype is delayed compared to *sp-classic*, consistent with delayed shoot termination and semi-determinate growth. Assessing *sp* allele frequencies from over 500 accessions indicated that one of the strong *sp* alleles (*sp-2798*) arose in early breeding cultivars but was not selected. The newly discovered *sp* alleles are potentially valuable resources to quantitatively manipulate shoot growth and yield in determinate breeding programs, with *sp-5732* providing an opportunity to develop semi-determinate field varieties with higher yields.

***Corresponding Author:** Tel. 055-772-1356, E-mail: sjpark75@gnu.ac.kr

OC-0002

Development of Identification Markers for Ginseng Variaties Using Improved GBS

Junkyoung Choe[1], Moon Nam[2], Moogeun Jee[3*]

[1]C BioTo Co., LTD, 2 Techno-ro, Yuseong-gu, Daejeon, Republic of Korea
[2]Genomic Base, 19 Dasanjungang-ro, Namyangju-si, Gyeonggi-do, Republic of Korea
[3]Ginseng and Medicinal Plant Research Institute, 31 Daesan-gil, Jewon-myeon, Geumsan-gun, Chungcheongname-do, Republic of Korea

Ginseng (Panax ginseng) is a valuable medicinal plant cultivated in South Korea with immune-enhancing, anticancer, and antioxidative properties. Each ginseng variety has distinct characteristics, necessitating marker development for varietal identification. Recent advancements in GBS (Genotyping-By-Sequencing) have enabled cost-effective SNP (Single Nucleotide Polymorphism) marker selection. In recent years, with the rapid advancement of next-generation sequencing and the increasing importance of genome research in various crops, there has been a growing number of cases in the development of SNP markers for varietal identification. In line with this trend, the GBS technique is widely utilized as a cost-effective and efficient method for selecting necessary SNP markers compared to whole genome sequencing analysis, which involves analyzing the entire genome at a higher cost. However, medicinal plants like ginseng have large genome sizes and high heterozygosity, leading to missing observations of the same SNP loci across different varieties during GBS analysis. When there are many missing values in the data, it imposes limitations on selecting appropriate SNPs. In this study, the analysis results were compared using both the conventional GBS method and the GBS method with applied selective primers, targeting 22 varieties (88 individuals) of ginseng. We successfully developed distinct markers for ginseng varietal identification and established an effective GBS analysis technique using ginseng populations. This can be applied not only to ginseng but also to various crops, including medicinal plants, for the efficient selection of SNP markers and diverse analyses.

***Corresponding Author:** Tel. 041-635-6464, E-mail: jeemoo84@korea.kr

OC-0003

농촌진흥청 감귤 품종 개발

윤수현*, 박석만, 최철우, 진성범

제주특별자치도 서귀포시 남원읍 하례광장로 107 국립원예특작과학원 감귤연구소

농촌진흥청의 감귤 품종개발은 제주시험장(현 온난화대응농업연구소, 제주시 소재)에서 1970년대 초반부터 시작되었다. 주로 도입육종과 온주밀감의 가지 돌연변이에 의한 품종개발 연구가 이루어졌다. 교배육종은 1984년도에 시작되었으나, 그 당시에는 교배를 위한 유전자원의 종류가 적어 재래귤을 주요 육종자원으로 이용하였는데 품종개발 결과는 거의 없었다. 이 시기에 육성되었던 품종으로는 온주밀감의 변이품종 ‘신익조생’(*Citrus unshiu*)과 ‘하귤’의 변이품종 ‘황금하귤’(*Citrus natsudaidai*)이 육성되었다. ‘신익조생’은 일부 보급되었고 2000년대 초반까지 생산되었으나 품질이 낮아 더 이상 재배되지 않고 있다. 본격적인 감귤 품종개발연구가 이루어진 것은 현 농촌진흥청 국립원예특작과학원 산하 감귤연구소가 설립된 1991년 이후이다. 초기에는 주심배실생 육종이 주로 이루어졌고 교배육종은 일본에서 도입된 우수한 단배성 품종인 ‘청견’(*Citrus unshiu*× *Citrus sinensis*) 품종을 이용하면서 1994년부터 본격적인 교잡육종이 시작되었다. 이 후 육종사업이 진행되어 2004년에 ‘하례조생’(*Citrus unshiu*)이 육성되었다. 이 품종은 한국에서 감귤 육종을 시작한 이래 경제적으로 보급되고 생산되며 소비자에게 판매되고 있는 첫번째 품종이다.

‘하례조생’은 온주밀감 품종인 ‘입간조생’의 주심배실생 품종이다. 주심배(Nucellar embryo)는 배주 외벽의 주심조직에서 배가 발생(Nucellar embryogenesis) 하여 생겨난다. 이때 주심조직은 체세포이며 모본 품종과는 이론적으로 동일하다. 주심배실생이 모본과 유전적으로 동일함에도 품종화되는 경우는 전 세계적으로 감귤에서 빈번하게 이루어지고 있다. 주심배실생 특성은 보통 감귤에서는 과실의 착색이 빨라지고, 수세가 강해지는 특성이 있다. ‘하례조생’은 기존 온주밀감과 비교하여 형태적으로나 맛의 특성이 구별이 되지 않으나 제주도 환경에서 당도가 높고 수세가 강하여 생산성이 높아 차별화된다. 주심배실생 육종법을 통해 한라봉 고당도 품종 ‘탐나는봉’(2012), 천혜향의 고당도 품종 ‘사라향’(2016) 등이 개발되어 보급되고 있다. 연내수확 만다린 교잡품종 개발은 2010년대후 활발하게 진행되었는데, 신예감(2012), 미니향(2015), 윈터프린스(2016), 노을향(2016), 미래향(2022) 등이 개발되었다. 이중 ‘윈터프린스’의 보급이 활발하여 2022년 53ha가 보급되었다. 레몬 품종에서도 내한성이 강한 ‘제라몬’(2016)을 개발하여 보급하고 있는데, 일정 수준의 농가 수요가 있어 묘목 보급이 활발하게 이루어 지고 있다. 또한, 기능성 품종 ‘무봉’(2014)를 개발하였는데 플라보노이드 성분 중 나린진 함량이 높아 쌉싸름한 맛을 느낄 수 있는데, 자몽에서 소비자가 느끼는 맛과 비슷하다. 최근의 개발 품종 ‘옐로우볼’(2019)은 과피와 과육이 노란색인 것이 특징이다. 겨울을 넘겨 4월에 수확하는 만숙성의 품종이다. 이 품종의 대표적 특성은 노란색과 함께 저장성이 강하다는 것이다. 지금까지 감귤 품종개발 성과는 1991년 우리나라에서 처음으로 조직적인 감귤육종연구팀이 꾸려진 이래 30여년 기간 동안 26개의 품종이 개발되었다.

***교신저자:** Tel. 064-730-4101, E-mail: yunsh04@korea.kr

OC-0004

Artificial Intelligence for Data-driven Horticultural Crop Breeding

Myongkyoon Yang*

Department of Bioindustrial Machinery Engineering, Jeonbuk National University, 567 Baekje-daero, Deokjin-gu, Jeonju, 54896, Republic of Korea

Recently, the global food supply has become increasingly unstable due to the Russia-Ukraine conflict and climate change, highlighting the demand for smart farming technologies to ensure stable food production. In the breeding of horticultural crops, it takes a lot of time and money, and it is necessary to try to break away from existing breeding methods that have limitations in terms of predictability and efficiency. Phenotypic analysis using artificial intelligence is being attempted as a technology to improve crop productivity, durability and adaptability. Artificial intelligence, which was unfamiliar concept, is approaching researchers and the general public faster than ever with the advent of AlphaGo and ChatGPT. Accordingly, this study will look at artificial intelligence for application to breeding of horticultural crops and data essential to complete it. This includes the basic concepts of artificial intelligence and data, the features that appear, and the parts that are being used recently. Additionally, it introduces studies applied to actual horticultural crop breeding, discusses future directions and potential applications. Through this, I would like to suggest the possibility of using data and artificial intelligence to analyze the breeding process of horticultural crops, and expect to gain the potential as an important development tool for improving agricultural productivity and food security.

***Corresponding Author:** Tel. 063-270-2591, E-mail: yangmk@jbnu.ac.kr

OC-0005

Indirect selection for heat-tolerance using impedance flow cytometry in tomato

Jiwon Kim[1], Jihyun Lim[1], Hyewon Yu[1], Yoonjeong Jeong[1], Dohee Kim[1], Hyobong Jeong[2], Eunyoung Yang[3], Wonbyoung Chae[1*]

[1]Department of Environmental Horticulture, Dankook University, Cheonan 31116, Korea
[2]Vegetable Division, National Institute of Horticultural & Herbal Science, Wanju 55365, Korea
[3]Department of Vegetable Crops, Korea National University of Agriculture and Fisheries, Jeonju 54874, Korea

Tomato is one of the major fruit vegetables and temperature is the major limiting factor for its summer production. Due to climate change, the surface temperature of the earth is expected to increase by 0.3 °C in every decade. The elevated temperature has the adverse impact including heat stress (HS) on vegetable crops. HS causes the significant changes in physiological, morphological, biochemical, and molecular responses during vegetative and reproductive growth stages in tomato. Pollen traits are known to be related to HS tolerance and can be used for indirect selection. Recently, impedance flow cytometry (IFC) has been introduced to investigate pollen traits such as pollen viability, number, developmental stages and ploidy levels among about 250 plant species. Therefore, the response of pollen traits to elevated temperature were investigated among various tomato cultivars and elite lines. Twenty-four tomato accessions were grown in two greenhouses, where the temperature set-points for ventilation were 25 °C and 35 °C, respectively. The numbers of flowers and fruits, fruit set ratio (%), and fruit yield as well as pollen viability and developmental stage, and the number of pollens per flower were measured using IFC. Four types of reposes to heat stress were observed: no pollen production due to early flower abscission and, reduced pollen number and viability in microspore and mature pollen stages. The correlations between fruit characteristics and pollen traits were investigated for two temperature conditions with all tomato accessions, and then within large fruit (>50g) and cherry tomato groups, separately.

***Corresponding Author:** Tel. 041-550-3642, E-mail: wbchae75@dankook.ac.kr

OD-0001

Phenotypic characteristics and comparative transcriptome analysis of six pine species inoculated with pine wood nematodes (*Bursaphelenchus xylophilus*)

Yang-Gil Kim[1], Bae Young Choi[2], Dayoung Lee[1], Sunjeong Kim[1], Su-Vi Kim[1], Donghwan Shim[2], Youn-Il Park[2], Kyu-Suk Kang[1*]

[1]Department of Agriculture, Forestry and Bioresources, Seoul National University. Gwanak-ro 1, Gwanak-gu, Seoul 08826, Republic of Korea
[2]Department of Biological Sciences, Chungnam National University, Daejeon 13431, Republic of Korea

Pine species (*Pinus*) are conifer trees mostly found in the Northern Hemisphere and have important economical values as lumber and ornamental. The most dangerous pest of pine trees is a pine wood nematode (*Bursaphelenchus xylophilus*), which causes pine wilt disease and kills pine trees. Resistance to pine wilt disease varies among pine species, but the mechanism is still unknown. In this study, seedlings of six pine species (*Pinus thunbergii, P. koraiensis, P. densiflora, P. parviflora, P. rigida* × *P. taeda* and *P. strobus*) in outdoor field were artificially inoculated with pine wood nematodes. The death rates and other phenotypic traits of seedlings were measured. For transcriptome analysis, a total RNAs were extracted from the cambium samples of three representative repeats per species in 0, 2 and 4 weeks after inoculation. The RNA samples were sequenced by Novaseq 6000 (Illumina, USA) and assembled into *de novo* assembly to find out DEGs (differentially expressed genes). The death rates of pine seedlings were in the order of 80% (*P. thunbergii*), 77.8% (*P. koraiensis*), 62.5% (*P. densiflora*), 22.0% (*P. parviflora*) and 0% (*P. rigida* × *P. taeda* and *P. strobus*). For RNA sampling, infected seedlings were sampled from three species (*P. thunbergii*, *P. koraiensis*, and *P. densiflora*) and uninfected seedlings were sampled in the othe three species (*P. parviflora*, *P. rigida* × *P. taeda*, *P. strobus*). Finally, the number of DEGs (P-value $\leq$ 0.05 and fold change $\geq$ 1) were 1673 (*P. thunbergii*), 1054 (*P. koraiensis*), 4947 (*P. densiflora*), 3241 (*P. parviflora*), 748 (*P. rigida* × *P. taeda*) and 1777 (*P. strobus*). The comparative transcriptome analysis of six pine species inoculated with pine wood nematodes were presented and discussed in the talk.

***Corresponding Author:** Tel. 02-880-4753, E-mail: kangks84@snu.ac.kr

OD-0002

Spectral Unmixing of Hyperspectral Images of Coniferous Trees for Monitoring Needle Color

Youn-Il Park*

Department of Biological Sciences, Chungnam National University, Daehagro 99, Youseong, Daejon 34134, Republic of Korea

Leaf color changes throughout the whole cycle of leaf phenological events that are subjected to modulation by either abiotic stress or biotic infection. As leaf colors are closely related to quantity as well as quality of photosynthetic pigments and hence primary productivity of plants, monitoring and quantification of leaf colors are very important in assessing forest structure and function dynamics. In the present study, a hyperspectral camera sensor was used for non-invasive and non-destructive assessment of needle color changes from the field test grown coniferous trees. For this purpose, three different needle color variations of pine trees, namely, needles showing seasonal autumn colors, pine wilt nematode-infected necrosis process and natural death were selected and monitored. To avoid inherent mixed spectral properties in hyperspectral data, endmembers from the individual images were extracted using the Purity Pixel Index algorithm, assuming endmembers are linearly mixed. Out of 1,321 endmembers extracted from 378 hyperspectral images of six pine trees, 8 endmembers were finally selected for reconstruction of hyperspectral images and then abundance maps. Among 8 endmembers, 4 endmembers represent very low, low, intermediate and high contents of photosynthetic pigments, respectively. Accordingly, these coniferous endmembers could be useful to assess seasonal leaf phenology and damage scale of pine trees infected by pine wilt nematodes.

***Corresponding Author:** Tel. 042-821-5493, E-mail: yipark@cnu.ac.kr

OD-0003

Improvement of poplar trees to mitigate global climate change using gene editing technology

Hyunmo Choi, Su Jin Park, Hyun-A Jang, Hyoshin Lee*

Forest Bioresources Department, National Institute of Forest Science, Suwon 16631, Korea

Forests are the most significant carbon sinks for absorbing greenhouse gases. Breeding plays a crucial role in developing trees capable of addressing the climate crisis. However, conventional tree breeding is time-consuming and labor-intensive. To overcome these challenges, we have opted to utilize the CRISPR/Cas9 system, which enables precise breeding of trees within a shorter time.

Firstly, we focused on developing lignin-reduced poplars to facilitate the production of sustainable biomaterials. To effectively reduce lignin, we employed gene editing techniques to target various genes in the biosynthetic pathway. In a knockout line of one of these genes, we observed a reduction of approximately 25% in lignin content, accompanied by a 20% increase in saccharification efficiency. Currently, field tests are being conducted to ascertain whether the gene-edited trees can produce biomass suitable for short rotation coppice system.

Secondly, our breeding objective was to decrease the crown width of trees, enabling the planting of more trees in a limited area. Consequently, we successfully developed trees with branches that grow upright towards the sky. Moreover, we confirmed an increase in the height growth of these trees. Field tests were initiated to evaluate biomass production under varying density conditions.

Given the strict GMO regulations in Korea, establishing non-transgenic biotechnology is of utmost importance. Consequently, one approach involves utilizing the geminiviral replicon system, while simultaneously seeking improvements to enhance the probability of T-DNA not integrating into the genome. Additionally, we are experimenting with various techniques, including the use of vectors containing a tRNA-like structure.

***Corresponding Author:** Tel. 031-290-1142, E-mail: choihyunmo@korea.kr

OD-0004

Research on development of fast-growing trees for reducing particulate matters formation

Il Hwan Lee*, Siyeon Byeon, Changyoung Oh

Forest Tree Improvement and Biotechnology Division, Department of Forest Bio-resources, National Institute of Forest Science, Suwon 16631, Republic of Korea

Fast-growing trees grow faster than average, and they are typically represented by poplar and willow species. They are known to have high carbon absorption capacity, as well as good environmental pollution purification capabilities. Here, we present the current research on the development of poplars and willows to reduce particulate matters formation. Particulate matters are made of solid particles and liquid droplets in the air and are classified into coarse particles(PM10), fine particles(PM2.5) and ultrafine particles(PM0.1) according to their size. It is known that more than 70% of the particulate matters is secondary particles, which is formed by chemical reactions of harmful pollutants emitted in gaseous form. Volatile organic compounds(VOCs), which are the main cause of secondary particulate matter, are divided into anthropogenic volatile organic compounds(AVOCs) and biogenic volatile organic compounds(BVOCs) according to their emission sources. In order to reduce particulate matters, efforts to reduce both VOCs are required. In this study, poplar and willow clones that emit less isoprene, a major BVOC, were selected through the evaluation of isoprene emission. In addition, endophytic microorganisms were isolated from plants growing on AVOCs-contaminated areas, and the AVOCs reduction ability was evaluated. The discovered AVOCs-reducing endophytic microorganisms will be used for the development of trees with superior AVOCs reduction ability by inoculating them. In the future, we will contribute to improving the urban environment by reducing particulate matter through planting these trees in AVOCs-contaminated area.

***Corresponding Author:** Tel. 031-290-1135, E-mail: lih0618@korea.kr

OD-0005

호랑버들과 갯버들, 종간 교잡종 식별을 위한 DNA 마커 개발

서한나*, 임효인, 이제완

경기도 수원시 권선구 온정로 39 국립산림과학원 산림생명자원연구부

버드나무속 식물들은 빠른 초기생장과 높은 발아율, 무성생식 등의 특성으로 바이오매스 생산을 위한 속성수로 활용된다. 국립산림과학원 산림생명자원연구부는 바이오매스 생산이 우수한 신품종 육성을 위해 호랑버들을 암나무로 갯버들을 수나무로 인공교배하여 종간 교잡종을 육성하였다. 호랑버들과 갯버들, 종간 교잡종은 개화 전 어린나무 시기에 명확한 식별이 어렵고, 분리된 생식기관과 영양기관의 생장기로 인해 형태적 특성을 확인하기 위한 긴 시간이 요구된다. 따라서 형태적 특성을 이용한 구별의 한계를 해결하고, 버드나무속 교잡 성공 여부를 조기에 판단하기 위한 식별 기술이 필요하다. 외부 형태 및 환경 변이에 영향이 없는 DNA 마커는 외부 형태만을 가지고 정확한 식별이 불가능한 시기에 종 식별을 위해 이용된다. 그 중 식물의 계통 분석 및 종 판별 연구에서 주로 사용되는 엽록체 DNA는 대부분의 활엽수종에서 모계 유전하는 특징을 가진다. 하지만 종간 교잡종의 식별은 부모종과 구분할 수 있어야 하므로 본 연구는 엽록체 DNA가 아닌 핵 DNA를 사용하였다. 본 연구의 목적은 호랑버들과 갯버들, 종간 교잡종의 조기 식별을 위한 DNA 마커를 개발하는 것이다. 이를 위해 버드나무속에서 개발된 총 35개의 nuclear Simple Sequence Repeat(nSSR) 마커를 평가하여 호랑버들과 갯버들, 종간 교잡종 간 차이를 나타내는 2개의 nSSR 마커를 선발하였다. 해당 마커 영역의 염기서열 분석 결과, SSR영역 이외의 종간 차이를 보이는 insertions or deletions (InDels) 구간이 존재하는 것을 확인하였다. 이에 종간 차이를 나타내는 InDel 영역이 포함되어 교잡종을 효과적으로 구분하는 primer set를 제작하였다. 제작된 primer set를 적용하여 증폭시킨 결과, 호랑버들과 갯버들에서 각기 다르게 관찰되는 증폭산물과 이를 모두 가지고 있는 교잡종의 특이적인 증폭산물을 관찰할 수 있어 교잡종을 효과적으로 식별할 수 있었다. 본 연구에서 얻은 결과는 호랑버들과 갯버들, 종간 교잡종의 유전자원 관리, 교잡종 조기 식별 관리 등에 활용할 수 있다.

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***교신저자**: Tel. 031-290-1118, E-mail: caragana2@korea.kr

OE-0001

Development of high-throughput SNP genotyping system for Korean rice varieties based on genome sequence analysis

Hyeonso Ji[1*], Kyeong-Seong Cheon[2], Chaewon Lee[3], Yunji Shin[4], Dong-Kyung Yoon[1], Young-Min Jeong[5], Young-il Cho[5], Hoon Jang[6], Yong-Chan Park[6], Kyung-Yun Kim[7], Hang-Chul Cho[7], Hyoja Oh[1], Jeongho Baek[1], Song Lim Kim[1], HwangWeon Jeong[1], Jae Il Lyu[1], Kyung-Hwan Kim[1]

[1]National Institute of Agricultural Sciences, RDA, Jeonju 54874, Korea
[2]National Institute of Forest Science, Suwon 16631, Korea
[3]National Institute of Crop Science, RDA, Suwon 16429, Korea
[4]Genecell Biotech Inc., Wanju, 55322, Korea
[5]Korean Agriculture Technology Promotion Agency, Gimje 54324, Korea
[6]CELEMICS, Seoul 08506, Korea
[7]INSILICOGEN, Yongin 16954, Korea

Korean japonica rice varieties exhibit remarkable phenotypic differences in important agronomic traits, including disease resistance, plant architecture, eating quality, heading date, seed size, and yield. However, polymorphic DNA markers among them were scarce, which hampered mapping genes for desirable traits and marker-assisted selection for molecular breeding. In order to overcome this limitation, we analyzed genome sequencing data from 13 Korean *japonica* rice varieties and discovered 740,566 SNPs. Among them, we selected SNPs with high polymorphism information content values and SNPs predicted to have high impact effects on gene. With thus selected SNPs, we developed 1,225 Kompetitive Allele-Specific PCR (KASP) markers for the selected SNPs. These markers have been widely used in mapping QTLs for bakanae disease resistance, pre-harvest sprouting resistance, root radial oxygen loss, seed size etc. and marker-assisted backcrossing. Furthermore, we developed a target capture sequencing genotyping system containing 2,565 SNPs, including 1,225 SNPs for *japonica* used in developing the above mentioned KASP markers and 1,339 SNPs informative for *indica*. In a diversity analysis with 50 rice varieties using this system, 2,341 (91.3%) of the 2,565 SNPs produced useful polymorphic genotype data and the mean number of markers polymorphic between any two varieties was 854. This system can be useful for wide range of rice germplasm and will be a powerful tool for rice genetics and breeding.

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

OE-0002

Genome-wide association study of resistance to new cyst nematode species in soybean

Kyung Do Kim*

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

White soybean cyst nematode (*Heterodera sojae*) is a newly discovered species of cyst nematode that parasitizes soybean roots and reduces their growth and yield. No genes or molecular markers linked to *H. sojae* resistance have been discovered yet, and it is unknown if the genetic markers linked to *H. glycines* (soybean cyst nematode) resistance can be used to predict resistance to *H. sojae*. Here, we performed a genome-wide association study (GWAS) on 385 accessions from the Korean soybean core collection. All accessions were phenotyped for *H. sojae* resistance while genotyped with markers associated with *H. glycines* resistance. Interestingly, not all the accessions carrying *H. glycines* resistance exhibit *H. sojae* resistance. The prediction rate for *H. sojae* resistance was 59.2%, which is insufficient to replace phenotypic testing. The GWAS analysis identified thirteen significant SNPs associated with *H. sojae* resistance. The allelic effect of the resistance was statistically tested and suggested that four SNPs located on Chromosomes 1 and 18 are associated with resistance to *H. sojae*. Candidate genes related to the resistance were identified and found to be mostly expressed in roots. The SNPs related to the resistance were developed as kompetitive allele specific PCR (KASP) markers, which can be utilized for high-throughput screening of *H. sojae* resistance in soybean breeding programs.

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

OE-0003

Transcription Factor-Mediated Control of Anthocyanin Biosynthesis in Rice Pericarp

Sun-Hyung Lim[1,2*]

[1]Division of Horticultural Biotechnology, School of Biotechnology, Hankyong National University, Anseong, 17579, Korea
[2]Research Institute of International Technology and Information, Hankyong National University, Anseong, 17579, Korea

Flavonoids are very useful to plants and humans and are mainly accumulated in various tissues such as leaves, flowers, stems, and seeds. Rice (*Oryza sativa* L.) show various colors on the pericarp according to the accumulation of anthocyanins and proanthocyandins. Various transcription factors are involved in the process of flavonoid biosynthesis, among them the MBW complex composed of R2R3 MYB, basic helix-loop-helix (bHLH), and WD40 protein. Previous work revealed that the two basic helix-loop-helix (bHLH) transcription factors OsKala4 and OsRc are key regulators for the black and red pericarp traits, respectively, and their inactivation results in rice with white pericarp. However, their pericarp-specific R2R3 MYB partner remained unknown. Here, we characterized the role of the R2R3 MYB gene OsKala3 in rice pericarp pigmentation through genetic and molecular approaches. A rice protoplast transfection assay showed that OsKala3 is a nuclear-localized protein. Furthermore, OsKala3 physically interacted with OsKala4 in a yeast two-hybrid analysis. Co-transfection assays in rice protoplasts revealed that OsKala3 and OsKala4 mediate the activation of anthocyanin biosynthetic genes. Notably, the OsKala3 promoter region exhibited an insertion polymorphism specifically in rice cultivars with black pericarp, creating two tandem repeats while red and white varieties harbor only one. The number of repeats within the OsKala3 promoter correlated with increased transactivation by OsKala3, thus providing a rationale for the black pericarp characteristic of cultivars with two repeats. These results thus provide evidence for the molecular basis of anthocyanin biosynthesis in rice pericarp and may facilitate the introduction of this beneficial trait to other rice cultivars through marker-assisted breeding.

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

OE-0004

Transcriptomic and epigenomic analyses revealed that polycomb repressive complex 2 (PRC2) regulates not only the developmental program but also stress-responsive metabolism in *Brassica rapa*

Adji Baskoro Dwi Nugroho, Sujeong Kim, Sang Woo Lee, Dong-Hwan Kim*

Department of Plant Science and Technology, Chung-Ang University, Anseong, Republic of Korea

Polycomb group proteins (PcG) play a crucial role in developmental programs in eukaryotic organisms, including plants. PcG-mediated gene repression is achieved by epigenetic histone modification on target chromatins. Loss of PcG components leads to severe developmental defects. CURLY LEAF (CLF), a PcG component in *Arabidopsis*, catalyzes the trimethylation of histone H3 on lysine 27 (H3K27me3), a repressive histone mark in numerous genes in *Arabidopsis*. In this study, we isolated a single homolog of *Arabidopsis* CLF, namely, BrCLF, in *Brassica rapa* ssp. *trilocularis*. Transcriptomic analysis revealed that BrCLF participated in *B. rapa* developmental processes, such as seed dormancy, leaf and flower organ development, and floral transition. BrCLF was also involved in stress signaling and stress-responsive metabolism, such as aliphatic and indolic glucosinolate metabolism in *B. rapa*. Epigenome analysis showed that H3K27me3 was substantially enriched in genes related to these developmental and stress-responsive processes. Thus, this study provided a basis for elucidating the molecular mechanism of the PcG-mediated regulation of development and stress responses in *B. rapa*.

***Corresponding Author:** Tel. 031-670-3260, E-mail: dhkim92@cau.ac.kr

OE-0005

Leaky mutations in the zeaxanthin epoxidase in Capsicum annuum result in bright red fruit containing a high amount of zeaxanthin

Seo-Young Lee[1], So-Jeong Jang[1], Hyo-Bong Jeong[1], Joung-Ho Lee[1], Seungki Back[1], Geon Woo Kim[1], Jelli Venkatesh[1], Jin-Kyung Kwon[1], Da-Min Choi[2], Jeong-Il Kim[2,3], Geun-joong kim[4], Byoung-Cheorl Kang[1*]

[1]Department of Agriculture, Forestry, and Bioresources, Research Institute of Agriculture and Life Sciences, Plant Genomics Breeding Institute, College of Agriculture and Life Sciences, Seoul National University, Seoul, South Korea
[2]Department of Integrative Food, Bioscience and Biotechnology, Chonnam National University, Gwangju 61186, Republic of Korea
[3]Kumho Life Science Laboratory, Chonnam National University, Gwangju 61186, Republic of Korea
[4]Biochemicals & Synthetic Biology Research Center, Korea Research Institute of Bioscience and Biotechnology, Gwahak-ro 125, Yuseong-gu, Daejeon 305-806, Republic of Korea

Fruit color is one of the most important traits in peppers due to its aesthetic value and nutritional benefits. Mature fruit color is determined by carotenoid composition resulting from diverse mutations of carotenoid biosynthetic genes. The EMS204 line, derived from an EMS mutant population, presents a bright red color, whereas the wild-type Yuwolcho cultivar shows a standard red color. HPLC analysis indicates that EMS204 fruit contains more zeaxanthin and less capsanthin and capsorubin than wild-type Yuwolcho. MutMap was used to reveal the color variation of EMS204 using an F3 population derived from a cross of EMS204 and Yuwolcho, and the locus was mapped to a 2.5-Mbp region on chromosome 2. Among the genes in the region, a missense mutation was found in *ZEP* (*zeaxanthin epoxidase*) that results in an amino acid sequence alteration (V291→I). A color complementation experiment with Escherichia coli containing carotenogenic genes and ZEP in vitro assay using thylakoid membranes revealed decreased enzymatic activity of EMS204 ZEP. Virus-induced gene silencing showed that *ZEP* silencing also results in bright red fruit containing less capsanthin but more zeaxanthin than the wild type. A germplasm survey of red color accessions revealed no similar carotenoid profiles to EMS204. However, a breeding line containing a *ZEP* mutation showed a very similar carotenoid profile to EMS204. Our results provide a novel breeding strategy to develop red pepper cultivars containing high zeaxanthin contents using *ZEP* mutations.

***Corresponding Author:** Tel. 02-880-4573, E-mail: lsy256913@snu.ac.kr

OE-0006

The patatin-related *phospholipase-AIIIδ* gene regulates lignification and leaf senescence in *Arabidopsis*

David Charles Simiyu[1,2,3], Ok Ran Lee[1,2*]

[1]Department of Applied Plant Science, College of Agriculture and Life Science, Chonnam National University, Gwangju 61186, Korea
[2]Interdisciplinary Program in IT-Bio Convergence System, Chonnam National University, Gwangju 61186, Korea
[3]Department of Botany, University of Dar es Salaam, P.O. Box 35091 Dar es Salaam, Tanzania

Deposition of lignin in plant cell walls is an important adaptation that gives plants the mechanical strength needed for vertical growth. Lignin also defend plants against excessive water loss during abiotic stresses. Lignin compounds are biosynthesized through the general phenylpropanoids pathway which also produces antioxidant compounds called flavonoids. Several enzymes are involved in lignin biosynthesis including phenylalanine ammonia lyase, hydroxycinnamoyl-CoA transferase, and cinnamoyl-CoA reductase. Moreover, lignin biosynthesis is regulated by transcription factors such as MYB58 and MYB63. Recently, we discovered that lignin biosynthesis is also regulated by several members of patatin-like phospholipase-AIII (pPLAIII)-encoding genes including *pPLAIIIα* and *pPLAIIIγ*. Overexpression (OE) of these *pPLAIIIs* decreased lignin content causing vertical growth limitations. Moreover, *pPLAIIIαOE* plants showed delayed senescence with lower ROS levels. Similarly, *pPLAIIIγOE* displayed lower ROS levels indicating enhanced antioxidant activity. Here we report that another member of *pPLAIIIs*, *pPLAIIIδ*, also regulates lignification. Overexpression of *pPLAIIIδ* delayed lignification, reduced height of plants and seeds, and decreased leaf area, while silencing of *pPLAIIIδ* (RNAi) showed opposite effects. We also report that senescence was delayed in *pPLAIIIδOE* and accelerated in *pPLAIIIδ:RNAi* lines. Increased ROS scavenging in *pPLAIIIδOE*, confirms previous findings that *pPLAIIIsOE* enhances ROS scavenging. Through this study we can suggest that overexpression of *pPLAIIIs* acts as a signal to shift the phenylpropanoids pathway from lignin biosynthesis to flavonoids biosynthesis, decreasing lignin content but enhancing antioxidants biosynthesis. These findings provide new insights to plant breeders on how the phenylpropanoids pathway can be targeted to make plants with desired traits including reduced lignin content.

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

OF-0001

Unveiling the Genetic and Functional Insights of Sesame Lignans for High-Lignan Variety Development and Industrial Utilization

Eunsoo Lee*, Sungup Kim, Jeongeun Lee, Eunyoung Oh, Jung In Kim, Sang Woo Kim, Min Young Kim, Myoung Hee Lee, Kwang-Soo Cho, Choon-Song Kim

Upland Crop Breeding Research Division, Department of Southern Area Crop Science, National Institute of Crop Science, RDA, Miryang, Gyeongnam, 50424, Republic of Korea

Sesame (*Sesamum indicum* L.), an oil crop, is gaining worldwide recognition for its numerous health benefits, leading to increased consumption. Industrially, sesame is primarily valued for its oil, which mainly consists of lignans. Consequently, lignan content is a crucial agronomic trait that determines the industrial utilization of sesame. However, studying the genetics and physiology of lignans in sesame poses challenges due to be influenced by multiple genes and environmental factors. Understanding gene function and synthetic pathways related to lignans in sesame remains limited. To address these knowledge gaps, we conducted genetic analyses using genetic segregation populations derived from resources with varying lignan content. Through the QTL-seq approach, we identified genetic loci controlling the levels of lignans, specifically sesamin and sesamolin. As a result, three major QTLs associated with lignan content were discovered. Additionally, we performed QTL analysis using GBS to uncover genetic factors influencing the content of lignan glycosides. By identifying these loci, we selected candidate variants to develop molecular markers, which were subsequently evaluated for their selection effects on populations and resources. Moreover, to confirm the cognitive function of sesame lignans, we utilized genetic resources to explore the relationship between variations in lignan content. This study not only highlights the significance of sesame oil but also provides valuable insights for the development of high-lignan varieties through the application of molecular markers in breeding strategies. Overall, this research contributes to our understanding of sesame oil's importance and paves the way for advancements in sesame breeding programs targeting enhanced lignan content.

***Corresponding Author:** Tel. 055-350-1239, E-mail: awesomelee@korea.kr

OF-0002

Glycyrrhiza interspecific hybrid cultivar development and Korea Pharmacopoeia (KP) registration for domestically producing licorice

Jeonghoon Lee*

National Institute of Horticultural and Herbal Science, RDA, Eumseong 27709, Republic of Korea

Licorice has been a medicinal crop, which was mainly used as a traditional medicine, food and cosmetics, mostly depends on imports in Korea. We have been trying to produce licorice in Korea for a long time. However, when it grows in Korea, the standard ingredient (Glycyrrhizin, Liquiritigenin) are below the standard value of KP and physiological disorder occur. To solve these issue, we have developed *Glycyrrhiza* interspecific hybrid cultivar suitable for domestic environment. For listing *Glycyrrhiza* new cultivar classified as *G. korshinskyi* in KP, we searched distribution of licorice hybrid species in nature, *Glycyrriza* new cultivar showed a safety through toxicity tests including 13 weeks repeated oral does. The result, *Glycyrriza* new cultivar (= *G. korshinskyi*) has been registered as a new origin plant for licorice in the Korean Pharmacopoeia, establishing a foundation for domestic licorice cultivation.

***Corresponding Author:** Tel. 043-871-5670, E-mail: artemisia@korea.kr

OF-0003

Large-scale micropropagation of *Panax ginseng* Meyer

Jung-Woo Lee*

Department of Herbal Crop Research, National Institute of Horticultural and Herbal Science, Rural Development Administration, Eumseong 27709, Republic of Korea

Panax ginseng Meyer is a valuable medicinal crop. However, the species' propagation is limited by its long reproductive cycle and low seed yield. The present study aims to establish a micropropagation system for *P. ginseng* cultivars via somatic embryogenesis and evaluate the genetic fidelity of regenerated plants. The somatic embryo induction was maximized in the original strength MS medium supplemented with 5% sucrose. The somatic embryo maturation was the best in the medium supplemented with 1/3 MS and 2% sucrose. The number and the quality of regenerated plants was the highest in the germination media supplemented with 1/2 MS or 1/2 SH basal media with 2% sucrose. A general 4-year-old *P. ginseng* could produce between 23.1-58.8 seeds per individual plant in 4 years, whereas micropropagation via somatic embryogenesis could produce between 37.1-41.1 *in vitro*-grown roots (IGRs) per a single seed in 1 year. IGRs produced from micropropagation were successfully acclimated to the soil, but their plants were morphologically different from those of general *P. ginseng*. Flow cytometry and molecular marker analysis suggested that the genetic fidelity of the plants derived from IGRs was comparable with that of the control. HPLC analysis showed that IGRs accumulated more ginsenoside than those of the control, but the ginsenoside content of 2 year old IGRs was similar to that of the controls after acclimatization. These results suggest that the micropropagation approach via somatic embryogenesis is valuable for the large-scale propagation of genetically stable cultivars of *P. ginseng*.

***Corresponding Author:** Tel. 043-871-5612, E-mail: enzymer@korea.kr

OF-0004

Utilizing Genomic Insights for the Breeding of Special Crops: A Study on Chimeric Ornamental Plants

Hyun-Seung Park[1,2*], Jae-Hyeon Jeon[2], Woohyeon Cho[2], Yeonjeong Lee[2], Jee Young Park[2], Tae-Jin Yang[2]

[1]Department of Integrative Biological Sciences and Industry, Sejong University, Seoul 05006, Korea
[2]Department of Agriculture, Forestry and Bioresources, Research Institute of Agriculture and Life Sciences, and Plant Genomics and Breeding Institute, College of Agriculture and Life Sciences, Seoul National University, Seoul, 08826, Republic of Korea

Plant breeding, a critical discipline in botany and agriculture, focuses on improving the genetic traits of plants to produce desirable characteristics. This includes both functional attributes such as increased yield, drought tolerance, metabolite contents, and enhanced functional properties, as well as aesthetic features that enhance a plant's ornamental value, like unique coloration, shape, and growth patterns. Chimeric plants, with their mix of green and albino tissues, present a unique opportunity in this area. Their striking visual appeal makes them highly sought-after in the market. Understanding the genetic mechanisms behind traits of interest, such as the chimeric phenotypes, can drastically enhance plant breeding efforts. Our study investigated the genetic mechanisms behind the unique chimeric phenotypes in ornamental plants by comparing plastid genomes across 20 species. We identified different mutations, mostly involving changes in amino acid length and one non-synonymous single-nucleotide polymorphism in the rpoC2 protein of *Reynoutria japonica*, which is a crucial subunit of plastid-encoded RNA polymerase. Structural protein modeling indicated that this mutation might destabilize the peripheral helix, while plastid gene expression analyses in chimeric *R. japonica* demonstrated a significant decrease in albino cells. This evidence suggests an impairment in the biosynthesis of the photosynthesis system. We suggest that mutant plastomes are maintained by heteroplasmy in chimeric plants. Our approach identified stable albino genes in the plastid genome of a chimeric ornamental plant, offering a high throughput system for scanning plastid-driven albino mutations.

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***Corresponding Author:** Tel. 02-3408-3837, E-mail: hspark10@sejong.ac.kr

OF-0005

Molecular analysis of high-linoleic acid perilla mutants and the functional characterization of *PfrFAD3a* and *PfrFAD3b* genes

Hyun-A Choi[1], Mid-Eum Park[2], Hyun Uk Kim[1,2,3*]

[1]Department of Bioindustry and Bioresource Engineering, Sejong University, Seoul, South Korea
[2]Department of Molecular Biology, Sejong University, Seoul, South Korea
[3]Plant Engineering Research Institute, SejongUniversity, Seoul, South Korea

Perilla frutescens var. *frutescens* is an allotetraploid oil crop with seeds containing 64% α-linolenic acid (18:3) and 14% linoleic acid (18:2). However, the presence of 18:3 in perilla seeds poses both benefits, such as health promotion, and drawbacks, including quick rancidity and trans-fat formation. Therefore, it is crucial to develop diverse perilla varieties tailored to specific purposes. This study aimed to analyze high-linoleic acid perilla mutants, SJDY-1-19 and SJNC-110-18, obtained through gamma irradiation. The 18:2 content in SJDY-1-19 and SJNC-110-18 significantly increased to 40% and 30%, respectively, compared to the wild type (13-14%). Perilla possesses two copies of the *FAD3* gene, namely *PfrFAD3a* and *PfrFAD3b*. In SJDY-1-19, a 4-bp deletion was observed in the *PfrFAD3b* gene, while *PfrFAD3a* remained unaltered. In SJNC-110-18, *PfrFAD3a* was not detected through genomic DNA PCR and Reverse Transcription (RT)-PCR. These observations indicated that the increase in 18:2 content in these two lines resulted from mutations in the *FAD3* gene. To further confirm the function of the two *FAD3* genes in perilla, they were individually transformed into the Arabidopsis *fad3-2* mutant. The transformants exhibited increased levels of 18:3 compared to the *fad3-2* mutant, supporting the notion that both *PfrFAD3*a and *PfrFAD3b* are involved in 18:3 synthesis. These findings provide a foundation for the targeted breeding of perilla varieties with desired fatty acid compositions, facilitating the improvement and utilization of perilla as a valuable crop.

***Corresponding Author:** E-mail: hukim64@sejong.ac.kr

OG-0001

Comparison of rice growth patterns with field phenotyping data in rice paddy field

Sungyul Chang*, Ji-Hyeon Lee

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

Technologies for indoor plant phenotyping revealed numerous traits of interest were studied with the platform and revealed new insight of the traits. Unfortunately, the insights could not readily applied in a breeding scheme or physiology study in outdoor due to limited environmental interaction of plant in a glasshouse. Therefore, alternative phenotyping tools such as terrestrial laser scanner (TLS) was required for phenotyping in outdoor. Two rice cultivars grow in rice paddy field and took images with TLS over eight weeks. Three dimensional (3D) data points were extracted and heights and canopy information fit into Gumbel distribution for further analysis. The result showed that multiple linear regression (MLR) from Gumbel distribution was accurately predicted heights of plants (r2=0.96). Also, the MLR was accurately predicted leaf areas (r2=0.91) and biomass (r2=0.90) of rice. The result indicated that feasibility utilized TLS for growth pattern of a crop in open field. In conclusion, the high throughput field phenotyping (HTFP) was emerging field in smart agriculture and it showed possibilities to apply the TLS for study of plant physiology and plant breeding in future.

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***Corresponding Author:** Tel. 063-238-5279, E-mail: schang8@korea.kr

OG-0002

Current status and applications of crop phenomics in the National Institute of Agricultural Sciences in Korea

Song Lim Kim, Jeongho Baek, Hyeonso Ji, In sun Yoon, Hwangwon Jung, Jaeil Ryu, Inchan Choi, Hongseok Lee, Chaewon Lee, Kyung-Hwan Kim*

National Institute of Agricultural Sciences, RDA, Wanju 55365, Republic of Korea

Crop phenomics that quantitatively measures crop traits using digital image data is a necessary foundation for digital breeding. In 2017, the National institute of Agricultural Sciences (NAS) established the National Crop Phenomics Center (NCPC) with the largest crop phenomics research building in Korea, and is expanding cooperative networks with institutions, universities, and companies. The infrastructure of the NCPC consists of high-throughput testing facilities, XYZ robotics system, precision environment room, and chambers with various image sensors such as RGB, NIR, IR, fluorescence, and hyperspectral cameras. It is possible to analyze growth patterns during whole life of crops and the characteristics related with tolerance to abiotic and biotic stresses (heat, drought, salt, and disease, etc.). Also, the shape and composition of plant organs such as flowers, seeds, and fruits can be analyzed producing numerical data through digital image analysis. Up to the present, more than 20 crop species have been analyzed, including rice, soybean, corn, sesame, cabbage, phalaenopsis, gerbera and so on, and the range of analysis items is also expanding. In addition, we are striving for digital breeding through production of artificial intelligence learning data set, phenome-genome linkage studies, and development of analysis software. In November 2022, NCPC has been certified as a national reference standard data center by the Ministry of Trade, Industry and Energy of Korea. In addition, NCPC will take the lead in promoting agricultural industry and digital breeding by improving the accuracy and reliability of data production, evaluation, management and dissemination.

***Corresponding Author:** Tel. 063-238-4651, E-mail: biopiakim@korea.kr

OG-0003

The current status of plant phenotyping technologies being developed at the KIST Phenomics Research Group

Yun-Hee Shin, Unseok Lee, Ji Hye Yoo, Hong-Beom Choi, Jae Kun Park, Hyein Lee, Soo Hyun Park*, Taek Sung Lee*, Hyoung Seok Kim*

Smart Farm Research Center, KIST Gangneung, Institute of Natural Products, 679 Saimdang-ro, Gangneung, Gangwon 25451, Republic of Korea

Plant phenotyping technology has received increased attention due to its broad range of applications in assessing various traits related to yield, product quality, and the physiological condition of plants. With the rapid advancement of artificial intelligence-based image analysis algorithms, there are now more opportunities to utilize computer vision technologies for measuring various plant phenotypes including complex morphological characteristics. However, a limitation remains for plant scientists and plant breeders who may not have easy access or proficiency in computer programming. We would like to introduce a recently developed software (PhenoTool) that can effectively analyze various plant images using both traditional computer vision algorithms and deep learning-based algorithms with a user-friendly interface. The PhenoTool software was tested for measuring quantitative and qualitative phenotypes using images acquired from both the PhenoBox and the x-y-z phenotyping stage in a series of case studies. These case studies aimed to assess the effectiveness of the PhenoTool software in plant breeding and physiology research. Additionally, they aimed to explore how recently available deep learning algorithms, such as Segmentation Anything, could enhance plant image analysis capabilities within the PhenoTool software.

***Corresponding Author:** Tel. 033-650-3660, E-mail: ecoloves@kist.re.kr, tslee@kist.re.kr, hkim58@kist.re.kr

OG-0004

Crop phenomics to genomics in the mathematical point of view

Younghae Do*

Department of Mathematics, Nonlinear Dynamics & Mathematical Application Center, Kyungpook National University, Daegu 41566, Republic of Korea

Crop phenomics is the multidisciplinary study of high-throughput accurate acquisition and analysis of multidimensional phenotypes on an organism-wide scale through crop development. On the other hand, crop genomics is the study of the genetic makeup of crops.The integration of genomics and phenomics in crop improvement can upscale the efficiency of breeding systems targeting climate resilience and hasten cultivar release cycle.In the mathematical point of view, the integrating study of crop phenomics and genomics is dealing with multiscale modelling of crop system. Ideally, crop phenomics (genomics) will correspond to the study at Macro (Micro) scale level, respectively. One of key questions in this study is how to make connections from multiscale data. For instance, many data produced at Macroscale will be plant height, leaf area, biomass, etc, and genomic data for Micro scale. Making connections between two different scale data has a major role in crop breeding programs. In this talk, to make connections between two different scale data at crop system in the future, we introduce a multiscale model of atopic dermatitis (AD) disease and show how to develop multiple phenotypes in AD. As a way of developing crop phenomics, based on Artificial Intelligence and Bigdata technology, AD Diagnosis Model will be introduced.

***Corresponding Author:** Tel. 053-950-6308, E-mail: yhdo@knu.ac.kr

OH-0001

Development of targeted base editing of cellular organelle DNA in plants

Young Geun Mok[1,3]†, Sunghyun Hong[1,3]†, Jin-Soo Kim[1,2]*

[1]Center for Genome Engineering, Institute for Basic Science, Daejeon, Republic of Korea
[2]NUS Synthetic Biology for Clinical & Technological Innovation (SynCTI) and Department of Biochemistry, National University of Singapore, Singapore
[3]GreenGene Inc. Seoul, Republic of Korea

Plant cellular organelles have their own DNA, such as chloroplast DNA (cpDNA), which contains up to 315 genes, typically ranging from 120 to 130. These genes include those encoding essential components in photosystems I and II, as well as the large subunit of RuBisco, which facilitates CO2 fixation in plants. However, using CRISPR/Cas9 to edit these genes can be challenging due to the difficulty in targeting guide RNAs to the cellular organelles. Recently, a new enzyme called $\mathrm{DddA_{tox}}$, which is a cytosine deaminase at dsDNA derived from bacteria, has made it possible to edit cytosine to thymine in cellular organelle DNA without requiring CRISPR/Cas9. $\mathrm{DddA_{tox}}$ was originally used as a pair of two inactive halves in a split form due to its cytotoxicity, non-toxic full-length variants called monomeric DddA have also been developed. Last year, organelle DNA adenine base editors called TALEDs were reported, which combine $\mathrm{DddA_{tox}}$ with the adenine deaminase TadA8e, thereby expanding the scope of base editing that was previously limited to cytosine only. This technology offers new opportunities for developing plants with enhanced photosynthesis, herbicide tolerance, and cytoplasmic male sterility through the editing of chloroplast and mitochondrial DNA in plants. These advancements have the potential to make significant contributions to overcoming climate change and addressing food shortages.

†These authors contributed equally to this work

***Corresponding Author:** E-mail: jskim01@snu.ac.kr

OH-0002

A new ternary vector system for efficient maize transformation and targeted mutagenesis

Keunsub Lee[1,2], Minjeong Kang[1,2,3], Qing Ji[2], Sehiza Grosic[2], Kan Wang[1,2*]

[1]Department of Agronomy, Iowa State University, Ames, Iowa, USA
[2]Crop Bioengineering Center, Iowa State University, Ames, Iowa, USA
[3]Interdepartmental Plant Biology Major, Iowa State, University, Ames, Iowa, USA

Maize (*Zea mays* L.) is one of the most important cereal crops and global maize production has substantially increased over the past decades. However, climate change and rapidly increasing global population urge the development of novel strategies for sustainable food and feed production with improved stress resilience and nutrient contents. Recently developed CRISPR technology presents a great opportunity for rapid crop trait improvements and hypothesis testing for critical biological questions. Unfortunately, this revolutionary genome engineering tool cannot be fully utilized due to the existing bottlenecks: low genetic transformation (and genotype-dependence) and CRISPR reagent delivery efficiencies. To overcome these bottlenecks, we developed a new ternary vector system for *Agrobacterium*-mediated maize transformation. A ternary vector system consists of a set of compatible plasmids: a binary vector carrying a gene of interest (GOI) T-DNA and a helper plasmid containing extra copies of essential *Agrobacterium* virulence genes. By combining with the QuickCorn media regime, we established a rapid maize B104 transformation method, which produces rooted transgenic plants in less than 2 months. Using the rapid transformation method, CRISPR-Cas9-mediated targeted mutagenesis was highly efficient, as about two thirds of the T0 plants were loss-of-function mutants. We then adopted *neomycin phosphotransferase II* (*NptII*) as a selectable marker gene and observed drastically reduced escape rate compared to *bar*/bialaphos selection system. In addition, we showed that a new visible marker *RUBY*, which converts tyrosine into purple pigment betalain, can be useful to monitor maize transformation and transgene integration in the transgenic and gene-edited plants.

***Corresponding Author:** Tel. +1-515-294-4429, E-mail: kanwang@iastate.edu

OH-0003

Beyond genome sequencing: Data-driven crop research toward digital breeding

Woo-Jong Hong*

Department of Smart Farm Science, Kyung Hee University, Yongin 17104, Republic of Korea

Due to the unprecedented climate crisis and global population growth, food security which supports the current civilization has entered an era of instability. To overcome this situation by facilitating the crop breeding process, the genomes of more than 100 crop species have been sequenced and a huge amount of omics data are being accumulated. Still, there are some limitations such as functional redundancy and incompleteness of gene annotation information to connect crop genomics data to breeding material development. Here, the presenter will introduce effective research strategy and results utilizing crop omics data and genome editing technology in a major staple crop species, rice. Furthermore, on-going research will be presented to achieve successful digital breeding and smart farming.

***Corresponding Author:** Tel. 010-7145-6012, E-mail: hwj0602@khu.ac.kr

OH-0004

Study on nucleic acid metabolic pathways during early seed development to improve rice grain quality

Jinmi Yoon[1], Cheol Woo Min[2], Jiyoung Kim[3], Sun-Tae Kim[3], Lae-Hyeon Cho[3*]

[1]Department of biological science and bioengineering, Inha University/Industry-Academia
[2]Life and Industry Convergence Research Institute, Pusan National University
[3]Department of Plant Bioscience, College of Natural Resources and Life Science, Pusan National University

Understanding the molecular mechanisms underlying early seed development is important for improving grain yield and quality in crop plants. To investigate the molecular mechanisms that occur during early seed development, we performed comparative label-free quantitative proteomic analysis on developing rice seeds between 0 and 1 day after pollination (DAP). A total of 5231 proteins were identified, and 902 proteins showed differential accumulation between 0 and 1 DAP seeds. Further analysis focused on the proteins preferentially expressed at 1 DAP and revealed an enrichment of proteins involved in DNA replication and pyrimidine biosynthetic pathways. In particular, the cytidine triphosphate synthase OsCTPS1, which has been reported to play an essential role in endosperm development, was found to accumulate specifically at 1 DAP. CTPS serves as the rate-limiting enzyme of cytosine nucleotide biosynthesis. Mutations in the *OsCTPS1* resulted in an endospermless phenotype and an enlarged embryo. Conversely, *OsCTPS1*-overexpressing plants exhibited increased seed size, weight, and levels of the neurotransmitter gamma-aminobutyric acid (GABA). Treatment of protoplasts from transgenic plants overexpressing OsCTPS1-GFP with various signaling inhibitors revealed that inhibition of phosphorylation increased the stability of the protein. In this study, we tried to understand the molecular mechanisms of early seed development at the post-transcriptional regulation. Based on regulatory mechanisms that control OsCTPS1 protein stability, we expect to improve quantity and quality of seed with genome editing technology.

***Corresponding Author:** Tel. 032-860-7696, E-mail: jinmiyoon@inha.ac.kr

OH-0005

Loss-of-function of gynoecium-expressed phospholipase pPLAIIγ triggers maternal haploid induction in *Arabidopsis* and its application in *japonica* rice

Jin Hoon Jang[1,2], Hae Seong Seo[1,2], Yu-Jin Kim[3], Ok Ran Lee[1,2*]

[1]Department of Applied Plant Science, College of Agriculture and Life Science, Chonnam National University, Gwangju 61186, Republic of Korea
[2]Interdisciplinary Program in IT-Bio Convergence System, Chonnam National University, Gwangju 61186, Republic of Korea
[3]Department of Life Science and Environmental Biochemistry, Pusan National University, Miryang, 50463, Republic of Korea

Doubled haploid technology efficiently generates pure homozygous lines in plants through the haploid embryo induction technique. However, traditional *in vitro* systems, which are labor-intensive and genotype-dependent, rely on tissue culture. To overcome these limitations, an innovative *in planta* haploid embryo induction system was developed, with a crucial role played by the pollen-specific phospholipase A, MATRILINEAL/NOT LIKE DAD/ZmPHOSPHOLIPASE-A1 (MTL/NLD/ZmPLA1). Mutated MTL/NLD/ZmPLA1 induces haploid embryo formation in various monocots, such as rice, wheat, and foxtail millet. Nevertheless, the genetic manipulation of MTL/NLD/ZmPLA1 homologs in dicots has not been explored. This study identifies novel MTL/NLD/ZmPLA1 homologs involved in haploid embryo production in both *Arabidopsis* and rice. In *Arabidopsis*, the *AtpPLAIIγ* gene is expressed in the gynoecium, particularly in the funiculus and ovule during flower stages 13 and 14. Loss-of-function mutations in *AtpPLAIIγ* induce maternal haploid induction when used as the female parent. Notably, in the funiculus of the *AtpPLAIIγ* mutant, an intriguing observation of mis-localization of PIN1 and PIN3, key auxin transporters, suggests a potential mechanism contributing to haploid induction. In rice, the homologous gene *OspPLAII*, expressed in pollen, enables maternal haploid induction through CRISPR-Cas9-mediated editing in *japonica* rice. These findings demonstrate the potential of genetically manipulating *AtpPLAIIγ* and *OspPLAII* to activate the haploid induction system, leading to viable haploid seeds in both monocot and dicot crops. This technology holds significant promise for enhancing crop improvement across diverse plant species.

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

OI-0001

Genetic inheritance and candidate gene-based markers for fruit flesh color in watermelon (*Citrullus lanatus* L.)

Girim Park[1], Bingkui Jin[2], Gibeom Kwon[3], Kaeun Jang[2], Jagyeong Shin[2], Yunseo Choi[2], Seoyeon Park[2], Durre Shahwa[2], Youngjae Kim[3], Younghoon Park[2*]

[1]Vegetable Research Division, National Institute of Horticultural and Herbal Science, Rural Development Administration, Wanju 55365, South Korea
[2]Department of Horticultural Bioscience, Pusan National University, Miryang 50463, South Korea
[3]Partner Seeds Co., Ltd. Gimje 54324, South Korea

The fruit flesh color of watermelon is an important trait associated with the accumulation of specific carotenoids. Breeding efficiency of this trait can be enhanced by employing the marker-assisted selection (MAS). This study aimed to identify candidate genes and develop molecular markers for different flesh colors: canary yellow (high xanthophylls content), orange (high prolycopene or β-carotene), and scarlet red (high *trans*-lycopene). Genome sequencing of near-isogenic lines (NILs) and QTL analysis of recombinant inbred lines (RILs) indicated that canary yellow flesh color was conferred by an epistasis interaction between the *PTR* and *LCYB*. Furthermore, the analysis of introgression regions in orange (high β-carotene) and canary yellow-fleshed NIL and segregation of their F_2 progeny revealed single recessive gene control for orange color with the *PSY1* as a candidate gene. For orange flesh color with high prolycopene content, the *CRTISO* converting prolycopene into *trans*-lycopene was examined as a candidate gene and a single nucleotide polymorphism (SNP) in an exon specific to this trait was identified. Finally, a genome analysis comparing scarlet red (high *trans*-lycopene)- and coral red (low *trans*-lycopene)-fleshed NILs allowed the identification of SNPs in an introgression region on chromosome 6, which was highly correlated with high *trans*-lycopene content. This study enabled the MAS of watermelon flesh colors using candidate gene-based markers. Further research is required to elucidate molecular function of these candidate genes in the expression of flesh color and carotenoids accumulation.

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

OI-0002

Genes associated with the eating quality traits of japonica rice

Yoon Kyung Lee, Hee-Jong Koh*

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

Eating quality is a major trait in rice (*Oryza sativa* L.) that is significantly and directly related to the consumers' satisfaction, hence achieving high eating quality has been a goal of many breeding programs. 10 eating and cooking qualities were assessed in 284 *japonica* rice accessions, and the genome-wide association of traits and genetic variants were studied with year replicates to dissect the genetic architecture of eating and cooking qualities and to discover novel genes that control the traits. With transcriptome analysis, the candidate genes for cooked rice glossiness and starch pasting properties were identified in chromosome 6 and 2, respectively. A candidate gene for glossiness is related to the interconversion of an important substrate beginning the starch biosynthesis. A candidate gene for maximum, minimum, and final viscosity is related to one of the storage protein subunits. The transcripts expression levels of the genes and different phenotypic variations based on the haplotypes were determined. Moreover, the functions of the genes to the eating quality properties were verified using homozygote T-DNA insertion lines. These newly identified genetic factors are related to the eating quality properties other than amylose and protein content, and it is expected to be usefully applied in breeding programs for acquiring high eating quality rice cultivars.

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

OI-0003

GWAS and QTL mapping for identification of key factors underlying isoflavone contents in soybean mutants

Jung Min Kim[1], Bo-Keun Ha[2*], Soon-Jae Kwon[1*]

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

[2]Division of Plant Biotechnology, Chonnam National University, Gwangju 61186, Republic of Korea

Soybean is a valuable source of diverse metabolites that can be used in food, cosmetics, and medicines. Isoflavones, exclusively produced by legumes, play pivotal roles in plant defense systems and human health. However, due to the influence of minor-effect alleles, the genetic basis of isoflavone content remains unclear. Herein, using genotype-by-sequencing (GBS) and single nucleotide polymorphism (SNP) chip array, soybean mutants and biparental population were genotyped based on high-quality SNPs. Through genome-wide association study (GWAS), we identified 12 and 5 quantitative trait nucleotides (QTNs) related to multiple isoflavones in 2020 and 2021, respectively. Linkage disequilibrium (LD) revealed that forty-four QTNs were located in 444-Kb interval surrounding Gm05:38940662. Of them, four QTNs were located at *Glyma.05g206900* and *Glyma.05g20700*, which encode glutathione S-transferase THETA1 (*GmGSTT1*). We assessed the gene expression levels of *GmGSTT1* and two isoflavone biosynthetic genes (*IFS1* and *IFS2*) between the original cultivar and highest isoflavone mutant accession. The mapping population was constructed by crossing between Korean cultivar ‘Hwangguem’ and soybean mutant ‘DB-088’ with different isoflavone contents (1,558 μg g^{-1} and 6,393 μg g^{-1}, respectively). A linkage map was constructed using 180K AXIOM® SoyaSNP array (3,049 cM). Thirteen and 29 quantitative trait loci (QTLs) related to agronomic traits and isoflavone contents were mapped to 11 chromosomes, respectively. Notably, the Gm11:9877690-Gm11:9955924 interval in chromosome 11 contributed to high isoflavone contents (613.6 μg g^{-1}) and included eight candidate genes encoding β-glucosidase, AMP-dependent synthetase, and ligase family protein. These results provide new insights into the key factors affecting isoflavone content in soybean.

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

OI-0004

Identification of the genes associated with cytoplasmic male sterility and development of the molecular markers for improvement of breeding efficiency in onion (*Allium cepa* L.)

Bongju Kim[1*], Sunggil Kim[2]

[1]Biotech LAB, Onist Co., Ltd, 367, Gongeumdaesan-ro, Gochang-gun 56463, Republic of Korea
[2]Department of Horticulture, Biotechnology Research Institute, Chonnam National University, Gwangju 61186, Republic of Korea

Cytoplasmic male sterility (CMS) defined as the inability to produce viable pollen grains is maternally inherited. In many crops, CMS has been utilized as an useful genetic emasculation tool for economical production of hybrid seeds. In the case of onions, CMS is the sole method for F1 hybrid seed production because there is no self-incompatibility phenomenon. Therefore, various studies about CMS were performed for improving onion breeding efficiency. First, the casual gene for CMS induction in onion was identified by comparative analysis of mitochondrial genome sequences of two recently diverged cytoplasms. Second, we developed high resolution melting (HRM) markers for distinguishing cytoplasm types and genotyping a restorer-of-fertility locus (Ms) in onion. Third, inheritance of fertility restoration of male-sterility induced by cytotye Y was analysed. Forth, we developed the molecular markers for distinguishing onion and Welsh onion based on polymorphic mitochondrial genome sequences. Consequently, the molecular markers developed in this study could be used for improvement of breeding processes, such as genetic purity tests of F1 hybrids, selection of maintainer or restorer lines, and establishment of a marker-assisted backcrossing (MAB) system. In addition, these results will be used as important data for genetic studies of CMS in other crops.

***Corresponding Author:** Tel. 010-3070-8799, E-mail: kbjooo@onist.co.kr

OJ-0001

Haplotype-resolved assembly highlights crucial components of pine genome evolution and allelic imbalance in *Pinus densiflora*

Seungill Kim*

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

Haplotype-level allelic characterization facilitates research on the functional, evolutionary, and breeding-related features of extremely large and complex plant genomes. Here, we report the 21 Gb of chromosome-level haplotype-resolved genome assembly in *Pinus densiflora*, Korean red pine. We found a distinct expansion of gene-rich, gene-poor and both regions through the burst of specific long terminal repeat-retrotransposons (LTR-RTs) in *P. densiflora*. Comparative and evolutionary analyses with annotation updates exhibited the *Pinus*-specific copy number expansion of transcription factors (TFs), and illustrated that tandem and LTR-RT mediated duplications led to a remarkable increment of TFs in *P. densiflora*. Comparison of *P. densiflora* haplotypes A and B uncovered allelic imbalances including presence absence variations of genes and allele-specific expressed genes, and their potential functions through the Arabidopsis functional gene-based investigation. Our study provides insights into key mechanisms underlying *Pinus*-specific genome enlargement and TF gene expansion, and allelic imbalances in *P. densiflora*

***Corresponding Author:** Tel. 02-6490-2686, E-mail: ksi2204@uos.ac.kr

OJ-0002

Dissecting seed pigmentation-associated genomic loci and genes in soybean: A dual approaches of reference-based and k-mer-based GWAS

Jin-Hyun Kim*

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

The soybean is agro-economically the most important among all cultivated legume crops, and its seed color is considered one of the most attractive factors in the selection-by-breeders. Thus, genome-wide identification of genes and loci associated with seed colors is critical for the precision breeding of crop soybeans. To dissect seed pigmentation-associated genomic loci and genes we employed dual approaches by combining reference-based genome-wide association study(rbGWAS) and k-mer-based reference-free GWAS(rfGWAS) with 438 Glycine accessions. The dual analytical strategy allowed us to identify four major genomic loci (designed as SP1-SP4 in this study) associated with the seed colors of soybeans. In addition, we propose that the mirtron-triggered gene silencing mechanism plays a crucial role in the gnome-wide silencing of CHS gene, thereby suggesting a clue to currently predominant soybean cultivars with the yellow seed coat.

***Corresponding Author:** Tel. 063-238-4575, E-mail: kimzz14@korea.kr

OJ-0003

Development of an integrated breeding platform for data-driven crop improvement

Yeisoo Yu[1*], SeungWook Lee[1], Suhyeon Park[1], Changyuel Lee[1], Youngsil Kim[1], Daegyu Kim[1], Seok Jae Yun[1], Dae Kwan Kim[1], KunHyurk Park[1], Changsoo Kim[2]

[1]Department of R&D, DNACARE Co. Ltd., Gangnam-gu, Seoul, 06126, South Korea
[2]Department of Crop Science, Chungnam National University, Daejeon, South Korea

Due to the advancement of genomics and bioinformatics, a significant amount of genomic resources has been developed for major crops. Coupled with accurate phenotype data, these genomic resources will be served to determine and utilize agriculturally important allelic variations for crop improvement, efficiently and effectively. In order to promote data driven breeding practices, plant breeders need an integrated informatics system to manage, analyze and utilize genomics and phenomics data in user-friendly manners. As a part of Digital Breeding Program funded by MAFRA (Project#322076003-1-CG), we have a keen interest in developing a user-friendly GUI system, which multi-layer genomics data are translated and applied for plant breeding practices. The research objectives are primarily 1) to generate genotype data for ~400 accessions of commercial hot pepper (*Capsicum annuum*) and ~200 cabbages (*Brassica oleracea*), 2) to collect phenotype data focused on agronomically important traits for the pepper and cabbage accessions, 3) to generate an integrated genotype and phenotype database to support trait association mapping, 4) to develop a GUI based genomics tools box to support variant selection, visualization and population genomics analyses, 5) to construct a user-friendly analysis module and result visualization tools for GWAS and genomic selection, and 6) to construct a GUI based breeder's tools box to support marker assistant selection (MAS) in plant breeding practices. With the system, genomics information will be translated for plant breeding, and selection efficiency will be greatly increased in crop improvement. The results and progresses will be discussed in the presentation.

***Corresponding Author:** Tel. 010-2214-0243, E-mail: yeisooyu@dnacare.co.kr

OJ-0004

Metabolic profiling and gene expression analysis in the biosynthetic pathways of antioxidants in mungbean sprout

Jungmin Ha*

Department of Plant Science, Gangneung-Wonju National University, Gangneung 25457, Korea

Mung beans (*Vigna radiata* L.) contain higher amounts of functional substances than other legumes. During germination, functional compounds, such as flavonoids, polyphenols, and vitamins, increase dynamically in mung beans. Here, 20 functional substances were profiled in 50 germinated mung beans and the expression levels of the transcripts of key enzymes in targeted secondary metabolite biosynthetic pathways were identified. VC1973A, a reference mung bean elite cultivar, had the highest amount of gallic acid but showed lower contents of most metabolites than the other genotypes. Wild mung beans contained a large amount of isoflavones compared with cultivated genotypes. The expression of key genes involved in biosynthetic pathways had significant positive or negative correlations with the target secondary metabolite contents. The results indicate that functional substance contents are regulated at the transcriptional level, which can be applied to improve the nutritional value of mung bean sprouts in molecular breeding or genetic engineering, and wild mung beans are a useful resource to improve the quality of mung bean sprouts.

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

Poster Session

PA-0001

The CRISPR/Cas9-Generated HEADING DATE 3a Mutation Enhances Leaf Production in *Perilla frutescens*

Sivabalan Karthik, Jae Bok Heo*

Department of Molecular Biotechnology, Dong-A University, Busan, 49315, Korea

Environmental cues regulate the transition of many plants from vegetative to flowering development. Consequently, the molecular mechanism of flowering control is prominent in Arabidopsis and rice, where essential genes like *FLOWERING LOCUS* T (*FT*) homolog, *HEADING DATE* 3a (*Hd3a*), have been connected to flowering regulation. We identified flowering-related genes under short-day conditions using RNA sequencing to develop an enhanced leaf production trait using the flowering mechanism in the perilla. Initially, an *Hd3a*-like gene was cloned from the perilla and defined as *PfHd3a*. Ectopic expression of *PfHd3a* in *Atft-1* mutant plants has been shown to complement Arabidopsis *FT* function, resulting in early flowering. In addition, our genetic approaches revealed that overexpression of *PfHd3a* in perilla caused early flowering. In contrast, the CRISPR/Cas9 generated *PfHd3a*-mutant perilla showed significantly late flowering, resulting in approximately 50% leaf production enhancement compared to the control. Our results suggest that *PfHd3a* plays a vital role in regulating flowering in the perilla and is a potential target for molecular breeding in the perilla.

Keywords: Perilla, FT, Hd3a, flowering mechanism

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***Corresponding Author:** E-mail: jbheo72@dau.ac.kr

PA-0002

Agrobacterium-mediated transformation of Perilla *Flowering Related gene*, PfHd3a, in Perilla

Jia Chae, Jae Bok Heo*

Department of Molecular Biotechnology, Dong-A University, Busan, 49315, Korea

Perilla (*Perilla frutescens*) is an annual plant and grown in Asian countries including Korea, Japan, China. Although perilla is mainly used to seed and leaf for food or industrial materials, much is unknown about research of perilla. Previously, we found a gene in RNA-seq results which may play an important role in flowering time, and it was identified to be an ortholog of OsHd3a in rice. Hd3a is well known boost to heading under short-day (SD) conditions. In this study, we focused on this pfHd3a. Since tissue culture system using agrobacterium was developed, we made a pfHd3a-overexpressing plant in perilla using agrobacterium-mediated transformation. Agrobacterium strain EHA105 harboring constructs pB2GW7-pfHd3a containing phosphinothricin (PPT) was used for genetic transformation. A reproducible shoot was induced from hypocotyl explants on MS basal medium supplemented with 3.0 mg/l 6-Benzylaminopurine (BA), 0.01mg/l indole-3-acetic acid (IAA), 250mg/l cefotaxime, 500mg/l carbenicillin and 1.2 mg/l PPT and candidates were selected. Rooting was induced on half-strength hormone-free MS medium. The transformants were confirmed by PCR of PPT resistance region. Next generation seeds were used for flowering phenotype check compared wild type under daylength condition.

Keywords: agrobacterium-mediated transformation, perilla, pfHd3a, reproductive shoot

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***Corresponding Author:** E-mail: jbheo72@dau.ac.kr

PA-0003

감귤류 꽃밥 배양 시스템 구축 및 유전적 검증

최철우, 박석만, 진성범*

농촌진흥청 국립원예특작과학원 감귤연구소

꽃밥 배양은 동형 접합 식물체들을 얻기 위한 목표로 가장 많이 활용되며, 모체와 동일한 체세포조직을 확보할 수 있다는 점에서 그 활용가치가 크다. 본 연구에서는 감귤류 유전자원으로써 그 활용가치가 높은 적육 오렌지 품종인 'Moro'과 만다린 품종인 'Lee' 품종에 대한 꽃밥 배양 시스템을 구축하기 위하여, 이 두 품종들의 꽃밥을 선행 연구에서 구축된 배지조성에 각각의 품종들에 대한 꽃밥을 배양하였다. 그 결과 이 두 품종들은 꽃밥이 부풀어 오르는 것을 확인하였고 부풀어 오른 꽃밥들은 식물 생장 호르몬 thidiazuron 0.5mg/L가 첨가된 EMS배지로 옮겨 배양한 결과 꽃밥으로부터 캘러스와 체세포 배가 유도됨을 확인하였다. 유도된 체세포 배는 EMS+ sorbitol 0.05M 과 galactose 0.05M 그리고 GA_3 0.5 mg/L 와 gelrtite 2g/L이 첨가된 배지로 옮겨 체세포배로부터 정상적인 식물체를 얻었다. 현재까지 확보된 이 두 품종들의 식물체에 대하여 유전적 분석 결과 'Lee' 만다린 품종은 반수체 유래 식물체로 추정할 수 있었으나 'Moro' 품종들은 모두 모체와 동일한 이형 접합 타입으로 확인되었다. 위 결과를 바탕으로 보다 더 많은 재생 식물체들에 대하여 유전적 조사를 수행해야 할 것으로 사료되며, 이 구축된 시스템을 다른 감귤류에도 적용 할 수 있을 것으로 기대된다.

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***교신저자:** Tel. 010-5599-0747, E-mail: pfad7@naver.com

PA-0004

‘미니향’ 재분화 시스템 구축

최철우, 박석만, 진성범*

농촌진흥청 국립원예특작과학원 감귤연구소

‘미니향’은 ‘기주밀감’과 ‘흥춘병감’ 교잡하여 육성된 국내 신품종 감귤이다. 이 품종은 과일 크기가 작고 당도가 높아서 관상용 및 상업적 목적뿐만 아니라 유전자원으로서 가치가 높다. 본 연구에서는 ‘미니향’의 조직배양 시스템을 구축하기 위해 성숙 과실의 무수정 미발달 종자 배양 세포를 이용한 ‘미니향’의 재분화 시스템 개발을 목적으로 하였다. 체세포 배는 배 발생 유도용 배지에서 얻었고, 세포의 증식은 변형된 EMS 배지에 계대배양하여 얻었다. 탄수화물원으로 lactose 70g/L과 agar 16g/L이 포함된 EMS배지에서 자엽 형성 배아가 아닌 비정상 구형 배아가 관찰되었다. 이러한 비정상적인 구형 배로부터 식물체의 재생은 sorbitol 0.05M과 galactose 0.05M이 공급된 EMS 배지에 GA_3 0.5 mg/L과 gelrite 2 g/L이 첨가된 배지에서 유도하였고, 뿌리가 유도된 체세포배들은 호르몬이 첨가되지 않은 EMS배지에서 정상적인 식물체를 얻을 수 있었다. 본 연구 결과를 기초로 생명공학을 적용하여 고품질 감귤 육종을 위한 유전자원으로서 활용할 수 있을 것으로 기대된다.

사사: 이 연구는 농촌진흥청 국립원예특작과학원의 연구사업(PJ014466)의 지원으로 수행되었습니다.

***교신저자:** Tel. 010-5599-0747, E-mail: pfad7@naver.com

PA-0005

바이오플라스틱 및 조사료용 방사선 육종 수수 계통 선발을 위한 발효 후 성분 분석

김재훈*, 이예진, 양바울, 이승현, 김운지, 김상훈, 권순재, 안준우, 류재혁

전북 정읍시 금구길 29 한국원자력연구원 첨단방사선연구소 방사선육종연구실

바이오플라스틱 원료생산을 위한 바이오매스 및 조사료로서 적합한 수수 계통선발을 위해 완숙기에 수확한 방사선 육종 수수를 파쇄한 후 진공포장하여 실온에서 40일간 발효를 시킨 후 일반성분, 젖산 및 사료가치를 분석하였다. 수수 25 계통 중 2계통(20-400 중요 및 Pahat 선발)은 다른 계통에 비해 탄수화물 함량은 높은데 반해 조섬유 함량은 낮게 나타났으며, 폴리락트산(polylactate) 생산을 위한 원료물질인 젖산(lactic acid) 생성량도 높게 나타나 바이오플라스틱 원료생산에 유용하게 활용될 수 있는 계통으로 판단되었다. 한편, 고품질 조사료 품질 기준이 되는 중성세재불용성섬유(neutral detergent fiber, NDF) 및 산성세재불용성섬유(acid detergent fiber, ADF)는 수수 25 계통 모두 각각 65% 및 40% 이하로 나타났으며, 상대적 사료가치(relative feed value, RFV) 또한 고품질 사료로서 최소기준인 80 이상으로 확인되어 모든 시료가 고품질 조사료 기준을 충족하는 것으로 판단되었다.

***교신저자:** Tel. 063-570-3205, E-mail: jaehun@kaeri.re.kr

PA-0006

Variety of Maize for Grain with Stable Production Capability ‘Suanok’

Hwan Hee Bae*, Jun Young Ha, Young Sam Go, Jae Han Son, Beom Young Son, Tae Wook Jung

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

In 2023, the National Institute of Crop Science developed Suanok, a new maize hybrid created by crossing two inbred lines, KS118 and KS236. Suanok is a yellow flint-like maize hybrid and underwent extensive trials for growth and yield evaluation. The trials included preliminary and advanced tests in Suwon for two years, followed by a regional trial across six locations from 2020 to 2022. Results showed that Suanok had a silking date of 76 days, two days earlier than Jangdaok. The major agronomic traits of Suanok, such as plant height, ear setting height ratio, 100 kernel weight, ear length, and ear width, were similar to Jangdaok. However, Suanok excelled in filled ear length ratio with a rate of 98%. Unlike Jangdaok, Suanok did not exhibit ear tip emergence, reducing damage from birds, mycotoxin contamination, and ear rot caused by consecutive rainfall. Suanok outperformed Jangdaok in grain yield, producing 860kg/10a compared to Jangdaok's 800kg/10a. It demonstrated strong resistance to both southern corn leaf blight and northern leaf blight, similar to Jangdaok, and exhibited resistance to furnacalis and lodging as well. In a seed production trial conducted in Yeongwol, Gangwon in 2022, the silking and tasseling days of KS118 and KS236 were well synchronized. Planting Suanok at a 4:1 density ratio resulted in a higher seed production yield of 185kg/10a, while a 2:1 ratio maintained a stable yield of 170kg/10a. Due to its exceptional characteristics, Suanok is regarded as a suitable cultivar for all regions of Korea.

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

PA-0007

The Color Waxy Corn, 'Hwanggeumheukchal,' Accumulates both Carotenoids and Anthocyanins

Hwan Hee Bae*, Jun Young Ha, Young Sam Go, Jae Han Son, Beom Young Son, Tae Wook Jung

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

The waxy corn currently widely consumed is available in single colors such as white, purple, and yellow. However, the National Institute of Crop Science has developed a new variety of waxy corn Hwanggeumheukchal, which accumulates both yellow and purple pigments, offering potential health benefits. Hwanggeumheukchal is obtained through the crossbreeding of KBW64 as the seed parent and KBW42 as the pollen parent. This variety showcases a unique characteristic of co-expressing carotenoids and anthocyanins in the grain. In 2019, a productivity evaluation was conducted in Suwon, followed by a three-year regional yield trial across six locations from 2020 to 2022. The test results showed that Hwanggeumheukchal had an ear length and width of 18.0 cm and 4.7 cm, respectively, which were 2.1 cm and 0.5 cm longer than the comparative variety, Heukjinjuchal. The filled ear length ratio was superior at 98% compared to Heukjinjuchal (91%). Hwanggeumheukchal revealed strong resistance to insects and diseases, reaching a similar level as Heukjinjuchal. The number of ears per 100 m^2 was similar to that of Heukjinjuchal, while the ear weight per 100 m^2 was 23% higher compared to Heukjinjuchal. The anthocyanin content of Hwanggeumheukchal was similar to Heukjinjuchal at 271 μg/g, while the carotenoid content was over 20 times higher at 8,872 μg/g compared to Heukjinjuchal. This indicates its excellent potential as a functional food. In the seed production trial conducted in Yeongwol, Gangwon Province in 2022, the planting ratio of 2:1 resulted in a stable seed production yield of 165 kg/100 m^2. Additionally, in the taste evaluation, the overall acceptability of Hwanggeumheukchal was rated superior to Heukjinjuchal.

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

PA-0008

Comparison of Growth Characteristics and Yield of Orchardgrass New Lines at Jeju location

Hee Chung Ji*, Ji Hyun Yoo*

Subtropical Livestock Research Institute, National Institute of Animal Science RDA, Jeju 63242, Korea

Orchardgrass has good forage crop for productivity and permanence of pasture but its cultivation area has been reduced to pasture of Korea because of the effect of increasing temperature and irregular rain, Thus, in Korea, improvement of quality and adaptability in Orchardgrass is very important to increase the productivity and to expand the cultivation area. therefore, we bred a new Orchardgrass polycross three lines with high quality and permanence variety in Korea. This study was conducted in the subtropical livestock research institute, National Institute of Animal Science, RDA, Korea. Orchardgrass Fve lines were sown in narrow strips in plots 2m by 3m in Randomized block design on 12th October 2021 in Jeju experiment field. Winter field survial was checked in early spring. Five Orchardgrass lines were harvested in heading time of variety for evaluating on fresh and dry matter productivity.

Plant height of composite 51 was 73 cm and heading date of composite 51 was on 2 May and showed high dry yield (5,426kg/ha) of one cutting compared to check variety ‘Amba’(2,349kg/ha).

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***Corresponding Author:** Tel. 064-754-5710, E-mail: cornhc@korea.kr

PA-0009

Methods of tetraploid induction in watermelon using chromosome doubling reagent treatments

Eun-Hye Kim[1*], Geon-Sig Yun[1], kyu-hoi Lee[1], Yu-min Jeon[1], Cheol-Ku Youn[1], In-Jae Kim[2]

[1]Watermelon and Strawverry Research institute, Chungcheongbukdo Agricultural Research and Extension Services, Eumseong, Chungcheongbuk-do, 27668, Republic of Korea
[2]Chungcheongbukdo Agricultural Research and Extension Service, Cheongju, Chungcheongbuk-do, 28130, Republic of Korea

The market demand for seedless watermelon has been continuously increasing because of consumer preference. To produce high quality seedless watermelon, we were using three diploid watermelon breeding lines (large-sized ‘LSWE19’, medium-sized colored LSCE242-1‘, secondary branchless watermelon ’NLSWE002‘). To identify the optimal tetraploid inductive conditions, three different chromosome doubling reagents were treated, and used different treatment methods, respctively. The highest induction rate of tetraploid occurred with 0.3% colchicine(40~44%) treatment with seed immersion. Results of comparing the morphological characteristics between tetraploid breeding lines and their diploids, leaf size, stem thickness, female flower size and male flower size were all larger in tetraploids. On the other hand, The internode length of the tetraploid breeding lines was similar or shorter than diploids. And the number of chloroplasts in guard cells are increased from 10-15 diploids to 17-19 tetraploids, and the size of guard cells are also lager than diploids. Afterward, the fruit characteristics of tetraploid watermelons will be investigated and thair breeding lines will be developed. These tetraploid breeding results will be useful for breeding new seedless watermelon cultivars.

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***Corresponding Author:** Tel. 043-220-5862, Fax. 043-220-5859, E-mail: ehkim0128@korea.kr

PA-0010

Mass Production of Rosmarinic Acid from *Perilla frutescens* Leaves through Stem Cell Culture

Seon Hwa Lee, Ju Ho Lee, Seon Kyeong Lee, Kyeong Ryeol Lee, Jong Sug Park, Sichul Lee, Woo Suk Cho*

Department of Agricultural Biotechnology, National Institute of Agricultural Science, RDA, 370 Nongssaegmyeong-ro, Jeonju, 54874, South Korea

Rosmarinic acid (RA), a high value-added functional compound obtained from agricultural bioresources, is a potent antioxidant and is used extensively in the pharmaceutical and food industries. Stem cell culture is required to mass-produce RA in stable quantities. Therefore, in this study, we developed a cambium-derived stem cell culture method for mass production of RA from perilla leaves for industrialization.

The perilla variety was used Bora that had the highest levels of RA among the 32 *perilla* varieties examined. And the leaves were used as the culture explant. The callus of stem cells, which are white, soft, and crushable, were formed when leaves were cultivated in solid MS medium with 2.0mg/L 2,4-D and 0.05mg/L BA. Then, we grew the callus of stem cells in the 1/4 MS liquid medium containing 0.5 mg/L of 2,4-D for mass production of RA. In this growth condition, RA levels were up to 40.4±1.4 mg/L.

It is well known that one characteristics of stem cells is their resistance to environmental stress. In order to identify stem cells indirectly, the catalase test was carried out. Bubbles were produced quickly after treating H_2O_2, a potent oxidizing agent, demonstrating the stem cells' antioxidant capacity. Moreover, microscopic examination showed that stem cells were made up of a significant number of small vacuoles while callus was made up of large vacuoles.

***Corresponding Author:** Tel. 063-238-4581, E-mail: phyto@korea.kr

PA-0011

Development of New Perilla Cultivar ‘Suyeon’ with High yield and High Rosmarinic acid Content in the Seeds

Jung In Kim*, Myoung Hee Lee, Sang Woo Kim, Sungup Kim, Eunyoung Oh, Kwang-Soo Cho, Jeongeun Lee, Min Young Kim, Eunsoo Lee, Choon-Song Kim

Upland Crop Breeding Research Division, Department of Southern Area Crop Science, National Institute of Crop Science, RDA, Miryang, Gyeongnam, 50424, Republic of Korea

Perilla oil is known to have beneficial effects on enhancing learning ability and improving memory. Additionally luteolin has antiviral and whitening effects, while rosmarinic acid is known for its antioxidant properties and dementia prevention in periila. To increase the added value and expand consumption of perilla, there was a need to develop cultivar with high seed yields and high functionality.

‘Suyeon’ was developed for perilla oil and powder. ‘YPS142-B-B-16-1-3-3’ and ‘YPS126-B-B-4-1-3-2’ crossed in 2013 and selected from F_3 to F_5 by pedigree method. The selected pedigree is ‘YPS248-B-B-6-3-1’ and named as Miryang No. 84. The regional yield trial (RYT) in four regions was conducted from 2020 to 2022. In RYT, ‘Suyeon’ was a high seed yield and good quality. ‘Suyeon’ has white flower and light brown spherical seed. Maturity date was Oct. 6, similar to ‘Dayu’(standard cultivar). The seed yield in adaptable regions was 1.37 ton/ha (6% increase compared to ‘Dayu’). ‘Suyeon’ is heavy seed (5.2g/1000 seeds) and are suitable for both oil and powder use due to their thin seed coat. They have a high fat content of 46.6% and content of rosmarinic acid is the highest among the cultivars developed so far, at 2,433 μg/g (26% increase compared to ‘Dayu’) of seed coat.

‘Suyeon’ is is expected to enhance perilla productivity and added value, contributing to increased farm income.

***Corresponding Author:** Tel. 055-350-1228, E-mail: kji1204@korea.kr

PA-0012

Investigation of several varieties of summer Kimchi cabbage using artificial infection of *Verticillium dahliae* and contaminated farmers field at Gwynemigol

Samnyu Jee, Youn Gyu Lee, Suhyoung Park*

Highland Agricultural Research Institute, National Institute of Crop Science, Gyeonggang-Ro 5481, 25342, Korea

The highland in Gangwon Province has a relatively cool weather in summer, so for more than decades, a series of crops have been cropped by turning Kimchi cabbage, radish, and potato (seed potato). Maebongsan and Gwynemigol in Taebaek province were the main production complexes for summer Kimchi cabbages, but the outbreak of yellow wilting disease making it difficult to grow Kimchi cabbages. *Verticillium* disease, a soil infectious pathogen, and has been reported to occur widely in various crops such as potatoes, radishes, and chrysanthemums. The symptoms of yellow wilting of Kimchi cabbages have been rapidly increasing in highland of Gangwon, and the symptom was very similar to the symptoms of *Verticillium* disease. Artificial inoculation was attempted to determine if the symptoms of the yellow wilting were caused by the *Verticillium* pathogens, and compared to the symptoms caused by the contaminated soil of Gwynemigol. As a result of cultivating 10 kinds of summer cabbage varieties in Gwynemigol, yellow wilting symptoms were found in all varieties, and two varieties were relatively resistant to diseases. As a result of artificial inoculation of 24 domestic resources with *Verticillium* strains, yellow wilting symptoms occurred at 6 resources. As a result of artificial inoculation, symptoms similar to contaminated soil occurred, and it is expected that artificial infection of *Verticillium* strains can be used for research on improving symptoms of yellow wilting of summer Kimchi cabbages.

***Corresponding Author:** Tel. 033-330-1850, E-mail: psh@korea.kr

PA-0013

The GWAS analysis revealed genetic loci conferring resistance to low nitrogen and phosphorus in a population of North Korean rice

Eun-Kyul Kim*, Han Cho, Jun-Oh Hwang, Soo-Cheul Yoo

Crop Molecular Breeding Laboratory, Department of Plant Life and Environmental Science, Hankyong National University, 327, Jungangro, Anseong-si, Gyeonggi-do 17579, Korea

Nitrogen and phosphorus are essential macronutrients for plant growth and development. Soils may not supply an adequate amount of nutrients for plant growth and development. Chemical fertilizers are considered as effective means to enhance crop yields and are widely used. However, excessive use of fertilizers leads to severe environmental pollution and makes sustainable agriculture impossible. Therefore, a pressing task for sustainable agriculture is the development of crops with improved nutrient use efficiency. We conducted a GWAS analysis on a population of 190 North Korean rice varieties to explore the genes involved in nitrogen use efficiency (NUE) and phosphorus use efficiency (PUE). Seeds were sterilized and germinated, then hydroponically cultured in the greenhouse of Hankyong National University with a Yoshida solution for 40 days. The mock used the conventional Yoshida solution, and the treatment groups consisted of low nitrogen (10^{-1} NH_4NO_3), low phosphorus (10^{-1} $NaH_2PO_42H_2O$), and low nitrogen and phosphorus conditions. Phenotypic traits such as tiller number, chlorophyll content, root length, and shoot length were measured. The plants cultivated under low nitrogen conditions exhibited relatively pale leaves, indicating low chlorophyll content in leaves. This confirms that nitrogen is an essential nutrient for chlorophyll synthesis. The plants cultivated under low phosphorus conditions had a relatively low tiller number, indicating the involvement of phosphorus in tiller formation. GWAS performed on a population of 190 North Korean rice varieties identified several known and unknown QTLs underlying NUE and PUE with statistically significant values. Further analysis is being conducted for haplotyping and candidate gene analysis.

***Corresponding Author:** Tel. 010-8637-0395, E-mail: sandydream@naver.com

PB-0001

Identification of Genomic Hotspots Linked to Phosphorus Use Efficiency through Meta QTL Analysis: Implications for Low-Input Rice Breeding

Ian Paul Navea[1,2], Phyu Phyu Maung[1,2], Priskila Tolangi[1,2], Na-Hyun Shin[1,2], Joong Hyoun Chin[1,2*]

[1]Food Crops Molecular Breeding Laboratory, Department of Integrative Biological Sciences and Industry, Sejong University, Seoul 05006, Republic of Korea
[2]Convergence Research Center for Natural Products, Sejong University, Seoul 05006, Republic of Korea

Phosphorus use efficiency (PUE) is a complex trait, governed by many minor quantitative trait loci (QTLs) with small effects. Advances in molecular marker technology have led to the identification of QTLs underlying PUE. However, their practical use in breeding programs remains challenging due to the unstable effects in different genetic backgrounds and environments, interaction with soil status, and linkage drag. Here, we compiled PUE QTL information from 16 independent studies. A total of 192 QTLs were subjected to meta-QTL (MQTL) analysis and were projected into a high-density SNP consensus map. A total of 60 MQTLs, with significantly reduced number of initial QTLs and confidence intervals (CI), were identified across the rice genome. Candidate gene (CG) mining was carried out for the 38 MQTLs supported by multiple QTLs from at least 2 independent studies. Genes related to amino and organic acid transport and auxin response were found to be abundant in the MQTLs linked to PUE. CGs were cross validated using a root transcriptome database (RiceXPro) and haplotype analysis. This led to the identification of 8 candidate genes (*OsARF8, OsSPX-MFS3, OsRING141, OsMIOX, HsfC2b, OsFER2, OsWRKY64, and OsYUCCA11*) modulating PUE. Potential donors for superior haplotypes were identified through haplotype analysis. The distribution of superior haplotypes varied in different subspecies being most commonly found in the Indica subspecies but were largely scarce in Japonica. Our study offers an insight on the complex genetic mechanisms that modulate PUE in rice. The MQTLs, CGs, and superior haplotypes identified in our study are useful in the accumulation of beneficial alleles for PUE in rice.

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

PB-0002

Genomics and Phenomics Approaches for Developing Rice Varieties with Enhanced Nutrient Use Efficiency

Ian Paul Navea[1,2], Jinwoo Lee[1,2], Phyu Phyu Maung[1,2], Priskila Tolangi[1,2], Na-Hyun Shin[1,2], Joong Hyoun Chin[1,2*]

[1]Food Crops Molecular Breeding Laboratory, Department of Integrative Biological Sciences and Industry, Sejong University, Seoul 05006, Republic of Korea
[2]Convergence Research Center for Natural Products, Sejong University, Seoul 05006, Republic of Korea

The escalating cost of fertilizers is one of the significant challenges facing rice farmers worldwide. Nitrogen (N) and phosphorus (P) are vital nutrients required by rice plants to achieve optimal yield. Recent advances in molecular breeding have opened up new possibilities for creating high-yielding rice varieties. However, these varieties often necessitate high fertilizer input, predominantly N and P, resulting in excessive carbon emissions from rice cultivation. In this study, we aim to leverage genomics and phenomics approaches to develop rice cultivars that are efficient in N and P utilization. The present study utilized a diverse collection of Korean rice varieties in combination with pseudomolecules produced from long-read genomic sequences (Nanopore technology) to conduct haplotype-based identification of core variety sets for genes associated with P-uptake. These core sets underwent testing in various temporal and spatial field experiments with different fertilizer regimes. We analyzed a core set of Korean rice varieties for *OsPTF1*, one of the most important genes modulating P-uptake, and identified donor lines based on *OsPTF1* haplotypes to develop NILs harboring both *OsPTF1* and *OsPSTOL1*.

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

PB-0003

The Effects of Nitrogen Fertilization on Growth Characteristics and Noodle Quality of Allergy-Reduced Wheat Cultivar ‘O-free’

Sumin Hong[1], Min-Young Lee[1], Sa-Rang Choi[1], Jin Hee Park[2], Go Eun Lee[2], Young-Mi Yoon[2], Chul-Soo Park[1*]

[1]Department of Crop Science and Biotechnology, Jeonbuk National University, Jeonju, 54896, Korea
[2]National Institute of Crop Science, Rural Development Administration, Wanju, 441-857, Korea

The objective of this study is to determine the effects of additional N-fertilization on agricultural traits, flour characteristics, and noodle quality of O-free, which is known to have allergy-reducing effects. As the fertilization rate increased, the culm length and spike length were increased, and the grain nitrogen removal also increased due to the increased protein content in the grains. While the leaf area index (LAI) of the plant was highest in the booting stage, the canopy LAI was highest at 21 days after flowering (21-DAF). While the LAI of the plant was higher in the treatments with additional nitrogen (N1 and N2) than in the control (N0), there was no significant difference in canopy LAI. Chlorophyll fluorescence values were highest at 21-DAF, and lowest at 35-DAF regardless of the fertilizer rate. The dry weight of leaves and stems was highest at 7-DAF in N0 and N1 but at 21-DAF in N2. Nitrogen content in leaves and stems decreased during grain filling, while it increased in the grains. As the fertilizer rate increased, moisture content, flour color value, protein content, and sedimentation value of flour increased, while the particle size of flour decreased. Dough extensibility, mixing time, and protein strength increased with increasing fertilizer rate, but dough stability decreased. Starch gel stability and aging were highest in the control, and starch swelling was lowest in N1. The brightness, thickness, and hardness of cooked noodles increased with increasing fertilizer rate, but elasticity and viscosity were not significantly affected.

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***Corresponding Author:** Tel. 063-270-2533, E-mail: pcs89@jbnu.ac.kr

PB-0004

Mapping quantitative trait loci for days to heading in a doubled haploid population derived from two Korean wheat cultivars

Sumin Hong[1], Kyung-Min Kim[2], Chang-Hyun Choi[2], Seong-Woo Cho[3], Chul-Soo Park[1], Young-Jun Mo[1*]

[1]Dept. Crop Science and Biotechnology, Jeonbuk National University, Jeonju, 54896, Korea
[2]National Institute of Crop Science, Rural Development Administration, Wanju, 441-857, Korea
[3]Department of Agronomy and Medicinal Plant Resources, Gyeongnam National University of Science and Technology, Jinju 52725, Korea

Developing early heading cultivars is necessary for Korean wheat breeding to improve the stability of double cropping and avoid pre-harvest sprouting caused by frequent rainfall after the heading. This study aimed to identify quantitative trait loci (QTLs) for heading date using 94 doubled haploid lines derived from Keumkang and Olgeuru. The study was conducted in upland conditions during three growth seasons (2017, 2018, and 2019) and various traits including days to heading date, culm length, spike length, kernels per spike, number of tillers, test weight, thousand kernel weight, and yield were investigated. Genotyping was performed using the 35K Axiom Wheat Breeder's Array. We identified seven QTLs that were significant at least two out of three years, and three of them were QTLs for heading date: *QDhd.jbnu-3B*, *QDhd.jbnu-6B*, and *QDhd.jbnu-7D*. They accounted for 17.4-40.9%, 12.2-33.1%, and 6.0-8.7% of the phenotypic variation, respectively. As they have additive effects of 1.10-2.22 days, 0.92-2.22 days, and 0.95-1.02 days, the accumulation of alleles for early heading in these QTLs could lead to a one-week reduction in the heading date. Another four QTLs were identified for culm length (*QCl.jbnu-6A*), kernels per spike (*QKps.jbnu-3B*), test weight (*QTw.jbnu-1A*), and thousand kernel weight (*QTkw.jbnu-6A*). These QTLs explained 13.2-30.6% of the phenotypic variation with addictive effects of 1.10-6.09. *QKps.jbnu-3B* was found in a similar genomic position as *QDhd.jbnu-3B*, and the early heading was associated with decreased kernels per spike. Therefore, caution to yield reduction resulting from the shortened heading date is needed.

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***Corresponding Author:** Tel. 063-270-2530, E-mail: yjmo@jbnu.edu

PB-0005

Reaction of blast resistance on monogenic lines and tropically adapted cold tolerant japonica rice variety in the cool climatic area of the Philippines

Jung-Pil Suh[1*], Jesson Del-Amen[2], Faith T. Estepa[2], Myrish Pacleb[1], Lenie Pautin[3], Thelma Padolina[3], Mary Jeanie Yanoria[1], Van ScheplerLuu[1], Sherry Lou Hechanova[1], Sung-Ryul Kim[1]

[1]International Rice Research Institute, College, Los Baños, Laguna, 4030, Philippines
[2]Benguet State University, La Trinidad, Benguet, 2601, Philippines
[3]PhilRice Central Experiment Station, Maligaya, Science City of Muñoz, 3119 Nueva Ecija, Philippines

Rice blast caused by the pathogenic fungus *Magnaporthe oryzae* is a devastating disease that poses a serious threat to rice production worldwide. To manage this disease, deployment of resistant varieties is essential, but a thorough understanding of the pathogen population's resistance genes in the target region is necessary. In this study, we evaluated the resistance of 25 monogenic rice lines against rice blast through a blast nursery test during the dry season from February to April 2023 in Benguet, La Trinidad, Philippines, which is located in a cool climate zone where only cold-tolerant rice varieties can grow. Our results indicate that the R genes *Pita2* and *Pi9* conferred high resistance, while *Piz5*, *Pita*, *Pit*, *Pi12*, *Pikm*, and *Piks* showed moderate resistance. However, susceptibility to leaf blast was present among *Piz-t, Piz, Pi7, Pik, Pikh, Pikp, Pi1, Pi20, Pi19, Pi3, Pii, Pia, Pib, Pish,* and *Pi5* genes. These findings are crucial for enhancing rice blast resistance in cool climatic areas of the tropics. We also evaluated the blast resistance of the 'Cordillera 4', a tropically adapted cold-tolerant japonica rice variety, which showed moderate resistance in the blast nursery. Our molecular marker analysis revealed that this variety lacks the *Pita2* and *Pi9* resistance alleles. Hence, we anticipate that introducing these genes can enhance the blast resistance of this variety in the cool climatic areas of the tropics.

***Corresponding Author:** Tel. 063-917-832-5623, E-mail: j.suh@irri.org

PB-0006

Physicochemical Properties and Sprout Yield of Several Legume Crops Cultivated in the Paddy Fields of Southern Korea

Seo Young Oh*, Jisu Choi, Tae Hee Kim, Sung Hoon Kim, Seong Hwan Oh

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

Soybean (*Glycine max* (L.) Merrill) and mungbean (*Vigna radiata* (L.) Wilczek) are important food sources used widely in Asia. They are used as anti-oxidant and anti-cancer food resources containing various types of physiologically active substances. In this study, the seed physiological activity and the sprout yield were evaluated from 5 soybean cultivars (‘Daechan’, ‘Daewon’, ‘Seonpung’, ‘Seonyu-2ho’, and ‘Cheongja-3ho’) and 4 mungbean cultivars (‘Dahyun’, ‘Sanpo’, ‘Areum’, and ‘Dado’). The protein and fat contents of seeds were higher in soybean than in mungbean. Isoflavone contents were detected in soybean although different one another depending on the cultivar, but not detected in mungbean. The protein, crude fat, and ash contents of soybean were 34.2~40.7%, 13.2~16.1%, and 4.5~5.0%, respectively. Particularly, protein and fat contents of ‘Daechan’ were higher than those of the other cultivars. Isoflavone content 272.5 $\mu g \cdot g^{-1}$ of ‘Seonpung’ was significantly higher than those of the other cultivars. In particular, genistin and dadizin contents were high in all soybean cultivars. Isoflavone, one of the flavonoid glycosides, is effective in cancers, oxidative damages, osteoporosis, and cardiovascular diseases. Seed germination rate of soybean cultivars was high in the order of ‘Seonpung’ > ‘Daechan’ > ‘Daewon’ > ‘Cheongja-3ho’ > ‘Seonyu-2ho’. The hypocotyl length and thickness in the sprouts of ‘Seonpung’ were 13.5 cm and 2.2 mm, respectively, and the sprout yield was higher than those of the other cultivars. The protein, fat, and ash contents of mungbean were 26.2~28.3%, 0.3~0.5%, and 3.6~3.7%, respectively, with no significant difference among cultivars. Seed germination rate of mungbean cultivars was great up to 94.2% in ‘Dado’. The growth rate of mungbean sprouts was high, and its hypocotyl length increased up to 9.2 cm. Based on the above results, it seems that soybean cultivar ‘Seonpung’ and mungbean cultivar ‘Dado’ could be favorable for the production of sprouts. In particular, mungbean is excellently adaptable to climate and soil conditions in the paddy fields although its yield is low compared to soybean, resulting that it could be favorable in paddy fields and its growing period is short, so that it could be recommended for various cropping systems in the paddy fields of Southern part of Korea.

***Corresponding Author:** Tel. 055-350-1166, E-mail: osoonja@korea.kr

PB-0007

Photosynthesis and Seed Yield of Soybean (*Glycine max* (L.) Merrill) Subjected to Drought Stress at the Flowering Stage

Seo Young Oh*, Jisu Choi, Tae Hee Kim, Sung Hoon Kim, Seong Hwan Oh

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

Soybean (*Glycine max* (L.) Merr.) is one of the most important crops in the world, and consists of about 40% protein, 30% carbohydrate and 20% lipid. The seed yield of soybean is affected by temperature, sunshine duration, etc. during the flowering and pod formation stages. In this study, photosynthesis and seed yield were investigated from soybeans subjected for 15 days to different irrigation conditions (0, 50, 100%) at the early bloom stage in summer season using a lysimeter. When soybean plants were subjected to drought stress, the leaf temperature was 3.5°C higher than those of fully-irrigated plants, and the leaf length and width were smaller and the leaf water content was slightly lower. The water use efficiency (WUE) was lower than those of fully-irrigated and 50% irrigated plants. The CO_2 fixation rate (*A*) was also low down to 3.6 $\mu mol \cdot m^{-2} \cdot s^{-1}$ under drought stress. On the other hand, the dark respiration rate (*Rd*) was high with low stomatal conduction (*gs*) and transpiration rate (*E*) when subjected to drought stress. The maximum photochemical efficiency of PSII (F_v/F_m) decreased with increased F_o and F_m in drought-stressed plants. In addition, the electron transfer activity of PSII (ET) was low under drought stress. The pod number and seed weight decreased, while the free sugar content of seeds increased, under drought stress. These results indicate that water stress during the flowering stage could be a factor that reduces soybean productivity. Moreover, in the open field in summer season, water stress combined with high temperature and/or high light could affect the growth of soybean in several growth stages. Therefore, for the stable production of soybeans, it is necessary to raise cultivars that are resistant to complex environmental stresses consisting of drought, high temperature, high light, etc. or to establish cultivation techniques that could minimize the damages caused by complex environmental stresses.

***Corresponding Author:** Tel. 055-350-1166, E-mail: osoonja@korea.kr

PB-0008

Oryza sativa, C3HC4-type E3 ligase plays positive a role in drought stress via stomata density and regulation of proportion

Jong Ho Kim, Cheol Seong Jang*

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

Drought stress is a negative factor in rice yield productivity, which leads to huge economic losses. Also, it will be becoming more issue due to the acceleration of global warming. In order to solve the problem of productivity reduction in drought stress, the development of drought-tolerant varieties and genetic research for drought tolerance should be a high priority in the future. Using a forward genetics approach, a drought-tolerance tiling line, a 200-380 mutant line, was identified from 150 rice gamma-ray mutant lines. Under drought stress conditions, 200-380 mutant lines exhibited a high fresh weight, survival rate, relative water, enzyme activity (SOD, POD, CAT), and low H_2O_2 content compared to WT plants. 200-380 mutant lines showed higher secondary metabolites such as proline and soluble sugar content than in the WT plants. Understanding drought tolerance mechanism, we identified three types of stomata (open, partially open, closed). The 200-380 mutant lines increased the proportion of closed stomata compared to WT under drought treatment conditions. Also, 200-380 mutants showed lower stomata density compared to WT plants. Whole genome sequencing of the 200-380 mutant line identified a single nucleotide polymorphism of E3 ligase (LOC_Os11g39640), which led to premature stop codon such as short peptide of 360 amino acids. Transcript of E3 ligase is an induced response to PEG treatment conditions by qRT-PCR analysis. And it was confirmed that the highest expression level was in leaf tissue. Collectively, mutation of E3 ligase in 200-380 mutants suggests improving drought tolerance via stomata density and proportion in rice.

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

PB-0009

고염지 적응 콩 품종 조기 개발 및 안정재배기술 개발

이정동[1*], 조현[1], 이상엽[1], 조현준[1], 박지영[1], 김수연[1], 이승수[2]

[1]대구광역시 북구 대학로 80 경북대학교 응용생명과학과
[2]충청남도 예산군 신암면 추사로 167 충청남도농업기술원

기후변화와 국제분쟁 등에 따라 국제 곡물가격이 불안정한 현실에서 수입에 의존하는 주요 식량작물인 콩에 대한 자급율 향상이 시급하다. 자급률 향상을 위하여 간척지 재배에 적합한 콩 품종을 조기개발하는 기술와 생산기술이 필요하다. 본 연구에서는 간척지에서 일반 밭 수량 대비 80% 이상의 단작용 콩 및 조사료용 콩을 개발하고 최대생산 기술을 개발하기 위한 연구를 수행 할 예정이다. 연구는 현대서산간척지와 당진간척지에서 수행을 하고 있다. 주 연구내용은 국내에서 육성된 주요 콩 품종의 염해 내성 검정, 분리집단에서 내염성 콩 선발, 내염성 곡실용 콩 품종 개발, 옥수수와 혼작이 가능한 내염성 조사료용 콩 품종 개발, 내염성 콩 종자생산 기반 확충 등을 수행하고 간척지에서 개발된 종실용 콩 및 조사료용 콩의 최대 생산을 위한 재배실험을 실시한다. 재배실험의 주 내용은 파종기에 따른 수량 및 품질 검정, 재식밀도 및 시비기술 등을 개발할 것이다. 본 연구를 통해 개발된 콩 품종 및 재배기술을 이용하여 간척지에서 조사료 및 곡식용 콩 생산으로 식량자급율 향상 및 농지이용율증대, 지역 농업단체가 포함된 간척지내 실증 시험 후 재배기술을 전수에 이용할 것이다.

사사: 본 연구는 고염지 적응 콩, 옥수수 품종조기 개발 및 안정재배기술 개발(RS-2023-00227533)의 일부 임.

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

PB-0010

Study on the function of pre-harvest sprouting (PHS) resistance by transcriptome and proteome co-profiles of Korean wheat cultivars (*Triticum aestivum* L.)

Sang Yong Park, Jae Yoon Kim*

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

Wheat (*Triticum aestivum* L.) is a representative grain consumed in various ways worldwide. Wheat is popular as a food, but frequent and unpredictable precipitation and early germination due to pre-harvest sprouting (PHS) cause major problems in wheat quality. Studies of PHS-resistant genes and mechanisms have been continuously executed. But PHS-related research needs a more detailed standpoint. In this study, we identified candidate genes related to the PHS response and resistance mechanism in Korean cultivars, 'Keumgang' (PHS sensitive) and 'Woori' (PHS resistant). To identify differentially expressed genes (DEGs) and differentially expressed proteins (DEPs), RNA-seq and proteomic analysis were performed and co-profiled on two Korean cultivars. The PHS rate analysis was evaluated by calculating the seed germination index in five spikes of two cultivars. 'Keumgang' (84.65%) and 'Woori' (2.91%) showed similar results to the PHS-induced experiment in the previous experiments. A total of 13,154 DEGs and 706 DEPs were identified in four comparison groups between the susceptible/tolerant cultivars. In particular, DEGs/DEPs functional annotation for each control group showed similar expression in 'proteasome' related functions and showed an increase in expression by more than 70% in 'Woori' (W PHS+7) compared to 'Keumgang' (K PHS+7). The germination-resistant wheat cultivar 'Woori' showed up-regulation in the 20S core particle of proteasome, and showed similar expression of E3-ubiquitin ligase involved in the proteasome role. 'Woori' is supposed to degrade unknown proteins that regulate PHS compared to 'Keumgang' actively. Further research is needed to discover the main genes recognized by E3-ubiquitin ligase and degradation by proteasomes. Co-profiling analysis between transcriptome and proteasome improved the reliability of transcriptome studies. Our data contributed to improving basic information and understanding of the PHS mechanism in wheat.

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

PB-0011

Characterization of a Novel *Wx-B1* Allele in Gunji-3 Wheat variety and Its Implications for Starch Quality Improvement

Yeonjun Sung[1], Keonghoon Kim[2], Jinhee Park[2], Seongwook Kang[3], Chulsoo Park[4], Seongwoo Cho[5*], Changsoo Kim[1,6*]

[1]Department of Smart Agriculture Systems, Chungnam National University, Daejeon, 34134, Korea
[2]Crop Breeding Division, National Institute of Crop Science, Wanju-gun, 54955, Korea
[3]Department of GreenBio Science, Gyeongsang National University, Jinju, 52828, Korea
[4]Department of Crop Science & Biotechnology, Jeonbuk National University, Jeonju, 54896, Korea
[5]Department of Smart Agro-Industry, Gyeongsang National University, Jinju, 52828, Korea
[6]Department of Crop Science, Chungnam National University, Daejeon, 34134, Korea

The quality and usage of wheat flour vary depending on the composition of its starch. Wheat starch consists of two types of glucose polymers, amylose and amylopectin. Amylopectin, synthesized by three enzymes, including granule bound starch synthase I (GBSSI), also known as waxy protein, plays a crucial role in determining the properties of starch. In wheat, the waxy phenotype is influenced by three copies of the *Wx* gene (*Wx-A1*, *Wx-B1*, *Wx-D1*) and their combinations. In this study, a new wheat variety, Gunji-3, was developed by crossing the Korean cultivars 'Keumkang' and 'Shinmichal 1'. The Gunji-3 variety was analyzed using sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) to compare the *Wx-B1* allele with the waxy-type cultivar (Shinmichal 1), resulting in the identification of one deletion and 12 single nucleotide polymorphisms (SNPs). Amino acid sequence comparison among the *Wx-B1* alleles revealed two variations, indicating the presence of a novel *Wx-B1* allele (*Wx-B1o*). Furthermore, a comparison of the physicochemical properties of starch between Keumkang and Shinmichal 1 cultivars demonstrated that Gunji-3 had higher protein content and lower amylose content. These findings contribute to the expansion of genetic resources in wheat breeding and offer potential for improving starch quality and enhancing wheat breeding programs.

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***Corresponding Author:** Tel. 055-772-3225, E-mail: chsw78@gnu.ac.kr
Tel. 042-821-7822, E-mail: sdcson1@o.cnu.ac.kr

PB-0012

OsMBTB3, Broad Complex BTB domain with Meprin and TRAF Homology MATH domain mutates improve drought resistance in rice Mutant

Ayoung Cho, Hyoenung Seo, Cheolseong Jang*

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

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, 200-98 (15), was selected from 150 rice mutant lines (M10) induced by gamma-ray irradiation. In the whole-genome re-sequencing of 200-98 (15) mutant, a single base adenine deletion of the *LOC_Os03g57854* gene is annotated leucine carboxyl methyl transferase, was found. The original gene was named *OsMBTB3*, and the mutant gene was named *OsMBTB3p.Glu141fs*, which means that the frameshift occurred at the 141st amino acid, glutamine. Under drought treatment conditions, the 200-98 (15) mutant showed a high survival rate, fresh weight, chlorophyll content and lower hydrogen peroxide (H_2O_2) content. The relative expression levels in WT and 200-98 (15) mutant, the expression level of the *OsMBTB3* gene was lower in the mutant than in the WT under drought condition.

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

PB-0013

A New Dark Purple Waxy Corn Variety,『Eomjichal』with Late-maturing and Short ears

Sang-Woo Kim*, Jong Hyeong Lee, Byoung Rourl Choi, Eun Kyu Jang, Young Rok Kim, Hae Chan Jung, Young-Soon Lee, Chang-Hui Cho

Gyeonggi Do Agricultural Research & Extension Services, Hwaseong 18388, Republic of Korea

A 'Eomjichal', a new dark purple waxy corn, is a pure line segregation variety developed by the crop breeding team of Crop Research & Development Division, GARES, Hwaseong, Korea in 2022. This corn was collected from Hwaseong City in 2014.

'Eomjichal' is a late maturing corn variety. This variety had a growth duration of 109 days from sowing to silking. The silking date was 33 days later than Heukjinjuchal. The ear length and ear diameter of 'Eomjichal' were 10 cm and 30 mm, respectively. Its ratio of kernel set length to ear length was 99.7%, which was higher than those of Heukjinjuchal. The number of fresh ears per plant was greater than Heukjinjuchal, but the weight of fresh ear was lower than Heukjinjuchal in the local adaptation test in 2 areas from 2020 to 2022.

Compared to sowing April sowing, when sowing in June, 'Eomjichal' had a shorter growth duration 71 days from sowing to silking and it resulted that stem height was smaller with 152 cm and more stronger to lodging. But, especially, the number of fresh ears per plant and the weight of fresh ears were higher than Heukjinjuchal in the local adaptation test in 2 areas from 2021 to 2022. This variety would be well adapted to Gyeonggi Province.

***Corresponding Author:** Tel. 031-8008-9271, E-mail: ksw314@gg.go.kr

PB-0014

A New Rice Variety,『Suryeomi』with Mid maturing and High-quality

Eun Kyu Jang*, Young Rok Kim, Byoung Rourl Choi, Sang-Woo Kim, Hae Chan Jung, Jung-Hee Jang, Young-Soon Lee, Chang-Hui Cho

Gyeonggi Do Agricultural Research & Extension Services, Hwaseong 18388, Republic of Korea

‘Suryeomi’ is a medium maturing, high quality rice variety developed by the crop breeding team of the Crop Research Division, GARES, Hwaseong, Korea in 2022. ‘Suryeomi’ was derived from a cross between ‘Soobo’ and ‘SR27936-B-GH1-10’ in 2013. The heading date of this variety is 9 August in Gyeonggi Province. Its culm length is 82 cm. This variety has 13 tillers per tiller and 111 spikelets per panicle. It is a medium-grain variety, with 1,000 grains of brown rice weighing 23.9 g. Its cold tolerance is similar to that of Hwaseongbyeo, and its lodging rate is lower than that of Hwaseongbyeo. It has moderate resistance to rice blast and excellent resistance to viviparous germination, but is susceptible to bacterial leaf blight and stripe virus. Its milled rice appearance is clear and its milled rice protein content is 5.9%, which is similar to Hwaseongbyeo. Its perfect rice grain milling recovery rate is 70.2%, which is higher than that of Hwaseongbyeo. The yield of milled rice was 5.22 MT/ha under the normal culture of the local adaptation test in 3 areas for 3 years. ‘Suryeomi’ is highly adaptable to Gyeonggi Province.

***Corresponding Author:** Tel. 031-8008-9270, E-mail: jek0428@gg.go.kr

PB-0015

Carbon nanodots and manganese iron oxide nanoparticles influence the growth, leaf pigment content, and antioxidant activity of drought-stressed maize inbred lines

Muhammad Zahaib Ilyas[1], Hyeon Park[1,2], Young Sun Baek[2], Kyu Jin Sa[1], Myong Jo Kim[1,2], Ju Kyong Lee[1,2*]

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

[2]Interdisciplinary Program in Smart Agriculture, Kangwon National University, Chuncheon 24341, Korea

Despite being the third most-consumed crop in the world, maize (*Zea mays* L.) is particularly sensitive to drought stress. This study investigated manganese iron oxide ($MnFe_2O_4$) nanoparticles (NP) and carbon nanodots (CND) for their efficacy in reducing drought effects in maize inbred lines. Pilot studies revealed that applications of 300 mg L^{-1} $MnFe_2O_4$ NP and 10 mg L^{-1} CND were the most effective treatments for drought-stressed maize. The experimental results revealed that the highest leaf blade length (54 cm) and width (3.9 cm), root length (45.20 cm), stem diameter (11.13 mm), root fresh weight (6.96 g), and chlorogenic (8.70 μg/ml), caffeic (3.01 μg/ml) and syringic acid (1.04 μg/ml) contents were demonstrated by CND-treated inbred lines GP5, HW19, HCW2, 17YS6032, HCW3, HW7, HCW2, and 16S8068-9, respectively. However, the highest shoot length (71.5 cm), shoot moisture content (98.07%), shoot fresh weight (12.46 g), chlorophyll content (47.3), and DPPH free radical scavenging activity (34.07%) were observed in $MnFe_2O_4$ NP-treated HF12, 11BS8016-7, HW15, HW12, and KW7 lines, respectively. The control group showed the highest gallic, *p*-coumaric, and ferulic acid and total phenolic contents. These results suggest that $MnFe_2O_4$ NP and CND improved maize drought tolerance through increased shoot moisture, chlorophyll content, and free radical scavenging.

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

PB-0016

영남 평야지에서 벼 극조기 재배 적응품종의 육묘일수별 수량특성

김태희, 최지수, 오서영, 김성훈, 오성환*

국립식량과학원 남부작물부 논이용작물과

최근 기후변화에 대응하여 우리나라 남부 평야지에서는 쌀의 추석전 출하를 위해 조기재배나 극조기재배가 증가하고 있는 추세이다. 그러나 조기재배나 극조기재배 와 연계한 2모작 작부모형이 부족하고 재배기술 또한 미흡한 실정이다. 본 시험에 앞서 영남평야지에서 극조기 벼 2모작을 위한 적응품종 선정과 재배적기를 구명한 바 있다. 이와 더불어 극조기 재배에 적합한 육묘일수와 수확시기별 수량 및 품질특성을 구명하여 더 안정적인 극조기 벼 재배 2모작 작부체계 기술을 확립하고자 본 시험을 수행하였다.

본 시험은 경남 밀양시 국립식량과학원 남부작물부 논 시험포장에서 실시되었다. 공시품종은 '20~'21년까지 선발된 백일미, 진옥, 주남조생 3품종을 무가온 온실을 이용하여 20, 30, 40일간 육묘하였고, 이앙시기는 4월 20일에 재식거리 30×12cm, 재식본수는 1주 5본으로 이앙하였다. 시비량은 질소-인산-칼리를 성분량으로 10a당 각각 9, 4.5, 5.7kg을 시비하였다. 재배관리는 농촌진흥청 표준재배법에 준하였으며, 수확시기는 출수후 25일에서 45일까지 5일간격으로 5시기에 100주씩 3반복을 수확하였다. 수량 및 쌀 품위 등은 농촌진흥청 농업과학기술 조사기준에 준해 조사하였다.

벼 극조기 재배시 공시품종의 육묘일수별 출수기는 육묘일수가 증가할수록 단축되었는데, 40일묘가 20일묘 대비 2일 단축되었으며 품종간 차이는 없었다. 단위면적당 수수는 육묘일수가 길어질수록 적었으며, 수당립수는 반대로 증가하는 경향이었다. 육묘일수별 현미천립중과 등숙률은 유의한 차이가 없었으며 쌀수량은 수수와 수당립수간의 상호보완에 따라 결국 육묘일수에 따른 수량은 유의적인 차이가 없었다. 수확시기별 쌀 수량은 출수후 25일부터 35일까지는 증가하다가 그 이후에는 유의적인 차이를 보이지 않았으며 대체로 35~40일경이 가장 높았다. 수확시기에 따른 등숙률은 출수후 35일까지는 지속적으로 증가하다가 35~40일에 최대가 되었으며 현미천립중은 수확시기간에 대체로 차이가 없었다. 수확시기에 따른 완전미율은 대체로 30~35일경에 높았고 그 이후에는 감소하는 경향을 보였다. 싸라기 비율은 대체로 수확일수가 늦어질수록 증가하였는데 수확시기가 늦어지면 고온인 상태로 포장에서 과도하게 건조되기 때문인 것으로 생각된다. 쌀수량과 완전미 수량, 싸라기율을 종합해 볼 때 극조기 벼 재배시 수확적기는 출수후 35~40일로 판단된다.

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***교신저자:** Tel. 055-350-1161, E-mail: osh0721@korea.kr

PB-0017

가공용 벼 재배 안정성을 위한 육성계통의 내냉성 특성 평가

곽강수*, 정국현, 서대하

강원도 춘천시 충열로 251 국립식량과학원 춘천출장소

근래 밥쌀용 쌀 소비의 지속적인 감소로 인한 쌀 과잉생산 문제와 밀가루 대체 가공용 쌀 수요의 증가 추세에 힘입어 산업체 연계 가공용 벼의 품종개발, 안정생산 및 공급을 위한 재배기술 개발이 지속해서 요구되고 있다. 한편, 가공용 벼의 안정적인 재배 및 생산을 위해서는 병해충 및 재해 저항성을 갖추어야 하는데, 특히 통일형 가공용 초다수성 벼의 경우 재배 안정성 향상을 위한 내냉성 검정이 필수적이라고 할 수 있다. 본 연구는 ’22년에 실시한 통일형 초다수성 벼 우량계통의 유묘 내냉성 및 포장 내냉성 특성 검정시험의 결과이다. 유묘 내냉성 검정을 위하여 초다수성 벼 육성계통 91계통을 파종 후 3엽기에 수온 13℃, 관개수심 4cm에서 10일간 흘려대기로 냉수 처리한 후 적고, 고사율 등을 체크품종(보람찬, 한아름2호)과 비교하여 평가하였다. 또한, 포장 내냉성 검정을 위하여 초다수성 벼 육성계통 91계통을 이앙 후 30일부터 등숙기까지 수온 17℃, 주야간 계속 흘려대기로 냉수 처리한 후 적고, 출수지연, 간장단축률 및 임실률 등 내냉성 관련 형질을 체크품종과 비교하여 종합내냉성을 평가하였다. 내냉성 평가 기준은 종합내냉성이 1~3은 ‘강’, 4~6은 ‘중’, 7~9는 ‘약’으로 분류하였다. (유묘 내냉성 검정) 체크품종의 내냉성 정도는 보람찬은 ‘중’, 한아름2호는 ‘약’의 반응을 나타냈으며, 공시한 초다수성 벼 육성계통의 경우 ‘강’으로 분류된 계통은 없었으며, 2계통이 ‘중’, 89계통이 ‘약’의 반응을 나타내어 극히 일부(2.2%) 계통을 제외하고 대부분(97.8%) 계통은 ‘약’의 반응을 나타내었다. (포장 내냉성 검정) 체크품종의 종합내냉성 정도는 보람찬과 한아름2호 모두 ‘약’의 반응을 나타냈으며, 공시한 초다수성 벼 육성계통의 등숙기 종합내냉성의 경우 ‘강’으로 분류된 계통은 없었으며, 4계통이 ‘중’, 87계통이 ‘약’의 반응을 나타내어 일부(4.4%) 계통을 제외하고 대부분(95.6%) 계통은 ‘약’의 반응을 나타내었다. 위의 결과에서, 출수지연이 덜 되고 간장단축률이 작아 등숙기 종합내냉성이 비교적 양호한 12개체를 선발하여 차년도 F_4 계통으로 냉수 처리하여 내냉성이 개선된 계통을 추가 선발할 예정이다. 이처럼 통일형 벼는 대부분 내냉성에 취약하여 저온에 대한 재배 안정성이 대체로 낮지만, 그중에는 상대적으로 어느 정도 내냉성을 갖는 계통도 있으므로 세대 진전을 통하여 내냉성이 더욱 개선된 계통을 선발하여 가공용 벼 품종을 육성하여 활용한다면 국내의 쌀가루 소비 확대와 쌀 가공산업에 크게 기여할 것이다.

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***교신저자:** Tel. 033-254-6328, E-mail: kskwak@korea.kr

PB-0018

Black soybean cultivar ‘Danheuk’ for cooking with rice with lodging and pod shattering tolerance

Jeong-Hyun Seo*, Beom-Kyu Kang, Jun-Hoi Kim, Su-Vin Heo, Man-Soo Choi, Jee-Yeon Ko, Hye-Rang Park, Choon-Song Kim

Upland Crop Breeding Research Division, Department of Southern Area Crop Science, National Institute of Crop Science, RDA, Miryang, Gyeongnam, 50424, Republic of Korea

Black soybeans are usually used to cooking with rice in Korea because of its sweetness and softness. Korean consumers prefer black soybean with a large seed size and green color inside the seed coat. ‘Danheuk’ is a black seed coat soybean cultivar developed from crossing ‘YS1882-B-B-16-2-4’ and ‘Cheongja3ho’ in 2012. Promising lines were selected using the pedigree method from F_3 to F_5. The preliminary and advanced yield trials were conducted in 2018 and 2019, respectively. Regional yield trials were conducted in eight regions from 2020 to 2022. ‘Danheuk’ has a determinate growth habit, oval leaflet shape, brown pubescence, and purple flowers. The seed of ‘Danheuk’ has a black seed coat color with green cotyledon. Flowering and maturing dates were Aug. 5, and Oct. 21, respectively. ‘Danheuk’ has large seed size (36.4 g/100-seed weight) and short plant height (65 cm). ‘Danheuk’ was tolerant to lodging and pod shattering in field and indoor RYT tests. ‘Daenheuk’ was resistant to bacterial pustule in the field and soybean mosaic virus in the inoculation test. The mean yield of ‘Danheuk’ in the RYTs was 271 kg/10a which was 4% higher than that of ‘Cheongja3ho’. ‘Danheuk’ is expected to be widely cultivated and used for cooking with rice because of its ease of cultivation and seed quality.

***Corresponding Author:** Tel. 055-350-1236, E-mail: next0501@korea.kr

PB-0019

Variation of soybean seed composition and soymilk quality according to the environmental factors

Jeong-Hyun Seo*, Beom-Kyu Kang, Jun-Hoi Kim, Su-Vin Heo, Man-Soo Choi, Jee-Yeon Ko, Hye-Rang Park, Choon-Song Kim

Upland Crop Breeding Research Division, Department of Southern Area Crop Science, National Institute of Crop Science, RDA, Miryang, Gyeongnam, 50424, Republic of Korea

Soybeans are widely cultivated as a material for making soy-foods such as tofu and soymilk in Korea. Among the soy-foods, soymilk is a suspension from the water-soluble solids are extracted. Therefore, the quality characteristics of soymilk could be varied depending on the composition of variety, and these compositions are easily affected by the growing environment during the maturation period. The objective of this study was to evaluate the variation of seed composition and soymilk quality over two experimental years. 32 domestic soybean varieties harvested in 2020 and 2021 were used to make soymilk. Soymilk was prepared using small-scale method with 50 ml conical tube developed in our previous study. Weather data from August to October were collected from the Korea Meteorological Administration (KMA) website (data.kma.go.kr). Compared to 2020, the average, maximum, and minimum temperature increased in 2021, especially in September and October. Also, the precipitation in August and October increased, compared to 2020, in September decreased, and the amount of sunlight decreased. As the maturing temperature increased and the amount of sunlight decreased in 2021, the protein content of seeds and soybean milk increased, the sugar content deceased, and the yield of soymilk increased, however the solid content decreased. This is consistent with previous studies that the protein content increases and the sugar content deceases as the maturing temperature increases. These results are thought to be helpful information for developing varieties with improved seed composition.

***Corresponding Author:** Tel. 055-350-1236, E-mail: next0501@korea.kr

PB-0020

Sensory evaluation and texture properties of frozen fried rice using different rice varieties

Gi-Un Seong[1], Ji-Yoon Lee[1], Sais-Beul Lee[1], Yeongsoo Park[1], Jun-Hyeon Cho[2], Ki-Won Oh[1], Dong-Soo Park[1], Ju-Won Kang[1*]

[1]Department of Southern Area Crop Science, National Institute of Crop Science, RDA, Miryang 50424, Republic of Korea
[2]Sangju Substation, National Institute of Crop Science, RDA, Sangju 37139, Republic of Korea

Frozen fried rice is a rice-based convenience food product for home consumption, where processing variables related to freezing and thawing significantly impact the final product. However, there is a lack of research on rice, the main ingredient of frozen fried rice. Rice that has been cooked and then tends to age over time, becoming hard and losing its stickiness, resulting in a decrease in taste quality. Therefore, it is important to evaluate how well the texture of the rice is restored when thawed using a microwave. In this regard, frozen fried rice was prepared using different types of rice (Miho, Miryang385, Saegoami, Shingil, and Sindongjin), and the physical properties and sensory evaluations were compared after thawing to assess their quality characteristics. The overall satisfaction ratings, from highest to lowest, were as follows: Miho (7.3), Miryang385 (6.4), Shindongjin (5.9), Shingil (4.4), and Saegoami (4.0). The results showed that Miho and Miryang385, which have a sticky texture, exhibited high satisfaction in terms of texture and sensory evaluation. However, Saegoami, which has a high amylose content, had weak elasticity and stickiness, resulting in lower scores. Therefore, semi-waxy rice (Miho and Miryang385) is considered suitable for producing frozen fried rice.

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***Corresponding Author:** Tel. 055-350-1156, E-mail: kangjw81@korea.kr

PB-0021

A new rice variety ‘ARTI-flo1’ with floury endosperm

Hong-Il Choi[1*], Gileung Lee[2], Jae Wan Park[1], Sang Hoon Kim[1]

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

[2]National Institute of Crop Science, Rural Development Administration, Wanju 55365, Republic of Korea

Floury endosperm is a necessary trait in rice to increase processing suitability, enabling dry milling to easily produce rice flour. Here we developed a new rice variety ‘ARTI-flo1’ with floury endosperm by mutation breeding. Rice callus induced from the variety ‘Donganbyeo’ were irradiated with 30 to 90 Gy gamma rays and screened on N6 medium containing azetidine-2-carboxylic acid. Rice plants were regenerated and proliferated for the construction of mutant population. A total of 192 mutant lines were selected based on investigation of agricultural traits and visual inspection, and advanced for genetic fixation. Among them, mutant line showing a phenotype of white opaque endosperm along with increased culm length and brown rice length was selected and named ‘ARTI-flo1’. The mutant variety had lower 1000-grain weight and grain hardness compared to Donganbyeo. Scanning electron microscope analysis revealed that the opaque endosperm of ‘ARTI-flo1’ was composed of loosely packed starch granules, which is typical appearance in floury endosperm rice. Our variety will contribute to the development and improvement of domestic rice cultivars suitable for economic end eco-friendly pulverization.

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

PB-0022

중북부 고랭지 적응 내냉성 강화 복합내병성 고품질 조생 벼 ‘수원670호’의 특성

정국현[1*], 김정주[2], 안억근[3], 현웅조[3], 이윤승[3], 박향미[2], 곽지은[4], 서대하[1], 곽강수[1]

[1]강원도 춘천시 충열로 251, 국립식량과학원 춘천출장소
[2]경기도 수원시 권선구 수인로 125, 국립식량과학원 재배환경과
[3]경기도 수원시 권선구 수인로 125, 국립식량과학원 중부작물과
[4]경기도 수원시 권선구 수인로 125, 국립식량과학원 수확후이용과

중북부 고랭지 적응 벼 품종은 최근 개발된‘진평’, ‘진한’, ‘진옥’ 등은 내병성과 품질이 우수하나 내냉성이 미흡한 실정으로 고랭지 적응성 뿐만 아니라 통일대비 북한지역 적응을 위해 내냉성이 강한 품종 개발이 필요하다. 본 연구는 내냉성이 강한 ‘진부57호’에 내병성을 도입하여 중북부 고랭지 재배가 가능한 조생 ‘수원670호’를 육성하여 그 특성을 밝히고자 수행하였다. ‘수원670호’는 내냉성이 강한 ‘진부57호’를 모본으로 복합내병성인 ‘익산537호’를 부본으로 교배하여 내냉성, 내병성, 내수발아성 등 재배안전성을 갖추고 수량성이 높으며 쌀알이 깨끗한 계통이다. ‘수원670호’는 등숙기 종합내냉성이 3으로 ‘진부’와 같이 강한 내냉성을 보였으며 저온발아율도 87%로 높다. ‘수원670호’의 출수기는 8월 3일로 ‘진부’보다 3일 빠른 조생이다. 간장은 76㎝로 ‘진부’ 보다 5cm 작고, 현미천립중은 22.3g으로 ‘진부’와 비슷하다. 쌀 수량은 607kg/10a로 ‘진부’보다 10% 증수되었다. 쓰러짐에 강하고 도열병, 흰잎마름병(K1균계)에 강하며, 수발아율이 9.9%로 강한 반응을 보였다. 내냉성이 강하면서 외관미질이 좋아 통일 대비 북한지역 쌀공급에 중요한 역할을 할 것으로 기대된다.

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***교신저자:** Tel. 033-254-6328, E-mail: khjung85@korea.kr

PB-0023

Multivariate analysis of morphological characteristics of maize (*Zea mays* L.) accessions from South Sudan

Emmanuel Andrea Mathiang[1], Hyeon Park[1,2], So Jung Jang[1,2], Jungeun Cho[1,2], Ju Kyong Lee[1,2*]

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

[2]Interdisciplinary Program in Smart Agriculture, Kangwon National University, Chuncheon 24341, Korea

Morphological characteristics studies provide useful information on germplasm that have the potential to be used in breeding. Here, Multivariate based analysis including principal component analysis (PCA) for agronomic traits were utilized to assess morphological patterns and group 31 maize landrace accessions for 7 quantitative characteristics. A significant positive correlation was found between days to tasseling (DT) and days to silking (DS), between plant height (PH) and ear height (EH) and stem width (SW), and between EH and SW and leaf length (LL). First and second principal components accounted for 69% of the total variance (40.9% and 28.6%, respectively). PH, EH, SW, LL, and leaf width (LW) were clearly characterized in a positive direction on the first axis. DT and DS were clearly characterized in a positive direction on the second axis. A scatter plot based on phenotypic data revealed the existence of 3 groups based on the most discriminating characteristics: Group I included 5 maize landrace accessions, Group II comprised 14 maize landrace accessions, and Group III included 10 maize landrace accessions. In principal component analysis, generally the investigated genotypes were not clearly grouped into their geographical origins owing to a weak geographic relationship among the accessions. Although the morphological characterization studies were conducted under South Korea climate, however, this study revealed noticeable phenotypic variation among the material studied. Therefore, this information about phenotypic divergence might be very useful for future breeding research programs as well as for genetic improvement of South Sudan maize.

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

PB-0024

밝은 적색 대립으로 다수성이며, 가공적성이 우수한 팥 신품종 ‘홍찬’

송석보*, 이병원, 추지호, 주영광, 최명은, 한상익

경남 밀양시 점필재로 20 국립식량과학원 남부작물부

‘홍찬’은 기계화적성이 우수하고 가공적성이 우수한 적색 대립 팥 품종을 육성하고자 2009년 하계에 국립식량과학원에서 쓰러짐에 강하고 담적색인 K204656/새길을 모본으로 하고 종자가 대립인 밀양9호를 부본으로 인공교배하여 계통육종법으로 선발한 품종이다.
2018~2019년 생산력검정시험에서 쓰러짐에 강하고 수량성이 높아 “밀양50호”로 계통명을 부여하였다. 2020~2022년 3년간 지역적응시험(밀양, 청원, 나주, 원주)을 실시한 결과, 가공적성이 우수하고 도복에 강한 품종으로 인정되어 2022년 농작물 직무육성 신품종 선정위원회에서 신규등록품종으로 결정되었다.
‘홍찬’의 개화일수는 44일로 ‘아라리’보다 10일 빠르지만 생육일수는 104일로 5일 늦은 중만생종이다. 경장은 56㎝로 아라리보다 4cm 정도 작고, 협수는 24개로 ‘아라리’와 비슷하다. 100립중은 21.3g으로 아라리보다 4.9g 더 무겁고 밝은 적색의 종피색을 가진 대립 품종이다. 수량성은 지역적응시험에서 평균수량이 2.11MT/ha로 다수성 품종이다. 적응지역은 강원도 산간고랭지를 제외한 전국 팥 재배 지역에서 재배가 가능하다. 기계수확이 가능한 ‘홍찬’은 노동력과 생산비절감으로 생력화와 농가소득 증대에 기여할 것으로 기대된다.

***주저자:** Tel. 055-350-1243, E-mail: songsb1254@korea.kr

PB-0025

조생 밥맛과 재배안정성이 우수한 벼 ‘새오대1호’

원용재, 백만기*, 구본일, 최원영

전라북도 완주군 이서면 혁신로 181 농촌진흥청 국립식량과학원

중북부 중간지 및 중산간지 적응 고품질 조생 벼 품종을 육성할 목적으로 2011년 하계에 조생 중립, 도열병저항성이고 쌀 외관이 우수한 ‘새오대’를 모본으로, 밥맛이 우수하고 흰잎마름병에 강한 ‘운봉51호’를 부본으로 교배하여 SR34150의 교배번호를 부여하였다. 유전적으로 고정된 우량계통을 얻고자 F1세대 8개체를 양성한 후 세대진전을 위하여 F2집단 1,400개체 중 95개체를 수확하고 2014/2015년 동계에 이들을 필리핀에 있는 IRRI에서 세대진전하였고 이중 IR1번 계통이 우수하여 선발하였다. F_5, F_6, F_7을 계통 재배하면서 초형, 주요 병해충 검정을 병행한 결과 유망한 SR34150-2-IR1-2-3-3계통을 선발하였다. 선발된 우량계통에 대하여 2018~2019년 생산력검정시험을 실시 한 결과 조생 중립이면서 도열병과 흰잎마름병에 강하고 쌀 외관이 우수하여 철원103호로 계통명을 부여하였다. 2020년부터 2022년까지 3년간 지역적응시험을 실시한 결과 모본인 새오대의 내병성, 품질 및 밥맛 개선 등의 우수성이 인정되어 2022년 12월 농촌진흥청 직무육성 신품종 선정위원회에서 국가목록등재품종으로 선정됨과 동시에 ‘새오대1호’로 명명되었다.

***교신저자:** Tel. 033-455-2031, E-mail: baekmg@korea.kr

PB-0026

Mid-Maturing, Aromatic and Glutinous Rice Variety ‘Gureumchal’

Young-Un Song*, Jong-Hee Shin, Chae-Min Han, Sang-Kuk Kim, Jung-Gi Ryu

Division of Crop Research, Gyeongsangbuk-do Provincial Agricultural Research and Extension Services, Daegu 41404, Republic of Korea

The ‘Gureumchal(Gyeongbuk13)’ is a new japonica rice cultivar selected by inducing mutations from the collected resources (K27885), glutinous black brown rice, fragrant and late ripening, with gamma rays. This cultivar, a mid-maturing rice with large grain size, fragrant glutinous rice, was developed by the rice breeding team at GBARES in 2022. The heading date of ‘Gureumchal’ was August 3 in the southern plain area, which was 5 days earlier than that of ‘Shinseonchalbyeo’ when they were transplanted May 30. ‘Gureumchal’ had a culm length of 65 cm, which was 19 cm shorter than that of ‘Shinseonchalbyeo’ and it had 73 spikelets per panicle. The viviparous germination rate of ‘Gureumchal’ was 8.6%. The milled rice of this variety exhibited medium grains. Compared to ‘Shinseonchalbyeo’, it has similar amylose content (5.4%), palatability of cooked rice and higher protein content (7.5%). The weight of 1,000 grains of brown rice of this variety was 28.5g, which was 36% heavier than that of the ‘Shinseonchalbyeo’. It also showed resistance to lodging. ‘Gureumchal’ showed 5.04 MT/ha of milled rice productivity in local adaptability test at 4 site. ‘Gureumchal’ would be adaptable to Yeongnam plain and south mid-mountainous area.

***Corresponding Author:** Tel. 053-320-0276, E-mail: crycek09@korea.kr

PB-0027

Characteristic Evaluation of AVRDC Mungbean Mini Core Collection

Ji-Ho Chu*, Byeong-Won Lee, Seok-Bo Song, Young-Kwang Ju, Sang-Ik Han

Upland Crop Breeding Research Division, Department of Southern Area Crop Science, National Institute of Crop Science, RDA, Milyang, Gyeongnam, 50424, Republic of Korea

Consumption of Mungbean has been on the rise because Mungbean is used for seeds but also sprout. As temperature around Korea has been risen sharply, the cropping system are changing in korea. As Mungbean adapt to high temperature, Mungbean has bean consumed in high temperature area like Austrailia and Southest Asia. 293 resources of AVRDC Mungbean core collection are tested for development of Mungbean cultivars suitable for Korean climate. Agricultural characters like Hypocotyl color, Growth pattern, Growth habit, Terminal leaflet shape, petiole color, leaf color, Promary leaf size, flower color, flowering date and Days to maturity is tested. 11 resources show indeterminate pattern. Flowering date of 59 resources is under 40days, and K733334's is 35days. In content analysis of Vitexin and iso-Vitexin, Content of Vitexin ranges from 921 to 1653㎍/g and iso-Vitexin's from 1223 to 1953㎍/g. weight of 100 seeds ranges from 1.4 to 7.6g. 23 resources like K273176 have been selected in the light of agricultural characters, content of Vitexin and iso-Vitexin and weight of 100 seeds.

***Corresponding Author:** Tel. 055-350-1245, E-mail: chugho@korea.kr

PB-0028

Comparison of transcriptome with colored wheat and its salt tolerant mutant under salt stress condition

Min Jeong Hong[1], Jin-Baek Kim[1], Chan Seop Ko[1], Hong-Il Choi[1], Sang Hoon Kim[1], Dae Yeon Kim[2*]

[1]Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, 29 Geumgu, Jeongeup 56212, Republic of Korea

[2]Department of Plant Resources, College of Industrial Sciences, Kongju National University, 54, Daehak-ro, Yesan-eup, Yesan-gun, Chungnam, 32439, Republic of Korea

Salinity stress is a major environmental stress that prevents plant normal growth and development, which reduces crop productivity. The need to develop salt-tolerant crops has emerged due to the increase in soil salinization worldwide, but the development of salt-tolerant crops and the discovery and utilization of salt-tolerant genes remains limited due to the narrow genetic diversity. In this study, we constructed a mutant pool of wheat using gamma-ray to broaden genetic diversity. Colored wheat seeds were irradiated with a total dose of 200 Gy of gamma rays in a ^{60}Co gamma irradiator. The mutants were continuously planted to M_6 generation and selected on the basis of excellent agricultural traits such as flowering time, plant height, yield, grain color, etc. To select salt-tolerant colored wheat mutant lines, mutants were screened at the seedling stage based on germination and plant growth rates at 150 mM of salinity level. PL6 selected as salt-tolerant colored wheat had higher tolerance to salt stress. Ion and chlorophyll contents were measured to determine physiological changes caused by salinity. In total, 4,017 differentially expressed genes (DEGs) were identified through transcriptome analysis between PL1 (control) and PL6. To understand the molecular mechanism of salt tolerance, transcriptome analysis identifying salt responsive gene networks and functional annotation was performed. This result provides new genetic resources of wheat in plant breeding for salt resistance and new information on salt-tolerant genes.

***Corresponding Author:** Tel. 041-330-1205, E-mail: dykim@kongju.ac.kr

PB-0029

Studies on cytogenetic characteristics of *Elymus humidus* for wheat breeding program

Ji-Yoon Han[1], Seong-Wook Kang[2], Sejin Oh[2], Yumi Lee[3], Myoung-Jae Shin[4], Sukyeung Lee[4], Seong-Woo Cho[1,2,3*]

[1]Department of Plant Resources, Gyeongsang National University, Jinju, 52725, Republic of Korea
[2]Department of GreenBio Science, Gyeongsang National University, Jinju, 52725, Republic of Korea
[3]Department of Smart Agro-Industry, Gyeongsang National University, Jinju, 52725, Republic of Korea
[4]National Agrobiodiversity Center, National Institute of Agricultural Sciences, Rural Development Administration, Jeonju, 54874, Republic of Korea

Recently, *Elymus humidus*, which was known as an indigenous plant in Japan was also found spontaneously around riverside in Korea. *E. humidus* is useful genetic resource for humidity resistance because of high growth adaptability in paddy field. We investigated stomata traits and leaf structure of *E. humidus* in this study. *E. humidus* showed long grain type with dark brown color. Seed length, width, and height of *E. humidus* were approximately 85.7, 45.3, and 12.8% of those of common wheat. Stomatal density, length, and width of *E. humidus* were significantly lower and smaller than CS, while distance between stomata of *E. humidus* was farther than CS in adaxial and abaxial sides. For chromosome observation, there were long and short chromosomes, relatively. In long chromosomes, some chromosomes showed the same length in long and short arms. Other chromosomes showed more two times length of long arm compared to length of short arm. In short chromosomes, some chromosomes were the same length in long and short arms, and other chromosomes showed little longer length in long arm than short arm. In addition, some chromosomes were with microsatellite among short chromosomes. In leaf anatomy section, *E. humidus* had the same structure of vascular bundle, but sclerenchymatous bundle sheath of *E. humidus* was more compact and with smaller cell size than CS. For genetic polymorphism in wheat breed program, we evaluated by using barley EST markers. There were 56 for polymorphism markers among total 236 EST markers.

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

PB-0030

A new soybean (*Glycine Max* L.) ‘Bitnadu’ cultivar with green cotyledon and glossy black seed coat characteristics

Hyeon-Tae Cho*, Chang-ki Son, Ji-Yun Lee, Jeong-Suk Bae, Tae-Yeung Oh, Jung-Ki Ryu, Jong-Soo Kim

Gyeongsangbuk-do Provincial Agricultural Research and Extension Services, 41404, Daegu, Republic of Korea

A new black soybean cultivar with green cotyledon, ‘Bitnadu(Gyeongbuk 7)’ was developed by the soybean breeding team at GBARES (Gyungsangbuk-do provincial Agricultural Research and Extension Services) in 2020. The population from which ‘Bitnadu’ was derived began as a single cross between ‘Seonheuk’ and ‘RCS640’ that was made in 2011. The elite breeding line was designated ‘Gyeongbuk 7’ after that it was evaluated and selected in the performance yield trial from 2016 to 2017. ‘Gyeongbuk 7’ also was tested in the regional yield trials in seven locations from 2018 to 2020. Its permanent name, ‘Bitnadu’, was assigned in 2020. ‘Bitnadu’ has a semi-determinate growth habits, purple flower, grey pubescence, light brown pod color, black seed coat, ellipse seed shape and large seed size (40.5 g/100seeds) which was larger than the check variety ‘Cheongja 3’ (35.5 g/100seeds). ‘Bitnadu’ has a deep green cotyledon compared with a light green cotyledon close to yellow of ‘Cheongja 3’. A contents of chlorophyll (lutein) in cotyledon for ‘Bitnadu’ is twice higher than ‘Cheongja 3’. ‘Bitnadu’ is moderately resistant to bacterial pustule (caused by Xanthomonas axonopodis pv. glycines) and soybean mosaic virus (strain G6H). The average yield in the regional yield trials (RYT) of ‘Bitnadu’ was 2.58 MT ha-1 which was 8% higher than ‘Cheongja 3’.

***Corresponding Author:** Tel. 053-320-0287, E-mail: 94best@korea.kr

PB-0031

A new sorghum (Sorghum bicolor L.) “Hongme” cultivar with higher antioxidants and cultivation characteristics

Chang-ki Son*, Jeong-Suk Bae, Tae-Yeung Oh, Hyeon-Tae Cho, Ji-Yun Lee, Jung-Ki Ryu, Jong-Soo Kim

Gyeongsangbuk-do Provincial Agricultural Research and Extension Services, Daegu 41404, Republic of Korea

The demand for sorghum has been increasing because it plays a significant and positive role in promoting nutrition and health in human beings. However, sorghum cultivated by farms is mostly a native variety with low genetic purity and production; hence, it is necessary to improve the variety. Accordingly, the sorghum breeding team at Gyeongsangbuk-do Provincial Agricultural Research and Extension Services a nonglutinous sorghum, Hongme, in 2022, which exhibited excellent antioxidant activity and growth characteristics. It was developed from a population derived by a single cross between the Wonju- and Bonghwa-collected species in 2011. This elite breeding line was designated as ‘Gyeongbuk 2’ and was evaluated and selected for the performance yield trial from 2018 to 2019 as well as for regional yield trials (RYTs) conducted at four locations from 2020 to 2022. Notably, we found that Hongme was an early maturing variety, which took an average of 65 days from the sowing date to the heading date and an average of 101 days for harvesting. Its typical characteristics include inverted triangle-shaped seeds; a thin density of ears; reddish brown and dark brown colors of the seedling sand bases hell, respectively; and the nonglutinous endosperm. Its stem length was 111 cm and the ear length was 34 cm, which was longer than that of Sodamchal. Further, the ear-neck length was 8 cm, and the branching number was 0.3; hence, it was considered a small-branched type variety. Its ear weight was 79 g and seed weight per ear was 48 g, which were 16 g and 9 g higher than those of Sodamchal, respectively. Moreover, the calcium, magnesium, and sodium contents of Hongme were slightly higher than those of Sodamchal. Furthermore, in Hongme, the content of polyphenols and flavonoids involved in antioxidant activity were 977.5 and 776.2 mg/100 g, which were 45% and 61% higher than the content of polyphenols and flavonoids in Sodamchal, respectively. The average yield of Hongme in RYTs was 3.45 MT ha-1, which was 17% higher than that of Sodamchal.

***Corresponding Author:** Tel. 053-320-0226, E-mail: sck3058@korea.kr

PB-0032

Candidate genes analysis for high seed protein content in soybean with two RIL populations derived from 'Saedanbaek'

Hye Rang Park, Beom Kyu Kang, Jun Hoi Kim, Su Vin Heo, Man Soo Choi, Jee Yeon Ko, Choon-Song Kim, Jeong Hyun Seo*

Upland Crop Breeding Research Division, Department of Southern Area Crop Science, National Institute of Crop Science, RDA, Miryang, Gyeongnam, 50424, Republic of Korea

Soybean [*Glycine max* (L) Merr.], which belongs to one of the legume crops, is a superb source for the supply of high-quality vegetable protein. The objective of this study was to discover quantitative trait loci (QTL) and candidate genes for high seed protein content in soybean. We used two recombinant inbred line (RIL) populations derived from a cross between 'Saedanbaek (high protein)', one of the elite cultivars in South Korea, and 'YS2035-B-91-1-B-1 (low protein)' or 'Ilmi (low protein)' in the field for three consecutive years. We found several QTLs on chromosome 15, 18, and 20. *qP-YS20* repeatedly appeared in the same region in the RILs of 'YS2035-B-91-1-B-1' and 'Saedanbaek' for three experimental years, which has already been reported in various studies to these days, and the others were novel regions. The logarithm of odds (LOD) values of these QTL ranged from 7.2 to 54.1, and the percentage of phenotypic variance explained (PVE) ranged from 6.9 to 61.7%. Considering the allele sequence variation between the parents, 32 annotated genes were found within the identified QTL regions. Among these regions, eleven contained stop gained, eighteen had frameshift variant, one had a stop retained variant, and two had stop lost variants in single-nucleotide polymorphisms (SNPs). These genes are suggesting potential application of selecting lines with high protein content in the soybean breeding program. The results provide useful information to understand the genetic mechanism of high protein and could be used to enhance marker-assisted selection strategies for developing soybean varieties with improved protein traits.

***Corresponding Author:** Tel. 055-350-1236, E-mail: next0501@korea.kr

PB-0033

A premium rice variety, ‘Hangadeuk’ through Stakeholder Participatory Program(SPP) for replacing foreign rice in the Gimpo area

Woong Jo Hyun*, Eok Keun Ahn, Kuk Hyun Jung, Yoon Sung Lee, Sang Beom Lee, Jeom Ho Lee, Hyang Mi Park, Man Gi Baek, Yong Jae Won, Jeong Heui Lee, Ji Eun Kwak, Jong Cheol Ko

National Institute of Crop Science, RDA, Korea

To enhance seed sovereignty, the government's rice seed distribution strategy aims to reduce the cultivation of foreign varieties with low stability and expand the distribution of domestic high-quality rice varieties. Among the national distribution varieties in South Korea in 2022, foreign varieties such as ‘Akibare’ and ‘Koshihikari’ accounted for 9% of the total supply, which is 1,978 tons. Therefore, there is an urgent need for the development of new varieties to replace the foreign varieties that are currently widely cultivated in the central and northern regions of our country. The National Institute of Crop Science invented a new type of rice variety development and distribution program called ‘Stakeholder Participatory Program(SPP)’. This program required series of activities including elite line selections, demonstrations, seed productions, training, and propaganda etc. Through this program, a premium quality mid-maturing rice, ‘Hangadeuk’ was developed in 2022 by collaboration among various stakeholders. ‘Hangadeuk’ was mated in 2010 with ‘Samgwang’ and ‘Juan/SR21733-48-1-12-1’ as the parent. An excellent line with good grain quality and resistance to diseases, SR33851-2-1-1-2, was selected from the fixed generation F6, and it was given the pedigree name “Suweon 639.” At the new variety council, this variety was chosen as the new rice variety in recognition of its excellent performance in the two-year yield trial and the three-year local adaptability test. ‘Hangadeuk’ is middle maturing variety with excellent taste and multiple disease resistance, so it can satisfy from farmers to consumers and be expected to play a role as a variety of premium rice brand.

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***Corresponding Author:** Tel. 031-695-4028, E-mail: onlybio@korea.kr

PB-0034

Agronomic Traits of Mungbean (*Vigna radiata* L.) Germplasm 'K278576' with Pod Shattering Resistance

Yeong Min Jo[1*], Kyu Hwan Choi[1], Byong Soo Heo[1], Hyun Ah Han[1], Min Sil An[1], Ju Kim[1], Chul-Soo Park[2]

[1]Jeollabukdo Agricultural Research Extension Services, Iksan, 54591, Korea.
[2]Department of Crop Science and Biotechnology, Jeonbuk National University, Jeonju 54896, Korea

Mungbean (*Vigna radiata* L.) is an important legumes consumed all over the world, it is diets foods with excellent source of minerals and vitamins including resistant starch. Despite its nutritional benefits, mungbean cultivation takes a lot of effort because agronomic traits, non-synchronous pod maturity and pod shattering cannot be fully improved by breeding programs. K278576, temporary ID of National Agrobiodiversity Center, was collected from Gimje-si, Jeollabuk-do, Korea, and has pod shattering tolerance. K278576 was sown on July 1, 2023 and flowering date was August 15 which was delayed 7 days compared to Korean leading mungbean cultivars. K278576 showed very low pod shattering rate (1.4%) at 70 days after flowering, which will be used as genetic resources in Korean mungbean breeding programs. The yield of K278576 was 261kg/10a, which was lower 52kg/10a than Geumsung, the highest yield in Korean cultivars. K278576 had longer plant height (101cm), fewer number of pod per plant (35) and higher thousand grain weight (66g) than average of Korean leading mungbean cultivars (106cm, 59 and 45g, respectively). Total polyphenol and flavonoid contents of K278576 were 121.52mg/100g and 102.64mg/100g, lower to that of Geumsung (209.80, 102.64mg/100g, respectively). Overall, minerals and vitamins were similar or lower than Geumsung.

***Corresponding Author:** Tel. 063-290-6033, E-mail: jomin0220@korea.kr

PB-0035

Natural variation in functional components of rice by environmental and genetic factors

Hyoun-min Park[1*], Jung-won Jung[1], So Ra Jin[2], Eun-ha Kim[1], Sang-gu Lee[1], Soo-yun Park[3], Seon-woo Oh[1]

[1]Biosafety Division, National Institute of Agricultural Science, Rural Development Administrative, 370 Nongsaengmyeong-ro, Jeonju, Jeollabuk-do, 54874, Republic of Korea
[2]Korea National Food Cluster, Iksan-si, Jeollabuk-do 54576, Republic of Korea
[3]Technology Cooperation Bureau, Rural Development Administration, Jeonju 54875, Republic of Korea

Rice is one of the most widely cultivated crops in the world. *Oryzae sativa*, which is mainly cultivated in Asia, is classified into Indica and Zaponica varieties depending on the shape of the grain. We analyzed functional components to confirm the natural variation of Indica rice(4 types), Zaponica rice(15 types) and Tongil rice(4 types) which developed by crossing Indica and Zaponica varieties in Korea, considering the environmental factors of 2 locations(Cheonan, Jeonju) for 2 years('15-'16). Tocopherol, tocotrienol and phytosterol were analyzed as functional components, and Stigmasterol was the highest content in all types. Next, Campesterol and β-sitosterol were followed, and phytosterol was higher in content than tocopherol, tocotrienol. Through p-value statistical analysis, δ-tocopherol showed to no significant difference between years and Cholesterol, stigmasterol showed no significant difference between locations. Otherwise, there was a significant differences ($p<0.001$) in all contents except campesterol($p<0.01$) between the three varieties. In this study, it was suggested that the content of 23 types of rice analyzed was affected by genetic factors than environmental factors.

***Corresponding Author:** Tel. 063-238-4710, E-mail: hyoun3239@korea.kr

PB-0036

A New Single Cross Hybrid for 'Alchanpop' Corn with High Yields

Jae-Keun Choi*, Si-Hwan Ryu, Hee Yeon Kim, Moon-jong Kim, Jung Heon Han, Seung Hyun Wang, Woo Sik Yong, Jae Nam, Ki Sun Kim

Maize Research Institute, Gangwondo Agricultural Research and Extension Services, Hongcheon, Korea

Popcorn is one of the popular snacks and the amount of consumption is reasonably high in South Korea, but the majority of popcorn is imported from outside. So we have to development to domestic varieties. This study was carried out to create new popcorn variety. 'Alchanpop' was made by single crossing with two inbred lines, the seed parent, GP2 and the pollen parent, GP7. The hybrid was made in 2017 and selected in 2022 after investigating characteristics for three years from 2020 to 2022. 'Alchanpop' was evaluated 3 places in Gangwon-do for three years. The morphological characteristics of 'Alchanpop' are as follows: yellow seed coat, anthocyanin-rich sillk, light green leaves. 'Alchanpop' silks at 83 days, similar to the check variety 'Oryunpopcorn'. The plant height is 220㎝ and ration ear height of plant height of 'Alchanpop' is 56%. The weight of 100 seeds was 18.1g, similar to that of the check variety. The yield of 'Alchanpop' was 562kg/10a in regional yield trials for three years, which was 36% higher than that of 'Oryunpopcorn'.(Application No. 2023-128)

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

PB-0037

국가기반 육종플랫폼 구축을 위한 소재-오믹스 딥데이터 공유 시스템

박수현[1], 이승욱[1], 김대규[1], 윤석재[1], 김대관[1], 송지용[1], 박수권[2], 송승엽[2], 이상범[2], 손재한[3], 유의수[1]*

[1]주식회사 디엔에이케어
[2]농촌진흥청 식량과학원 작물기초기반과
[3]농촌진흥청 식량과학원 중부작물부

작물육종은 유전체 정보에 기반하여 기타 오믹스 데이터 및 정밀표현체 정보와 인공지능기술 등 신기술의 융・복합적인 접목을 통해 선발효율 향상, 육종연한 단축, 복합형질 육종을 목표로 하는 데이터 기반 정밀육종으로 전환되고 있다. 또한 최근 기후변화, 탄소중립, 소비 트랜드의 변화 등에 빠르게 대응하기 위해서는 다양성을 포함하는 육종소재 개발 및 대사체를 포함한 다양한 오믹스 데이터의 생산, 공유를 통해 전문화된 협업관계를 유지하며 목표에 부합하는 종자를 신속하게 개발할 수 있는 데이터베이스 및 정보 활용 체계의 구축이 필요하다. 본 과제는 육종 소재와 오믹스 정보의 통합 관리 데이터베이스를 구축하여 표준화된 육종 소재를 중심으로 유전형 및 다양한 오믹스 데이터 생산을 가속화하고 인공지능 심화학습에 필요한 딥데이터의 집적을 유도하며, 연관분석 시스템 구축으로 유용 형질과 연관된 유전자 탐색 및 마커 개발, 예측 효율 향상, 정보 공유를 통한 연구 그룹 간의 효율적인 협업 환경 조성의 지원을 목표로 한다. 세부적으로는 1) 소재 메타데이터와 다중 오믹스 데이터의 표준화, 2) 소재-오믹스 정보를 연계한 통합 데이터베이스 구축, 3) 데이터베이스와 연동한 전유전체 연관분석 체계 및 사용자 인터페이스 구축, 4) 대사체-기능체 간 다변량 분석 체계 및 사용자 인터페이스 구축, 5) 소재 및 데이터 생산, 분석이력 및 성과 공유를 위한 모니터링 모듈 구축을 목표로 본 과제를 수행한다. 본 과제를 통해 구축된 소재-오믹스 정보 통합관리 시스템은 지속 및 확장 가능한 데이터베이스의 역할을 통해 표준화・정규화를 거친 고품질의 다중오믹스 딥데이터를 축적하고, 인공지능을 활용한 기계학습의 데이터 셋으로 사용하여 형질 예측 기술 강화 및 소재-오믹스 데이터의 공유를 통한 공동연구 기회 확대에 활용될 것으로 기대한다.

사사: 본 결과물은 농촌진흥청의 재원으로 공공성 확보를 위한 국가 기반 육종 플랫폼 개발(딥데이터 처리 및 연계 기술 개발) 사업의 지원을 받아 연구되었음(과제번호 RS-2023-00228991)

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

PB-0038

Genetic diversity of Korean soybean (*Glycine max*(L.) Merr.) landraces and traces of domestication selection associated with agronomic traits

Jung-Yoon Yi*, XiaoHan Wang, Hye-Myeong Yoon, Yu-Mi Choi, Myoung-Jae Shin, Su-Kyeung Lee, Kebede Taye Desta, Young-Wang Na, Na-Young Ro, Hyun-Seok Oh

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

Various kinds of soybeans have been cultivated in East Asia(including Korea) as a result of being used as diverse food materials and being adapted in different environment for a long time.

The National Agrobiodiversity Center (NAC) has maintained a large collection of Korean soybean landraces(approximately 15,000 accessions) to prevent genetic erosion and to preserve genetic diversity. In this study, 14 agricultural traits of 936 Korean soybean landraces from NAC were evaluated. And genotyping was performed using the Axiom_Soya SNP array (180k) developed by the Rural Development Administration (RDA). Correlation between 5 quantitative traits, flowering stage, growth habit, plant height, the maturity and seed number per pod, was analyzed. Population structure analysis results showed determination of 5 or 8 subpopulation. Phylogenetic analysis further confirmed the significant genetic differences among the eight subgroups. Principal component analysis (PCA) showed the differnece in quantitative traits of 8 subpopulations. Genetic diversity analysis (LD decay) showed that the genetic differences among the subpopulations were small and the genetic diversity of subpopulations 1, 5 and 7 was higher than that of other subpopulations. By calculating the genome-wide sliding window Tajiama' D, the regions of allele frequency fluctuations due to strong selection events experienced in Korean landrace populations were marked. And some of these intervals are related to the loci obtained from the results of the nine quantitative traits genome-wide association studies, but not related to the genes related to the qualitative traits (GWAS).

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***Corresponding Author:** Tel. 063-238-4911, E-mail: naaeskr@korea.kr

PB-0039

Knock out the candidate genes associated with fatty acid composition in rice

Muhyun Kim[1], Minyoung Song[1], Dohye Kweon[1], Yumi Ko[1], Seehyun Park[1], Ah-Rim Lee[2], Soon-Wook Kwon[2], Tae-Ho Ham[3], Hyunjin Park[3], Joohyun Lee[1*]

[1]Department of Crop Science, Konkuk University, Seoul 05029, Korea
[2]Department of Plant Bioscience, College of Natural Resources and Life Science, Pusan National University, Miryang 50463, Korea
[3]Department of Agricultural Science, Korea National Open University, Seoul 03087, Korea

Fatty acids in rice grain are significant factor that determine rice grains and rice branoil qualities as they influence their starch and lipid compositions. Univariate GWAS for single trait(UV-GWAS), univariate GWAS for principal component(PC-GWAS), and multi-trait GWAS(MV-GWAS) was conducted for fatty acid composition in brown rice grain in rice accessions of 295. By comparing results from UV-GWAS, PC-GWAS and MV-GWAS, we obtained several loci detected for unsaturated fatty acid composition and saturated acid composition. Based on the phenotypic differences among haplotypes and functional annotation of genes, we selected candidate genes for unsaturated fatty acid and saturated fatty acid composition, respectively. For functional validation of GWAS candidate genes, CRISPR/Cas9-mediated knockout mutants were created by introducing mutation into the genes. Designed gRNAs containing the Cas9 targeting sequences were cloned into pRGEB32 vector and transferred to rice calli, mediated by agrobacterium. We identified 6 putative unsaturated fatty acid gene mutants through PCR screening. Producing mutants of saturated fatty acid composition and additional mutants for unsaturated fatty acid is underway.

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

PB-0040

Distribution of traits closely related to high temperature tolerance in a RIL population of rice

Tae-Ho Ham[1*], Mi-Young Park[1], So-Myoung Lee[2]

[1]Dept. of Agricultural Science, Korea National Open University, 86 Daehar-ro, Jongro-gu, Seoul, 03087, Republic of Korea
[2]National Institute of Crop Science, RDA, Miryang 50424, Republic of Korea

Rice is sensitive to high temperatures stress during almost growth and development stages. According the climate crisis, high temperature stress has become one of the main factors restricting yield and quality of rice. In this study, 137 recombinant inbred lines (RILs) derived from cross between a *indica* rice Miryang 23 and a *japonica* rice Tong88-7 were planted in Milyang city. Two traits closely related to high temperature tolerance, heading date (HD) and spikelet fertility (SF), were measured. In HD showed a bimodal distribution, whereas SF had a continuous and left-skewed distribution. By GWAS analysis, there are significant SNP and some qtl were detected.

***Corresponding Author:** Tel. 02-3668-4630, E-mail: kg780516@knou.ac.kr

PB-0041

Development of Advanced Backcross Nasted Associated Mapping Population With Recurrent Cultivar, Youngjin, For Genomic Selection In Rice

Youngho Kwon*, So-Myeong Lee, Hyeon-Jin Park, Jin-kyung Cha, Nkulu Rolly Kabange, Jong-Hee Lee

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

Recently, there has been a growing diversity in customer demands, and it is crucial to respond quickly to these changes. Therefore, breeding an excellent prototype is essential. By backcrossing elite variety with germplasms, breeder can select near isogenic lines that have useful and unexpected traits. Here, we developed Advanced-NAM population that backcrossed 'Youngjin' 2 times. 'Youngjin' is promising cultivar developed in 2016. Youngjin has *qbk1* and *xa3*, 63cm of height and grains are clear, clean, and have a high level of completeness in terms of milling. Youngjin was crossed with 16 elite germplasms in 2020 summer and backcrossed 2 times in 20/21 winter. BC2F1 were harvested in 2021 summer and progressed generation on greenhouse in 21/22 winter. In 2023, BC2F7 plants of each population were performed target captured sequencing to select lines that have different fragment respectively. Finally, 16 Youngjin Advanced-NAM populations were developed. Average recurrent ratio of populations were 77.9%. These populations can be a great tool for genetic study but also developing a new cultivar.

***Corresponding Author:** E-mail: kwon6344@korea.kr

PB-0042

Variation of ripening and quality of processing rice cultivars depending on weather conditions in north central area of Korea

Bon Il Ku[1*], Man Kee Baek[1], Hyun Jin Park[2], Jieun Kwak[2], Jeong Heui Lee[2]

[1]Cheorwon Branch, National Institute of Crop Science, RDA
[2]Department of Central Area Crop Science, NICS, RDA

Cheorwon has shorter rice growing period which is located in northernmost and inland region in major rice fields of Korea. So ripening environment after heading have a greater impact on rice yield. Especially, daily minimum temperature descended quickly in 2022. Therefore, the ripening period of rice was reduced and passed the lower temperature condition. So this study was conducted to evaluate the adaptability of processing rice cultivars in low temperature ripening condition in north central area of Korea. 20 processing rice cultivars were transplanted on May 20 in 2021 and 2022. And we checked weather change after heading of rice, rice yield and quality. Compared to 2021. Temperature descended quickly in late September and early October in 2022. The cultivars which showed low ripened grain ratio in 2022 were Heukjinju, Heuknami, Joeunheugmi. And rice yield were low in Seonhyangheugmi, Gilimgeukmi, Heuknami. The range of protein content was 5.2~7.3% and it were higher in Gilimheukmi, Heukjinju and lower in Seohaechal 2, Namil.

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***Corresponding Author:** Tel. 033-456-2031, E-mail: kubonil@korea.kr

PB-0043

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

Si Hyeon Kim[1], Hye Jeong Kim[2], Hae Gyun Park[1], Hyemin Park[1], Soo Hyun Park[1], Young-Soo Chung[2*]

[1]Department of Applied Bioscience, College of National Resources and Life Science, Dong-A University, Busan 49315, Republic of Korea

[2]Department of Molecular Genetics, College of National Resources and Life Science, Dong-A University, Busan 49315, Republic of Korea

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 twenty-six 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-six transgenic lines, it was confirmed that fifteen 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. To identify the insertion locus of the transgenic line #18 (T_0), the Adapter Ligation PCR was conducted to confirm the regions flanking the T-DNA inserts. As a result, it was confirmed that pCKLSL-β-con:*TI*(RNAi), pCKLSL-β-con:*LE*(RNAi), and pCKLSL-β-con:*P34*(RNAi) were inserted into the chromosome #8, #2, and #8, respectively.

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***Corresponding Author:** Tel. 051-200-7510, E-mail: chungys@dau.ac.kr

PB-0044

Production of soybean overexpressed in seeds with *GmIFS* and *GmMYB29* genes by co-transformation method

Wan Woo Yeom[1], Si Hyeon Kim[1], Hae Gyun Park[1], Soo Hyun Park[1], Ye Won Kim[1], Young-Soo Chung[2*]

[1]Department of Applied Bioscience, College of National Resources and Life Science, Dong-A University, Busan 49315, Republic of Korea

[2]Department of Molecular Genetics, College of National Resources and Life Science, Dong-A University, Busan 49315, Republic of Korea

Isoflavone is one of the primary metabolites in soybeans (*Glycine max* (L.) Marr.) and is a variety of physiologically active substances. In plants, isoflavones act as phytoalexin in microbial interactions and plant protection. In addition, in soybeans and plants, it acts as a signal substance for nitrogen fixation in plants. In humans, isoflavone acts as a vegetable estrogen, preventing cancer and cardiovascular disease through antioxidant action and alleviating menopause syndrome. The three key isoflavones in soybeans are daidzein, genistein, and glycitein. In isoflavone biosynthesis, phenylalanine is deaminated by phenylalanine ammonia decomposition enzyme (PAL), and is finally synthesized by isoflavone synthetase (IFS) by a line of enzyme reactions. Previous studies have confirmed that GmMYB29, one of the transcriptional regulators MYB, acts as a phagocytic regulator in IFS2 expression. In previous studies, it has been reported that GmMYB29, one of the transcriptional regulators MYB, acts as a positive regulator for IFS2 expression. In this study, agrobacterium was transformed to express GmMYB29 and IFS genes in seeds with β-conglycinin promoters, which are seed expression promoters. Two GmMYB and IFS agrobacteria were simultaneously transformed into soybean seeds to produce transgenic plants. Agrobacteria with each GmMYB and IFS gene were co-modified into soybean seeds to produce transgenic plants. Transgenic T_0 plants confirmed the introduction of T-DNA using PCR analysis, and RNA expression was confirmed using RT-PCR analysis. T_1 seeds were sown to harvest T_2 seeds, and RNA was extracted from T_2 seeds to quantify the expression of genes in the IFS biosynthesis pathway using qRT-PCR.

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

PB-0045

A new mid maturing and high-eating quality *japonica* rice variety 'Chamjinmi' derived from Korea native resources

Chang-Min Lee*, Hyun-Su Park, Man-Kee Baek, Ki-Yeong Kim, O-Young Jeong, Ji-Ung Jeong, Choon-Song Kim, Jung-Pil Suh, Su-Kyung Ha, Dong-Kyu Lee, Hyun-Sook Lee, Min-A Jin, Jeonghwan Seo, Song-Hee Park, Gileung Lee, Seung Young Lee

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

'Chamjinmi' is a mid-maturing rice variety that can be harvested faster than mid-late maturing varieties and also exhibits good the rate of milling, and the taste. From the analysis of the glossiness and taste of cooked rice of Korean native rice resources, we selected the promising resource 'Hoengseongaengmi3', which had better rice eating quality compared to Korean (Ilpum) and Japanese (Hitomebore) varieties. 'Jeonju 654', which was bred by crossing 'Hwayeong' and 'Hoengseongaengmi 3', was developed through pedigree breeding, yield trials, and regional adaptability test, and 'Jeonju 654' was released as 'Chamjinmi' in 2022. The average heading date of 'Chamjinmi' for ordinary planting and late planting for double cropping was August 10th and August 20th, which were 4 days earlier than that of the check variety 'Nampyeong'. The milled rice yield of 'Chamjinmi' was 5.67 MT/ha for ordinary planting (103% of 'Nampyeong') and 5.64 MT/ha for late planting for double cropping (96% of 'Nampyeong'). 'Chamjinmi' had a culm length of 78 cm, a panicle length of 21 cm and 13 panicles per plant. The brown rice type of 'Chamjinmi' was slightly bigger than 'Nampyeong', with a 1,000 grain weight of 23.1 g and a length/width ratio of 1.84. The milled rice of 'Chamjinmi' was translucent, with a protein content of 5.9% and an amylose content of 17.2% (1.3% lower than 'Nampyeong'). The release of 'Chamjinmi' is anticipated to contribute a beneficial mid-maturing rice variety that can be employed across diverse cropping systems in paddy fields, effectively enhancing farm work efficiency.

Keywords: Chamjinmi, Rice, Eating quality, Korean native resource

***Corresponding Author:** Tel. 063-238-5215, E-mail: cropas@korea.kr

PB-0046

Biological effect of gamma-ray irradiation on radiosensitivity in Korea soybean varieties

Jeong Woo Lee[1,2], Jung Min Kim[1], Ji Su Seo[1,2], Bo-Keun Ha[2], Soon-Jae Kwon[1*]

[1]Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongeup, 580-185, Korea

[2]Division of Plant Biotechnology, Colleage of Agriculture and Life Sciences, Chonnam National University, Gwangju, Korea

Plant mutation breeding is an alternative method that uses physical or chemical mutagens to develop new crop varieties unlike hybridization and selection. The primary metrics used to determine the optimal dose are Lethal Dose (LD_{50}) and Reduction Dose (RD_{50}). Activity of antioxidant enzymes such as superoxide dismutase (SOD), peroxidase (POD) and ascorbate peroxidase (APX) can be used to evaluate oxidative stress which is indirect damages caused by reactive oxygen species (ROS). In this study, we screened radiosensitivity for application of gamma-ray into ionizing radiation in Korea soybean varieties. The nine Korea soybean varieties (recently released) were exposed to radiation with gamma-ray 0 to 800 Gy. As a result, the LD_{50} based on survival rate was 140 (Mipung) - 342 Gy (Jangol), and RD_{50} of plant height which tended to decrease with increasing irradiation levels was between 116 (Soman) and 221 Gy (Jangol and Saedanbaek). The activities of antioxidant enzymes and contents of malondialdehyde (MDA) used as stress indicator of lipid peroxidation had most a ‘falling-rising-falling’ pattern. However, the MDA contents of shoot parts indicated mostly higher than the root parts, and the POD activity of root parts indicated mostly higher than the shoot parts. This study suggests that the radiosensitivity of each variety for gamma-ray had difference and the biochemical responses (antioxidant enzymes activity and MDA contents) represent various changing values according to irradiation levels and plant parts. This results could be useful to determine optimal doses for mutation breeding with gamma-ray.

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

PB-0047

Suppression of cuticular wax biosynthesis mediated by rice LOV KELCH REPEAT PROTEIN 2 supports a negative role in drought stress tolerance

Yejin Shim[1], Kiyoon Kang[2*], Nam-Chon Paek[1*]

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

Drought tolerance is important for grain crops, including rice (*Oryza sativa*); for example, rice cultivated under intermittent irrigation produces less methane gas compared to rice grown in anaerobic paddy field conditions, but these plants require greater drought tolerance. Moreover, the roles of rice circadian-clock genes in drought tolerance remain largely unknown. Here, we show that the mutation of *LOV KELCH REPEAT PROTEIN 2* (*OsLKP2*) enhanced drought tolerance by increasing cuticular wax biosynthesis. Among *ZEITLUPE* family genes, *OsLKP2* expression specifically increased under dehydration stress. *OsLKP2* knockdown (*oslkp2-1*) and knockout (*oslkp2-2*) mutants exhibited enhanced drought tolerance. Cuticular waxes inhibit non-stomatal water loss. Under drought conditions, total wax loads on the leaf surface increased by approximately 10% in *oslkp2-1* and *oslkp2-2* compared to the wild type, and the transcript levels of cuticular wax biosynthesis genes were upregulated in the *oslkp2* mutants. Yeast two-hybrid, bimolecular fluorescence complementation, and coimmunoprecipitation assays revealed that OsLKP2 interacts with GIGANTEA (OsGI) in the nucleus. The *osgi* mutants also showed enhanced tolerance to drought stress, with a high density of wax crystals on their leaf surface. These results demonstrate that the OsLKP2-OsGI interaction negatively regulates wax accumulation on leaf surfaces, thereby decreasing rice resilience to drought stress.

***Corresponding Author:** Tel. 032-835-8894, E-mail: kykang@inu.ac.kr, ncpaek@snu.ac.kr

PB-0048

Comparison of Agronomic Traits and Nutrient Characteristics of Colored Wheat Cultivars

Hyeonjin Park*, Jin-Kyung Cha, Youngho Kwon, So-Myeong Lee, Gi-Un Seong, Jong-Hee Lee

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

The color of wheat grains can vary due to the presence of different pigments in the bran layers. Red color is caused by minor anthocyanins, tannin, and catechin in the seed coat. Blue color comes from anthocyanins in the aleurone layer, while purple color is a result of anthocyanins in the pericarp layer. Colored wheat, rich in functional compounds like anthocyanins, offers various health benefits primarily due to its antioxidant properties. This study aims to evaluate the phenotypic and nutritional characteristics of wheat cultivars with different coat colors in order to consider the introduction of germplasm for breeding purposes.

This study used three Korean cultivars: Keumgang (white), Tapdong (red), Arijinheuk (brown), and a blue-colored wheat germplasm (RDA-GeneBank accession: IT016425). These cultivars were cultivated at the Crossing block in NICS, RDA, Miryang, Korea in 2021 and 2022. Phenotypic traits were assessed after heading, and grain samples were harvested at physiological maturity. The samples were dried at room temperature until the seed moisture content reached approximately 14%. Threshing was performed using a thresher, and the grains were ground with a Buhler mill to pass through a 2.2 mm sieve. Analysis of protein, gluten, minerals, and functional compounds such as polyphenols, flavonoids, and anthocyanins was conducted.

In the field trial, IT016425 had a heading date and maturity that were 24 and 8 days later than Keumgang, respectively. IT016425 also had the tallest plant height (91 cm), but the shortest spike length (6.7 cm) and nod number (14 per plant). The thousand grain weight was similar to Tapdong, measuring 39.0 g. IT016425 had the lowest protein content, with a mean value of 12.1%, while Keumgang had the highest protein content (15.5%). However, Tapdong and IT016425 compensated for their lower protein content by having higher levels of total dietary fibers. These cultivars exhibited the highest total dietary fiber content, with mean values of 3.16 and 3.29 g/100 g, respectively, whereas Keumgang and Arijinheuk had lower values. IT016425 also had the highest content of anthocyanin, with a mean value of 1.61 mg/100g. Additionally, IT016425 had the highest levels of minerals such as K (230.64 mg/100g), P (190.31 mg/100g), Mg (45.40 mg/100g), Zn (1.06 mg/100g), Mn (0.54 mg/100g), and Cu (0.12 mg/100g) compared to the tested cultivars. Cultivating IT016425 in Korea may not be suitable due to the common practice of rice-wheat double-cropping, as it has delayed heading and maturity. However, considering its high anthocyanin and mineral content, it is necessary to introduce the beneficial traits of IT016425.

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

PB-0049

전북지역 2모작 작부체계 적응 흑찰벼 '백일흑찰'

김효진*, 이덕렬, 유영석, 강영호, 최유나, 조대호, 안민실

전라북도 익산시 서동로 413 전라북도농업기술원

전북지역 2모작지에 적합한 흑미품종을 육성하기 위하여 2011년 하계에 단간이면서 초형이 우수하고 수량성이 높은 익산533호를 모본으로 하고 조생종이면서 품질이 우수한 조생흑찰을 부본으로 인공교배하여 계통육종법으로 생육기간이 짧고 색택이 양호한'백일흑찰'을 개발하였다. 출수기는 호남평야 보통기 보비재배에서 7월 23일로 대비품종인'흑남'보다 17일 정도 빠른 조생종이다. 간장은 61cm로'흑남' 보다 10cm 작고 이삭은 18cm로 흑남보다 작으며, 주당수수는 15개로'흑남'보다 적다. 수당립수는 66개로'흑남'보다 적고 등숙비율은 92.7%로 높으며 현미 천립중은 22.6g으로'흑남' 보다 무겁다.'백일흑찰'은 저온발아성이 32.0%로'흑남'보다 낮고, 내냉성이 '흑남'보다는 약하며, 불시출수는 못자리일수 50일묘 이앙에서 발생하지 않았으며, 수발아율은 6.4%로'흑남'8.0%보다 낮아 강한 특성을 보인다.'백일흑찰'의 제현율은 78.2%로 조생흑찰 73.1%보다 높고, 현미장폭비는 2.75로 대비품종인'흑남'보다 쌀알이 긴 모양이며, 종피색은'흑남'과 같은 흑자색이나 메벼인 '흑남'과 달리 찰벼품종이다. 단백질함량은 8.6%로 '흑남'보다 높은 경향이었다. 지역적응시험에서'백일흑찰'의 현미수량은 431kg/10a으로 흑남대비 81% 수준이었으나, 2모작 적응성 시험에서 10a당 현미수량이 7월 5일 이앙 시'조생흑찰'과 차이가 없었고, 7월 15일 이앙에서는'조생흑찰'대비 130% 수량성을 보였다. 적응지역으로는 전북지역 평야지 2모작, 중산간지 및 산간 지역이 적합하다.

***교신저자:** Tel. 063-290-6072, E-mail: khj0819@korea.kr

PB-0050

Evaluation of multi-environment trials and stability for yield traits of commercial rice cultivars

Seung Young Lee[1,2], Hyun-Sook Lee[1], Su-Kyung Ha[1], Chang-Min Lee[1], Gileung Lee[1], Youngjun Mo[2*], Ji-Ung Jeung[1*]

[1]National Institute of Crop Science, RDA, Wanju 55365, Republic of Korea
[2]Department of Agronomy, Jeonbuk National University, Jeonju 54896, Republic of Korea

The practical application of multi-environment trials (METs) was implemented to assess the adaptability and productivity of 276 Korean rice cultivars across diverse environments. The cultivars were categorized into three maturity groups (81 early-maturing, 90 medium-maturing, and 105 medium-late-maturing) and were cultivated in three different regions (Jeonju, Suwon, and Miryang) during two planting seasons (early and regular) over a two-year period. Since the commercial cultivars exhibited limited genetic variability and were grown under relatively similar climate conditions, the statistical analysis did not reveal significant genotype-by-environment interaction (GEI) effects. However, when employing GGE biplot analysis for genotype and environment evaluation, distinct patterns emerged, indicating diverse formation of mega-environments, winning genotypes, genotype rankings, discriminating power, and representativeness based on variations in planting seasons and regions. Furthermore, by utilizing a weighted average of absolute scores from the singular-value decomposition of matrix of BLUPs (WAASB) and multi-trait stability index (MTSI), we identified six recommended genotypes for early maturing cultivars, six for medium-maturing cultivars, and four medium-late-maturing cultivars. These winning genotypes can serve as valuable parental source for developing region-specific cultivars by fine-tuning desirable traits, while the recommended genotypes can be utilized as elite climate-resilient parents, assisting breeders in enhancing both yield potential and stability across diverse planting seasons and regions.

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***Corresponding Author:** Tel. 063-270-2530, E-mail: yjmo@jbnu.edu
Tel. 063-238-5231, E-mail: jrnj@korea.kr

PB-0051

Evaluation of genotype and devleopment of KASP marker for *GPC-B1* in wheat

Jin-Kyung Cha*, Hyunjin Park, Youngho Kwon, So-Myeong Lee, Jong-Hee Lee

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

The gene *GPC-B1* (*NAM-B1*) plays an important role in increasing protein content in wheat (T. *aestivum*). Initially, *GPC-B1* was mapped on chromosome 6B as a QTL, and subsequently, the single gene *NAM-B1* was identified as the primary regulator of wheat protein content. Therefore, *NAM-B1* gene is commonly known as *GPC-B1* in the literature. However, functional wild type *NAM-B1* gene is rarely found in recently cultivated common bread wheat because it was introduced from wild emmer wheat (*T. dicoccoides*) to common wheat, and the *NAM-B1* gene was subsequently removed during the breeding of environment-stable lines. Therefore, a total of 166 wheat genetic resources were screened for the *NAM-B1* gene using SSR markers and Sanger sequencing in this study. Three cultivars from foreign countries (IT15821, IT176584, IT336105) were found to harbor the wild type *NAM-B1* gene, while the remaining 163 cultivars showed either a 1bp-inserted non-functional *NAM-B1* allele or gene deletion. A new KASP marker was developed to efficiently differentiate between the wild type *NAM-B1* and the non-functional *NAM-B1* for molecular breeding. Since no significant difference in protein content was observed between the non-functional *NAM-B1* and *NAM-B1* deletion cultivars, the selected wild type *NAM-B1* cultivars and the developed KASP marker can be utilized to increase the protein content in Korean wheat cultivars.

***Corresponding Author:** Tel. 055-350-1182, E-mail: jknzz5@korea.kr

PB-0052

Soft property of silken tofu and high tofu yield soybean cultivar ‘Dadrim’

Beom-Kyu Kang*, Jeong-Hyun Seo, Jun-Hoi Kim, Man-Soo Choi, Su-Vin Heo, Jee-Yeon Ko, Byung-Won Lee, Choon-Song Kim

Upland Crop Breeding Research Division, Department of Southern Area Crop Science, National Institute of Crop Science, RDA, Milyang, Gyeongnam, 50424, Republic of Korea

Soybeans[*Glycine max*. (L.) Merr] are used for various food materials, mainly for tofu in Korea. Recently days, seed yield and mechanized harvest are important traits but also food process-ability is a critical role in market. ‘Dadrim’ which is tofu-quality improved soybean cultivar developed in 2022 and show high tofu yield, bright and large seed, and soft taste of silken tofu. ‘Dadrim’ was developed by pedigree method. In 2012, Milyang 231 and Chamol were crossed, and promised line(YS2492-B-B-32-3-1) was selected by pedigree method in F_3~F_5 generation. Two-year preliminary and advanced yield trials in 2018~2019, and 3-year regional yield trial in 10 locations in 2020~2022 were conducted. ‘Dadrim’ is determinate growth type, oval leaf shape, white flower, grey pubescence, light brown pod, yellow seed coat and hilum, and spherical seed shape. Growth characteristics of ‘Dadrim’ are late-maturing(22th Oct.), shorter plant height(64cm), higher first pod height(16cm), compared to ‘Daewonkong(Standard)’. Lodging, pod-shattering, and main diseases such as bacterial pustule and SMV are resistant. Seed qualities of ‘Dadrim’ are superior to standard cultivar, that seed size is larger(30.9g/100-seed, 95.8% uniformity/7.1mm) and lightness is brighter(L-value 68.4). When tofu was made by ‘Dadrim’, yield was 283% and 67%p higher than ‘Daewonkong’. In silken tofu test, appearance was yellowish gloss and hardness was 537g, and 106g softer than ‘Daechan(competitor)’. In flavor test, the result showed total 7.1 point and 1.5 point higher than competitor cultivar. Unique properties of ‘Dadrim’ can assist tofu producer to improve tofu quality and market value by differentiation.

***Corresponding Author:** Tel. 055-350-1233, E-mail: hellobk01@korea.kr

PB-0053

Early maturing, pod-shattering resistant, and large seed soybean cultivar 'Pungol'

Beom-Kyu Kang[1*], Jeong-Hyun Seo[1], Man-Soo Choi[1], Jun-Hoi Kim[1], Su-Vin Heo[1], Jee-Yeon Ko[1], Nam-Geol Kim[2], Hong-Sik Kim[3], Yeong-Min Jo[4], Chang-Heui Son[5], Choon-Song Kim[1]

[1]Upland Crop Breeding Research Division, Department of Southern Area Crop Science, National Institute of Crop Science, RDA, Miryang, Gyeongnam, 50424, Republic of Korea
[2]Central Area Crop Breeding Research Division, Department of Central Area Crop Science, National Institute of Crop Science, RDA, Suwon, Gyeonggi, 16429, Republic of Korea
[3]Crop Post-harvest Technology Research Division, Department of Central Area Crop Science, National Institute of Crop Science, RDA, Suwon, Gyeonggi, 16613, Republic of Korea
[4]Jeollabuk-do Agricultural Research & Extension Service, Iksan, Jeonbuk, 54591, Republic of Korea
[5]Gyeongsangnam-do Agricultural Research & Extension Service, Gyeongnam, Jinju 52733, Republic of Korea

Soybeans[*Glycine max*. (L.) Merr] can be used for double cropping with winter crops such as wheat, barley, and onions in Korea. In double cropping, short maturing of soybeans should be important trait for harvesting and seeding of previous and subsequent crops. A soybean cultivar 'Pungol' is adequate for double cropping as short maturing, and improved for main shortcomings of existed early maturing soybean cultivars. 'Pungol' was developed as followed process, 'Milyang 235' and 'Jungmo 3004' were crossed in 2011, and promised line(YS2441-B-2B-83-2-3-2) were selected in F_4~F_7 with pedigree method. Two-year preliminary and advanced yield trials in 2017~2018, and 4-year regional yield trial in 4 locations in 2019~2022 were conducted. 'Pungol' is in-determinate growth type, oval leaf shape, white flower, grey pubescence, light brown pod, yellow seed coat and hilum, and sub-spherical seed shape. Growth characteristics of 'Pungol' are early maturing(2th Oct.), longer plant height(74cm), higher first pod height(14cm), large seed(27.4g/100-seed), and lower yield(282kg/10a) compared to 'Seonyu2ho(competitor)'. Tofu and fermenting tests were evaluated at level of normal. Especially, pod-shattering was a general shortcoming in early mature soybean cultivars in the past, of which pods were shattered 80~95% in maturing stage, but that of 'Pungol' was only shattered 3.8% and determined as resistant genotype by molecular marker(*qPDH-KS*). 'Pungol' can be harvested early-october and pod shattering resistant, then it can contribute to stabilize soybean production in double cropping.

***Corresponding Author:** Tel. 055-350-1233, E-mail: hellobk01@korea.kr

PB-0054

Allelic variation of *Hd1*, *OsPRR37*, *Ghd7*, and *DTH8* in Korean rice cultivars

Jiheon Han, Hayeong Lee, Yeeun Jun, Yurim Kim, Youngjun Mo*

Department of Crop Science and Biotechnology, Jeonbuk National University, Jeonju 54896, Republic of Korea

Heading date plays a crucial role in determining the adaptability and productivity of rice in diverse environments. Understanding the genetic regulation of heading date is essential for developing effective rice breeding strategies. In this study, we investigated the allele types of four key genes (*Hd1, OsPRR37, Ghd7*, and *DTH8*) known to influence heading date in 287 rice cultivars developed by National Institute of Crop Science (NICS) in Korea. Through the classification of allele types based on Sanger sequencing of the protein coding regions of the four heading date genes, we identified nine different *Hd1* alleles, comprising four functional (H) and five non-functional (h) types. *OsPRR37* exhibited seven different alleles, including five functional (P) and two non-functional (p) types. *Ghd7* displayed five different alleles, with three functional (G) and two non-functional (g) types. *DTH8* exhibited six different alleles, including five functional (D) and a single non-functional (d) type. Based on the functionality of these genes, 287 Korean rice cultivars were classified into eight different allelic combinations, with the majority of cultivars (177) falling into the fully functional HPGD combination. The hPGD combination was the next prevalent, comprising 97 cultivars. The hPGd combination included eight cultivars, while HpGD, HPgD, hPgD, hpGD, and hpgD combinations each consisted of only one cultivar. Further research on examining the effects of different alleles and their combinations on heading date and other agronomic traits will contribute to optimizing heading date and developing breeding strategies aimed at enhancing rice productivity in the future.

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***Corresponding Author:** Tel. 063-270-2530, E-mail: yjmo@jbnu.edu

PB-0055

Toward mapping of novel QTLs for pre-harvest sprouting resistance in rice based on image analysis

Soojin Jun, Hyoja Oh, Dong Kyung Yoon, Mi Hyeon Cho, Song Lim Kim, Jeongho Baek, HwangWeon Jeong, Jae Il Lyu, Hyeonso Ji*

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

Rice (*Oryza sativa*) is a globally important crop, serving as a staple food for over 3.5 billion people and playing a critical role in addressing population growth and food security challenges. Pre-harvest sprouting (PHS) which means sprouting from the seed before harvest, is a serious problem because it reduces quality and yield. Therefore, developing varieties resistant to PHS is a major goal in rice breeding. In this study, we aim to find novel PHS resistant QTLs with a recombinant inbred lines (RILs) population derived from a cross between 'Junam' which is susceptible to PHS and 'Nampyeong' which is resistant to PHS. In order to construct a generic map of the RIL population, we are doing genotyping of the RILs using the target capture sequencing genotyping system developed in our laboratory. In addition, we plan to develop a method for measuring PHS rate using RGB image analysis. At first, we will try to develop a method for discriminating between germinated seeds and ungerminated seeds from RGB images using artificial intelligence. This technology will enable objective and high-throughput measurement of rice seed germination rate, which will pave the way for efficient rice breeding for PHS resistance.

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

PB-0056

Observation of stomatal traits and chromosome aberration of common wheat treated by zebularine

Seong-Wook Kang[1], Sejin Oh[1], Yumi Lee[2], Seong-Woo Cho[1,2*]

[1]Department of GreenBio Science, Gyeongsang National University, Jinju, 52725, Republic of Korea
[2]Department of Smart Agro-Industry, Gyeongsang National University, Jinju, 52725, Republic of Korea

Zebularine is one of the DNA methylation inhibitor and tumorigenesis inhibitor. DNA methylation inhibitor causes chromosome breakage from DNA breakage, and then chromosome rearrangement occurs by DNA repair in plant cells. Zebularine solution (1,000 μM) was treated by imbibition with seeds of common wheat (Keumkang, Korean wheat cultivar) for 72 hours in dark condition. After germination, we investigated some broken chromosomes with short length compared to normal chromosomes and other chromosomes with loose chromatic structure. Zebularine affected chromosome structure *i.e* occurrence of abnormal chromosomes (M_0). Chromosomes of M_1 plants were also observed to identify epigenetic effects of zebularine treatment. Zebularine-treated plants were planted in greenhouse conditions. Seed of M_0 plants collected and planted in greenhouse conditions (M_1). We planted 23 M_1 plants in greenhouse conditions and investigated stomatal traits such as length, width, and distance and SPAD. Stomatal traits of M_1 plants were observed for phenotypic mutation of zebularine treatment. Among 23 M_1 plants, on the adaxial side, the length of stomata of eight M_1 plants was significantly shorter than Keumkang and the width of stomata of 18 M_1 plants was wider than control. And five M_1 plants had wider distances between stomata than control. Among 23 M_1 plants, on the abaxial side, 10 M_1 plants showed significantly longer length and 12 M_1 plants showed significantly wider width in stomata. And four M_1 plants showed significantly more stomata distribution than Keumkang. Chlorophyll content was not significantly different with control.

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

PB-0057

In Silico Prediction and Potential Assessment of Off-Target Genome Regions on Genome-Edited Crop Generated by CRISPR/Cas9 System

Byung Jun Jin[1], Min Chul Kim[1,2*]

[1]Institute of Agriculture & Life Science, Gyeongsang National University, Jinju 52828, Korea
[2]Division of Applied Life Science (BK21 Four), Gyeongsang National University, Jinju 52828, Korea

Prediction and assessment of nonspecific double-strand break (DSB) on unknown genome regions is a prerequisite for sustainable and reliable application of CRISPR/Cas9 system on the improvement of agronomic traits of various staple crops. In this study, we present normalized workflow and examples of assessment of the ‘off-target effect’. First of all, we defined the characters of off-target genome regions by summarizing previous studies on relations between mutation efficiency and various intolerance cases of DNA/gRNA interaction to Cas9 nuclease activity, such as the number and distribution of mismatching in spacer region, small nucleotide polymorphism (SNP) on protospacer adjacent motif (PAM), DNA/RNA bulge and cutting frequency determination (CFD) score. Secondly, we selected seven web tools providing alignment- or scoring-based evaluation results of genome databases of staple crops, including, by comparing sixty-five computational CRISPR/Cas9 off-target prediction tools. Thirdly, using guide RNA sequences of *OsESP4-1* GE rice line, we suggested detailed prediction results of each off-target group, with how to utilize the most-recommended web tool for successful mining of off-targets belonging to one of our off-target criteria. Finally, we assessed the DSB potential of these off-targets through InDel PCR experiment to confirm nonspecific genome editing by CRISPR/Cas9 system. Our study not only provides reliable guidelines for systemic mining and assessment of the off-target effect of GE crops generated by the introduced CRISPR/Cas9 system, but also will be a platform for the development of crop-specific off-target assessment workflow for various GE crops generated in the future.

***Corresponding Author:** Tel. 055-772-1874, E-mail: mckim@gnu.ac.kr

PB-0058

Characterization of the Cross-Pollination by Pollen Dispersal of Maize to Develop Environmental Risk Assessment (ERA) Strategy of Genetically Modified Maize

Byung Jun Jin[1], Hyeong Kyu Kim[2], Ye Jin Cha[2], Hae Rang Seo[2], Tae Hee Han[2], Su Jin Lee[2], Min Chul Kim[1,2*]

[1]Institute of Agriculture & Life Science, Gyeongsang National University, Jinju 52828, Korea
[2]Division of Applied Life Science (BK21 Four), Gyeongsang National University, Jinju 52828, Korea

Although global demand for genetically modified (GM) maize (*Zea mays* L.) has been increasing, there is still little domestic study of environmental risk assessment (ERA), especially, the critical factors that affect the efficiency of pollen dispersal and cross-pollination. In this study, we summarized methods and results that have been performed to assess these issues. To assess the long-distance pollen dispersal and cross-pollination, which is expressed by xenia of kernel pericarp pigmentation, we first designed semi-radial distribution of nine groups of pollination parent (plain pigmentation) centered in one group of pollen parent (dark pigmentation) in 66,638m^2 of the experimental field. Next, in addition to figuring out of geographic features of the experimental field that affect pollen dispersal, we also calculate the potential cross-pollination period from the observed first tassel emergence date and theoretical period of flowering and pollination. Finally, we analyzed weather conditions of this period and inferred the relation between long-distance cross-pollination efficiency and observation results of our experimental field. Consistent with previous studies, geographic features, wind direction, and rainfall are the main factors that govern long-range pollen dispersal efficiency. Also, significant differences in several factors, including wind consistency, temperature, amount of cloud, and relative humidity, suggest the requirement of a more detailed study to establish how these factors affect pollen stability and ear development after cross-pollination. Our results provide useful information to develop practice for ERA on the field and to improve modeling-based pollen dispersal prediction.

***Corresponding Author:** Tel. 055-772-1874, E-mail: mckim@gnu.ac.kr

PB-0059

베타카로틴을 함유한 황색찰옥수수 ‘행복찰(경북찰13호)’

오태영[1*], 손창기[1], 조현태[1], 허창석[1], 배정숙[2], 이지윤[2], 고은정[3]

[1]대구광역시 북구 칠곡중앙대로 136길 47, 경상북도농업기술원
[2]경상북도 청도군 이서면 가금구라길 186-6, 경상북도농업기술원 청도복숭아연구소
[3]경상북도 봉화군 봉성면 부랭이길 81, 경상북도농업기술원 봉화약용작물연구소

찰옥수수는 여름철 대표적인 간식으로 알려져 있다. 국내에서 육성된 찰옥수수는 대부분 백색 찰옥수수이며 최근 건강기능성이 부각되면서 유색 찰옥수수에 대한 수요가 늘고 있다. 유색 찰옥수수는 대부분 자색 찰옥수수가 일반적이다. ‘행복찰(경북찰13호)’은 경상북도농업기술원에서 개발한 단교잡종 찰옥수수로 이삭의 종피색깔은 황색이며 자식계통 GYW16을 종자친으로 하고 GYW13을 화분친으로 하였다. 행복찰의 출사일수는 67일이고, 일미찰에 비해 평균 5일정도 빠른 조숙종으로 이삭무게는 200g, 이삭수(10a)량은 1,251kg이며 백색 찰옥수수에는 없는 베타카로틴이 360㎍/g 함유되어 있다. 일미찰에 비교했을때, 아밀로펙틴 함량은 93.7%로 비슷하였으며, 과피두께가 52㎛로 다소 두껍게 나타났지만, 전체 기호도는 더 좋았다.

***교신저자:** Tel. 053-320-0283, E-mail: ohty@korea.kr

PB-0060

Evaluating Browning-Resistance of Potato Lines for Fresh-cut

Jae-Youn Yi*, Yong Ik Jin, Yeong Eun Park, Gun Ho Jung, Jang-Gyu Choi, Gyu Bin Lee, Do Hee Kwon, Chung Ki Cheon

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

Fresh-cut produce refers to agricultural products with fresh and convenient to use. Nowadays, the fresh-cut produce market in Korea is getting bigger. But, the current varieties are not suitable for this industry. So, the development of browning-resistant potato varieties for fresh-cut is necessary. In 2022, 56 lines were planted for a preliminary yield trial(PYT) at Daegwallyeong and Gangneung. The lines were harvested at 100 days after planting in Gangneung and 120 days after planting in Daegwallyeong. The survey included an investigation of plant growth, yield, specific gravity, degree of browning, and other factors. ‘S18010-8’ and ‘S18036-21’ had a tuber’s total yield of 3,922 kg/10a and 6,337 kg/10a, respectively, which is 29% and 108% higher than “Sumi”. Furthermore, they exhibited lower susceptibility to common scab and physiological disorders compared to “Sumi”. After grinding, Hunter's delta L and E values measured 6 hours later were lower than those of “Sumi” and “Daeseo”. This research is expected to significantly contribute to enhancing self-sufficiency in raw materials for food processing varieties and improving the competitiveness of the potato industry.

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***Corresponding Author:** Tel. 033-330-1690, E-mail: cjsfydsns@korea.kr

PB-0061

Multiple Disease Resistant Mid-late Maturing Rice Cultivar ‘Chamdongjin’ Carrying Bacterial Blight Resistance Gene *Xa21* with the Genetic Background of ‘Sindongjin’

Hyun-Su Park*, Man-Kee Baek, Ji-Ung Jeung, O-Yeong Jeong, Chang-Min Lee, Su-Kyung Ha, Jeonghwan Seo, Jae-Ryoung Park, Hyun-Sook Lee, Songhee Park, Kyeong Min Kang, Mira Yoon, Mina Jin, Ki-Young Kim

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

‘Chamdongjin’ was developed for enhancing the disease resistance of ‘Sindongjin’. ‘Sindongjin’ devleped by RDA in 1999 is a mega variety with the unique grain size and excellent taste of cooked rice and it has been cultivated in the largest area in Korea since 2018. As ‘Sindongjin’ has been cultivated for a long time in a large area, problems such as pest damage are increasing, and the importance of developing the alternative cultivars is emerging. Accordingly, multiple disease resistant mid-late maturing rice cultivar ‘Chamdongjin’ carrying bacterial blight resistance gene *Xa21* into the genetic background of ‘Sindongjin’ was developed. ‘Chamdongjin’ was developed by backcross method using donor parent ‘HR27195-59-3-5-5’ harboring bacterial blight resistance genes *Xa3*+*Xa21* and recurrent parent ‘Sindongjin’. ‘Chamdongjin’ was selected through the pedigree method, yield trials, and local adaptability tests, with a high selection pressure for agronomic traits similarities with ‘Sindongjin’. In order to effectively improve the disease resistance, marker assisted selection for disease resistance genes and bioassay for bacterial blight, blast, and stripe virus were performed in parallel. ‘Chamdongjin’ was confirmed to have three disease resistance genes, *Xa3*+*Xa21*+*Stvb-i*. Most of agronomic traits of ‘Chamdongjin’ were similar to ‘Sindongjin’, while ‘Chamdongjin’ showed the enhanced disease resistance against bacterial blight and panicle blast than ‘Sindongjin’. ‘Chamdongjin’, like ‘Sindongjin’, possessed the grain size related gene, *gs3* allele and exhibited larger grain than general Korean *japonica* cultivars. In addition, ‘Chamdongjin’ showed a similar or higher level of tastes of cooked rice to ‘Sindognjin’, indicating the excellent quality characteristics. In the genetic background analysis using 787 KASP markers, ‘Chamdongjin’ showed 96.3% homozygosity with ‘Sindongjin’, which had the most similar genetic background to ‘Sindongjin’ than other existing cultivars. ‘Chamgdongjin’ is expected to be widely cultivated as the alternative cultivar of ‘Sindongjin’ that could maintain the brand value while preventing disease damage of ‘Sindongjin’ (Registration No. 9310).

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

PB-0062

Analysis of yield performance of ‘Namchan’ under normal and low nitrogen level conditions

Hyun-Su Park[1*], Man-Kee Baek[2], Jae-Ryoung Park[1], Jeonghwan Seo[1], Songhee Park[1], Kyeong Min Kang[1], Mira Yoon[1], Mina Jin[1], O-Young Jeong[1]

[1]Crop Breeding Division, National Institute of Crop Science, Rural Development Administration, Wanju, 55365, Republic of Korea
[2]Cheolweon Substation, National Institute of Crop Science, Rural Development Administration, Cheorwon, 24010, Republic of Korea

‘Namchan’ is a mid-late maturing japonica rice cultivar that exhibits high yield even under low-nitrogen conditions. To analyze the yield performance of ‘Namchan’, yield trials were conducted in two locations (Jeonju and Miryang) over three years (2016-2018). The trials compared ‘Namchan’ with the cultivar ‘Nampyeong’ under normal nitrogen level conditions (NNLC; nitrogen-phosphate-potassium: 9-4.5-5.7 kg/10a) and low-nitrogen level conditions (LNLC; 6-4.5-5.7 kg/10a). In both NNLC and LNLC, ‘Namchan’ exhibited late heading date (HD), longer culm length (CL), shorter panicle length (PL), increased panicle number per hill (PN), heavier 1,000-grain weight (TGW), higher ratio of ripened grain (RRG), brown/rough rice ratio (BRR), and higher yield compared to ‘Nampyeong’. Analyzing the trait variations according to nitrogen level conditions revealed that under NNLC, both ‘Namchan’ and ‘Nampyeong’ showed later HD, longer CL and PL, increased PN and NS, heavier TGW, higher BRR, and higher yield compared to under LNLC. The traits that contributed the most to enhancing the yield of ‘Namchan’ were NS (standardized regression coefficient 0.59, R2=0.490) under NNLC and PN (0.76, 0.316) under LNLC. For ‘Nampyeong’, the traits that contributed the most to enhancing yield were NS (standardized regression coefficient 0.40, R2=0.444) under NNLC and PN (0.60) and RRG (0.60, 0.447) under LNLC. To improve yield under LNLC, it is important to focus on increasing PN.

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

PB-0063

‘Hyemalgeun’: A New Covered Barley Variety with Low Proanthocyanidin Content Suitable for Making Clear *Sikhye*

Chang-Hyun Lee, Seul-Gi Park, Jin-Cheon Park, On-Sook Hur, Kyong-Ho Kim, Young-Mi Yoon*

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

To develop a barley variety suitable for making clear *sikhye* (traditional Korean rice beverage) with high enzyme activity and low proanthocyanidin content, artificial crossbreeding was conducted between ‘Topgolbori(IT56909)’ which has lodging resistance and high yield, and ‘Ant17-154’, which has low proanthocyanidin content. Subsequently, in 2010, the progeny was crossed again with ‘Hyemi’. After the F_1 generation was produced in 2011, the F_2-F_3 generations were developed as a bulk from 2012 to 2013. In 2014-2015, elite lines with low proanthocyanidin content were selected from the F_4-F_5 generation through vanillin analysis. In 2016, the selected elite lines were tested as Observational yield trial(OYT), and the ‘IC10008-B-B-9-1’ line was selected. This selected line was recognized for its excellence after a two-years yield trial(2016-2017) and given the breeding line name “Jeonju518.” The regional yield trials(RYT) were conducted for ‘Hyemalgeun’ as a breeding line ‘Jeonju518’ in five different regions from 2019 to 2021(RDA). The culm length of ‘Hyemalgeun’ was 84cm, which was similar to that of ‘Hyeyang’(82cm) and a weight of 34.8g for 1,000 grains which was heavier than ‘Hyeyang’(29.7g). ‘Hyemalgeun’ showed intermediate resistance to barley yellow mosaic virus (BaYMV) and susceptible to Powdery mildew which was similar to ‘Hyeyang’. The yield of ‘Hyemalgeun’ in the regional yield trial was 522kg/10a(overall average between upland and paddy field) which was similar to that of ‘Hyeyang’(516kg/10a). ‘Hyemalgeun’ showed similar levels as those of ‘Hyeyang’ with respect to protein, β-glucan(11.3%, 4.8% respectively). However, ‘Hyemalgeun’ showed lower proanthocyanidin content (0.0099mg/g) than ‘Hyeyang’(0.1401 mg/g) and higher enzyme activity(460WK) than Hye-yang(397WK). Furthermore, when making *Sikhye*, ‘Hyemalgeun’ showed higher sweetness level(11.4°Bx) than ‘Hyeyang’(11.0°Bx), and the turbidity level was 0.58, indicating a clear appearance.

‘Hyemalgeun’ has similar agricultural traits to existing varieties but has low proanthocyanidin content and high enzyme activity, making it suitable for producing clear *sikhye*. It is planned to be distributed in barley cultivation areas with a minimum average temperature above -6°C in January.

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***Corresponding Author:** Tel. 063-238-5227, E-mail: mi3710@korea.kr

PB-0064

Phenotypic information of germination and growth rates under low temperature conditions

Dongjin Shin*, Yeongsoo Park, Hyunggon Mang, Joeng-Hee Lee

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

Rice is an important staple food in the world including Korea. In order to strengthen of domestic rice price competitiveness, the direct seeding method was spread. Direct seeding method showed limitations in domestic rice paddy field due to the difficulty of weeding. However, recently direct seeding is being considered as one of strategies to reduce methane emissions produced in the rice field. Here, germination and growth rates phenotypes under low temperature conditions were investigated for using to develop direct seeding suitable cultivar. Average germination rates under control conditions (6 days after treatment, 28 degrees) and low temperature conditions (14 days after treatment, 13 degrees) were similar at about 85%. The average germination days was 11.0 days and 5.3 days under low and control temperature conditions, respectively. Among cultivars, germination days of Hongjinju and Hyagnam are 6.4 and 6.7 days after imbibition but Basmati389 and IR64-EMF are 16.9 and 18.0 days after imbibition. In the case of shoot growth length under low temperature conditions, Hua117 and Baldo showed the largest length, 36.4 cm and 35.8 cm at 50 days after sowing, but Geumgang and Apo are 12.0 cm and 12.6 cm, respectively. In the case of root growth length under low temperature conditions, Geonganghongmi and Milyang326 are 25.1 cm and 24.5 cm at 50 days after sowing, but IR74371-54-1-1 and Apo 5.3 cm and 8.2 cm, respectively. In the future, we will find QTL controlling low temperature germination and growth with phenotypic information.

***Corresponding Author:** Tel. 031-296-6898, E-mail: acob1223@korea.kr

PB-0065

A new soybean cultivar ‘Oreum’, suitable for mechanized harvesting with high plant height and strong to lodging

Jun-Hoi Kim[1*], Beom-Kyu Kang[1], Jeong-Hyun Seo[1], Su-Vin Heo[1], Man-Soo Choi[1], Jee-yeon Ko[1], Hyae-Rang Park[1], Jeong-Ho Baek[2], Choon-Song Kim[1]

[1]Upland Crop Breeding Research Division, Department of Southern Area Crop Science, National Institue of Crop Science, RDA, Miryang, Gyeongnam, 50424, Rep. of Korea
[2]National Institute of Agricultural Science, RDA, 370 Nongsaengmyeong-ro, Wansan-gu, Jeonju-si, Jeollabuk-do, Rep. of Korea

Soybean is an important legume crop that provides protein and oil for food and animal feed. Especially in Asian countries, soybeans have been widely used for soybean sprouts. Therefore both sprout and cultivation characteristics are important. ‘Oreum’ is a new soybean cultivar specifically developed for soybean sprouts. It was developed through a crossbreeding between ‘Kosuzu’ and ‘HS1273-4-1-2-2-1-2-1’ in 2012. F_1 plants and F_2 population were developed from 2013 to 2014, and promising lines were selected from F_3 to F_5 using the pedigree method from 2015 to 2017. Preliminary yield and advanced yield trials were conducted from 2018 to 2019, followed by regional yield trials in four regions from 2020 to 2022. The morphological characteristics of ‘Oreum’ are as follows: determinate, white flowers, grey pubescence, yellow pods, and small, yellow, spherical seeds (11.5g · $100seeds^{-1}$). The flowering and maturity dates were August 4th and October 11th, respectively. Plant height, first pod height, number of nodes, and number of branches, were 74cm, 14cm, 18, and 4.4, respectively. The lodging tolerance of ‘Oreum’ was also stronger than the standard cultivar ‘Pungsannamulkong’. In the soybean sprout test, ‘Oreum’ exhibited a germination rate of 84.7%, with a total length of 19.2cm, hypocotyl length of 9.0cm, thickness of 2.07mm, and sprout yield of 540%. The yield in adaptable regions was 316kg/10a, which was 5% higher than that of ‘Pungsannamulkong’. With its high plant height, first pod height, and suitable cultivation characteristics, ‘Oreum’ might be widely used for soybean sprout production and is also suitable for mechanized harvesting.

***Corresponding Author:** Tel. 055-350-1235, E-mail: itomi123@korea.kr

PB-0066

Association of the allelic variation in *Hd1*, *OsPRR37*, *Ghd7*, and *DTH8* with major agronomic traits in Korean rice cultivars

Hayeong Lee[1], Jiheon Han[1], Yurim Kim[1], Chang-Min Lee[2], Su-Kyung Ha[2], Seung Young Lee[2], Ji-Ung Jeung[2], Youngjun Mo[1*]

[1]Department of Crop Science and Biotechnology, Jeonbuk National University, Jeonju 54896, Korea
[2]National Institute of Crop Science, Rural Development Administration, Wanju 55365, Korea

In this study, we investigated the effects of allelic variations in *Hd1*, *OsPRR37*, *Ghd7*, and *DTH8* on major agronomic traits (DTH-days to heading; CL-culm length; PL-panicle length; PN-panicles no. per plant; SN-spikelets no. per panicle; RGP-ripened grain ratio; TGW-thousand-grain weight; HRP-head rice percentage) in 287 Korean rice cultivars. Phenotype data evaluated at the National Institute of Crop Science for four years (2018-2021) were used in this study. Two-way ANOVAs were conducted with the genotype as a fixed factor and the year as a random factor excluding the interaction effect. Compared to the cultivars carrying functional *Hd1*, those with non-functional *hd1* headed 12.2 days earlier, showed longer PL, higher SN, but lower PN, TWG, and HRP. Cultivars carrying non-functional *osprr37* headed 16.4 days earlier and had shorter CL, lower SN and HRP compared to those with functional *OsPRR37*. Cultivars carrying non-functional *ghd7* headed 23.2 days earlier, had shorter CL and PL, and lower SN. Finally, cultivars carrying non-functional *dth8* showed longer PL, CL and higher SN, but lower HRP compared to those with functional *DTH8*. We also conducted two-way ANOVAs with the allelic combination of the four genes as a fixed factor and the year as a random factor excluding the interaction effects. The allelic combination showed significant effects on all traits except RGP. Further research is underway to analyze more precise effects of the allelic variations and interactions among major heading date genes.

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***Corresponding Author:** Tel. 063-270-2530, E-mail: yjmo@jbnu.edu

PB-0067

Analysis of agricultural characteristics and grain yield under the waterlogging treatment in maize

Jae-Han Son*, Hwan-Hee Bae, Young-Sam-Go, Jun-Young Ha, Beom-Young-Son, Tae-Wook Jung

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

Maize (*Zea mays* L.) grain is very useful for processing, so productivity and quality are important factors. When the soil is excessively wet(waterlogging), the maize plants cannot uptake sufficient oxygen, which causes root damage, slowed growth or death of the corn plants, which in turn reduces the grain productivity. Therefore, the resistance or tolerance of corn to waterlogging is very important factor to cultivate in paddy field. In this study, we selected 10 inbreds with tolerance to waterlogging through waterlogging treatment for 9 days at the seedling (V3) stage. When it treated the waterlogging, the emergence period of tassels and silks were delayed by 4 and 8 days, respectively. Stem length decreased by 18% - 20%, and ASI was 7.3 days on average, which increase by 3 days on average after waterlogging treatment(WT). Stem thickness decreased by an average of 3.9 mm (20%) after WT from untreated 19.4 mm to 15.5 mm treated, respectively. The ear productivity of 10 inbreds was less than 20%, plant survival rate was 50%, and ASI were within 3 days, respectively. We select the ear and grain productivity, viability, and ASI, as the main selection criteria for development of waterlogging tolerance line.

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***Corresponding Author:** Tel. 031-695-4045, E-mail: pathfinder1@korea.kr

PB-0068

Selection of maize varieties adapted to high latitude (the south of Mt. Suyang)

Jae-Han Son[1*], Hwan-Hee Bae[1], Young-Sam-Go[1], Jun-Young Ha[1], Bonil Ku[2], Man-Kee Baek[2], Beom-Young-Son[1], Tae-Wook Jung[1]

[1]Department of Central Area Crop Science, National Institute of Crop Science, RDA, Suwon, 16429, Republic of Korea
[2]National Institute of Crop Science, RDA, Cheorwon, 24040, Republic of Korea

Since maize (Zea mays L.) originates from central and south America, it needs to maintain warm climate conditions during the growing season. When the temperature of night is below 10℃ or -1.7℃, growth stops or it dies. So it should be kept within 10-30℃ from seeding to maturity. Germination temperature is at least 8-11℃, optimal at 32-34 ℃. Since temperature is closely related to germination rate, period, it has an important effect on maize growth. Therefore, in this study, the quantity and feed value of 11 major varieties were evaluated to select varieties suitable for cultivation of maize for feed in high latitudes (North Korea below 38 degrees north). In particular, a cultivation test was conducted in Suwon(South Korea) to evaluate the adaptability of the area south of Mt. Suyang. The days to silking of Shinhwangok 2 was fastest with 65 days, and Gangpyeongok was the slowest with 75 days. Stem length of all varieties were taller than 230㎝, and Gwangpyeongok was the largest, Daanok and Shinhwangok 2 had the highest ear ratio. The Dry matter and TDN quantity of Dacheongok had the highest values of 3,142kg/10a and 2,166kg/10a, respectively. The crude protein content was the highest in Pyeonggangok at 8.0%. TDN(%) was in the range of 57-68%, and Hwangdaok was as high as 68%. As a result, it is thought that Dacheongok and Pyeonggangok are suitable for cultivation in terms of quantity and feed value.

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***Corresponding Author:** Tel. 031-695-4045, E-mail: pathfinder1@korea.kr

PB-0069

Sweetpotato Variety 'Hopungmi' for Edible and Food Processing Use with Multiple-Disease Resistance

Hyeong-Un Lee[1*], Mi-Nam Chung[1], Gyeong-Dan Yu[1], Tae-Hwa Kim[1], Yeon-Sang Song[1], Su-Jung Kim[1], Jae-Myung Kim[1], Jin-Young Moon[2], Young-Sik Kang[3], Kyu-Hwan Choi[4], Sang-Sik Nam[1], Koan Sik Woo[1], Won Park[1], Kyo Hwui Lee[1]

[1]Bioenergy Crop Research Institute, National Institute of Crop Science, Rural Development Administration, Muan 58545, Korea
[2]Gyeongsangnam-do Agricultural Research & Extension Services, Jinju 52733, Korea
[3]Chungcheongnam-do Agricultural Research & Extension Services, Yesan 32418, Korea
[4]Jeollabuk-do Agricultural Research & Extension Services, Iksan 54591, Korea

Sweetpotato is one of the economically important crops in Korea, with the second-highest agricultural production amount among food crops, following rice, as of 2020. Sweetpotato farms also have the highest income per unit area among food crops in Korea. However, the damage caused by major diseases such as Fusarium wilt, Streptomyces soil rot, and root-knot nematodes poses challenges by reducing the yield and quality of sweetpotatoes. It was reported that disease-resistant varieties against these diseases are the most effective and environmentally friendly approach to control. Therefore, there is a high demand among sweetpotato farmers for resistant varieties against these diseases. In 2021, a sweetpotato variety, 'Hopungmi', was developed with resistance to Fusarium wilt, Streptomyces soil rot, and root-knot nematode. It was derived from a cross between 'Pungwonmi' with resistance to Fusarium wilt and root-knot nematode and 'Hogammi' with resistance to Streptomyces soil rot. 'Hopungmi' has good characteristics for edible and food processing use. The storage roots of 'Hopungmi' are elliptical-shaped storage roots with red skin and light orange flesh. The steamed texture of storage roots is slightly moist, and it exhibits good palatability when roasted. As a result of the sensory evaluation of dried sweetpotato, 'Hopungmi' was superior to the existing variety, 'Hogammi'. The marketable storage root yield of 'Hopungmi' was 34.0 tons/ha when cultivated for 120 days, which was 14% higher than that of 'Hogammi'. Furthermore, it increased to 57.8 tons/ha when cultivated for 150 days. 'Hopungmi' also demonstrated good storability, exhibiting a minimal decay rate during long-term storage. The multiple-disease-resistant variety, 'Hopungmi', with high yield and resistance to major diseases, is expected to contribute to increasing agricultural productivity and consumption, as it can be utilized for both edible and food processing use.

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

PB-0070

Functional Characterization of SIZ1 Homologs Reveals Enhanced TSWV Resistance in mutant *Nicotiana benthamiana* lines

Jelli Venkatesh, Ghimire Sunita, Jin-Kyung Kwon, Danah Kim, Byoung-Cheorl Kang*

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

Tomato spotted wilt virus (TSWV) is a highly destructive plant virus that affects a wide range of host species, leading to significant agricultural crop losses. The *SIZ1* gene, functioning as a small ubiquitin-like modifier (SUMO) E3 ligase, plays a critical role in regulating various plant developmental processes and stress responses. Despite considerable research efforts, the precise function of *NbSIZ1* in *Nicotiana benthamiana* plants remains largely elusive. To gain further insights, we conducted a comprehensive *in silico* analysis of *SIZ1*-like genes, uncovering the existence of two homologs (*NbSIZ1a* and *NbSIZ1b*) sharing a sequence identity of 70-80% with Arabidopsis *AtSIZ1* genes. These NbSIZ1 homologs exhibited significant conservation in their structural domains and conserved residues, indicating their functional similarity to AtSIZ1. To investigate their roles, we generated the *NbSiz1a/b* double mutant using CRISPR/Cas9 genome editing. Remarkably, our findings revealed that the *NbSIZ1a/b* double mutants exhibited enhanced resistance to TSWV infection. Overall, our study sheds light on the crucial role of *NbSIZ1a/b* in combating TSWV infection and highlights the potential utility of *SIZ1* as an important genetic resources for future molecular breeding efforts to develop TSWV-resistant crop plants. Future investigations focused on the precise functional characterization of *NbSIZ1a/b* will undoubtedly provide more comprehensive insights into their contributions to TSWV resistance in plants.

***Corresponding Author:** Tel. 02 880-4573, E-mail: bk54@snu.ac.kr

PB-0071

Changes in wheat characteristics of two cultivars by different double cropping systems

Jisu Choi*, Seong Hwan Oh, Seo Young Oh, Sung Hoon Kim, TaeHee Kim

Paddy Crop Research Division, Department of Southern Area Crop Science, National Institute of Crop Science, Republic of Korea

The increasing size of the domestic baking market in South Korea has led to a rising demand for high-quality baking wheat. However, with a self-sufficiency rate of only 1.1% for hard wheat as of 2021, there is a need to improve wheat production in the country. Currently, wheat is predominantly cultivated in the regions of Jeonnam, Jeonbuk, and Gyeongnam as a secondary crop following rice cultivation. To expand of wheat cultivation, the cropping systems that incorporate wheat as a subsequent crop after primary crops has been proposed. Previous studies have demonstrated the successful connectivity of cropping season of rice, soybeans, and corn in South Korea. However, information how wheat quality is affected by the cultivation of different primary crops is crucial for producing high-quality wheat. This study conducted field trials at the Southern Crop Department of the National Institute of Crop Science, planting rice, soybeans, and corn as primary crops, followed by wheat cultivation. Quality characteristics, including protein content, sedimentation value, and falling number, were analyzed. Plant growth characteristic and soil physicochemical properties were also assessed. Statistical analysis was performed using two-way analysis of variance and Duncan's multiple range test at a 95% confidence level.

The results revealed that the Geumgang wheat cultivar exhibited superior quality characteristics as a hard wheat compared to the Jogyung cultivar, including higher milling yield, protein content, sedimentation value, and gluten content. Both cultivars demonstrated remarkable characteristics as hard wheat when cultivated after soybeans. Soil analysis before and after wheat and primary crop cultivation indicated a significant decrease in phosphorus content after soybean cultivation. While physical soil properties showed variations in soil moisture content, the proximity to the well location introduced positional effects that need to be considered.

The findings from this study provide valuable insights into the quality characteristics of wheat cultivated after different primary crops, which can contribute to the development of effective crop rotation systems for future high-quality wheat production in South Korea.

***Corresponding Author:** Tel. 055-350-1174, E-mail: choijisu24@korea.kr

PB-0072

Development of mid-late maturing, salt tolerant high biomass whole crop silage rice (*Oryza sativa* L.) harboring *Saltol* QTL with multiple disease-insect and lodging resistance

Eok Keun Ahn[1*], Jeom Ho Lee[1], Yong Jae Won[2], Kuk Hyun Jung[3], Ung Jo Hyun[1], Yoon Sung Lee[1], Sang Beom Lee[1]

[1]Department of Central Area Crop Science, National Institute of Crop Science, RDA, Suwon, 16429, Republic of Korea

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

[3]Chuncheon Branch, National Institute of Crop Science, RDA, Chuncheon, 24219, Republic of Korea

Salinity is the most common abiotic stresses leading to the reduction of rice yield at many rice-growing areas in world wide. Developing new rice varieties for feed, the main goals are to enhance biomass production and lodging resistance. It is also important to have salt tolerance to adapt to reclaimed land for expansion of cultivation through adaptation to harsh environment. And so salt tolerant *Saltol* QTL has been a breeding target for the improvements of salt tolerance in whole crop silage (WCS) rice. In rice, major QTL for salinity tolerance named *Saltol*, which responsible for seedling stage salinity tolerance was identified on the short arm of chromosome 1 and explain more than 40% of the phenotypic variation. In this study, we have developed new WCS rice line, ‘Suweon655’ with salinity tolerance and high biomass by applying marker assisted selection. The ‘Suweon655’ were introgressed *Saltol* QTL and salt tolerant similar with level of ‘Pokkali’ and ‘FL478’ when 0.6% ($12dSm^{-1}$) salt treated. Tolerant ‘Suweon655’ showed lower Na^+ contents and Na^+/K^+ ratio in shoot and root similar to ‘Pokkali’ and ‘FL478’ compared to sensitive parent ‘Yeongwoo’ cultivar. High amylose (27.2%) ‘Suweon655’ for forage are resistant to lodging, despite their long leaf and culm, and have high biomass, 18.8 t/ha, are multiple-resistant to diseases and insects such as blast, bacterial blight (race K1, K2, K3, K3a), rice stripe virus and (small) brown planthopper. This will be useful to be cultivated at about 130 thousand reclaimed areas of Korea and as a result, contribute in control of rice over-production and self-sufficient feed supply in Korea.

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

PB-0073

Moderation of leaf rolling trait for developing japonica rice variety with ideal plant type

Su Jang, Yoon Kyung Lee, Hee-Jong Koh*

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

Moderate leaf rolling has been recognized as an optimal trait for achieving ideal plant type in rice (*Oryza sativa* L.), as it improves photosynthetic efficiency and, consequently, grain yield. In this study, identification of quantitative trait loci (QTLs) controlling adaxial leaf rolling was conducted using a recombinant inbred line (RIL) population obtained from a cross between Tong 88-7 (T887) and Milyang 23 (M23). The rolling phenotype of both the flag leaf and upper secondary leaf was predominantly governed by two major QTLs, namely *qARO1* and *qARO9*. Different allelic combinations led to a substantial variation in leaf rolling. Histological analysis of near-isogenic lines (NILs) elucidated the specific mechanisms underlying leaf rolling. *qARO1* was found to influence leaf thickness across the small vein, while *qARO9* affected on leaf thickness across the entire leaf, and bulliform cell area, resulting in adaxial leaf rolling. In order to develop Japonica rice varieties with the ideal plant type, introduction of *qARO1* and *qARO9* into japonica varieties was achieved through a backcrossing approach. These QTLs consistently exhibited their effects on leaf rolling across diverse genetic backgrounds, enhancing plant architecture even in advanced backcross lines. The results of this study contribute to advancing our understanding of the genetic basis underlying adaxial leaf rolling. In addition, *qARO1* and *qARO9* could be useful for developing japonica rice varieties with ideal plant type, resulting in enhanced rice grain productivity.

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

PB-0074

High quality red color waxy corn ‘Ararichal’

JungHeon Han[1*], Min Namgung[2], KiJin Park[3], SiHwan Ryu[1], JaeKeun Choi[1], HeeYeon Kim[1], MoonJong Kim[1], SeungHyun Wang[1], WooSik Yong[1], JaeNam Sim[1], KiSun Kim[1]

[1]Maize Research Institute, Gangwondo, Agricultural Research and Extension Services, Hongcheon, Korea
[2]Gangwondo, Agricultural Research and Extension Services Chuncheon-si, Korea
[3]Potato Research Institute, Agricultural Research and Extension Services Gangneung-si, Korea

Anthocyanin is a natural plant metabolite and has the best antioxidant action among antioxidants in nature. In corn, it is known to be high in purple corn, where the foliage, kernel, and stalk are known to be high in content. Purple corn has the difficulty of extracting anthocyanins contained in foliage or stalk or processing kernel. In order to improve the added value of waxy corn and meet the demand for healthy functional foods through research on breeding varieties that can consume anthocyanin in the form of fresh ear rather than processed products, anthocyanin-high-containing Cheongchunchal has been developed. It showed a anthocyanin content 25 times higher than that of the existing black corn, but the pericarp was slightly thick and the size of the ear was small. so it was necessary to improve the ear and quality characteristics. This study was conducted to develop varieties that contain anthocyanin and have excellent ear and quality characteristics. Ararichal was based on HW12 of the white-waxy corn inbreed, and 16CLP39, a pigmented corn inbreed that exhibits a waxy factor and forms anthocyanin in the kernel, was hybridized. Ararichal increased by 3% and 49% to ear yield(6,563/10a) and ear weight 946kg/10a, respectively, compared to Cheongchunchal, and the ear length was more than 19cm and the kernel setting rate was 98%, so the ear characteristics were excellent. Compared to Cheongchunchal, anthocyanin content is 45%, but it is considered to be a variety suitable for consumers' demand due to its excellent growth, ear, and quality characteristics.

***Corresponding Author:** Tel. 031-248-6922, E-mail: wjdgjs9908@korea.kr

PB-0075

Quality analysis of wheat near-isogenic lines(NILs) overexpressing 1Bx7 glutenin subunit

Kyeong-Min Kim*, Myoung Hui Lee, Changhyun Choi, Kyeong-Hoon Kim, Go Eun Lee, Jun Yong Choi, Chon-Sik Kang, Ki-Chang Jang

Wheat Research Team, National Institute of crop Science, Rural Development Administration, Wanju, 55365, Republic of Korea

Overexpression of Glu-1Bx7 via allele 1Bx7^{OE} significantly contributes to high dough strength in some wheat varieties and is useful for improving wheat quality. Therefore, breeding more wheat varieties with 1Bx7^{OE} subunits would be a promising way to improve wheat quality. However, the proportion of wheat varieties containing 1Bx7^{OE} is significantly lower in Asia, including Korea. This study aimed to develop wheat varieties with increased 1Bx7 expression for wheat quality improvement using a speed-breeding method.

Four cultivars containing both the 43 bp insertion in the promoter and 1Bx7 gene duplication were selected from crossing blocks (CB) of wheat in the National Institute of Crop Science (Republic of Korea). Among the selected varieties, CHISHOLM was crossed with Keumkang. And then three times backcross with keumkang and two self-pollinations, we developmet a homozygous Keumkang near isogenic lines (NILs). Sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) and ultra-performance liquid chromatography (UPLC) analyses showed that the expression of 1Bx7 was significantly higher in NILs compared with that in Keumkang. Wheat quality was analyzed with near infrared reflectance spectroscopy by measuring the protein content and SDS-sedimentation of NILs. The protein content of NILs (12.94%) was 21.65% higher than that of CHISHOLM (10.63%) and was 4.54% higher to that of Keumkang (12.37%) but the difference was not significant. In addition, the SDS-sedimentation value of NILs (44.29 ml) was 14.97% and 16.44% higher than that of Keumkang (38.52 ml) and CHISHOLM (38.03 ml), respectively. This study is expected to improve the quality of domestic wheat HMW-GSs by crossbreeding with 1Bx7^{OE}-containing cultivars.

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***Corresponding Author:** Tel. 063-238-5458, E-mail: raiders87@korea.kr

PB-0076

Discovery of SNP related to salinity stress on heading stage in the Korean wheat core collection by GWAS analysis for culm length and seed area

Kyoung Do Min, Jae Yoon Kim*

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

Due to global warming, the temperate climate has been changing to a subtropical climate in South Korea. Also, drought regions and other regions occurred torrential rains from spring to summer due to climate change. The representative varieties of Korea were early mature wheat, and most of them were harvested before about the middle of June. It is important because abiotic stress negatively affects flowering and ripening stage, the plant decreased seed potential. When wheat was exposed to rain during maturity, the protein content of the spikes decreases. The culm length and seed area of the Korean wheat core collection grown in the Kongju University fields (KNU field) and reclaimed lands were investigated to search for excellent salt stress resistance varieties.

In this study, we are evaluating the culm length and seed area in the Korean wheat core collection grown in each KNU field and reclaimed land. The seeds were scanned using a print scanner and the area of the seeds was calculated using the ImageJ program. For genotyping, a total of 566 accessions of the 614 Korean core collection were selected after consideration of DNA QC. We performed GWAS in R on GAPIT tools that FarmCPU model.

Accession numbers 871 and 951 received high scores in the ratio (NaCl treatment/control) of stem length (871:0.55, 951:0.564) and seed area (871:1.23, 951:1.26) and belonged to the top 50 among all 614 accessions. These two resources can be utilized as excellent resources in reclaimed land. GWAS results, there were no significant SNPs found simultaneously in the culm length and seed area. One SNP (AX-94543470_1B chromosome), exceeding the FarmCPU model threshold, was found only in the culm length. We plan to explore related genes and the possibility of use as markers in the future.

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

PB-0077

중기 보존 밀 유전자원의 종자활력 및 농업형질의 연관성 분석

성필모, Mesfin Haile Kebede, 조규택, 우희종, 홍소연, 노나영*

농촌진흥청 국립농업과학원 농업유전자원센터

국내・외 유전자원의 보존 및 활용을 위해서는 유전자원의 품질관리가 중요하다. 본 연구에서는 농업유전자원센터에서 발아 활력 검정을 실시하고 이에 대한 정보를 구축하고 있는 농업유전자원관리시스템(GMS)의 발아데이터를 활용하여 중기 보존 밀(*Triticum aestivum subsp. Aestivum*) 유전자원 대한 10년 주기의 발아 활력 변화율과 농업형질 간의 연관성에 대하여 조사하였다. 초기 발아율이 85% 이상인 밀 1,046 유전자원을 대상으로 10년간 중기 저장고(온도 4℃, 상대습도 30%)에 저장된 자원의 발아율과 활력변화를 조사하였고, 농업형질로는 천립중, 조단백질 총함량, 수장, 망장, 식물생장습성, 이삭형태, 수색, 망색, 알의 대소, 종피색을 조사하였다. 활력변화 조사 결과, 초기 발아율과 10년 저장된 자원의 발아율 활력변화는 10-100% 범위로 나타났으며, 이 중 활력변화가 50% 보다 감소한 자원은 34개, 활력변화가 50-85%로 감소한 자원은 307개, 활력변화가 85-100%로 감소한 자원은 593개, 100%로 활력변화가 없는 자원은 112개로 조사되었다. 활력변화와 농업형질과 비교한 결과, 종피색의 경우 백립계 자원이 활력변화가 가장 적었으며, 알의 대소에서는 소립종자, 수색은 갈색, 망색은 흑색, 망장은 장망, 이삭형태는 봉형, 식물생장습성에서는 폐의 특성이 활력변화가 가장 적게 나타났다. 조단백 총함량과 수장에서는 그룹별로 유의미한 차이가 나지 않았지만, 천립중에서는 무게가 적은 그룹일수록 활력변화가 적게 나타났다. 밀 유전자원의 발아 활력 변화와 농업형질간 연관성 조사를 통해서 자원관리 체계 및 보존 연구 활성화에 도움이 될 것으로 판단된다.

사사: 본 연구는 농촌진흥청 연구사업(세부과제명: 농업생명자원 국가관리 및 활용체계 구축, 과제번호: PJ015579)의 지원으로 수행되었음

***교신저자:** Tel. 063-238-4943, E-mail: nonanona@korea.kr

PB-0078

A New Rapeseed Line ‘Mokpo 133’ with Long Flowering Period and Deep Yellow Color

Jaehee Jeong, Young-Lok Cha, Da-Hee An, Ji-Bong Choi, Soo-Yeon Kim, Kwang-Soo Kim*

Bioenergy Crop Research Institute, National Institute of Crop Science, Rural Development Administration, Muan, Republic of Korea

In Korea, rapeseed is widely cultivated for its scenic value, thus necessitating the development of varieties with a long flowering period. ‘Mokpo 133’ is a deep yellow rapeseed with a long flowering period, selected from a cross of the ‘Yeongsan’ cultivar and ‘AV62’ line. Results from regional adaptation test conducted in three regions (2020-2023) demonstrated ‘Mokpo 133’ bloomed 3-7 days earlier and had a 10-day longer flowering period than ‘Jungmo 7001’. Using a spectrophotometer to measure L*, a*, and b* values revealed that the flower color of ‘Mokpo 133’ (73.5, 3.5, 69.0, respectively) is a deep yellow, distinguishing it from the color of ‘Jungmo 7001’ flowers (76.0, -4.6, 71.5, respectively). Additionally, ‘Mokpo 133’ offers the advantage of easier harvesting with a combine due to its thinner main stem diameter (9.3 cm) than that of ‘Jungmo 7001’ (11.3 cm). The number of siliques per plant in ‘Mokpo 133’ (59.8) was higher than in ‘Jungmo 7001’ (53.9), while the number of seeds per silique was the same at 18.6. ‘Mokpo 133’ can be widely utilized for landscaping and as a honey plant due to its extended flowering period.

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

PB-0079

Establishing core collection of maize (*Zea mays* L.) including domestic landraces with phenotypic diversity in Korea

Seongmin Hong[1], Jinkwan Jo[1], Jae-Hong Kim[1], Ji Won Kim[1], Na-Young Ro[2], Gibum Yi[1*]

[1]Department of Bio-Environmental Chemistry, College of Agriculture and Life Sciences, Chungnam National University, Daejoen, Republic of Korea
[2]National Agrobiodiversity Center of NAAS, RDA, Jeonju, Korea

Establishing a core collection in crop species has shown its effectiveness and power in various aspects, such as designing breeding programs and conducting genetic and genomic research. In maize (*Zea mays* L.), there have been several core collections for different purposes. Here we report the progresses made in establishing a core collection to maximize the utility of Korean germplasm emphasizing Korean landraces which have substantial genetic diversity but have rarely been studied. There are about 8,000 maize germplasm collections in Korea, including over 3,000 Korean maize landraces in the National Agrobiodiversity Center (of NAAS, RDA, Korea). We analyzed available morphological phenotypes of 1,716 maize germplasm, which could be divided into four independent groups determined by their geographic origins (domestic and foreign) and breeding processes (breeding line and landrace). Total 12 categorical and 17 quantitative traits were used to assess morphological diversity among these groups. The maize germplasm showed different phenotypic correlation patterns by each maize groups, indicating various patterns of the selection related to combinations of the breeding processes and geographic origins. Principal component analysis demonstrated that the phenotypic variations of collected maize germplasm were largely explained by flowering time. In particular, Korean maize landrace showed narrower range of flowering time than that of foreign germplasm and dominant proportion of waxy seed texture. Our results revealed that phenotypic characteristics of Korean landrace germplasm, compared to foreign germplasm, will facilitate for development of Korean maize core collection.

Keywords: Corn, Germplasm, Landrace, Phenotypic diversity, Core collection

***Corresponding Author:** Tel. 042-821-6738, E-mail: gibumyi@gmail.com

PB-0080

Phenotyping of multiple waxy corn ears in single digital image

Seung Hyun Wang[1*], Ki Jin Park[2], Min Nam-Gung[3], Si Hwan Ryu[1], Jae Keun Choi[1], Hee Yeon Kim[1], Moon Jong Kim[1], Jeong Heon Han[1], Woo Sik Young[1], Jea Nam Sim[1], Ki Sun Kim[1]

[1]Maize Research Institute, Gangwondo agricultural research & extension service, Hongchoen 25160, Korea
[2]Potato experiment station, Gangwondo agricultural research & extension service, Gangneung, 25437, Korea
[3]Research cooperation section, Gangwondo agricultural research & extension service, Chuncheon, 24203, Korea

Images of 2,538 ears from 924 inbred lines of waxy corn were used to measure length, width, length-width ratio, and area. ImageJ straight was used for manual measurements and imagej batch macro was used to estimate feret's diameter and bounding rectangle. Inbred lines were grouped according to ear color (white, black, yellow, pigmented, and red) to compare traits. Based on manual measurements, the red maize inbred lines had the highest average ear length and width values of 11.9 cm and 3.35 cm, respectively. The yellow lines had the shortest mean ear length at 10.5 cm and the color waxy lines had the narrowest ear morphology with a mean width of 2.89 cm. The estimated average ear area was highest for the red maize lines at 243,010 pixels and smallest for the pigmented maize lines at 188,617 pixcel. The ear length-width ratio was found to be a maximum of 8.01 and a minimum of 1.40. The manually measured ear length showed a high correlation with the estimated spikelet length of 0.953 (Feret) and 0.954 (bounding rectangle), respectively, while the correlation between the manually measured ear width and the minFeret of the automatic measurement was 0.831. This study is expected to enable efficient and precise measurement of ear traits in maize with various colors.

***Corresponding Author:** Tel. 033-248-6928, E-mail: team0321@korea.kr

PB-0081

Evaluation of Chip Processing and Sprouting Properties within Korean Potato clones

Do Hee Kwon*, Young Eun Park, Kwang Ryong Jo, Jang Gyu Choi, Young Ik Jin, Gun Ho Jung, Gyu Bin Lee, Jae Youn Yi, Hong Sik Won

Highland Agriculture Research Institute, National Institute of Crop Science, Rural Development Administration, Pyeongchang 25342, Republic of Korea

Due to the increased demand for potato chips and the development of the potato processing industry, various chip-processing varieties have been bred. Regarding chip processing properties, there are some important parameters, such as light chip color, round shape, specific gravity and so on. Among them, chip color is one of the major characteristic. Potato is stored 4 degrees to prevent sprouting, unfortunately this accumulates glucose leading to dark chip colors and potential acrylamide build up. In this study, we evaluated chip processing properties of 49 korean potato clones and examined the chip color after 100, 150 days of storage at 4 and 10 degrees. In addition, sprouting property was investigated at 4, 10 degrees and room temperature. After harvesting, the right color of the chip clones are ‘Jangwon’, ‘Arirang-2’, ‘Saebong’ released by HARI. Even after 100 and 150 days, the color of the chip remained bright clones are ‘Arirang-1’. ‘Dubaek’, ‘Dawon’. As a result of the sprouting investigation, it was observed that most clones grew long at RT and 10 degrees. In the 4 degrees, the sprouting tended to grow slowly, and among them, ‘Daebaek’, ‘Dawon’, ‘Early fry’, ‘Golden egg’ and ‘Dubaek’ were not sprouted. Further, we accumulate foreign and superior clones to construction a chip processing data. This study will provide insight and basic information for chip-processing potato breeding program. With the increasing demand for potato chip and the development of the potato processing industry, various chip processing cultivars have been bred. Important traits related to chip processing include the tuber shape, chip color, specific gravity, and glucose content in tuber. Potatoes are stored under low temperature to prevent sprouting after harvesting, which increases tuber glucose content, leading to dark chip color. In this study, chip processing traits after harvesting and low-temperature storage conditions (100 days and 150 days at 4 °C s and 10 °C, respectively) were investigated for Korean potato clones. There was a significant difference between the chip processing characteristics after harvest and low temperature storage. After harvesting, Jangwon, Mangang, and Dubaek were selected as promising resources with light chip color. In addition, clones with good chip processing characteristics, which showed market acceptable chip color and no sprouting were selected under low-temperature storage conditions. This study will provide insight and basic information for chip-processing potato breeding program.

***Corresponding Author:** Tel. 033-330-1680, E-mail: dohee220@korea.kr

PB-0082

Comparison of main characteristics and yield by waxy corn cultivars

Yejin Kyung*, Jong Woo Han, Hyeong Ryeol Lee, Min-Young Park, Se-Gu Hwang

Agriculture Business Center, 65-6, Deokgeum-ro, Jincheon-gun, Chungbuk, 27844, Republic of Korea

In this study, two new cultivars ('Taeyangchal' and 'Saengmyeongchal') developed by the Chungbuk Agriculture Business Center were compared to three major certified seeds ('Mibeakchal', 'Daehakchal', and 'Ilmichal') in terms of their main characteristics and yields. The days to silking among the different species, 'Taeyangchal' had the longest time, taking 74 days, while 'Mibeakchal' had the shortest time, taking only 67 days. The culm length of 'Taeyangchal' was the longest at 262.7 cm, while 'Saengmyeongchal' had the shortest at 216.2 cm. The height of the ears of 'Taeyangchal' was the tallest(144 cm), while the 'Mibeakchal' had the shortest ear height (117.2 cm). In terms of ear characteristics, Daechal had the longest ear length among the five cultivars, but its kernel set ratio was the second lowest. In the first ear of kernel set ratio, all cultivars showed more than 98%. However, in the second ear, 'Taeyangchal' had the highest rate of 99%, while 'Mibeakchal' had the lowest rate (29.4%). In terms of pericarp thickness, 'Taeyangchal' had the thinnest at 39.8 ㎛, while 'Ilmichal' had the thickest at 49㎛. The yield of ear weight (kg/10a) was highest for 'Mibeakchal' (373.7 kg) and lowest for 'Daehakchal' (284 kg). After examining five cultivars, it showed that the new variety 'Taeyangchal' had the tallest culm and ear height. But it has thin pericarp and can be harvested not only the first ear but also the second ear. Therefore, it is considered to have a high market value.

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

PB-0083

Comparative Transcriptome Analysis of Biomass-related Component Gene Expression Using RNA-Seq in Sorghum (*Sorghum bicolor* L.) Mutant

Ye-Jin Lee[1,2], Baul Yang[1,2], Woon Ji Kim[1], Juyoung Kim[1], Soon-Jae Kwon[1], Jae Hoon Kim[1], Joon-Woo Ahn[1], Sang Hoon Kim[1], Chang-Hyu Bae[2*], Jaihyunk Ryu[1*]

[1]Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongeup 56212, Korea

[2]Department of Plant Production Sciences, Graduate School of Sunchon National University, Suncheon 57922, Korea

The increase in environmental pollution caused by fossil fuels has resulted in a growing interest in organic materials for bioenergy on the globe. Sorghum (*Sorghum bicolor* L.) is the fifth-most important cereal crop as well as renewable resources as alternative energy crop. To explore the molecular basis of biomass-related traits in sorghum, we selected three germplasms and three mutant lines with different soluble solids content (S1; 13.3 brix°, S2; 13.4 brix°, S3; 11.7 brix°, S4; 17.8 brix°, S5; 10.6 brix°, S6; 8.8 brix°), which were included by gamma-irradiation and performed comparative transcriptome analysis using the RNA-sequencing. A total of 66.3 Gb reads were generated for six sorghum samples and finally yielded 41,048 representative transcripts, with an average length of 142.7 bp, of which 32,478 (79.12%) were annotated from databases. Among the five comparisons, including S1 vs. S2, S1 vs. S3, S1 vs. S4, S1 vs. S5, and S1 vs. S6, 11,747 differentially expressed genes (DEGs) were classified into six groups through clustering analysis. Based on Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) analyses, these DEGs were enriched in functional annotations. The top 20 enriched GO terms in five comparisons, the GO terms represented small molecule biosynthetic processes, response to oxygen-containing compounds, and carboxylic acid metabolic process. Major classification of DEGs were enriched in metabolism pathway based on KEGG pathway. A total of 260 genes related to the starch and sucrose metabolism pathway, such as Beta-fructofuranosidase, insoluble isoenzyme (*CWINV1*), Alpha-amylase 2B (*AMY2B*), Beta-amylase (*BMY1*) were identified by KEGG enrichment analysis. These studies will help in the analysis of biomass-related components of sorghum.

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***Corresponding Author:** Tel. 061-750-5183, 063-570-3311, E-mail: chbae@scnu.ac.kr, jhryu@kaeri.re.kr

PB-0084

Examining variations in agronomic traits across ecotypes through speed breeding in soybean (*Glycine max* (L.) Merr.)

Yeon-Ju Kwon[1,2], Yu-Hyeon Park[1], Nayoung Kwon[1], Daewoong Lee[1,2], Ju Seok Lee[2], Tae-Hwan Jun[1*]

[1]Department of Plant Bioscience, Pusan National University, Miryang, 50463, Republic of Korea
[2]Bio-Evaluation Center, Korea Research Institute of Bioscience and Biotechnology, Cheongju, Chungbuk, 28116, Republic of Korea

Soybeans are recognized as a major plant-based protein resource, however, the growing period of soybeans generally extends to about 120 days until harvest, which poses significant constraints in the development of new cultivars. The Speed Breeding methodology considerably helps to reduce breeding time, but more studies are needed to determine optimal environmental conditions guided by light wavelengths impacting soybean flowering and maturation stages. This study used several different soybean ecotypes, including early to late maturing cultivars such as Kwonol, Sunnok, Chungja, Daewon, and Soeritae. These were seeded in eight replicates with a planting density of 5cm x 5cm and grown under Speed Breeding conditions with an average LED intensity of 676 µmol/(m2・s). Here, the ratios of red (660nm) to blue (450nm) light wavelengths were 1:2 and 2:1, respectively, under a 12-hour photoperiod. At 21 days after planting, no significant height differences were observed between the two light ratios, whereas plant height at the flowering stage showed a notable difference, exhibiting a 1.5-fold difference between the two light ratios. SPAD values were similar for both light conditions, averaging at 28.1. Remarkably, we noticed that the flower time was shortened by an average of approximately 5 days across all ecotypes under the 1:2 light ratio. In the case of the Soeritae cultivar, which usually takes 164 days from planting to maturity, we achieved around 90% germination rate even when harvested 80 days after planting under the 1:2 light ratio. This implies the possibility of producing approximately four times per year.

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

PB-0085

A Comparative Analysis of Pod Counts in Soybeans [*Glycine max* (L.) Merr.] Under Two Seeding Conditions on the Speed Breeding Platform

Daewoong Lee[1,2], Tae-Hwan Jun[2,3], Ju Seok Lee[1*]

[1]Bio-evaluation Center, Korea Research Institute of Bioscience and Biotechnology, Korea
[2]Department of Plant Bioscience, Pusan National University, Miryang 50463, Korea
[3]Life and Industry Convergence Research Institute, Pusan National University, Miryang 50463, Korea

The speed breeding platform (SB) is a controlled environment system that accelerates plant growth and development through optimized conditions. In SB, initial seeding conditions are crucial for crop productivity, particularly in single seed descent (SSD) methods, as they significantly affect pod formation and yield. To optimize soybean production, a comparison was made between two planting configurations: condition A (single-seed planting) and condition B (double-seed planting) in separate holes of a 50-seedling tray. In speed breeding platform, the temperature was maintained at 25℃±1℃ and the humidity was kept above 50% using a thermo-hygrostat, while a short-day photoperiod of 9 hours of light and 15 hours of darkness was implemented. As a result, in condition A, the average number of pods was 4.5 ± 1.5, while in condition B, it was 3 ± 0.8. This result shows that there is a significant difference in the number of pods between the two planting schemes. Advantages of double-seed planting were observed, with Socheong 2 and Cheonja showing 3 and 3.8 pods respectively, compared to 1.4 and 0.4 pods in single-seed planting. Compared to single-seed planting, which had high variation among genetic resources, the double-seed planting method had a lower but more even number of pods overall. The experiment confirmed that double-seed planting conditions are suitable for obtaining a higher number of seeds in early-maturity groups, while single-seed planting conditions are ideal for mid and late-maturity groups. These findings support the stable implementation of the SSD method for generation progress on the speed breeding platform.

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***Corresponding Author:** Tel. 043-240-6712, E-mail: juseoklee@kribb.re.kr

PB-0086

Comparisons of SPAD value in rice genetic resources according to the nitrogen application levels

Tae-Heon Kim, Dong-Hyun Baek, Changju Lee, Suk-Man Kim*

Department of Ecological and Environmental System, Kyungpook National University, Sangju, Republic of Korea

Nitrogen is one of the essential nutrient for the growth of crops, and is a major component of chlorophyll and protein which are closely related to leaf color, crop growth status, and yield. Insufficient nitrogen supply causes lower chlorophyll content, less biomass production, and consequently, reduced grain yield and quality. 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 nitrogen application can lead to 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 compare the SPAD value in rice genetic resources according to the nitrogen application levels and evaluate the differences among them. Total of 160 rice genetic resources, 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 conditions: low-N (4.5 kg/10a) and normal-N (9 kg/10a). SPAD value of each lines was estimated by measuring the middle parts of the flag leaves using a SPAD-502 plus (Konica Minolta, Japan) at 10 days after heading (DAH). SPAD value of 160 rice genetic resources showed a range of 30.5~55.7 under normal-N condition and 27.5~52.6 under low-N condition. The average SPAD value of normal-N condition was 7% higher than that of low-N condition. The SPAD value was higher in the order of japonica, Tongil type, and indica under both conditions low-N and normal-N. The rate of SPAD value decrease in low-N condition compared to normal-N condition was highest in japonica at 9%, followed by indica at 7%, and Tongil type at 4%.

***Corresponding Author:** Tel. 054-530-1206, E-mail: s_kim@knu.ac.kr

PB-0087

A New Black Wheat Cultivar ‘Shintong’ with Adjective Whole Grain Cookie Quality

Kyeong-Hoon Kim*, Kyeong-Min Kim, Chon-Sik Kang, Chang-Hyun Choi, Go Eun Lee,
Myoung Hui Lee, Jinhee Park, Jiyoung Shon, Ki-Chang Jang

Wheat Research Team, National Institute of crop Science, RDA, Wanju, 55365, Republic of Korea

‘Shintong’, a black wheat(*Triticum* aestivum L.) cultivar was developed by the National Institute of Crop Science, RDA. It was derived from the cross ‘black wheat(IT229974)/wild wheat(K253305)’ and ‘Olgeuru’ in 2010 at RDA. ‘Shintong’ was evaluated as “Jeonju410” in Advanced Yield Trial Test in 2019. It was tested in the regional yield trial test between 2020 and 2022. ‘Shintong’ showed black grain color, facultative type with growth habit of Ⅰ. The Heading date of Shintong was similar to Keumkang at upland. And Shintong were 2 days later than those of Keumkang at paddy field. The grain yield of Shintong in the regional adaptation yield trials was 5.19MT/ha in upland and 4.79MT/ha in paddy field, which corresponded 110% and 117% to those of Keumkang, respecvively, The cultivar had 68cm of culm length, 677 spikes per m^2, test weight 788g/ℓ and 1,000-grain weight 45.9g. At result quality of flour, Shintong milling rate(61.7%), protein content(9.3%), SDS-sedimentation volume(11.5ml) were lower than those of Keumkang and Ariheuk. On the other hand, at result qualty of whole grain flour, Shintong fiber(10.1%), K(424.2mg/100g), Cu(0.59mg/100g), Fe(6.09mg/100g) content were higher than those of Keumkang and Ariheuk. A Mixing score of Shintong whole grain flour showed Absorption 7.0, Gluten7.0, Viscosity 7.0, Amylase 1.0 and Retrogradation 8.0. Whole grain cookie making adaptabilities of Shintong was also comparable to those of Keumkang.

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***Corresponding Author:** Tel. 063-238-5457, E-mail: k2h0331@korea.kr

PB-0088

메밀 내도복 및 다수성 신품종 ‘햇살미소’

김수정[1*], 이종남[1], 남정환[1], 김도연[1], 박수형[1], 이성문[2], 오민아[2], 손황배[3], 김율호[4]

[1]강원도 평창군 대관령면 경강로 5481 국립식량과학원 고령지농업연구소
[2]제주도 제주시 애월읍 월각로 563-20 제주도농업기술원 농산물원종장
[3]전라북도 전주시 덕진구 농생명로 300 농촌진흥청 기술협력국 수출지원과
[4]경기도 수원시 권선구 수인로 125 국립식량과학원 재배환경과

‘햇살미소(Haetsal-Miso)’는 대립 내재해 다수성 메밀 신품종 육성을 목표로, 다수성 ‘양절메밀2호(장주화)’을 모본으로 내재해 ‘양절메밀(단주화)’을 부본으로 하여 교배한 후 선발계통 ‘CB16003-12(장주화)’를 다시 모본으로 하고, 대립 호명재래(IT318103, 장주화)를 부본으로 하여 2017년도에 인공교배한 CB17004 조합으로 삼원교배하여 계통육성법으로 선발하였으며 계통명은 ‘대관 3-10호’이다. 꽃색은 흰색이고 잎모양은 심장형이며, 종자모양은 삼각형이고 종실 과피색은 빗살무늬를 띈 흑갈색이며 1000립중은 32.5 g으로 ‘양절메밀’에 비하여 2.1 g 정도 무거운 대립이다. ‘양절메밀’보다 성숙기가 약간 늦어 성숙기간이 5일이 길다. 병해충에 강하며, 내도복성은 ‘양절메밀’보다 약간 우수하다. 종실의 루틴 함량은 ‘양절메밀’보다 2.5배 많은 57.5 mg/100 g이며, 새싹의 루틴 함량은 492.0 mg/100 g으로 ‘양절메밀’보다 1.7 배 많다. ‘양절메밀’ 대비 수량성은 생산력검정 및 지역적응시험에서는 25 % 증수하였으며, 전국 3개소 2작형의 3년 평균 종실수량 은 10a당 127kg이다.

사사: 본 연구는 농촌진흥청 작물시험연구(연구과제명: 고품질 다용도 메밀 품종 개발(2단계 종실용 메밀 품종 육성), 과제번호: PJ016068012023)의 지원으로 수행되었음

***교신저자:** Tel. 033-330-1840, E-mail: sjkim30@korea.kr

PB-0089

속이 노란 유색감자 신품종 '자황'

최옥*, 조윤상, 송윤호, 박아름, 원헌섭, 박기진

강원도 강릉시 사천면 중앙서로 216 강원도농업기술원 감자연구소

최근 건강에 대한 관심이 높아지면서 기능성 식품 수요가 증가하였다. 감자는 탄수화물의 주요 공급원으로 고품질의 단백질과 비타민C 함량이 높다. 또한 유색감자에 함유된 카로티노이드나 안토시아닌 등 기능성 성분은 소비자의 기호도를 증가시켜 다양한 기능 및 용도의 품종개발을 요구하였다. 따라서 강원도농업기술원 감자연구소에서는 속이 노란'자황'을 육성하였다. 신품종 '자황'은 일본에서 육성한 Red Moon 품종과 국내 고령지농업연구소에서 선발한 대관 92호를 부본으로 하여 2009년 인공교배를 실시하고 진정종자 340립을 획득하였다. 2010~2012년에 실생1~3세대를 거쳤고 2013~2014년 강릉, 평창에서 생산력검정시험을 실시하여 수량성 및 괴경형질이 안정적이어서 'GWP10-018'호로 최종 선발하였고, 2016년부터 2018년까지 '강원2-10호'로 계통명을 부여하여 강릉, 춘천, 평창 등 3개 지역에서 지역 적응성 및 특성검정을 실시하였다. 기존의 수미품종과 대등하면서 모양, 눈깊이 등의 괴경형질과 표피색・육색, 수량성이 우수하여 2018년 강원도 신품종 선정위원회를 거쳐 '자황'으로 명명하였다. 2019년에 출원하여 2022년도에 품종보호(제9058호)되었다. 자황은 재배기간이 수미보다 5일 정도 늦은 중생종이며 줄기는 반개장형으로 초형이 양호하며 보라색이 꽃이 핀다. 지상부 생육은 출현율 99%, 경장 36.7㎝, 경수 3.1개로 수미와 비슷하며 생리장해 발생은 수미에 비해 다소 적었으며 PLRV바이러스는 발생하지 않았으며, PVY의 저항정도는 수미와 비슷하다. 괴경은 장타원형으로 표피는 자색이고 육색은 황색으로 겉과 속이 다르며 150~250g의 괴경이 4~5개가 착생한다. 휴면기간은 70일 내외로 중휴면을 띠며 점질형 감자로 저장시에 식미(당분)가 증가한다. 자황은 겉은 자색이고 속이 노란 유색감자로 다양한 용도로 활용이 가능한 품종이다.

***교신저자:** Tel. 033-610-8753, E-mail: chldhr78@korea.kr

PB-0090

Comparing growth of drought resistant rice varieties between two different cultivation method for breeding new cultivars which adapt to dry direct seeding

Yoonsung Lee*, Jeomho Lee, Eokkeun Ahn, Woongjo Hyun, Sangbeom Lee

Department of Central Area Crop Science, National Institute of Crop Science, RDA, Suweon 16429, Republic of Korea

Due to the global warming which is caused by greenhouse gases such as carbon dioxide and methane, the global climate is undergoing rapid changes. According to the International Panel on Climate Change (IPCC), the average global temperature has increased by 0.74°C over the past 100 years, and the temperature increase over the past 20 years is more than twice as fast as the temperature increase over the previous century. South Korea has experienced an average temperature increase of 1.5°C over a similar period. As a result of the temperature rise, changes in winter precipitation patterns have led to worsening drought conditions from late winter to spring. Dry direct seeding is one of the methods used in cultivating rice, which is advantageous during spring droughts as it involves sowing seeds in dry paddy fields. Additionally, it produces lower methane gas emissions compared to transplanting rice seedlings. ‘Nongnimna 1’ and ‘Sangnambatbyeo’ are cultivars developed for upland rice and have strong drought resistance. Comparing the growth of each cultivar cultivated with rice transplantation and dry direct seeding, the clum length and number of panicles of ‘Nongnimna 1’ were increased, but the length of panicles was decreased when cultivated by dry direct seeding. In contrast, only the length of panicles of ‘Sangnambatbyeo’ decreased, and the clum length and number of panicles were not statistically different from transplanting. There was no significant difference in the yield of white rice between each two cultivars between transplantation and dry direct seeding. The genotypes related to drought tolerance, such as OsDWA1 and OsPP2C, were the same in both cultivars. Based on the genotypes of these two varieties, it can be used as basic data for cultivating varieties that adapt to dry direct seeding.

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***Corresponding Author:** Tel. 031-695-4026, E-mail: leeys6056@korea.kr

PB-0091

Comparative analysis of maize seeds composition according to genotype and environmental factor

Muhammad Imran[1], Soo-Yun Park[2], Hyoun-Min Park[1], Eun-Ha Kim[1], Seon-Woo Oh[2], Sang-Gu Lee[1*]

[1]Biosafety Division, National Institute of Agriculture Science. Rural Development Administration, Jeonju 54874, Republic of Korea

[2]Technology Cooperation Bureau, Rural Development Administration, Jeonju 54874, Republic of Korea

Maize is one of the most important crop with the longest industrial chain and holds a great strategic significance for the around the world. However, the impact of weather and climate variability, genotype, cultivation site, and management strategy can affect the composition of maize seeds. For this reason, in the current study an 8 conventional varieties of maize (DO3, GDO, IMC, MB2, HJC, JDO, GPO and KIO) were grown over two years (2021 and 2022) in three different locations Daegu, Hongcheon, and Suwon of Korea, to assess the natural variation in seed composition for safety evaluation. These 8 conventional varieties were evaluated for their proximate, fatty acid, amino acids and mineral content. The results indicate a sizable variation in these component content among the various varieties, which was more pronounced at the cultivation year and site. Since DO3, GDO, HJC, and IMC are the dominant varieties, shows higher productivity of minerals, fatty acids and amino acids component when compare by verities along with cultivation sites and year of cultivation. The univariate analysis of the combined data revealed a moderated difference in proximate, amino acids and fatty acids by MB2, JDO, GPO and KIO variety, with a significant difference by cultivation year and site. The cultivation year and location have a substantial impact on the mineral, amino acid and fatty acids components. Analysis of percent variability showed that the compositions of maize seeds were influenced by genotype, environment, and the interplay between genotype and environment. As by principal component analysis (PCA) reveals, that location and cultivation year were responsible for a large amount of variation in compositions. In conclusion, the genotype, environment, and the interaction between genotype and environment can significantly influence the compositional diversity of maize seeds. Thereby, these variations can be further assessed to the plant breeding for developing more nutrient rich and environmental resistance maize genotype.

***Corresponding Author:** Tel. 063-238-4720. Email: sangulee@korea.kr

PB-0092

Evaluation of yield, agronomic and seed characteristics of rice under fence based agro-photovoltaic system in South Korea

Hyun Jo, Junbeom Park, Thi Cuc Nguyen, Hai Anh Tran, Jong Tae Song, Jeong-Dong Lee*

Department of Applied Biosciences, Kyungpook National University, Daegu 41566, Republic of Korea

The Ministry of Trade, Industry, and Energy of the Korean government announced that it will increase the proportion of renewable energy up to 20% by 2030 based on the renewable energy expansion policies such as the Renewable Energy 3020 Implementation Plan and the 2050 Carbon Neutral Strategy. The agro-photovoltaic (APV) system is a new alternative to conventional photovoltaic power plants that can simultaneously generate renewable energy and agricultural productivity by installing solar panels on the same farmland. Recently, bifacial photovoltaic systems as fence type solar panels have attracted growing interest globally than monofacial solar panels. This study was aimed to evaluate the agronomic performances, protein and yields of rice (*Oryza sativa* L.) between fence based APV system and the open field in South Korea. In this study, fence based bifacial solar panels were installed in a rectangular area of rice paddy field to understand the growth and production of rice in 2022. Based on the sunrise and sunset during rice growing season, the length of shade from different directions of solar panels were different. The agronomic measurements, protein and yield were obtained from twenty-seven plots in fence based APV system. The number of spikelets per hill, percentage of ripened grains, plant height, yield and seed protein content showed significance among plots based on analysis of variance. As the result was from a one-year, rice yield trial and phenotypic evaluation will still be required for multiple years under the fence based APV system.

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

PB-0093

A Multi-Omics Approach for the Search for Drought Stress Resistance Genes in Wild Soybean (*Glycine soja*)

Tae Kyeom Kim, Jae Yoon Kim*

Department of Plant Resources, Kongju National University, Yesan, Chungnam, Republic of Korea

Soybean (*Glycine max*) has been improved through a very long breeding history. Because cultivated soybean has very narrow genetic variation, it is restricted to discovering novel abiotic stress resistance genes in cultivated soybeans rather than in wild soybeans. Wild species with high genetic variations can be useful resources for exploring new resistance traits. In this study, a multi-omics-based analysis was performed on wild soybean *Glycine soja*, which has a high genetic variation and is resistant to various stresses. Transcriptome and proteome analysis were performed on wild soybean by treating drought stress to the V_3 growth stage. Various genes were identified by comparative analysis of differentially expressed genes (DEG), alternative splicing (AS), and differentially expressed proteins (DEP). Gene ontology analysis of co-profiled genes and proteins suggested that genes and proteins involved in stomatal regulation, antioxidant response, and ion binding response were modulated. When transcriptome and proteome analysis results were compared, it was confirmed that the sulfur metabolism pathway, calcium-sensing receptor (CAS), and trigger factor genes and proteins were commonly down-regulated during drought treatment. In particular, CAS is a thylakoid membrane protein known to regulate stomatal closure to adapt to drought stress. Changes in the regulation of sulfur metabolism and trigger factors are also highly related to drought stress adaptation. Genes discovered through a multi-omics approach will provide even more complementary and decisive information for understanding drought response mechanisms in wild soybean.

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

PB-0094

Development and agronomic characteristics of foxtail millet Chungbuk no. 18

Hyerim Moon[1*], Jaesun Lee[1], Injae Kim[1], Minja Kim[1], Sangik Han[2]

[1]Department of Crop Research at Chungcheongbuk-do Agricultural Research and Extension Services, 46, Gagok-gil, Ochang-eup, Cheongwon-gu, Cheongju-si, Chungcheongbuk
[2]Field Crop Development Division, Southern Crop Division, National Institute of Food Science

Abstract: Foxtail millet, proso millet, and sorghum, which belong to the representative multigrain world, are annual flowering plants that have a long history of cultivation as important grains in China, Korea, and Manchuria. They have been used as alternative crops or citrus crops since ancient times due to their tolerance in poor environments. The cultivation area of grains in Chungbuk is 3,658ha, accounting for 13% of the 27,851ha nationwide (Statistics Office, 2022), and the main cultivation areas in the province are Danyang and Jecheon. Examples of mainly produced varieties are “Hwanggeum Joe” and “Samdachal”, but raw varieties are required to increase quantity and reduce labor. The Chungbuk Agricultural Research and Extension Services developed the varieties of “Cheongpung Me” (2018) and “Geumbit Me” (2021), and fostered Chungbuk No. 18 which has faster harvest maturity and multiple characteristics than existing varieties.

Method and materials: Chungbuk No. 18 collected native seeds from Jecheon, Chungbuk in 2011, pure segregation from '2013~'14, reviewed growth characteristics from '15~'17, conducted regional adaptability tests in Pyeongtaek, Cheongju, and Daegu from `18~`21. Its major survey items were intrinsic resistance, insect resistance, breed characteristics, functional substances, and yield characteristics.

Conclusion: Chungbuk No. 18 has a cylindrical shape and a yellow seedling color. The average number of days of export is 58 days, which is about 11 days faster than Samdame, it is showing the characteristics of early cultivated produce and it is believed to be advantageous in double cropping. It is 142cm tall, 3cm shorter than the contrast variety, and has an upright herb which is excellent for mechanized cultivation aptitude. As for the yield-related characteristics, the length of the ears was 23.8cm, 14.5g of the seed weight per hill, and 2.9g of the thousand seed weight, which was superior to Samdame. Among the intrinsic and insect-resistant properties, there were some lodging, and it was found to be a little weak against insects such as stinkbug, however, it was resistant to foliage aging, wetness, and water germination. The results of the national regional adaptation test between ′18 and ′21 shows the average yield is 328kg/10a, an increase of 6% compared to Samdame. In the general component characteristic test, Chungbuk No. 18 contained somewhat more crude protein, potassium, and magnesium than Samdame, and the DPPH and ABTS radical elimination activity of antioxidant activity were somewhat lower. As a result, Chungbuk No. 18 is expected to grow quickly and mechanically, enabling mass cultivation of raw materials for processing.

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***Corresponding Author:** Tel. 043-220-5562, E-mail: mosg60@korea.kr

PB-0095

Analysis of agricultural characteristics of risotto rice varieties in Korean environment

Songhee Park, Jeonghwan Seo, Jae-Ryoung Park, Kyeong Min Kang, Mira Yoon, Mina Jin, O-Young Jeong, Hyun-Su Park*

Crop Breeding Division, National Institute of Crop Science, Rural Development Administration, Wanju, 55365, Republic of Korea

Risotto is an Italian rice dish cooked with broth until it reaches a creamy consistency. It is one of the most common ways of cooking rice in Italy. The famous rice varieties for risotto are 'Carnoroli', 'Arborio', and 'Vialone Nano'. This study was conducted to provide essential data for breeding risotto rice varieties suitable for Korea by analyzing the agricultural traits of three risotto varieties and 'Cheolweon96' (Carnaroli SA-mutant line) under the environmental conditions of Korea. The risotto varieties and line showed early maturing like 'IS592BB'. They had longer culm length, lower number of panicles per hill and spikelets per panicle compare to Korean rice varieties, 'Sindongjin' and 'IS592BB'. They showed lower ratio of ripened grain, brown/rough rice ratio, and yield. The risotto rice varieties and line except for 'Vialone Nano' represented longer, wider, and heavier grain characteristics. The risotto rice varieties and line showed high level of chalky rice. Chalky rice is known to absorb more water rapidly during cooking. Absorption of broth is important in risotto cooking. Therefore, chalkiness could be considered important characteristics for risotto rice varieties. In the analysis of pasting properties, 'Carnaroli', 'Cheolweon96', and 'Vialone Nano' showed similar characteristics, while 'Arborio' was classified into the same group as 'IS592BB'. The cooked rice of 'Carnaroli', 'Cheolweon96', and 'Vialone Nano' exhibited hard and not sticky texture, while its of 'Arborio' was softer and stickier than Korean rice varieties. The risotto rice varieties mainly showed larger grain size, higher chalkiness, pasting temperature, and setback, and harder texture compared to Korean rice varieties. These characteristics are expected to be useful selection indicators for breeding Korean risotto rice varieties.

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

PB-0096

New high amylose aroma rice with super yield, “Amimyeon”

Ji-Yoon Lee[1*], Jun-Hyeon Cho[2], Ju-Won Kang[1], Dong-Soo Park[1], Jong-Hee Lee[1], Young-Ho Kwon[1], So-Myeong Lee[1], Dong-Jin Shin[1], Ki-Won Oh[1]

[1]20, Jeompiljae-ro, Miryang-si, Gyeongsangnam-do, Republic of Korea
[2]22161, Junghwa-ro, Hwaseo-myeon, Sangju-si, Gyeongsangbuk-do, Republic of Korea

In order to develop super yield high amylose flavor rice, F_1 (YR31808) was cultivated in 2016 after crossing Miryang288 and Bukkyeong 2012-2 in 2015. In 2017, the F_2 population was deployed, and 95 plant selected were cultivated as F_3 generation in the first winter of 2017/2018. Since then, the second generation has been further advanced in accordance with the pedigree method in the winter greenhouse, and it was named Miryang355 in 2019 after two years of productivity testing from 2018 to 2019. As a result of the three-year local adaptatibility trial from 2020 to 2022, it was developed as a variety as “Amimyeon” in 2022 due to its high amylose content and aroma, high quantity, and excellent resistance to blast and rice strip virus disease. “Amimyeon” is a middle late flowering variety with heading date of Aug. 13 in four regions(Jungbu, Honam, and Yeongnam) The culm length, panicle length, and number of grains per panicle are 81cm, 23cm, and 122, respectively. The ripened grain ratio, 1000 grain weight, and rice yield are 85.2%, 21.5g, and 724kg/10a, respectively.

Amimyeon is a medium- and long-term species with a brown rice long-width ratio of 2.77, and fragrant high amylos (26.7%) varieties which is very suitable for making rice noodles. Rice noodles made of amimyeon have stronger increasing power than existing products, and rice pasta has chewy properties due to its good elasticity and cohesivenes.

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

PB-0097

Identification of *flo4-6*: A New *cyOsPPDKB* Associated with Floury Endosperm Allele Properties Optimal for Dry-Milled Rice Flour Production

Su-Kyung Ha[1], Hyun-Sook Lee[1], Chang-Min Lee[1], Gileung Lee[1], Seung Young lee[1,2], Youngjun Mo[2*], Ji-Ung Jeung[1*]

[1]National Institute of Crop Science, RDA, Wanju 55365, Republic of Korea
[2]Department of Agronomy, Jeonbuk National University, Jeonju 54896, Republic of Korea

Floury endosperm rice cultivars serve as valuable resources for the production of dry-milled rice flour, contributing to the advancement of the processed rice food industry. In rice, the *flo* gene plays a crucial role in determining the endosperm texture, particularly the starch characteristics. NICS previously developed a rice cultivar called Baromi2, which carries the flo4-4 allele. It stands as an early maturing rice cultivar suitable for dry-milled flour production, specifically tailored to the double cropping system in Korea. However, there is also a need for mid-late maturing rice cultivars with floury endosperm to enhance yield and broaden adaptability. To broaden the genetic pool for developing rice varieties with floury endosperm, the National Institute of Crop Science (NICS) created SK-flo3, a mutant line with floury endosperm, through chemical mutagenesis of Samkwang, a highly esteemed Korean japonica rice cultivar. The resulting dry-milled flour from SK-flo3 exhibited superior physicochemical properties, including reduced starch damage and finer particle size, compared to Samkwang. Genetic analysis identified a specific point mutation (G-to-A) in exon 7 of the *cyOsPPDKB* gene, resulting in the substitution of glycine with aspartic acid, which was identified as the cause of the floury endosperm in SK-flo3. We named this allele flo4-6 and developed a molecular marker to efficiently introduce it into commercially relevant rice cultivars. These findings present valuable genetic resources and insights for developing specialty rice varieties that can produce high-quality rice flour while reducing milling expenses.

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***Corresponding Author:** Tel. 063-270-2530, E-mail: yjmo@jbnu.ac.kr
Tel. 063-238-5231, E-mail: jrnj@korea.kr

PB-0098

CRISPR HDR knock-in efficiency of Golden SNP-allelic *OsLcyE* gene in rice

Jong Hee Kim[1], Jin Young Kim[1], Jun Young Shon[1], Min Ju Park[1], Kwon Kyoo Kang[1,2], Yu Jin Jung[1,2*]

[1]Division of Horticultural Biotechnology, School of Biotechnology, Hankyong National University, Anseong 17579, Korea
[2]Institute of Genetic Engineering, Hankyong National University, Anseong 17579, Korea

Lycopene epsilon-cyclase (LcyE) is a key enzyme in the carotenoid biosynthetic pathway of higher plants. Using the CRSPR/Cas9 and the geminiviral replicon, we optimized a method for targeted mutagenesis and golden SNP replacement of the LcyE gene in rice. We have exploited the geminiviral replicon amplification as a means to provide a large amount of donor template for the repair of a CRISPR-Cas-induced DNA double-strand break (DSB) in the target gene via homology directed repair (HDR). Mutagenesis experiments performed on the Donggin variety achieved precise modification of the LcyE loci with an efficiency of up to 90%. In HDR experiments, our target was the LcyE allele (LcyE-H523L) derived from anther culture containing a golden SNP replacement. The phenotype of the homologous recombination (HR) mutant obtained through the geminiviral replicon based template delivery system was tangerine color, and the frequency was 1.32% of the transformed calli. In addition, the total carotenoid content of the LcyEsg2-HDR1 and LcyEsg2-HDR2 lines was 6.8-9.6 times higher than that of the wild-type (WT) calli, respectively. The reactive oxygen species content was lower in the LcyEsg2-HDR1 and LcyEsg2-HDR2 lines. These results indicate that efficient HDR can be achieved in the golden SNP replacement using a single and modular configuration applicable to different rice targets and other crops. This work demonstrates the potential to replace all genes with elite alleles within one generation and greatly expands our ability to improve agriculturally important traits.

***Corresponding Author:** E-mail: zino@hku.ac.kr

PC-0001

Evaluation of homozygosity levels of onion (*Allium cepa* L.) inbred lines using molecular markers evenly distributed in a high-resolution linkage map

Geonjoon Kim[1], Jin Seong Moon[2], Bongju Kim[3], Sunggil Kim[1*]

[1]Department of Horticulture, Biotechnology Research Institute, Chonnam National University, Gwangju 61186, Republic of Korea
[2]Onion Research Institute, Gyeongsangnam-do Agricultural Research & Extension Services, Changnyeong-gun 50319, Republic of Korea
[3]Onist Co. Ltd., Gochang-gun 56463, Republic of Korea

Onion (*Allium cepa* L.) is a cross-pollinated crop with severe inbreeding depression. Inbred breeding lines are thus commonly maintained through sib-mating or a combination of sib-mating and self-pollination. Therefore, the homozygosity levels of onion inbred lines are generally low compared with self-pollinated crops. To evaluate the homozygosity levels of inbred lines, 43 high-resolution melting (HRM) markers that were evenly distributed throughout eight onion linkage groups were selected among 652 markers consisting of a high-resolution linkage map. Eight individual plants from 119 inbred lines collected from five onion-breeding institutes were analyzed using the 43 HRM markers, resulting in an average homozygosity level of 0.55. This indicates that almost half of the 43 markers were still segregating in those inbred lines. The homozygosity levels of inbred lines varied between the onion-breeding institutes but they were generally higher than those of the Plant Introduction (PI) accessions. Additionally, the average proportion of genotypes fixed as either homozygous or heterozygous was 0.46 in 12 F_1 cultivars, indicating that their parental lines had low homozygosity levels. Phylogenetic analyses based on the pairwise genetic distances of all entries did not show clear clustering of related entries. This lack of clear clustering patterns was attributed to the relatively large within-population variations and low genetic diversity of the analyzed entries. The observed heterozygosity of the 43 markers was generally higher than the expected heterozygosity. Moreover, one marker exhibited a marked increase in observed heterozygosity, suggesting the possible involvement of this genomic region in inbreeding depression.

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

PC-0002

3배체 포도 유전자원의 생육 및 과실특성 평가

김주현*, 장은하, 정햇님, 이제창, 이기옥, 원재희, 박영식

강원도농업기술원 원예연구과

국내 재배되는 포도품종은 유럽종(*Vitis vinifera*), 미국종(*Vitis labrusca*)과 교잡종이 대부분 재배되고 있다. 강원도에서도 고품질의 포도 재배를 위해 다양한 품종을 도입하였지만 대부분의 도입 품종은 강원도의 저온을 견디며 고당도・대립성 포도를 지속적으로 재배하기에는 많은 어려움이 있었다. 이중 가장 문제가 되는 것은 강원도에서는 생육 기간이 짧으며, 만생종 포도를 재배할 때는 남부지역 보다 생육기간이 짧아 수확 이후 충분한 영양분 축적이 되지 않았다. 따라서 강원도의 낮은 온도를 견딜 수 있는 내한성이 강한 품종의 보급이 필요하였다. 이러한 문제점들을 개선하고자 강원도농업기술원에서는 2002년도부터 거봉(Kyoho)과 세레단(Seredan), 캠벨얼리(Campbell early)를 교배하여 내한성이 강한 고품질 포도를 육성하였으며, 지속적인 생육 및 과실특성 검정을 통해 계통을 선발하여 우수한 7개의 품종을 등록하였으며, 지속적으로 육성하고 있다. 본 연구에서는 품종은 자체 육성된 '스위트드림' 등 7품종과, 계통 GWT-35 등 6계통을 증식 및 주요 형질특성 평가를 수행하고 지역 적응성이 우수한 신품종 선발 및 이용 촉진의 기초자료로 활용하고자 한다. 자체육성 7품종('스위트드림', '블랙스타', '흑아롱', '흑다솜', '레드드림', '자이언트드림', '로망스')과 계통 6종(GWT-35, GWT-76, GWT-142. GWT-144, GWT-134, GWT-170), 캠벨얼리, 샤인머스캣을 춘천 과수시험포장에서 동일한 환경 조건에서 재배하여 각 품종별로 원예적 형질특성을 조사하였다. 다음 중 가장 빠른 수확기를 보인 품종과 계통은 각각 '블랙스타'와 GWT-76으로 수확기는 8월 24일로 동일하였고, 수확기가 9월 10일인 '캠벨얼리'보다 약 17일경 빨랐다. 과방중은 300g~800g까지 다양한 분포를 보였으며, '블랙스타'가 가장 작은 327.6g이 나타났으며, '자이언트드림'에서 795.4g으로 가장 큰과방이 나타났다. 10개의 과립중 또한 '자이언트드림'에서 132.5g으로 가장 큰 것으로 나타났다. 종자의 수는 자체 육성 품종과 계통에서는 0개, 캠벨얼리와 샤인머스캣에서 각각 송이당 27개, 1.2개를 보였다. 강원도에서 육성된 품종과 계통은 3배체 포도이기 때문에 종자의 출현은 0으로 나타낸 것으로 보인다. 당・산도는 14~20brix의 분포를 보이고 있으며, '캠벨얼리'에서 가장 낮은 14.8brix가 나타났고, '블랙스타'에서 19.8brix, GWT-144에서 19.7brix로 높은 당도를 보였다. 위에서 조사된 품종과 계통은 2002년 교배를 시작으로 2차 선발을 통하여 내한성과 과실의 품질의 우수성이 확인되어 품종등록과 증식된 계통들이다. 위의 특성조사를 보면 강원도 시험연구장에서 재배한 '캠벨얼리'와 '샤인머스캣'에 비해 품질이 떨어지지 낮지 않은 것을 볼 수 있다. 따라서 강원도농업기술원에서 육성된 포도를 연간 온도 편차가 심한 강원지역과 고지대에서 재배한다면 고품질의 우수한 포도를 생산할 수 있을 것이다.

***교신저자:** Tel. 033-248-6074, E-mail: juhyeon93@korea.kr

PC-0003

탄수화물원과 유전자형에 따른 만다린 감귤류 체세포 배 형성 효과 및 재생 능력 세포 구축

최철우*, 박석만, 진성범

농촌진흥청 국립원예특작과학원 감귤연구소

감귤류들의 체세포 배 발생은 탄수화물원과 유전자형에 따라서 영향을 받는다고 알려져 있다. 또한, 장기간에 걸친 계대배양을 통한 배 형성능 및 재분화능을 상실한 세포의 재생 능력 회복과 관련된 연구가 필요하다. 따라서, 본 연구는 만다린 품종들의 조직배양 효율을 증진시킬 목적으로 만다린 품종 4종의 세포에 대하여 탄수화물원 4종류(sorbitol, manitol, galactose, lactose)의 농도 처리와 배양 기간(2, 4, 8주)에 따른 세포 증식과 체세포 배 유도율을 조사하였으며, percol 농도구배에 따른 감귤류들의 재생 능력 회복을 조사하였다. 그 결과 세포의 증식율은 탄수화물 원으로써 sucrose를 첨가한 MS1배지(대조구)에서 감귤류들의 세포 증식율이 높았으며 품종들 간 탄수화물의 영향은 큰 차이를 보이지 않았다. 체세포 배 형성은 대체적으로 온주밀감 품종 중 '궁천조생'이 탄수화물원 maltose100mM과 lactose 146mM에서 가장 좋았고, '태전병감'은 galactose 100mM과 lactose 146mM 혼용 처리 했을 때 배가 형성된 것을 관찰할 수 있었지만 배 형성율은 매우 저조하였다. Percol 농도40%층 에서 선발된 세포들은 '남감20호'을 제외한 나머지 품종들에서 체세포 배 형성율은 높게 향상되었고, 식물체 재분화는 '태전병감'을 제외한 온주밀감 '궁천조생'과 '하례조생' 품종은 정상적인 식물체를 획득할 수 있었다. 감귤류의 배 형성 및 식물체 재분화 효율 차이는 품종 간 유전적 차이로 발생하는 것으로 추정할 수 있었으며, 체세포 배 발생 효율이 떨어지는 모든 감귤 세포들은 percol 농도구배에 따른 세포 선발 방법을 적용하는게 바람직하다고 사료된다.

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***교신저자:** Tel. 064-730-4142, E-mail: cwchoi7@korea.kr

PC-0004

A New Ornamental Crab Apple Cultivar ‘Hanabell’

Young Soon Kwon*, Jeong-Hee Kim, Jong Taek Park

Apple Research Institute, NIHHS, RDA, Gunwi 39000, Korea

Crab apples are consistently demand for landscaping, such as street tree, golf courses, and park, because their flower are beautiful and have high ornamental value. However, they have no or limited variety available and are sold collectively as ‘crab apple’ regardless of varieties. The new ornamental crab apple variety ‘Hanabell’ developed by the Apple Research Institute, NIHHS, RDA in 2020 originated from open pollination of *Malus baccata* collected at Palgong mountain, Gunwi-gun, Gyeongsangbuk-do. Line selections were conducted from 2009 to 2020, and characteristic evaluation were experimented from 2018 to 2020. Tree vigor and tree form of ‘Hanabell’ were medium and spreading. The first flowering time is early, around April 17, and the flowering period is as long as 16 days. The flowers of ‘Hanabell’ are pink in the balloon stage and white in full bloom. Its flower have a good flavor and high ornamental value. As a result of analyzing volatile flavor components of flowers, it was confirmed that a large amount of benzyl acetate, a substance that attracts bees, is contained. ‘Hanabell’ is resistant to major apple pests and its canopy does not grow large significantly. Therefore, The new variety ‘Hanabell’ will be promising variety as ornamental tree. ‘Hanabell’ was officially applied for variety protction on Korea Seed & Variety Service in 2021(Application no.2021-144).

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***Corresponding Author:** Tel. 054-380-3132, E-mail: peat1004@korea.kr

PC-0005

Jasmonate regulates plant resistance to *Pectobacterium brasiliense* by inducing indole glucosinolate biosynthesis

So Young Yi[1,5], Myungjin Lee[1], Sun Kyu Park[2], Lu Lu[2], Gisuk Lee[3], Sang-Gyu Kim[3], Si-Yong Kang[4,5*], Yong Pyo Lim[2]

[1]Institute of Agricultural Science, Chungnam National University, Daejeon 34134, Republic of Korea
[2]Molecular Genetics and Genomics Laboratory, Department of Horticulture, Chungnam National University, Daejeon 34134, Republic of Korea
[3]Department of Biological Sciences, Korea Advanced Institute for Science and Technology, Daejeon 34141, Republic of Korea
[4]Department of Horticulture, College of Industrial Sciences, Kongju National University, Yesan 32439, Republic of Korea
[5]Research Center of Crop Breeding for Omics and Artificial Intelligence, Kongju National University, Yesan 32439, Republic of Korea

Pectobacterium brasiliense (*P. brasiliense*) is a necrotrophic bacterium that causes the soft rot disease in *Brassica rapa.* However, the mechanisms underlying plant immune responses against necrotrophic bacterial pathogens with a broad host range are still not well understood. Using flg22-triggered seedling growth inhibition (SGI) assay with 455 *B. rapa* inbred lines, we selected six *B. rapa* flagellin-insensitive lines (*Br*fin2-7) and three *B. rapa* flagellin-sensitive lines (*Br*fs1-3). *Br*fin lines showed compromised flg22-induced immune responses (oxidative burst, MAPK activation, and seedling growth inhibition) compared to the control line; nevertheless, they were resistant to *P. brasiliense*. To explain this, we analyzed the phytohormone content and found that most *Br*fin lines had higher *P. brasiliense*-induced JA than *Br*fs lines. Moreover, MeJA pretreatment enhanced the resistance of *B. rapa* to *P. brasiliense.* To explain the correlation between the resistance of *Br*fin lines to *P. brasiliense* and activated JA signaling, we analyzed pathogen-induced glucosinolate content in *B. rapa*. Notably, in *Br*fin7, the neoglucobrassicin content among indole glucosinolates (IGS) was significantly higher than that in *Br*fs2 following *P. brasiliense* inoculation, and genes involved in IGSs biosynthesis were also highly expressed. Furthermore, almost all *Br*fin lines with high JA levels and resistance to *P. brasiliense* had higher *P. brasiliense*-induced neoglucobrassicin levels than *Br*fs lines. Thus, our results show that activated JA-mediated signaling attenuates flg22-triggered immunity but enhances resistance to *P. brasiliense* by inducing IGSs biosynthesis in *B. rapa.* This study provides novel insights into the role of JA-mediated defense against necrotrophic bacterial pathogens within a broad host range.

***Corresponding Author:** Tel. 041-330-1226, E-mail: sykang@kongju.ac.kr

PC-0006

A GBS-Based Genetic Linkage Map and quantitative trait loci (QTL) Associated with resistance to *Xanthomonas campestris* pv. *campestris* race 1 identified in *Brassica oleracea*

Lu Lu[1], Su Ryun Choi[1], Yong Pyo Lim[2], Si-Yong Kang[3,4*], So Young Yi[1,4]

[1]Institute of Agricultural Science, Chungnam National University, Daejeon 34134, Republic of Korea
[2]Molecular Genetics and Genomics Laboratory, Department of Horticulture, Chungnam National University, Daejeon 34134, Republic of Korea
[3]Department of Horticulture, College of Industrial Sciences, Kongju National University, Yesan 32439, Republic of Korea
[4]Research Center of Crop Breeding for Omics and Artificial Intelligence, Kongju National University, Yesan 32439, Republic of Korea

The production of *Brassica oleracea*, an important vegetable crop, is severely affected by black rot disease caused by the bacterial pathogen *Xanthomonas campestris* pv. *campestris.* Resistance to race 1, the most virulent and widespread race in *B. oleracea*, is under quantitative control; therefore, identifying the genes and genetic markers associated with resistance is crucial for developing resistant cultivars. QTL analysis of resistance in the F_2 population developed by crossing the resistant parent BR155 with the susceptible parent SC31 was performed. Sequence GBS approach was used to develop a genetic linkage map. The $F_{2:3}$ population (N = 126) was evaluated for resistance to black rot disease in summer (2020), fall (2020), and spring (2021). QTL analysis, using a genetic map and phenotyping data, identified seven QTLs with LOD values between 2.10 and 4.27. The major QTL, *qCaBR1*, was an area of overlap between the two QTLs identified in the 2nd and 3rd trials located at C06. Among the genes located in the major QTL interval, eight were found to respond to biotic stimuli. We compared the expression patterns of eight candidate genes in SC31 and BR155 lines using qRT-PCR and observed their early and transient increases or suppression in response to *Xcc* inoculation. These results support the involvement of the eight candidate genes in black rot resistance. The findings of this study will contribute towards marker-assisted selection, additionally the functional analysis of candidate genes may elucidate the molecular mechanisms underlying black rot resistance in *B. oleracea.*

***Corresponding Author:** Tel. 041-330-1226, E-mail: sykang@kongju.ac.kr

PC-0007

Application of Chlorophyll Fluorescence Imaging Analysis for the Selection of Rapidly Superior Germplasms of Peach(*Prunus persica*)

Haet-Nim Jeong[1*], Je-Chang Lee[1], Ju-Hyeon Kim[1], Ki-Ok Lee[1], Eun Ha Chang[1], Jae Hee Won[1], Kyeong-Ho Kim[2], Ki-Young Choi[2]

[1]Gangwon-do Agricultural Research & Extension Services, Chuncheon 24203, Republic of Korea
[2]Kangwon National University, Chuncheon, 24341, Republic of Korea

As extreme cold temperatures and high-temperature occurrences in winter increase due to climate change, damage during the dormant period of peaches is also on the rise. Developing a fast and accurate evaluation method and establishing a data-driven screening system for selecting cold-hardy varieties are crucial. However, current evaluation methods are time-consuming and obtaining reliable data is challenging. The objective of this study is to compare and analyze the cold-hardiness of major peach varieties at different dormancy stages using the non-destructive method of chlorophyll fluorescence imaging analysis, and to establish criteria for selecting superior genetic resources. Eight domestically bred varieties, including 'Sumi' since 2017, and four Japanese imported varieties, including 'Odoroki,' were planted in Chuncheon and Yanggu to compare winter damage levels in the same environment. Monthly collections of one-year-old branches (4-7mm thick) from October 2021 to March 2022 allowed the comparison and analysis of winter damage and chlorophyll fluorescence imaging data based on dormancy depth and cold stress levels. Correlation analysis between damage rates of flower buds and leaf buds and key indicators of chlorophyll fluorescence imaging data showed significant relationships for all parameters, including Fo, Fp, Ft_Lss, Qy_max, and Rfd_Lss. Fo had a coefficient of determination (R2) of 0.7978, and Qy_max had an R2 value of 0.9123, indicating high significance. Qy_max, representing maximum quantum yield, had the least measurement error and required a shorter measurement time, making it a useful indicator for rapidly evaluating cold-hardiness and winter stress in a large number of germplasms.

***Corresponding Author:** Tel. 033-248-6072, E-mail: jhn5362@korea.kr

PC-0008

The new kiwifruit cultivar ‘Nokong’

Mockhee Lee[1*], Seong-Cheol Kim[1], Chun Hwan Kim[1], Eun Young Song[1], Yeon Jin Jang[1], Hong-Lim Kim[2], Jae ho Joa[2], Ha-kyoung Lee[3], Yong-Bum Kwack[4]

[1]Research Institute of Climate Change and Agriculture, National Institute of Horticulture & Herbal Science, Jeju 63240, Korea

[2]Namhae Branch, National Institute of Horticulture & Herbal Science, Namhae 52430, Korea

[3]Horticultural and Herbal Crop Environment Division, National Institute of Horticulture & Herbal Science, Wanju 55365, Korea

[4]Department of Fruit, National Institute College of Agriculture and Fisheries, Jeonju 54874, Korea

One of the purchasing factors in kiwifruit is its health benefits. The high vitamin C content in kiwifruit has promoted its consumption. In accordance with this factor, ‘Nokong’ was bred using the germplasm of *Actinidia eriantha* from the Actinidiaceae known for its high vitamin C content. In 2006, ‘JCS17(*A.* Hybrid)’, an intermediate parent, was crossed with ‘Tomuri(*A. deliciosa*, IT233168)’, and the fruits, in autumn, were picked and stored. In 2007, 3,500 seeds were obtained. In April, they were sown in a greenhouse after then 770 seedlings were grown. Two hundred of them were transplanted in October 2010 into a seedling field. In 2013, ‘65-WN-2.14’ was selected for its green flesh, high soluble solids content, and pink petals. In order to investigate growth and development, it was transplanted to another field in 2014 and examined from 2018 to 2020. In 2020, it was finally selected and named ‘Nokong’. Its fruit is elliptical in shape and weighs 117.7g. Its petal color is reddish pink. The full bloom date is mid-May and the harvest date is late October in the southern region of Korea. The soluble solids content and titratable acidity after ripening is 16.0°Brix and 1.12%. The vitamin C content of fresh fruit is 250.0mg/100g, which is five times higher than that of ‘Hayward’, a reference cultivar. It needs artificial pollination for fruit set, thinning lateral flower buds because of dichasium, and prevention from fruit rot.

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***Corresponding Author:** Tel. 064-741-2552, E-mail: mockey92@korea.kr

PC-0009

Machine Learning Approaches to Predict Powdery Mildew Resistance in Watermelon (*Citrullus* spp.) Using Genome Wide SNPs

Oak-Jin Lee[1*], Koeun Han[1], Hye-Eun Lee[1], Hyo-Bong Jeong[1], Nari Yu[1], Woo-Moon Lee[1], Myunghee Jung[2], Yu-jin Lim[2], Younhee Shin[2]

[1]Vegetable Research Division, National Institute of Horticultural and Herbal Science, RDA, Wanju 55365, Republic of Korea
[2]Research and Development Center, Insilicogen Inc., Yongin 16954, Republic of Korea

Powdery mildew caused by *Podosphaera xanthii* is one of the common diseases on watermelon (*Citrullus* spp.) around the world. It hampers photosynthesis and causes leaf discoloration, subsequently result in stunned plant growth, diminished fruit quality and eventually yield loss. Previously, a study identified a gene for powdery mildew resistance, which is located on chromosome 2. Based on the results, several molecular markers were designed to genotype to confirm the SNPs (single nucleotide polymorphism) associated with the resistance locus. However, we discovered few germplasm showing different resistance between molecular and biological inoculation experiments in our preliminary studies. In order to increase the utilization of genetic information for breeding, we explored the associated genetic region and developed a predictive machine learning model with genome wide SNPs. In total, 112 SNPs in watermelon inbred lines were selected based on the powdery mildew resistance and genetic distance. We obtained more than 400Mbp reads per inbred line by GBS (genotyping by sequencing) using ApeKⅠ with Illumina NovaSeq6000. GWAS (genome wide association study) was conducted to identify SNPs significantly associated with resistance from the 27,673 high-quality SNPs. Afterwards, a prediction model was built by applying the final 38 SNPs selected from feature importance rankings. The constructed model can be used for classification of resistance against powdery mildew and has an accuracy of 0.85. This study can be extended to other horticultural traits of interest in the future and is expected to contribute to breeding.

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***Corresponding Author:** Tel. 063-238-6615, E-mail: ojlee6524@korea.kr

PC-0010

Characteristics in genetic resources of cucurbitaceae family for development of watermelon breeding material

Guem-Jae Chung[1*], Geon-Sig Yun[1], Eun-Hye Kim[1], Yu-Min Jeon[1], Kuy-hoi Lee[1], Cheol-Ku Youn[1], In-Jae Kim[2], Ho-Cheol Ko[3]

[1]Watermelon and Strawverry Research institute, Chungcheongbukdo Agricultural Research and Extension Services, Eumseong, Chungcheongbuk-do, 27668, Republic of Korea

[2]Chungcheongbukdo Agricultural Research and Extension Service, Cheongju, Chungcheongbuk-do, 28130, Republic of Korea

[3]National Agrobiodiversity Center, National Institute of Agricultural Sciences, Rural Development Administration, Jeonju, Jeollabuk-do, 54874, Republic of Korea

Watermelon (Citrullus lanatus) is one of the three most important horticultural crops produced in the world, and the watermelon cultivation area in Korea is 11,748 ha in 2021, and the production is about 489,000 tons. Currently, it is required to develop various watermelon varieties according to consumer needs and market trends. In order to breed excellent varieties, it is important to secure various genetic resources, maintain and increase the collected genetic resources, and evaluate their characteristics. Therefore, in this study, the characteristics of cucurbitaceae family genetic resources collected domestic and international are evaluated, and resources with useful traits are selected to discover them as breeding materials. In order to identify excellent cucurbitaceae family resources and provide them as breeding materials, characteristics were conducted on 100 seeds purchased from the National Agrobiodiversity Center. 13 qualitative traits and 10 quantitative traits were investigated, and 3 types of image information (leaf, seed, fruit) were constructed. The color of the seed coat was black with 53%, followed by cream and brown. Green color and leopard patterns accounted for 96% of the pericarp color. The fruit flesh was mainly red, accounting for 41%, followed by yellow and pink. Among the resources investigated, 4 lines with high sugar content of 11°Bx or higher (K192614, K193497, K193444, K193467) and 4 colored watermelon lines (K192556, K192573, K195985, K222439) are judged to be useful for cultivating new varieties.

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***Corresponding Author:** Tel. 043-220-5864, E-mail: wjdrmawo95@korea.kr

PC-0011

The strategy of digital breeding for a breeding program in the *Capsicum annuum L.*

Yuna Kang[1], Changsoo Kim[1,2*]

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

Capsicum spp. is a major economic crop used in cooking and medicinal purposes in most regions of the world. Various breeding techniques are employed based on the preferences of breeders, including disease resistance, flavor, and color traits. However, traditional breeding methods such as Marker-Assisted Selection (MAS) are time-consuming and expensive, relying on a limited number of markers. Genomic selection allows for predicting the breeding value of a population using only the genotypic and phenotypic data of the training population. This makes it economically advantageous as it enables the selection of phenotypes based solely on genotypic data.

In this study, a total of 346,863 SNPs were obtained through GBS analysis of domesticated pepper breeding lines. Genome-wide association analysis and genomic selection analysis were conducted for fruit length, fruit stalk, and maturity. Using Gapit's Farmcpu model, seven significant SNPs were identified for fruit stalk, seven for maturity, and eight for fruit length. Finally, six statistical models (GBLUP, LASSO, BayseA, RKHS, SVM, RF) were compared to determine the most efficient predictive accuracy for genomic selection. Additionally, the predictive accuracy based on markers linked to Linkage Disequilibrium (LD) was compared. The correlation analysis between the genomic breeding value and phenotype was validated using the breeding population. Consequently, GWAS and GS were conducted for fruit length, fruit stalk, and maturity in *Capsicum* spp, establishing the foundation for digital breeding.

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

PC-0012

껍질째 먹는 신품종 단감 “단초롱”

김은경[1*], 정재은[1], 김태엽[1], 김영빈[1], 안광환[1], 김영광[2]

[1]경상남도 김해시 진영읍 하계로 138번길 30 경상남도농업기술원 단감연구소
[2]경상남도 진주시 대신로 570 경상남도농업기술원 연구개발국

‘단초롱’은 소비시장의 변화에 대응한 껍질째 먹는 단감 품종개발을 목적으로 경상남도농업기술원 단감연구소에서 육성하였다. 2010년 씨가 적은 단감 단연104를 모본으로 하고, 껍질이 부드러운 태추를 부본으로 교배하여 2011년부터 98개 계통을 재배하였다. 이 중 과피가 유연하고 생리장해가 적은 단연10-1-39를 2017년 1차 선발하였다. 이후 특성을 조사한 결과 종자형성력이 약하고 일반적 수분수 조건에서 씨가 형성되지 않는 무핵과 비율이 84%에 이름을 확인하였다. 또한, 껍질째 먹어도 이물감이 없어 먹기에 편하고, 당도 또한 17.9°Bx로 대조품종인 상서조생(15.8°Bx)에 비해 월등히 높았다. 2020년부터 2022년까지 수체생육과 과실 세부특성조사를 수행하여 품종의 균일성과 안정성을 확인하고 최종선발하여 ‘단초롱’으로 명명하였다. ‘단초롱’은 현재 국립종자원에 품종보호출원하여 재배심사 진행 중이며, 향후 먹기 편한 고당도 단감 품종으로써 소비자 수요가 확대될 것으로 기대되는 바이다.

***교신저자:** Tel. 055-254-1552, E-mail: kim2471@korea.kr

PC-0013

Utilization of breeding materials through cold resistance evaluation of apple genetic resources

Jeong-Hee Kim*, Young Soon Kwon, Jong Taek Park, Seon Ae Kim, Van Giap Do

Apple Research Institute, National Institute of Horticultural and Herbal Science, RDA, Gunwi 39000, Republic of Korea

Recently, the difficulties of apple growers due to abnormal weather are increasing. In particular, poor fruiting due to defective flower buds caused by low temperature damage during the flowering period in spring is a problem. Poor fruiting can cause great damage to apple production. There are about 1,100 apple genetic resources in Korea, including varieties, wild resources, rootstocks, and introduced species. And their morphological phenotypes and genotypes are very diverse. In order to investigate the cold resistance of various genetic resources and to utilize genetic resources with excellent cold tolerance as breeding materials, the cold tolerance test of the genetic resources being preserved was performed. Branches of 285 genetic resources such as ‘Duchess of Oldenburg’ after endogenous dormancy were collected, and the temperature was gradually lowered to -30℃ and -40℃ using a cold chamber. And then shoot germination in the state of water cutting was confirmed. ‘N.J.38’ and ‘N.J.53’ shoot germinated in -40℃ treatment were confirmed to have very strong cold resistance. After evaluating the cold resistance of all resources, including genetic resources that have not been confirmed in this experiment, we plan to classify the genetic resources by cold resistance stage and use them as breeding materials.

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***Corresponding Author:** Tel. 054-380-3130, E-mail: kimjhee@koea.kr

PC-0014

Evaluating watermelon germplasm for breeding material utilization

Ju-Hyung Jeong[1*], Eun-Young Lee[1], Jeong-Hyeon Lim[1], Seung-Hyun Cho[1], Hyeong-Goog Kim[1], Kyoung-Won Seo[2]

[1]Watermelon Experiment Station, Jeollabuk-do A.R.E.S., Gochang-gun 56469, Jeollabuk-do, Republic of Korea
[2]Fruit Vegetables Research Institute, Jeollabuk-do A.R.E.S., Gunsan-si 54062, Jeollabuk-do, Republic of Korea

Generation advancement(5-8 generations) is essential for phenotypic characterization of watermelon germplasm, and it is necessary to improve the quality and secure massively multiplied seeds for research and distribution of breeding materials. In the watermelon experiment station of Jeollabuk-do Agricultural Research and Extension Services, horticultural characterizations were evaluated for 100 watermelon germplasms distributed by the Gene bank to identify excellent resources and provide breeding materials in connection with consumers. The characterization evaluation consisted of 13 qualitative traits(leaf lodging depth, seed coat, female flowering period, fruit shape, rind base color, rind base color intensity, fruit stripe, fruit stripe color intensity, fruit bone distribution, color of flesh, leaf body marbling, shape of blossom end, seed coat base color) and 10 quantitative traits(blossom end size, fruit stripe width, fruit weight, fruit length, fruit width, rind thickness, number of seeds, seed length, seed width, sugar contents), lycopene contents, and three types of image information (pre-harvest leaves, post-harvest fruits, post-harvest seeds). Among the investigated germplasm, four germplasm(IT110900, IT199783, IT207138, and IT207181) with high lycopene contents of 55 μg/g more are considered useful for developing new varieties.

***Corresponding Author:** Tel. 063-290-6373, E-mail: jju1019@korea.kr

PC-0015

A New Variety of *Rebutia* sp. ‘Red Velvet’

Jae Hong Jung[1*], Ji Hye Lee[1], Jae Hong Lee[1], Gu Hyun Jung[1], Sang Youn Sim[2]

[1]Cactus and Succulent Research Institute, Gyeonggi-do Agricultural Research and Extension Services, Goyang, 10224, Korea
[2]GARES, Hwaseong, 18333, Korea

A new variety *Rebutia* ‘Red Velvet’ was developed at Cactus & Succulent Research Institute, Gyeonggi-do A.R.E.S in 2022. GR14121-28 had pink flowers and GR11046-11 had orange flowers were crossed in 2016 and we got 41 seedlings from this combination. Through the selection from 2017 to 2019, two breeding lines ‘GR16127-2’ and ‘GR16127-5’ were selected. ‘GR16127-2’ was finally selected through 3 years testing on characteristics from 2020 to 2022 and named as ‘Red Velvet’. The flowers of new variety ‘Red Velvet’ had red(RHS color chart, 50A) color which diameter was 4.0cm and produced 16.2. Plant body of ‘Red Velvet’ was elliptical shaped with green(NN137A) based color. Diameter of ‘Red Velvet’ plant body was 56.9mm which was larger than that of *Rebutia* ‘Red Pie’. ‘Red Velvet’ had short spines and produced 19.3 offsets. Morphological characteristics of this cultivar can be maintained through vegetative propagation of offsets.

***Corresponding Author:** Tel. 031-8008-9540, E-mail: sserai@gg.go.kr

PC-0016

Breeding of a Grafted Cactus *Astrophytum* sp. ‘Twinkle Gem’

Ji Hye Lee[1*], Jae Hong Lee[1], Jae Hong Jung[1], Seung Min Hong[2], Gu Hyun Jung[1]

[1]Cactus & Succulent Research Institute, Gyeonggi-do Agricultural Research & Extension Services, Goyang, 10224, Korea
[2]Crop Research Division GARES, Hwaseong, 18333, Korea

The new cultivar of *Astrophytum* sp. ‘Twinkle Gem’ was developed at Cactus and Succulent Research Institute, Gyeonggi-do A.R.E.S. in 2019. GA103119-1 and GA113014-13 were crossed in 2014 and we got 17 seedlings. GA14105-2 had been selected among 5 breeding lines from 2015 to 2016 and it had tested for specific characteristics from 2017 to 2019. One cultivar was finally selected through the test of specific characters in 2019 and named as ‘Twinkle Gem’. This cultivar has lots of small-sized white wolly hairs evenly distributed on dark green(136A) color surface. It has flat-round globose stem with 7~9 ribs and brown areoles on the body. The plant height and diameter were 4.2cm and 5.4cm 10 months after grafting, respectively. ‘Twinkle Gem’ is able to produce 7.2 offsets per plant within 10 months for grafting, and it has excellent productivity.

***Corresponding Author:** Tel. 031-8008-9533, E-mail: dwfljh012@gg.go.kr

PC-0017

Breeding of ‘Gold King’, a New Small and Medium-Sized Watermelon Variety that Reduces Labor

Geon-Sig Yun[1*], Sol-Ji Noh[1], Eun-Hye Kim[1], Geum-Jae Jeong[1], Gyu-Hoi Lee[1], Yu-min Jeon[1], Cheol-Ku Youn[1], In-Jae Kim[2]

[1]Watermelon and Strawverry Research institute, Chungcheongbukdo Agricultural Research and Extension Services, Eumseong, Chungcheongbuk-do, 27668, Republic of Korea
[2]Chungcheongbukdo Agricultural Research and Extension Service, Cheongju, Chungcheongbuk-do, 28130, Republic of Korea

In Korea, most watermelons are distributed in the market in the form of large -sized fruits, but recently, as the number of single-person households increases, preference for small and medium-sized fruits tends to increase. In order to meet these changes in consumption trends and reduce the labor force of farmers, a new variety of small and medium-sized color watermelon ‘Gold King’, suitable for vertical manned cultivation, was developed. The maternal line was a black rind, a medium-sized fruit with yellow flesh, and the paternal line selected strains with high sugar content and excellent leaf shape. Combining ability test were conducted between the parental combinations to finally develop the ‘Gold King’ variety. ’Gold King’ is a diploid watermelon with inherent characteristics such as oval fruit shape, black skin and yellow flesh color. As for the variable characteristics, the number of seeds is 294, and the weight of fruits is 6.3 kg in the crawling cultivation (40 cm×300 cm) and 4.0 kg in the vertical attraction cultivation (25 cm×150 cm), which is preferred in the small and medium-sized watermelon distribution market. The length and diameter of the ‘Gold King’ fruit are 27.5 cm and 17.3 cm, respectively, and the thickness of the fruit is 0.8 cm, which is thinner than that of ‘Sambokggul’. Characteristics in contrast to ‘Sambokggul’ the size of the ovum, the shape of the fruit, the base color of the fruit skin, and the main color of the flesh. When cultivating ‘Gold King’ vertically, the quantity is 9,481 kg/10a, which is expected to increase the income of farmers by 53% compared to the cultivation of ‘Sambokggul’ in the belly. In addition, the L-Citrulline content, a functional substance of the fruit skin, was 67 g/mg, 59.9% higher than that of the ‘Sambokggul’, and the β-carotene content was 14,321 ㎍/100g, 93.6% higher. In the future, this cultivated variety will be used as a variety to reduce the labor force of farmers and respond to the new consumption market.

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***Corresponding Author:** Tel. 043-220-5861, F. 043-220-5859, lothmv@korea.kr

PC-0018

A New Variety of *Kalanchoe blossfeldiana* 'Yellow Tin'

Kyu Seok Jung[1*], Ji Hye Lee[1], Jae Hong Lee[1], Youn Hee Kim[1], Sang Youn Sim[2], Gu Hyun Jung[1]

[1]Cactus & Succulent Research Institute, Gyeonggi-do Agricultural Research & Extension Services, Goyang, 10224, Korea

[2]Environmental Agricultural Research GARES, Hwaseong, 18333, Korea

A new variety of *Kalanchoe blossfeldiana* 'Yellow Tin' was developed at Cactus and Succulent Research Institute, Gyeonggi-do A.R.E.S. in 2022. 'Yellow Tin' was crossed between *K. blossfeldiana* 'Yellow Star' and 'Coto', 20 seedlings were gained in 2018. GK18101-10 was selected in 2019 and it had tested for characteristics as new variety from 2021 to 2022. It was finally selected and named as 'Yellow Tin' applying for the protection of new variety. This variety has large double type flowers with vivid yellow(12A) color. The plant height and width at flowering period reached 19.1 and 18.2cm, respectively. 'Yellow Tin' produces 32.5 flowers per peduncle and 12.7 branches per plant. The diameter of flower is 2.2cm. To flowering stage of 'Yellow Tin', it was taken 74.3 days after the short day treatment in January. Morphological characteristics can be maintained through vegetative propagation.

***Corresponding Author:** Tel. 031-8008-9538, E-mail: win258@gg.go.kr

PC-0019

A New Variety of *Graptosedum* spp. 'Gold Louis' Intergeneric Hybrid of *Sedum* and *Graptopetalum*

Youn Hee Kim[1*], Jae Hong Lee[1], Kyu Seok Jung[1], Ji Hye Lee[1], Sang Youn Sim[2], Gu Hyun Jung[1]

[1]Cactus & Succulent Research Institute, Gyeonggi-do Agricultural Research & Extension Services, Goyang, 10224, Korea

[2]Environmental Agriculture Research Division GARES, Hwaseong, 18388, Korea

A new variety of *Graptosedum* spp. 'Gold Louis' was developed at Cactus & Succulent Research Institute, Gyeonggi-do A.R.E.S. in 2022. *Sedum lucidum* 'Obesum'(IT310607) and *Graptopetalum macdougallii* were crossed in 2018 and we got 4 seedlings the combination. After pedigree selection from 2018 to 2020, 2 breeding lines, GSE18043-1 and GSE18043-3 had been tested for specific characteristics from 2020 to 2022. The breeding line GSE18043-1 was finally selected in 2022 and named as 'Gold Louis'. 'Gold Louis' has medium quantity of powder on the leaf surface and moderate yellow green(RHS color chart, 145C) base of the leaves which shows light yellow green(154D) around the margins. The number of leaves per plant was 129.0 and leaf shape was long obovate which showed the roundish end. Leaf size was 3.0cm long, 1.4cm wide and 3.0mm thick. Gold Louis's main stem grows straight 5.1cm high and 7.2cm wide, and produces 5.6 straight stems per plant. In cultivation test it makes high acceptability among growers with attractive color and vigorous growing characteristics within 8 months after planting. Morphological characteristics of this variety can be maintained through vegetative propagation of leaf and stem.

***Corresponding Author:** Tel. 031-8008-9539, E-mail :sky3884@gg.go.kr

PC-0020

Integrated Physiological and Metabolomic Analyses Unravel the Multi-Functional Proline Metabolisms in *Prunus persica* Flowering Delay

Hyunsuk Shin[1,2*], Yeonju Park[1,2], Pandiyan Muthuramalingam[1,2], Yunji Shin[1,2], Jinwook Kim[1,2]

[1]Division of Horticultural Science, Gyeongsang National University, Jinju 52725, Korea
[2]Department of GreenBio Science, Gyeongsang National University, Jinju 52725, Korea

Peach responds to various environmental stresses. Particularly, freezing temperatures in early spring raise possibility of frost damage of peach and consequently impact its productivity. Considering this issue, flowering delay is one of the prominent strategies to circumvent spring frost damage. Hence, this holistic study was to investigate and confirm that treatment with 5% sodium alginate (5AG) in the blooming stage causes the flowering delay to avoid frost damage. In addition, we systematically analyzed the modification of amino acid profiles at intervals of days in both control and 5AG-treated peach plants. Our results indicated that specific differences exist in the changes of arginine, glutamate, and proline (Pro) between control and 5AG-treated peach shoots during phenological development of flower buds. Significantly, Pro had a notable expression dynamism. Therefore, Pro biosynthesis and their attributes, gene ontology, gene synteny, *cis*-regulatory elements and gene organizations were analyzed via computational metabolomics approach which will lead to unravel a putative role of Pro in peach flowering delay. qRT-PCR analysis showed the transcriptional regulation of Pro producing and flowering responsive genes and their role in flowering delay. Overall, this pilot study provides an importance of 5AG to avoid frost damage and deeper insights on Pro role in flowering delay.

***Corresponding Author:** Tel. 055-772-3254, E-mail: shinpomo@gnu.ac.kr

PC-0021

양배추 ‘MRC33’ 육성계통의 소포자 배양을 통한 캘러스 유도 및 재분화

최수빈[1,2], 모숙연[1], 박한용[1*]

[1]서울시 광진구 능동로 209 세종대학교 바이오산업자원공학과
[2]제주 제주시 한림읍 어도봉남길 133-20 농업회사법인 ㈜ 미라클종묘

소포자 배양은 homozygous line인 doubled haploid을 개발하는데 널리 사용되며 이는 육종연한을 단축시키고 노동력을 절감할 수 있다. 일반적으로, 소포자 배양을 통해 생성된 microspore-derived embryo는 액체배지에서 발아하여 고체배지로 옮겨져 plantlet이 된다. 그 다음, 뿌리를 유도하고 순화과정을 거친다. 이에, 본 실험은 양배추 ‘MRC 33’ 소포자 유래 배의 재분화 조건을 확립하기 위해 실행되었다. 3~4mm bud를 채취하고 NLN-13 액체배지를 이용하여 소포자를 분리하였다. 분리된 소포자는 32.5°C에서 24시간 열처리하였고 embryo가 보일 때까지 25℃에서 암배양하였다. Petri-dish 당 2개의 embryo가 발생하였다. 1cm 이상의 발아된 embryo를 B5-2(Sucrose 2%, agar 0.7%) 고체배지로 옮겼으나 잎이 부풀고 갈변하여 embryo의 cotyledon를 잘라 캘러스 유도 배지인 MS + 2,4-D 1ppm + NAA 1ppm or + BAP 1ppm에 치상하였다. 약 2달 후 MS + 2,4-D 1ppm + NAA 1ppm + BAP 1ppm에서만 캘러스가 유도되었다. Shoot regeneration를 위해 캘러스를 MS + BAP 2ppm + NAA 0.5ppm + agar 0.7% or 0.9%에 치상하였다. 두 agar 농도 모두 shoot가 발생하였으나 agar 0.9%를 포함한 배지에서 더 많은 shoot가 발생하였다. 발생한 shoot를 캘러스에서 분리하여 생장조절제가 없는 MS 고체배지에 계대배양하였다. 뿌리가 왕성히 발생된 식물체는 순화과정을 거쳐 인공토양(perlite:vermiculite = 2:1)을 이용하여 3.5인치 포트에 식재하였다. 각 식물체가 본엽 8~10개를 가졌을때 식물체의 형태학적 조사를 위해 각 식물체의 폭, 잎의 모양, 엽폭, 엽장, 엽색을 기록하였다. 또한 분자 마커(RAPD와 SSR 각각 3개의 primer)를 사용하여 돌연변이 유무 판단을 위한 검정을 하였고 PCR 결과 모든 식물체는 동일한 유전형을 가진 것으로 나타났다. 본 실험에서 얻어진 식물체들은 추후 춘화처리를 하여 자식(selfing)을 통해 종자를 받을 예정이다. 최종적으로, 육종 재료로 사용되어 순도 높은 F_1 생산에 도움이 될 것으로 기대된다.

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***교신저자:** Tel. 010-6746-7477, E-mail: hypark@sejong.ac.kr

PC-0022

Cultivating a Fast-Ripening Sweet Persimmon Lineage: ‘Dan-yeon 09-12-7’

Tae-yeup Kim*, Ji-young Son, Jae-eun Jung, Yeong-Bin Kim, Eun-gyeong Kim, Gwang-hwan Ahn, Young-kwang Kim

Gyeongsangnam-do Agricultural Research & Extension Services

In south korea, persimmon cultivation covers 9,242 hectares as of 2022, with 85% (7,895hectares) dedicated to late-ripening varieties. This imbalance results in issues like price declines, labor shortage, and limited consumer choice. To tackle these challenges, this research was conducted to focus on developing fast-ripening persimmon varieties. In progenies, Traits such as early harvest, round fruit shape, and high uniformity were considered during the selection process. From 2019 to 2021, the progenies tree and fruit traits were studied following Korea Seed & Variety Service guidelines. ‘Dan-yeon 09-12-7’ emerged as the selected variety, a non-astringent Persimmon with moderate tree size and branching. It bears fruit exclusively from female flowers, with a flowering period starting on May 16th(May 15th in the control cultivar, Uenishwase) and reaching maturity on September 30th(October 17th in the control cultivar), with a sugar content(Brix) of 15.4°Bx(15.6°Bx in the control cultivar) and firmness of 26.0N 5mm∅(26.2N in the control cultivar). Despite being a non-astringent variety, ‘Dan-yeon 09-12-7’ showcases large fruit size and excellent flavor, which is anticipated to contribute to the market expansion of sweet persimmons. there is an intention to apply for variety protection for the ‘Dan-yeon 09-12-7’ lineage through the Korea Seed & Variety Service in the future. This step safeguards and recognizes the unique qualities of ‘Dan-yeon 09-12-7’, ensuring its value in the market

***Corresponding Author:** Tel. 055-254-1554, E-mail: kite0106@korea.kr

PC-0023

A High-yielding New Spray Rose Cultivar 'Pitch Pangpang' with Peach-colored Petals and Double Type for Cut-flower

Hye Rang Beom[1*], Dong Chun Cheong[1], Jin Jae Lee[2], Sung Young Jin[1], Hyun Jung Kim[1]

[1]Division of Horticulture, Jeollabuk-do Agricultural Research and Extension Services, 413, Sedong-ro, Iksan-si, Jeollabuk-do, Republic of Korea
[2]Medicinal Resource Research Institute, 108, Haengjeonggongan-gil, Unbong-eup, Namwon-si, Jeollabuk-do, Republic of Korea

The Domestic Rose cultivation area increased with the introduction of the hydroponic cultivation system in the 1990s, and increased to 863ha in 2006. However, it has gradually stabilized downward due to changes in consumption trends, increased heating cost. As of 2021, it occupies the second cultivation area after chrysanthemum with 224.5ha. Roses are crop whose consumption and preference change very quickly. In order to reduce royalty payments for the cultivation of new varieties, 'Pitch Pangpang', a spray rose variety for cut flowers with a peach-colored and pastel-toned in double type. The 'Pitch Pangpang' variety is a cross between the dark pink 'Bellina' variety and the 'babe' variety, which is less damaged by mites. The 'SR141514-104' line was finally selected through a characteristic test from 2015 to 2017. In 2018~2019, the 3rd characteristic test and on-site demonstration were carried out, and 'Pitch Pangpang' was developed through characteristic test and productivity test according to new rose variety application investigation criteria of the Korea Seed and Variety Service. The characteristic evaluation results in 2019, the height of the flower was 0.5cm higher than that of the control variety('Babe'), and the number of petals was 20 more than the control variety. The cut-flower vase life was about 1 day longer than that of the control variety, and consumer's preference was high due to its peach-color. The 'Pitch pangpang' applied for new variety protection to the Korea Seed and Variety Service in 2020, and the new variety protection right (No.9265) was registered in December 2022.

***Corresponding Author:** Tel. 063-290-6148, E-mail: gpfkd0629@korea.kr

PC-0024

A New Freesia Hybrid ‘Light Purple’ with Double and Multi-flowering for Cut Flower

Ji Hye Jang, Sea Hyun Gi*, Dong Chun Cheong, Hye Rang Beom, Seh Hui Jung, Mi Sun Kim, Jae Jong Noh, Jin Jae Lee

Division of Horticulture, Jeollabuk-do Agricultural Research and Extension Services, 413, Sedong-ro, Iksan-si, Jeollabuk-do, Republic of Korea

A freesia (*Freesia hybrida* Hort.) ‘Light Purple’ was developed for the cut flower in the Jeollabuk-do Agricultural Research and Extension Service in 2022. This hybrid was selected from 15 seedlings obtained by crossing ‘Ancona’ and ‘Giraffe’, which is purple double flowering and yellow single flowering, respectively, in 2013. Morphological characteristics of the selected hybrid were investigated for 3 years from 2019 to 2021, and then it was named ‘Light Purple’. The characteristics survey was conducted according to the survey standards of the International Union for the Protection of New Plant Varieties (UPOV), and ‘Ancona’ was investigated as a control cultivar. ‘Light Purple’ had purple color of RHS VG75B and double flowering without spots. ‘Light Purple’ has not developed stamens and anther, and the color of the style is purple. The average days to first flowering of ‘Light Purple’, was 138.5 days, and it was approximately 14 days earlier than the control cultivar. The average height was 109.6 cm, 13.3cm longer than the control cultivar (96.3 cm), and the cut flower length of the first flower was 35.7 cm, similar to the control cultivar (36.5 cm). The number of floret per stalk was 13, and stalk length was 9.6 cm. The vase life of the flowers is 9.5 days (vs. 8.5 days in the control cultivar) and they are especially resistant to bulb rot. The average yield of both cultivars was 5 cut flower stem per plant, which was similar.

***Corresponding Author:** Tel. 063-290-6147, E-mail: jhjang24@korea.kr

PC-0025

랜덤포레스트를 활용한 양파 생육 기상 데이터 기반 면적당 양파 수량 및 생산성 예측

전재범*, 한지희, 박수진, 심준용, 이혜림, 류수현

농촌진흥청 디지털농업추진단, 전라북도 전주시 덕진구 농생명로 300

작물 수량은 여러 요인의 상호작용에 의해 영향을 받는 것으로 알려져 있으며, 알려진 요인들이 선형 관계로 영향을 주는 것이라고 할 수 없다. 따라서 선형을 넘어 머신러닝 기법 중 분류분석 기반의 랜덤포레스트(RandomForest)의 방법을 활용하여 양파 수량성을 예측하는 모델과 농가수량성을 예측할 수 있는 모델을 개발하였다. 모델 개발을 위해 농촌진흥청 농업빅데이터수집사업에서 4 년간(2019~2022) 수집한 양파 생육데이터와 국립농업과학원의 농업날씨365의 기상데이터를 활용하였다. 농가수량성은 12,000 kg/10a이상은 상, 4,000~12,000 kg/10a는 중, 4,000 kg/10a 이하는 하로 설정하였다. 전체 생육데이터는 전남, 경북, 경남 지역의 8시군구, 109 농가 데이터로 농가 대표값과 시군구 대표값으로 정리하였으며 기상 데이터는 일별 측정값을 양파 생육단계인 이식기, 월동기, 경엽신장기, 구비대기로 구분해 평균값을 계산하여 활용하였다. 랜덤포레스트 예측 모델을 개발하기 위해 60%의 데이터를 활용하였고 grid search로 모델 최적값을 탐색하였으며 40%의 데이터를 개발된 모델에 적용검증하여 예측률을 도출하였다. 생육 데이터(초장, 엽초경, 엽수, 구직경, 생구무게 등)와 기상 데이터(평균기온, 최고기온, 최저기온, 강수량, 풍속, 일조 등)를 입력하여 농가에서 기록된 수량(kg/10a)를 예측한 결과 약 65%의 정확도로 수량 예측이 가능하였으며, 재식밀도, 최저기온, 엽수량, 강수량, 엽초장길이, 경엽무게가 중요 요인으로 나타났다. 또한 농가생산성을 상, 중, 하의 구간으로 예측한 결과 85%의 정확도로 예측이 가능하였다. 모델의 예측률은 불균형한 데이터 비율, 데이터의 편차 등에 의해 영향을 받았는데, 본 연구에서 모델 개발을 위해 활용된 데이터는 노지에서 수집되어 그 편차가 크고 생산성 상위 농가의 데이터 비율이 상대적으로 낮아 예측률이 낮게 도출된 것으로 보인다. 따라서 추가적인 양파 농가의 데이터 축적을 통해 개발 모델의 예측률을 개선할 수 있을 것으로 생각된다.

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***교신저자:** Tel. 063-238-1542, E-mail: jbchun01@korea.kr

PC-0026

'Nokju' pear

Kyungho Won[1], Haewon Jung[1], Il Sheob Shin[1*], Kyeong-Bok Ma[1], Byulhana Lee[1], Hye-Gyoung Yoo[1], Janghoon Song[1], Arang Kang[1], Ho-Jin Seo[1], Kang Hee Cho[2], Sehee Kim[2], Byeonghyun Yoon[2], Yoon Kyeong Kim[1], Sam-Seok Kang[1], Seong Sig Hong[1]

[1]Pear Research Institute, National Institute of Horticultural & Herbal Science, Rural Development Administration, Naju 58216, Republic of Korea
[2]Fruit Research Division, National Institute of Horticultural & Herbal Science, Rural Development Administration, Wanju 55365, Republic of Korea

'Nokju', a new Asian pear cultivar, was developed from open pollination of 'Hwangkeumbae', the mid-maturing pear cultivar with green skin and high fruit quality in Korea. It was made in 1994 at the Pear Research Institute, National Institute of Horticultural and Herbal Science, Rural Development Administration in Korea. It was first selected as '25-1-1' in 2013 for its attractive eating quality, good appearance and acceptable strorability. After regional adaptability tests at five sites for nine years from 2014 to 2022 as 'Wonkyo Na-78', it was selected and named in 2022. Its full bloom day, on 8 April in average, was similar to 'Hwangkembae' ' in 2018-2022. It is strong in tree vigor and has an upright tree habit. 'Nokju' is classified as mid-susceptible to pear scab (*Venturia nashicola*) and highly susceptible to pear rust (*Gymnosporangium asiaticum*) similar to 'Hwangkeumbae'. 'Nokju' had 62.5% cross-pollination rate with 'Wonhwang' (S_3S_4) to 98.6% with 'Seolwon' (S_3S_9). The average optimum harvest time of 'Nokju' was 165 days after full bloom and it matured around two weeks later than 'Hwangkeumbae' and one week earlier than 'Niitaka', major pear variety in Korea. The fruit is round in shape and yellowish green in skin color. Average fruit weight was 634 g and soluble solids concentration was 12.2°Brix. The flesh had abundant juice and negligible grit. It can be stored for 30 days at room temperature (20°C) and for 3 months at low temperature (1~2°C).

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***Corresponding Author:** Tel. 061-330-1540, E-mail: shinis3@korea.kr

PC-0027

과수 화상병 저항성 사과 육종의 시작

박종택*, 권영순, 김정희

농촌진흥청 국립원예특작과학원 사과연구소

과수화상병(Fire Blight)은 '*Erwinia amylovora*'라는 세균에 의해 장미과 식물에 발생하는 병으로 병에 걸린 나무는 서서히 말라죽는다. 병의 증상은 가지나 잎, 꽃, 열매 등 전체 나무에서 나타나는데 그 모습이 마치 불에 덴 것 같다고 해서 화상병으로 불린다. 개화기 방화곤충의 활동에 의해 전염된다고 알려져 있으며 전정이나 접목 등 농작업으로도 전염이 가능하여 예방이 어렵다. 또한, 일단 발병하게 되면 치료제가 없어 치료는 거의 불가능하고 이병부위를 제거하여 병의 진전을 막을 수 있지만, 육안으로 병징이 나타난 부위 외에도 병원균이 존재할 가능성이 높아 이병부위의 완벽제거는 어렵다.

이러한 여러 가지 제약으로 인해 과수화상병을 극복하기에는 어려움이 많으며, 과수화상병 저항성 품종육성이 근본적 해결책이다. 하지만 저항성 품종육성은 오랜 시간과 많은 자본이 투입되어야하는 방법으로 교배집단의 규모 관리나 육종연한을 단축할 수 있는 방안이 필요하다.

과수화상병이 최초로 보고된 미국에서는 1968년부터 저항성 품종 육성 프로그램을 운영하고 있으며 화상병에 저항성인 사과 '*Malus×robusta* 5'를 활용하여 저항성 사과대목 품종을 육성하여 보급하고 있다. '*Malus×robusta* 5'는 과수화상병 저항성 자원으로, 저항성 유전자(*MR5*)를 보유하고 있는 것으로 알려져 있다.

국립원예특작과학원 사과연구소에서는 2020년부터 '*Malus×robusta* 5'를 활용하여 교배집단을 양성하고 있으며, 교배집단에서 저항성 계통 선발을 위해 *MR5* 검출 프라이머를 제작하여 선발에 활용하고 있다. *MR5* 마커를 활용하여 교배실생 집단을 검정한 결과 '후지'×'*M.×robusta* 5' 집단에서 170개체 중 80개체, '홍로'×'*M.×robusta* 5' 집단에서 252개체 중 57개체가 *MR5*를 보유하고 있는 것으로 조사되었다. *MR5* 검출 마커의 정황도 확인을 위하여 교배집단에서 11계통을 임의 추출하여 접종한 결과 *MR5*를 보유하지 않은 계통은 '이병성', 혹은 '고도이병성'으로 판단되었고, *MR5*를 보유하고 있는 계통은 '중도저항성' 내지 '고도저항성'으로 판단되었다.

이러한 결과를 바탕으로 저항성 계통양성을 위해 양성한 분리집단에서 이병성 계통의 조기 도태가 가능하여 실생계통 집단의 규모 조절이 가능하고, 육종연한 단축이 가능하여 과수화상병 저항성 사과육종을 위한 시간 및 예산을 절감할 수 있을것으로 기대된다.

***교신저자:** Tel. 054-380-3133, Fax. 054-380-3109, jongtaek@korea.kr

PC-0028

VCF 변이정보 처리 및 가시화를 위한 사용자 인터페이스 구축

윤석재[1], 이승욱[1], 박수현[1], 김대규[1], 김대관[1], 송지용[1], 정선균[2], 유의수[1*]

[1]주식회사 디엔에이케어
[2]농업회사법인 주식회사 피피에스

최근 작물육종의 경향은 다양한 유전체정보를 기반으로 정밀 영상 표현체, 대사체 정보 등 다양한 표현형 데이터를 이용하여 형질연관 마커를 탐색하고 육종현장에 활용을 통하여 선발효율 향상, 육종연한 단축, 복합형질 육종을 목표로 하는 데이터 기반 육종으로 전환되는 추세이다. 효율적인 데이터 기반 육종의 실현을 위해서는 대용량 유전형, 표현형 데이터를 잘 활용할 수 있는 유전체정보분석 인력 및 대용량 서버의 활용이 필수적이나 현실적으로 분석인력 및 서버 자원은 매우 제한적이어서 데이터 기반 육종의 확산도 어려운 것으로 판단된다. 따라서 표준화된 분석 체계를 기반으로 유전체 정보분석 환경에 접근이 취약한 연구자들이 활용할 수 있는 분석도구 및 사용자 인터페이스의 개발은 데이터 기반 육종에 필요한 유전체 정보활용, 확산을 유도하고 작물육종에 적용할 수 있는 마커 개발에 효율성을 제공하여 육종효율 향상에 기여하는 효과가 기대된다. 본 발표는 디지털육종전환 기술개발 사업의 일환으로 대용량 유전체 정보의 접근성을 향상 시킨 사용자 친화적 가시화 도구 개발로 1) ‘VCF viewer’는 국제표준 변이정보 파일인 VCF파일의 정보를 웹 인터페이스를 통해 고품질 변이 추출, 유전체상 변이 분포 가시화, 변이 통계 정보, 유전자 기능 정보 등을 연계 가시화하고, 시퀀스 추출 등의 기능을 수행하는 도구, 2)‘MAP viewer’로 분자표지 또는 유전지도의 정보를 유전체 서열 상에 연계하여 분자표지 위치와 마커 상세 정보, 유전지도와 물리지도 비교 등 수행하고 가시화 결과를 제공하는 인터페이스를 상세히 소개한다. 본 과제에서 개발되는 두 가지 사용자 친화적인 인터페이스는 유전체정보분석 연구자들의 유전체 정보 활용도를 향상시키고, 또한 육종 전문가들이 데이터기반의 정밀육종 구현을 위한 정보 분석 및 결과 활용에 적극 활용되어 육종 효율 향상에 기여할 것으로 기대된다.

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

PC-0029

디지털육종 기술 활용 확산을 위한 연관분석 통합 디지털 육종 플랫폼 개발

이창열[1], 이승욱[1], 박수현[1], 김대규[1], 윤석재[1], 김대관[1], 송지용[1], 김창수[2], 장창순[3], 박형준[4], 김석용[5], 유의수[1*]

[1]주식회사 디엔에이케어
[2]국립충남대학교 농업과학대학 식물자원학과
[3]농업회사법인 한국종묘 주식회사
[4]주식회사 농업회사법인 솔라늄네트웍스
[5]농업회사법인 주식회사 피피에스

최근들어 유전체정보를 기반으로 정밀 영상 표현체, 인공지능 등 신기술의 융·복합적인 접목을 통해 육종 효율을 극대화할 수 있는 디지털육종에 많은 관심이 집중되고 있다. 데이터 기반 디지털 육종의 확산을 위해서는 고품질 유전체 정보 및 다양한 표현형 정보의 생산이 필수적이며 또한 이들 정보를 연계하여 분석, 활용할 수 있는 통합시스템의 구축이 반드시 필요하다. 본 발표를 통해 데이터 기반의 디지털육종 분석기술 개발 및 활용 확산을 위해 유전체, 표현체 및 정보분석 인프라가 필요한 연구자들이 활용할 수 있는 디지털육종플랫폼을 소개하고자 한다. 표준화된 분석체계, 분석환경 및 결과활용 환경을 위해 사용자 친화적인 요소를 적용하여 디지털육종 플랫폼을 개발하였으며 따라서 분석 경험의 정도에 관계없이 사용자 데이터 입력만을 통해 디지털육종 기술을 효율적으로 적용할 수 있도록 구축하였다. 본 과제 수행을 위해 유전체 및 표현체 정보의 생산, 관리, 분석, 활용 등 데이터기반 정밀육종 전 주기에 필요한 요소 분석을 통하여 세부 목표를 설정하였다. 세부목표는 1) 학습집단 양배추 200계통과 고추 400계통 대상 유전형 정보와 농업형질 및 육종 관심형질에 대한 3개년간의 표현형 정보 DB 구축, 2) 전유전체 형질연관분석(GWAS) 표준화 분석체계 및 사용자인터페이스 구축, 3) 유전체선발(Genomic selection) 표준화 분석체계 및 사용자인터페이스 구축, 4) 분석 결과 연동 및 유전자 기능 탐색을 위한 variants browser, 5) 유전체 데이터 활용 효율 향상을 위한 사용자 친화적인 디지털육종 toolbox 구축(다양한 정보 가시화 도구, 변이정보처리, 집단유전학 분석, 표현형정보 통계 분석 및 마커 디자인 등의 사용자인터페이스)을 목표로 시스템 개발을 수행 하였다. 본 과제에서 개발되는 디지털육종시스템은 육종현장에 적용하여 선발효율 증대, 육종연한 단축을 통한 신품종생산 경쟁력 향상 및 종자산업 활성화라는 장기적 목표에 기여할 것으로 생각한다.

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

PC-0030

Identification of flesh color by high-resolution melting (HRM) marker based on RNA-Sequencing in Kiwifruits accessions

Dongseob Lee[1], Sewon Oh[1,2], Yumi Kim[1], Garam Lee[1], Mockhee Lee[3], Daeil Kim[1*]

[1]Department of Horticulture, Chungbuk National University, Cheongju 28644, Korea
[2]Fruit Research Division, National Institute of Horticultural and Herbal Science, Rural Development Administration, Wanju 55365, Korea
[3]Namhae Branch, National Institute of Horticultural and Herbal Science, Rural Development Administration, Namhae 52430, Korea

Kiwifruits with red flesh color are in increasing commercial value due to their unique color against green or yellow flesh colors. Anthocyanin causes the red flesh coloration of kiwifruits. RNA-sequencing is a recently developed approach to profile transcriptome that uses deep-sequencing technologies. Single nucleotide polymorphism (SNP) is a single nucleotide variation in a specific position of the genome. High density of SNPs can provide the simplest and maximum number of markers. High resolution melting (HRM) is used to detect variations such as SNPs by monitoring the melting curves of fluorescence in DNA strands during heating process. This study was performed to develop SNP markers for identifying flesh colors of kiwifruits accessions. The fleshes of kiwifruits were collected at 120, 160 days after full bloom and ripening stage by each flesh colors of green, yellow, and red. RNA was extracted using collected flesh samples and RNA-sequencing was performed. SNPs were detected derived from RNA-sequencing data of kiwifruits. The common 17,690 SNPs were detected during the fruit maturation stages. Thirteen out of 17,690 SNPs associated with anthocyanin pathway were selected. Within 13 candidate SNP for distinguishing the flesh color of kiwifruits accessions, one SNP located on the coding sequence of *Myb transcription factor* can be used as developing HRM marker. The developed HRM marker has separated melting curves in green, yellow, and red flesh color of kiwifruits accessions. Therefore, these results could improve the maker assisted breeding of kiwifruits.

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***Corresponding Author:** Tel. 043-261-2527, E-mail: dkpomo@cbnu.ac.kr

PC-0031

Detection of QTL Linked to Stone Cell Content of Pear Flesh

Hakgyun Kim[1], Sewon Oh[1,2], Yumi Kim[1], Doyeong Kim[1], Il Sheob Shin[3], Keumsun Kim[3], Daeil Kim[1*]

[1]Department of Horticultural Science, Chungbuk National University, Cheongju 28644, Korea
[2]Fruit Research Division, National Institutue of Horticultural and Herbal Science, Rural Development Administration, Wanju 55365, Korea
[3]Pear Research Institute, National Institute of Horticultural and Herbal Science, Rural Development Administration, Naju 58216, Korea

Pears (*Pyrus*) are divided into Asian pear (*P. pyrifolia*, *P. ussuriensis*, and *P. bretschneideri*) and European pear (*P. communis*) according to their geographical origin. Asian pears have a higher stone cell content than European pears. The high content of stone cell is negatively affecting the consumer value due to gritty texture and poor taste. Therefore, the purpose of the pear breeding programs is to reduce the stone cell content. In this study, we detected quantitative trait loci (QTLs) linked to stone cell content in Asian pears. 'Whangkeumbae' (*P. pyrifolia*, low content stone cell) and 'Minibae' ((*P. pyrifolia* × *P. ussuriensis*) × *P. pyrifolia*, high content stone cell) were collected for measuring the stone cell content. Stone cell was stained using Phloroglucinol-HCl and stone cell content was measured using MATLAB. QTLs related to the stone cell content was analyzed using MapQTL 6.0 software. The measured stone cell content of 'Whangkeumbae' and 'Minibae' using image processing were 0.26 and 1.30, respectively. The stone cell content was distributed 0.157 to 1.524 in 95 F_1 individuals. QTLs of stone cell content was detected on chromosome 14 in pear. These results can be useful in detecting genes of stone cell content, developing markers to discriminate stone cell content.

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***Corresponding Author:** Tel. 043-261-2527, Fax. 043-271-0414, E-mail: dkpomo@cbnu.ac.kr

PC-0032

Evaluation of Variant Calling Tools for Detecting Accuracy SNPs in Highly Polyploidy Kiwifruits (*Actinidia* spp.)

Yumi Kim[1], Sewon Oh[1,2], Hakgyun Kim[1], Dongseob Lee[1], Mockhee Lee[3], Daeil Kim[1*]

[1]Department of Horticulture, Chungbuk National University, Cheongju 28644, Korea
[2]Fruit Research Division, National Institute of Horticultural and Herbal Science, Rural Development Administration, Wanju 55365, Korea
[3]Namhae Branch, National Institute of Horticultural and Herbal Science, Rural Development Administration, Namhae 52430, Korea

Kiwifruit (*Actinidia* spp.) has 29 basic chromosome numbers with various polyploidy. NGS is used for detecting the genetic variation such as single nucleotide polymorphisms (SNPs), insertion and deletion (Indel), and structural variants. However, detecting SNPs of polyploidy plants, including kiwifruit, is difficult. Therefore, we compared the variant calling tools for the evaluating efficiency of SNPs in various polyploidy kiwifruits. Genotyping-by-sequencing was performed using Illumina HiSeq X with two enzyme. The raw reads were alignment to kiwifruit reference genome cv. Hongyang (*A. chinensis*) using BWA-mem. Freebayes and genome analysis toolkit (GATK) were used to detect variants. The raw SNPs were extracted and filtered by the following criteria: bi-allelic, missing rate < 30%, and minor allele frequency > 5%. The genetic diversity was analyzed using SNPs of freebayes and GATK in 56 kiwifruit accessions. In total, 12,946 and 338,230 filtered SNPs were called from freebayes and GATK, respectively. As a result of genetic diversity, phylogenetic tree and population structure were not clearly divided using SNPs of freebayes. On the other hand, the phylogenetic tree and population structure were clearly separated using SNPs of GATK in 56 kiwifruit accessions. In population structure, the 56 kiwifruit accessions were divided into three clusters, which represented *A. chinensis*, *A.* hybrid, and *A. arguta.* Therefore, GATK more accurate and efficient for detecting SNPs than freebayes in various polyploidy kiwifruits.

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***Corresponding Author:** Tel. 043-261-2527, E-mail: yumi@cbnu.ac.kr

PC-0033

Screening of Pepper Germplasm for Resistance to Tomato Spotted Wilt Virus (TSWV) Using Bioassay

Hyeonseok Oh[1*], Ho-Sun Lee[1], Gi-An Lee[1], Bichsaem Kim[1], Ho-cheol Ko[1], On-Sook Hur[2]

[1]National Agrobiodiversity Center, National Institute of Agricultural Science, Rural Development Administration, Jeonju 54874, Republic of Korea

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

Tomato spotted wilt virus (TSWV), belonging to the genus *Orthotospovirus* (*Tospoviridae*), is a significant disease that globally affects the yield of pepper (*Capsicum* spp.) worldwide. TSWV-resistant cultivars containing the TSWV resistance gene (*TSW*) are commonly used for disease management. However, the emergence of TSWV resistance-breaking (RB) strains in various countries necessitates the exploration of new resources for TSWV-RB strain resistance in order to develop TSWV-resistant pepper cultivars. In this study, a bioassay was conducted on 414 pepper germplasm conserved by the National Agrobiodiversity Center to evaluate their resistance to TSWV. The screened germplasm included *C. annuum*, *C. baccatum*, *C. chinense*, and *C. frutescens*, comprising landraces, breeding lines, and cultivars collected from Korea, Peru, Hungary, Nepal, Mexico, and other countries. After inoculating TSWV RB strain (TSWV-P1) sap onto the upper leaves of seedlings (n=12) with three to four healthy leaves, symptoms such as ringspot, mosaic, and necrosis were observed to calculate the incidence rate. Among the screened accessions, two accessions (IT136625, IT284050) showed 0% incidence rate, two accessions (IT284058, IT308753) showed 1-10% incidence rate, and nine accessions (IT32468, IT32476, IT32480, IT103079, IT136626, IT218962, IT284056, IT284059, IT308738) showed 10-30% incidence rate. These resistant accessions can serve as valuable breeding materials for the development of TSWV-resistant pepper cultivars.

Keywords: Pepper, Germplasm, Tomato spotted wilt virus, Resistance

***Corresponding Author:** Tel. 063-238-4904, E-mail: zzjiy@korea.kr

PC-0034

Development for high-throughput marker set for seed quality screening in *Cucurbita maxima*

Eun Su Lee*, Koeun Han, Do-Sun Kim

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

Pumpkin (2n=2x=40) is the economically important *Cucurbitaceae* crops worldwide. Among them, *Cucurbita maxima* is used for food (sweet pumpkin) as well as the rootstock for F_1 generation of watermelon cultivation. In order to develop high-throughput SNP markers for the determination of rapid seed purity from F_1 hybrids, genotyping-by-sequencing (GBS) of 49 pumpkin accessions was performed using Illumina NextSeq 500. SNPs were collected and filtered based on filtering parameter (depth$\geq$5, missing rate$\leq$0.05). A total of 7,478 SNPs were obtained and among them, 341 SNPs were selected based on the stringent filtering parameters such as bi-allelic genotype, single copy number, polymorphism information content (PIC) value. Further, 48 evenly distributed SNPs on each chromosome were identified and converted to kompetitive allele-specific PCR (KASP) markers. To validate the KASP markers, genotyping and phylogenetic analysis of 78 accessions were performed. In addition, the KASP marker set was utilized for testing 15 F_1 hybrids and parental lines. The results suggested that the designed KASP markers were able to distinguish the accessions and aided in the seed purity test of F_1 hybrids.

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

PC-0035

Inheritance of dwarf vine in pumpkin (*Cucurbita maxima*)

Eun Su Lee*, Eunmin Choi, Koeun Han, Do-Sun Kim

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

Pumpkin (*Cucurbita maxima*) is an economically important crop worldwide. Dwarfism is one of the most valuable traits in pumpkin breeding because of its contribution to yield as well as the decreased labor required to cultivate and harvest smaller plants. However, the underlying genetic mechanism is unknown. We studied the inheritance of dwarf vine using an F_2 population derived from a cross between normal vine line 'A01' and dwarf vine line 'A07'. The 107 F_2 individuals, five F_1, and five parent plants were grown and evaluated in a greenhouse. The vine length of parents, F_1, F_2 were measured at the adult stage (25th node). The F_1 plants showed intermediate dwarf type (45-110cm) and segregation in F_2 exhibited one normal vine: two intermediate vine: one dwarf vine ratio through chi-square test ($p < 0.05$). These data support a single gene with incomplete dominance that was underlying the normal vine type in the 'A01' × 'A07' population. The identified inheritance of dwarf vine would help to detect a recessive dwarf allele and to develop molecular markers for pumpkin breeding.

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

PC-0036

대추나무의 생육특성 및 세포유전학적 배수체 분석

이동근*, 이채영, 박희순, 강효중, 박재은, 신현만

충청북도 보은군 산외면 상부평길87, 충청북도농업기술원 대추호두연구소

대추(*Ziziphus jujuba.* Mill)나무의 꽃은 크기가 작고 암술의 수분능력이 개화 당일로 짧아 인공교배하기에 어려움이 있다. 이러한 특성으로 대추의 품종육성은 지역재래종인 ‘무등’, ‘월출’, ‘금성’과 대과형 대추인 ‘천황’, ‘황실’ 등 선발품종 뿐이다. 교배육종의 어려움을 극복하고자 대추 자원의 배수체를 검정하여 배수체 육종에 활용하고자 본 연구를 수행하였다. 대추호두연구소가 보유하고 있는 유전자원 중 9개 자원에 대한 세포유전학적 분석을 하였고, 주요 6개 자원에 대하여 생육특성을 조사하였다. 대추의 배수성 판정을 위한 유세포분석법의 기준이 없어 ‘복조’를 기준으로 하여 분석하였다. 자원 중 ‘복조’, ‘천황’, ‘산조’, ‘일본’, ‘BJV-1’ 자원은 2배체로 확인하였고, ‘천상’과 ‘Zj-2’, ‘Zj-3’, ‘Be-4’ 자원은 4배체로 분석되었다. 4배체의 특성을 가진 자원의 잎 특성은 ‘복조’ 자원에 비해 잎의 크기와 공변세포의 크기가 컸으며, 공변세포 수는 적었다. ‘천황’은 대과형 대추로 잎의 크기가 큰 편임에도 2배체로 확인되었다. ‘BJV-1’ 자원은 잎의 크기는 큰 편이나 공변세포의 크기가 작았고, 공변세포 밀도가 가장 높았다. 이러한 배수체 분석과 생육특성을 바탕으로 신품종 육종을 위한 콜히친 처리 등 배수체 육종과 약배양, 배배양 육종에 기초자료로 활용될 것이다.

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***교신저자:** Tel. 043-220-5803, E-mail: andante25@korea.kr

PC-0037

고구마 품종‘신율미’의 대량증식을 위한 마디배양의 최적 호르몬 규명

강태연, 모숙연, 박한용*

서울시 광진구 능동로 209 세종대학교 바이오산업자원공학과

고구마는 영양이 풍부하고 에너지가 높은 구황작물로 식량, 식품, 사료, 공산품의 원료로써 세계적으로 중요한 작물이다. 고구마는 6배체의 영양번식 작물로 종자의 형성이 불량하여 주로 고구마 액아의 줄기를 이용하여 대량번식을 통한 육묘를 한다. 토양의 바이러스 혹은 병원균에 감염된 고구마로 대량번식된 고구마 줄기를 이용한 재배시 수확량이 적고 양질의 생산물을 얻기 힘들다. 따라서 생장점 배양을 통해 virus, bacteria-free한 우수묘를 생산한 후 node culture를 통한 *In vitro* propagation은 우수한 묘를 대량생산하므로 균일하고 건강한 식물을 생산하는 것에 효과적이다. 이에, 본 실험은 고구마 품종‘신율미’의 axillary bud를 포함한 node를 배양하여 고품질의 묘를 대량증식하기 위해 최적의 호르몬 사이토키닌의 종류(BAP, TDZ, Kinetin, Zeatin)와 농도를 규명하고자 하였다. 고구마 품종‘신율미’의 생장점배양으로부터 획득된 기내 조직배양묘로부터 3~4mm 크기의 node를 채취하고 다양한 종류와 농도의 사이토키닌이 첨가된 고체 MS 배지(MS powder, Sucrose 3%, agar 0.4%, gelite 0.2%, 5.8 pH)에 배양하였다. 배양체는 25℃에서 16시간:8시간 명암주기로 8주간 배양하였다. 모든 사이토키닌 호르몬 종류와 농도별 실험결과 모든 호르몬에서 크기의 차이가 있지만 대조구(Hormon-free)에서 발생하지 않은 캘러스가 발생하였다. 대량번식 요인에 중요한 요소인 multi shoots 수와 마디 수를 보았을 때, BAP 1.0 mg/L를 첨가한 배지에서 가장 많은 multi shoots 수(2.11)가 나타났지만 다른 호르몬 조성의 결과에 비해 마디 수(7.9)가 적게 나타났다. 실험결과를 종합적으로 판단하였을 때, Zeatin 0.5 mg/L를 첨가한 배지에서 multi shoots 수(1), 마디 수(17.35), 슈트 길이(119.5mm), 뿌리 수(12.3), 생체중(2133.95mg)으로 측정되어 생육이 가장 좋고 대량번식에 유용할 것으로 나타났다. 따라서, 본 실험의 결과는 고구마의 *In vitro* micropropagation을 통한 고품질의 묘를 대량증식 하는데 도움이 될 것으로 기대된다.

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***교신저자:** Tel. 010-6746-7477, E-mail: hypark@sejong.ac.kr

PC-0038

Quantitative evaluation of spotted wilt disease in the interaction between *Tomato spotted wilt virus* and *Solanum lycopersicum*

Jinjeong Lee, Sung-Mi Kim, Seon-Hwa Bae, Eunhee Kim, Myeong Jin Kang, Hye-Jin Yun, Jae-Hyeon Oh, Young-Joo Seol, Il-Pyung Ahn*

Gene Engineering Div., National Institute of Agricultural Sciences, RDA, Jeonju 54874, Republic of Korea

Spotted wilt (SW) disease, caused by *Tomato spotted wilt virus* (*TSWV*), is an important disease in *Solanum lycopersicum*. *TSWV* genome is composed with three segments, L, M, S, and each encodes RNA-dependent RNA polymerase, cell-to-cell movement protein NS_M and glycoproteins G_N/G_C, and silencing suppressor NS_S and nucleoprotein N. We characterized interactions among one *TSWV* isolate SW-TO2 and two *S. lycopersicum* inbred lines AVTO0101, Hawaii7996 and four commercial F_1 cultivars Seokwang, SuperDotaerang, Tory, Lucky. Inoculum was propagated in *Nicotiana rustica*, then crude extract was infected onto the seedlings' third true leaves. Symptom development on the inoculated leaf was photographed every other days and the leaves were retrieved for RNA preparation. Tory, and Lucky were resistant to SW-TO2 infection, but other four lines and cultivars were susceptible. Real time PCR-based quantification system was established based on the nucleotide sequence of NS_M. After cDNA synthesis using the RNA from SW-TO2-infected *N. rustica*, 200-bp-long amplicon was produced using the NS_M-specific primer pair and cloned into pGEM-T easy vector. Standard curve depicting the relationship between crossing point (CP) values and copy number of NS_M/SW-TO2 was constructed. Plotting CP values of the cDNAs (RNAs) on the standard curve clearly evaluated the copy numbers of SW-TO2 in the pictured and then sampled leaves. Accompanied with the observation for SW disease developments, copy numbers of NS_M in the compatible interactions were evidently higher than those in the incompatible ones. Our evaluation system should supply convincible annotation for SW symptom development.

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

PC-0039

Revisiting the genes of the Green Revolution to customize plant size for vertical farming

SeungPyo Hong[1], Choon-Tak Kwon[1,2*]

[1]Graduate School of Green-Bio Science, Kyung Hee University, Yongin 17104, Republic of Korea
[2]Department of Smart Farm Science, Kyung Hee University, Yongin 17104, Republic of Korea

Tnomato is a major fruit crop known for its tall and large plant size, which is unsuitable for vertical farming. Therefore, reducing the plant size is desirable. One practical approach to controlling plant height and internode length in tomatoes is manipulating gibberellin synthesis or signaling. Hence, we aimed to regulate plant size by targeting genes involved in GA biosythesis, well-known as the genes of the Green Revolution. Specifically, we targeted eight tomato *gibberellin 20-oxidase* (*SlGA20ox*) genes to generate semi-dwarf tomato varieties. We obtained 81 T_0 transgenic lines with genetic chimerism and generated single and double mutants of *slga20ox2* and *slga20ox4* using CRISPR genome editing. In the case of the *slga20ox2 slga20ox4* double mutants, we observed a significant decrease in plant size but a slight increase in fruit yield and harvest index. The higher yield of *slga20ox2 slga20ox4* double mutants was due to increased fruit size and weight, not fruit number. However, the *slga20ox2 slga20ox4* double mutants showed later fruit ripening than wild-type plants, indicating that introducing an early ripening trait is required for rapid cycling in vertical farms. We suggest that targeting *slga20ox* genes could be a powerful strategy for developing vertical-farm cultivars.

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

PC-0040

Fine-tuning tomato stem length for vertical farming by editing gibberellin biosynthesis genes

Yoonseo Lim[1], Choon-Tak Kwon[1,2*]

[1]Graduate School of Green-Bio Science, Kyung Hee University, Yongin 17104, Republic of Korea
[2]Department of Smart Farm Science, Kyung Hee University, Yongin 17104, Republic of Korea

Vertical farming offers the advantage of providing a stable environment for plant cultivation, shielding them from adverse conditions such as climate change. Optimizing plant growth and architecture is necessary for vertical farming. The *gibberellin 3-oxidase* (*GA3ox*) genes encode gibberellin 3-oxidases responsible for activating GA within the pathway and modulating stem length. By multiplex CRISPR genome editing, we targeted the six tomato *GA3ox* genes for modulating plant architecture and stem length. Among the six *SlGA3ox* genes, we confirmed the phenotypes of *slga3ox3* and *slga3ox4* single homozygote mutant (*slga3ox3*, *slga3ox4*) plants and *slga3ox3 slga3ox4* double homozygote mutant (*slga3ox3/4*) plants. The *slga3ox3*, *slga3ox4*, and *slga3ox3/4* plants exhibited decreased stem internode lengths and primary shoot lengths compared to wild-type plants. However, stunted growth, thickened stems, and super-compact inflorescences in the *slga3ox3/4* plants present significant challenges for their practical application. In addition, the *slga3ox3/4* double mutant plants showed lower stomatal conductance to water and transpiration and higher leaf temperature values than wild-type plants. The severe phenotypic effects of the *slga3ox3/4* plants indicate that cultivating the *slga3ox3* or *slga3ox4* plants is suitable in vertical farms with high-tech hydroponics. We suggest that the modifications of *SlGA3ox3* and *SlGA3ox4* genes can be exploited to optimize the stem internodes for vertical farming.

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

PC-0041

Modulating Strigolactone Signaling to Optimize Tomato Shoot Architecture for Vertical Farming

JiWoo Lee[1], Choon-Tak Kwon[1,2*]

[1]Graduate School of Green-Bio Science, Kyung Hee University, Yongin 17104, Republic of Korea
[2]Department of Smart Farm Science, Kyung Hee University, Yongin 17104, Republic of Korea

The acceleration of global warming and consequent climate change has significantly diminished the favorable conditions for traditional agriculture. As a result, a food crisis has emerged, prompting the adoption of vertical farms as a viable solution to address the adverse effects of climate-induced food shortages. While leafy green vegetables with short growth cycles and compact plant height are well-suited for vertical farming, fruiting plants like tomatoes pose challenges due to their continuous and infinite growth. The *DWARF14* (*D14*) gene is involved in the metabolic pathway and signaling of Strigolactones (SLs), a plant hormone that plays a role in shoot branching in *Arabidopsis* and rice. Mutations in *Arabidopsis* orthologs of *D14* caused increased shoot branching, while rice *d14* mutants showed higher tiller numbers and reduced plant height. We thus targeted the tomato *D14* (*SlD14*) to optimize plant height and maximize fruit yield per unit area. Using the CRISPR/Cas9 system through 3 guide sequences, we successfully induced mutations in the *SlD14*. A total of 29 T_0 plants were obtained, and two lines were advanced to subsequent generations, acquiring two distinct alleles. The T_1 plants showed more shoot branching and shorter plant height than the wild-type plants. Future generations will undergo further analysis to evaluate quantitative, physiological, and agronomic traits.

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

PC-0042

CRISPR/Cas9 targeted mutagenesis of tomato *EPIDERMAL PATTERNING FACTOR-LIKE* genes to engineer plant size and architecture

Myeong-Gyun Seo[1], Choon-Tak Kwon[1,2*]

[1]Graduate School of Green-Bio Science, Kyung Hee University, Yongin 17104, Republic of Korea
[2]Department of Smart Farm Science, Kyung Hee University, Yongin 17104, Republic of Korea

Arable area and external environmental factors are critical points for crop production. Vertical farming is a new cultivation system that enables growing crops under restricted space conditions, even in urban areas. However, fruit crops are unsuitable for vertical farming due to their long stem length and vine-like growth. The *ERECTA* gene is involved in above-ground organ elongation, and EPFL ligands regulate its activity in *Arabidopsis.* To optimize tomato shoot architecture, we exploited multiplex CRISPR genome editing to mutate the tomato orthologs of *Arabidopsis EPIDERMAL PATTERNING FACTOR-LIKE* genes (*SlEPFLs*). Among the eleven *SlEPFL* genes, *SlEPFL4*, *SlEPFL5*, and *SlEPFL6*, which are genetically close, were targeted. We evaluated the phenotypes of *slepfl6* single homozygote mutant (*slepfl6*) plants and *slepfl4 slepfl6* double homozygote mutant (*slepfl4/6*) plants. We found shorter stem internodes, inflorescence length, and plant height in the *slepfl4/6* plants compared to wild-type plants. Additionally, there was an overall reduction in stem internode length in *slepfl4/6*, which could be advantageous for utilization in vertical farming. However, such phenotypic changes were not observed in the *slepfl6* mutants. In the physiological traits such as stomatal conductivity, photosynthetic efficiency, and chlorophyll contents, we observed no significant differences among wild-type, *slepfl6*, and *slepfl4/6* plants. Compared to the wild-type plants, the *slepfl6* and *slepfl4/6* plants exhibited a slight decrease in total yield, not harvest index and sugar content. Furthermore, introducing *slepfl5* into the *slepfl4/6* is in progress to fine-tune plant size and architecture.

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

PC-0043

A New Spray Chrysanthemum Cultivar, ‘Dahong Mulgyeol’ with Double Type and Dahong Color Petals for Cut Flower

Seh Hui Jung[1*], Sung Young Jin[1], Chang Hak Choi[1], Hye Rang Beom[1], Sea Hyun Gi[1], Jin Jae Lee[2]

[1]Division of Horticulture, Agricultural Research and Extension Services, 413, Sedong-ro, Iksan-si, Jeollabuk-do, Republic of Korea

[2]Herb & wild plants experiment station, Jeonbuk ARES Medicinal Resource Research Institute Namwon, Jeollabuk-do, 55720, Korea

A new spray chrysanthemum cultivar ‘Dahong Mulgyeol’ was developed at the Jeollabuk-do Agricultural Research and Extension Services (Iksan) in 2022. The cultivar ‘Dahong Mulgyeol’ was bred from the cross hybridization between ‘Art’, a spray chrysanthemum cultivar with yellow colored double type petals, and ‘Jinta’, a spray chrysanthemum cultivar with pink colored single type petals in 2014. Trials were conducted from 2015 to 2022 for evaluation and selection of the cultivar, including a shading culture in spring and a retarding culture in summer. Finally, ‘Dahong Mulgyeol’ was selected. The natural flowering date of ‘Dahong Mulgyeol’ was October 27th, and year-round flowering by shading or retarding culture is possible. ‘Dahong Mulgyeol’ has double type flower with dahong (ORG34A) colored petals and the diameter of flower was 7.3cm. The number of flowers per stem was 17.0 and the number of petals per flower were 393.4 in natural flowering time. The plant height was 95.9cm and stem diameter was 4.8cm. The color of leaf was green (GG137B) and that of stem was green (GG137D). The consumer’s preference was high at 4.5 ranged up to 5.0. The days to flower under summer cultivation was 8 weeks (56 days) from the beginning of short-day treatment. The resistance of white rust is high level than the control(‘Malibu Purple’).

***Corresponding Author:** Tel. 063-290-6135, E-mail: sehhui@korea.kr

PC-0044

Evaluation of Horticultural Characteristics and Disease Resistance in Sweet Pepper(*Capsicum* spp.) Germplasm

Jin-Hee Kim[1*], Jong-Suk Park[2], Se-Hong Bae[1], Ye-Ji Hong[1], Hun-Tak Oh[1], Kyoung-Won Seo[1], Eun-Ji Hwang[3], Jun-Dae Lee[3]

[1]Fruit Vegetables Research Institute, Jeonbuk A.R.E.S., Gunsan 54062, Republic of Korea
[2]Division of Horticulture, Jeonbuk A.R.E.S., Iksan 54591, Republic of Korea
[3]Department of Horticulture Institute of Agricultural Science and Technology, Jeonbuk National University, Jeonju 54896, Republic of Korea

In Korea, Sweet pepper is a mainly export crop among fresh produce. However, Cultivated seeds are highly dependent on imports from multinational corporations. Domestic sweet pepper has a short breeding period. Therefore, Characteristics primary germplasm should be provided for development of new varieties. In order to investigated the basic characteristics, 160 pepper germplasm were collected from RDA genebank in 2022. 8 qualitative traits(hypocotyl color, flowering time, flower color, etc.) and 17 quantitative traits(8 Growth characteristics: plant height, number of leaf nodes, etc./9 fruit characteristics: firmness, weight, lobe, etc.) were investigated, and disease resistance test was performed using HRM. In this study, pepper germplasm with blocky type observed 25 species including IT158328, IT199404, IT 240866, and IT 240866. The fruit weight ranged from 2.4 to 162.7g among 18 genetic resources were over 120g(S size), 3 germplasms(IT259225, IT260105, and IT270507) have over 160g(L Size). And we selected 50 disease resistance genetic resources(15 Anthracnose resistance, 20 Tomato Spotted Wilt Virus resistance(TSWV), and 15 powdery mildew resistance). Among them, 3 germplasm(IT218947, IT261491, and IT261552) were identified as complex resistance to anthracnose, TSWV, and powdery mildew. The genetic resource information will be constructed with image database to be used basic information for breeding.

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***Corresponding Author:** Tel. 063-290-6063, E-mail: kjh102320@korea.kr

PC-0045

Establishment of an integrated management system for the systematization of virus field diagnosis in bulbous flowers

Kwang-hyun Cho, Jeong-won Seo, Jae-eun Oh, Da-young Jeon, Ji-eun Kim, Jeong-hee Lee*, Sung-Hwan Jo*

SEEDERS Inc., Daejeon, 34912, Republic of Korea

The interest in bulbous flowers has been increasing, yet due to the characteristics of bulbous reproduction, the risk of viral infection from the parent bulb remains a significant concern. Furthermore, detecting a bulbous flower virus in the early stages of infection proves challenging, hampering both cultivation and commercialization. Despite these issues, systematic virus management or infection status monitoring systems remain underdeveloped. In this study, we have constructed a database for the standardization of bulbous flower virus diagnosis. We developed a comprehensive management system for bulbous flower viruses, which includes an on-site diagnosis app and real-time transmission and storage of data obtained through the app to a web-based platform. Data on virus detection diagnoses for gladiolus, lilies, tulips, and daffodils were provided by Kangwon National University and Kyungpook National University, respectively. This allowed us to establish a diagnostic list database (DB) comprising variety, diagnosis dates, collection sites, types of infectious viruses, and disease images. The DB incorporates diagnostic information for 51 tulips, 143 gladiolus, 74 daffodils, and 108 lilies. The database includes the collection location, symptom information, collection date, and virus infection results for each crop. An integrated system web, connected to the DB, was developed for effective data management and analysis. This system enables access to unique numbers, variety information, and virus diagnosis information for a total of 376 individuals. Additionally, a list of bulbous flowering plants susceptible to each virus, a list of associated symptoms, and current data on virus infection status in Korea were incorporated. The app facilitates precise storage of virus diagnosis information using the QR code of the diagnostic kit and captures the history of local testing using smartphone GPS functionality. This integrated management system will expedite the detection of viral infections in bulbous flowers and mitigate the damage to farmers due to these infections.

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

PC-0046

Assessment of Genetic Diversity and Structure Based on Microsatellite Markers of Pear Germplasm Collected from Korea

Keumsun Kim, Kyungho Won, Seong Sig Hong, Il Sheob Shin*

Pear Research Institute, National Institute of Horticultural & Herbal Science, Rural Development Administration, Naju 58216, Republic of Korea

Korea has a diverse pear germplasm and has made great contributions to domestication of the *Pyrus* genus. The diverse germplasm in the region is considered as a significant source of important genes and offers invaluable opportunities for breeders to achieve their breeding goals. However, in addition to the lack of genetic information of local pear germplasms, it is also difficult to manage germplasm by synonyms and homonyms. The objective of this study is to identify synonyms and homonyms and to assess genetic diversity in pear germplasm, including local pear genotypes, by analyzing genetic variation with twenty simple sequence repeat (SSR) markers, including the ECPGR set and the USPGR set. As a result, 43 synonyms were identified among 146 pear accessions. Of 146 accessions in 43 groups, 122 accessions in 33 groups had the same genotype and phenotype, while 24 accessions in 10 groups had different phenotypes. In the analysis of the phylogenetic tree, the accessions were classified into two major groups (group I and II), and nine subgroups in group II. In our population structure analysis, the local pear genotypes showed high diversity within the regions from which they were collected. Ulleungdo Island had low genetic diversity compared to other regions due to its isolation as an island. The genetic structure between the inland regions, which were based on Baekdudaegan, was similarly analyzed. The present SSR fingerprint database will have great contributions to future germplasm management efforts and the development of breeding materials.

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***Corresponding Author:** Tel. 061-330-1540, E-mail: shinis3@korea.kr

PC-0047

Genome-wide identification of *GASA* gene family and characterization of heat-induced *GASA* genes in response to abiotic stresses in lettuce

Jin Seok Yoon[1], Sun Ho Lee[2], Woo Joo Jung[3], Dae Yeon Kim[4], Yong Weon Seo[1,2*]

[1]Ojeong Plant Breeding Research Center, Korea University, Seoul 02841, Republic of Korea
[2]Department of Plant Biotechnology, Korea University, Seoul 02841, Republic of Korea
[3]Institute of Life Science and Natural Resources, Korea University, Seoul 02841, Republic of Korea
[4]Department of Plant Resources, College of Industrial Science, Kongju National University, Yesan 32439, Republic of Korea

Lettuce, a globally consumed and economically significant vegetable, is particularly sensitive to high temperatures and water content as a cool-season crop. High temperatures promote premature bolt formation, reducing lettuce productivity. Therefore, investigating delayed bolting and flowering mechanisms is crucial for maintaining optimal harvestable yield and quality. In this study, 20 *GASA* gene family were identified from the lettuce genome. The chromosome localization, phylogeny, gene structure, *cis*-acting elements and family evolution analysis were evaluated via in silico analysis. All GASA proteins, except one, exhibited a conserved GASA domain containing 12 cysteine residues. *Cis*-element analysis revealed that *LsGASAs* were closely associated with light, phytohormones, and stress resistance. Duplication analyses uncovered five segmental and three tandem duplication events within the LsGASA family. Synteny analysis showed that *LsGASA5* is highly collinear with all species in lettuce, Arabidopsis, tobacco and rice. According to gene expression analysis, 6 out of 20 *LsGASA* showed increased expression patterns in the shoot apical meristem under heat stress. Furthermore, 6 *GASA* exhibited highly increased expression levels in response to NaCl, abscisic acid, and gibberellin treatment. Additionally, LsGASA proteins were predominantly located in the plasma membrane and/or cytosol. These findings provide valuable insights for future investigations on the involvement of lettuce GASA genes in the signaling pathways associated with heat-induced bolting.

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

PC-0048

Evaluation and Comparison of chemical composition profiling in 23 Choy Sum (*Brassica rapa* subsp. *chinensis* var. *parachinensis*) Germplasms

Seong-Hoon Kim[1*], Sehun Kim[1], Haemi Cho[1], Young-Wang Na[1], Aejin Hwang[1], Yoon-Jung Lee[1], Kyung-chul Kim[2]

[1]National Agrobiodiversity Center, National Institute of Agricultural Sciences, RDA, Jeonju 54874, Korea
[2]Asia Seed korea, Seoul 05855, Korea

Choy sum (*Brassica rapa* subsp. *chinensis* var. *parachinensis*) is one of the cruciferous vegetables from the Brassicaceae family that is well known as economically important crop and a staple food ingredient in Asia. *Brassica* vegetables contain a large number of glucosinolates (GSLs). GSLs are secondary compound containing sulfur and nitrogen and they or these breakdown products are reported to have fungicital, bacteriocidal and allelopathic properties. Moreover, GSLs have a health benefits such as antioxidant and anticancer properties. To introduce crops with beneficial compounds into the diet, it is necessary to analyze the diversity of GSLs. Therefore, the purpose of this study was to construct GSLs profile database of germplasms that can be utilized as breeding materials. The twenty-three choy sum germplasms conserved in RDA Genebank were used. A total of 17 glucosinolates were detected, including 12 aliphatic, 4 aromatic, and 1 indolic GSL. Among the aliphatic GSLs, the gluconapin (GNA), glucobrassicanapin (GBN), progoitrin (PRO), and epiprogoitrin (EPI) were predominant, indicating average contents of 2997.62, 1884.15, 1430,06 and 1085.29 μmol・kg^{-1} DW, respectively. The gluconasturtiin (GNS) of aromatic GSL showed the highest content ranging from 74.38 to 2379.24 μmol・kg^{-1} DW and the glucobrassicin (GBC), which only detected indolic GSLs, indicated a content ranging from 85.15 to 908.09 μmol・kg^{-1} DW. The germplasms IT293078, IT228140, IT303519, and IT303519 could be useful as breeding materials due to their high GSL contents in GNA, GBN, PRO, and EPI, respectively. The GNA, predominant GSL, showed a significant positive correlation with glucoiberin (GIB) ($r = 0.59$, $p < 0.01$), glucocheirolin (GCR) ($r = 0.58$, $p < 0.01$), sinigrin (SIN) ($r = 0.94$, $p < 0.01$), and glucoraphanin (GRA) ($r = 0.64$, $p < 0.01$). The high positive correlation between GNA and GRA could be related to the biosynthesis pathway that GRA is the precursor of GNA. In the PCA result, the four principal components had eigenvalue ≥ 1, explaining 85.07% of the total variations. The all GSLs except for GBN and GNL were positively loaded to PC1. While GBN and GNL were loaded positively on PC2 and negatively on PC2, respectively. In score plot, 23 germplasms were clustered into three groups based on GSLs contents. The cluster 2 is considered to be highly influenced by the GNL content. The differences and diversity in GSLs contents among germplasms could provide valuable information for breeding with choy sum of high GSLs. In addition, research utilizing choy sum germplasm is expected to advance as the germplasms and information are available from RDA-Genebank.

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

PC-0049

Evaluation of growth characteristics of sweet potato (*Ipomoea batatas* Lam.) at early growth stage after early transplanting

Sejin Oh[1], Seong-Wook Kang[1], Yumi Lee[2], Seong-Woo Cho[1,2*]

[1]Department of GreenBio Science, Gyeongsang National University, Jinju, 52725, Republic of Korea
[2]Department of Smart Agro-Industry, Gyeongsang National University, Jinju, 52725, Republic of Korea

Low temperature negatively affects on growth of sweet potato (*Ipomoea batatas* Lam. cv. Hopungmi and Sodammi) root, vine, and leaf as a tropical crop. This study was to observe the effect of low temperature on sweet potato early growth. Therefore, we grew slips in growth chambers, and then transplanted at extremely early (1st & 2nd & 3rd) / early (4th & 5th) dates. According to growth stages (3-6 weeks after transplanting), we measured sweet potato vine and leaf traits. After 6 weeks, we measured SPAD index and stomatal traits. In the Hopungmi, on the adaxial side, stomatal length and width of the 1st and 4th transplanting groups were larger than other groups, while stomatal density of the 2nd and 3rd transplanting groups was higher than that of other groups. On the abaxial side, stomatal length and width of the 3rd transplanting group were larger than those of other groups, while stomatal density of 3rd transplanting group was lower than that of other groups. In the Sodammi, on the adaxial and abaxial sides, stomatal length and width of the 5th transplanting group were larger than those of the extremely early transplanting group. Whereas stomatal density of 3rd and 4th transplanting groups was higher than that of other groups. In the SPAD index, Hopungmi and Sodammi 5th transplanting groups were bigger than other groups. For measurement of leaf and vine from slip after transplanting 6 weeks, Hopungmi and Sodammi leaf length and width increased, while vine length and diameter didn't.

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

PC-0050

Study on the prediction of Actuator data in Smart Greenhouse using LSTM neural network

Moon-Seok Jeon, YuSeok Jeong, Hyo Jun Bae, Jaesu Lee, Jongpil Moon, Siyoung Lee, Inchan Choi*

Department of Agricultural Engineering, National Institute of Agricultural Sciences, Jeonju 54876, Republic of Korea

Korea's facility horticulture industry continues to conduct research on smart greenhouses that combine ICT with greenhouses that produce crops intensively. This technology can optimize the crop management of greenhouses, resulting in increased crop production, improved crop quality and cost reduction. However, to optimize greenhouse conditions, users need to periodically identify and adjust actuators based on internal and external environment monitoring. Therefore, we conducted research on predicting actuator data according to the current internal and external environments. To do this, we utilized a LSTM trained on environmental and actuator data from the cultivation season of a leading tomato farm. LSTM was trained with 335,668 datasets after setting it to Window size: 60, Horizon: 1, and Epoch: 100. After that, predictive performance was evaluated with 143,859 test datasets and MAE. As a result, we were able to predict the actuator data with an error of 1.01℃ for the supply temperature, 2.61% for the roof opening, 0.90% for the curtain opening, 1.99% for the 3-way valve opening, 0.02 for the boiler operation, 0.04 for the circulation pump operation, and 0.01 for the flow fan operation. The significance of this technology lies in its potential to narrow the gap in crop production between leading farms and new farms when it is implemented and adopted in agricultural practices. we will conduct research on the applicability of the trained LSTM by comparing crop production between greenhouses where network is applied and those where it is not. This research aims to investigate the feasibility of implementing the technology in agricultural practices.

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***Corresponding Author:** Tel. 010-3017-6366, E-mail: inchchoi@korea.kr

PC-0051

Study on Control Data Prediction Technology for Smart Greenhouse Control

Yu Seok Jeong, Moon-Seok Jeon, Hyo Jun Bae, Jaesu Lee, Jongpil Moon, Siyoung Lee, Inchan Choi*

Department of Agricultural Engineering, National Institute of Agricultural Sciences, Jeonju 54876, Republic of Korea

Agriculture plays an important role in the survival and development of mankind, but Korea is struggling with agriculture due to the four seasons and lack of land. Accordingly, a smart greenhouse has been developed and is attracting attention as a technology that can obtain maximum efficiency in a small area. Smart greenhouses utilize the latest information and communication technologies to provide integrated heating and air conditioning, and farmers can optimize the environment inside the greenhouse. However, as the greenhouse environment is entirely controlled by farmers, there is a large difference in production from farm to farm because expertise is required. Therefore, this paper conducted a study to imitate the greenhouse control of leading farmers by learning data from managed smart greenhouses through LSTM, an artificial intelligence model. Smart greenhouse data located in Sacheon, Gyeongsangnam-do was used, and the data list includes external data, setting data, and control data. External data represents environmental information, configuration data includes input parameters for interaction, and control data includes values applied to greenhouse control. External, setting, and control data were learned as learning input data and output as control data. The predicted error rates for applied ventilation temperatures are MSE 0.022, RMSE 0.151, MAE 0.082 and MAPE 0.44%. For the applied heating temperature, the error rates are MSE 0.001, RMSE 0.034, MAE 0.010, and MAPE 0.06%. It aims to support the optimization of heating and ventilation control of smart greenhouses, and will conduct research on optimal greenhouse control through additional data prediction in the future.

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***Corresponding Author:** Tel. 010-3017-6366, E-mail: inchchoi@korea.kr

PC-0052

당도가 높고 신맛이 적은 플럼코트 '슈가벨벳' 육성

김대홍*, 이지윤, 서은철, 이형일, 박원흠

경상북도 청도군 이서면 가금구라길 186-6 경상북도농업기술원 청도복숭아연구소

플럼코트는 동양계 자두(*Prunus salicina*)와 살구(*Prunus armeniaca*)를 교배하여 만든 과종으로 국내 육성 품종으로는 농촌진흥청이 품종보호권 등록한 '하모니','티파니', '심포니', '샤이니'4품종이 있고, 국외에는'New Castle Gold(뉴질랜드)', 'Red Velvet(미국)', 'Red Pricot(일본)'등 많은 품종이 있다. 그러나, 국내에 재배되는 플럼코트는 농촌진흥청에서 육성한 품종이 대부분으로 선택의 폭이 한정적인 실정이다. 경상북도농업기술원 청도복숭아연구소에서는 열대과일을 포함한 다채로운 과일에 대한 소비자의 요구를 반영한 핵과류 신과종을 만들기 위해 2011년 플럼코트 육종을 시작하였다.

'슈가벨벳(Sugar Velvet)'은 과육이 붉고 과즙이 풍부한 자두'솔담(♀)'에 당도가 높고 화분이 풍부한 살구 '하코트(♂)'를 인공교배하여 2012년 파종, 2018년 1차 선발하고 2021년 최종 선발하였다. 과중은 86g, 당도는 16.3°Brix로 대조품종인 '하모니'95.4g보다 크기가 다소 적으나 대조품종(12.3°Brix)보다 당도가 높다. 과육 바탕색은 오렌지색이고 수확기는 6월 하순으로 대조품종 보다 3일 빠른 조생 품종이다. 과피는 미세한 털이 덮여 있고 붉게 착색되는 특성이 있어 외관이 양호하다. 이상의 특성들로 2023년 1월 국립종자원에 품종보호 출원하였다.

***교신저자:** Tel. 054-373-5486, E-mail: whshdw@gmail.com

PC-0053

Analysis of differences in tomato growth and yield according to summer planting season

Hyo Jun Bae, Yu Seok Jeong, Moon-Seok Jeon, Seong Jin Park, Siyoung Lee, Inchan Choi*

Department of Agricultural Engineering, National Institute of Agricultural Sciences, Jeonju 54876, Republic of Korea

Summer cropping is an environment in which it is difficult to grow crops due to high temperature, high humidity due to the rainy season, and weak light. As a result, productivity is reduced due to poor fruiting, deformity and occurrence, and is avoided by farms. However, in the case of greenhouses equipped with cooling facilities, an increase in farm household income can be expected due to an increase in average price due to a decrease in domestic production. This study was conducted to derive the planting period with the best yield during summer cultivation. Rural Development Administration Advanced Digital Greenhouse (east height 8.3m side height 7m) 1building (24m*40m) was divided into 3parts, planted three times from the left at an interval of about 4weeks, at a planting density of 1.11weeks/m2, in April, May, and June. The growth and yield of tomatoes were investigated. The growth survey was divided into early growth (68days after planting) and late growth (242days after planting) for 4weeks, and yield was measured by harvesting once or twice a week from the first harvest to 265days after planting. As a result of investigating early growth and late growth, it was found that planting were sown in April and had the smallest plant height, and the flowering position, stem Diameter, leaf length, leaf width were the smallest. The final yield was 16.4% and 33.2% higher in April than in May and June, respectively. This result is thought to be that assimilation products were distributed to fruits rather than nutrient organs compared to May and June in the planting season in April, and it is judged to be the most suitable planting period for summer cropping.

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***Corresponding Author:** Tel. 063-238-4024, E-mail: inchchoi@korea.kr

PC-0054

Polyploidy Induction in sweet persimmon by Colchicine and Oryzalin Treatment

Hye-Gyoung Yoo*, Byul-Ha-Na Lee, Kyeong-Bok Ma, Sung-Sik Hong
Pear Research Institute, NIHHS, RDA. Naju 520-821, Korea

According to a recent consumer trend survey, it has been observed that consumers prefer seedless fruits for convenient consumption. Persimmon, a crop with a chromosome count of 2n=6x (hexaploid, x=15), underwent chromosomal doubling through evolution. Some astringent persimmon varieties are naturally seedless due to being polyploid (2n=9x, x=15). To increase demand for seedless sweet persimmons, it is essential to develop seedless (2n=9x) varieties that align with consumer preferences. This can be achieved by using diploid(2n=6x) pollen without meiosis for pollination or by obtaining a dodecaploid(2n=12x) individual through artificial chromosomal doubling and using it as a parent. In this study, the objective was to secure polyploid (2n=12x) individuals for breeding seedless(2n=9x) individuals and make them as parental models. To induce polyploidy, embryo culture was performed using immature seeds. After 30 days of embryo culture, the shoot tips were trimmed to a length of 0.5 cm and treated with colchicine and oryzalin. Embryos for culture were obtained from four mating combinations: 'Fuyu'×'Taishu', 'Roman'×'Taishu,' 'Ro-19'×'Taishu,' and 'Sinchu' × 'Taishu.' Immature seeds were collected 70-80 days after fruiting, and the embryos were isolated and cultured. Colchicine treatment at a concentration of 0.5% was applied to the four combinations based on previous literature. Oryzalin treatment was carried out at a concentration of 0.5%, considering specific combinations like 'Ro-19' × 'Taishu,' 'Shinchu' × 'Taishu,' and others, to determine the appropriate concentration. The treatments were immersed for 24 hours at four levels: 0.01%, 0.05%, 0.001%, and 0.005%. Following treatment, shoot and root development was induced in 1/2 MS medium. After 30 days of culture, fully developed leaves were collected for ploidy analysis using Flowcytometry. The success rate of polyploidy induction with 0.5% colchicine treatment was 23.0%. In contrast, the highest success rate of 48.0% was achieved with the 0.005% oryzalin treatment. These results indicate that oryzalin is more effective in inducing polyploidy in sweet persimmons compared to the colchicine treatment mentioned in previous research. Oryzalin is considered relatively safer than colchicine and is widely used for polyploidy induction in various plant species. The findings of this study provide fundamental data for improving the efficiency of inducing chromosomal ploidy.

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***Corresponding Author:** Tel. 061-330-1582, E-mail: uiop9397@korea.kr

PC-0055

아라비카 커피 ‘카투아이’ 잎의 엽령별 카페인, 클로로젠산 및 망기페린 함량 변화

김성철[1*], 장연진[1], 이목희[1], 송은영[1], 김영희[1], 선정훈[2], 문준관[2]

[1]제주시 애조로 1285 국립원예특작과학원 온난화대응농업연구소
[2]경기도 안성시 중앙로 327 한경대학교 식물생명환경과학과

스페셜티커피로 가장 많이 이용되는 아라비카 커피 ‘Catuai’ 품종의 국내시설재배시 잎의 활용 가능성을 검토하기 위하여 잎의 엽령별 카페인. 클로로젠산 및 망기페린 함량을 비교하였다. 실생묘 3년생을 2019년 5월 중순 1.5×1.5m로 토양에 정식하고 2021년 7월에 발아 후 0.5개월, 1개월, 2개월, 4개월, 8개월째의 잎을 채취하여 동결 건조한 후 50% MeOH로 24시간 동안 추출하여 분석에 사용하였다. 카페인은 엽령이 0.5개월에서 21.8mg/g으로 가장 높았고 엽령이 증가할 수록 감소하였다. 발아 후 0.5개월에서 8개월째는 0.5개월 대비 31.7%까지 감소하였다. 클로로젠산 함량은 0.5개월 잎에서 41.1mg/g로 가장 높게 나타났고 카페인과 마찬가지로 엽령이 증가할수록 감소하였으며 8개월째는 36.0%까지 낮아졌다. 망기페린 또한 0.5개월에서 20.9mg/g으로 가장 높았으며 8개월째인 완전히 성숙된 잎에서는 4.3mg/g으로 20% 수준까지 낮아졌다. 한편 엽령별 비교에서 카페인, 클로로젠산, 그리고 망기페린은 0.5개월에서 1개월째까지 각각 48.6%, 69.6%, 80.4%까지 낮아지고 2개월째에는 각각 32.6%, 29.9%, 27.3%까지 낮아져 엽령이 1개월에서 2개월 사이에 급격히 감소하는 것으로 나타났다. 이상의 결과를 종합해 볼 때 아라비카커피 ’카투아이’ 잎을 이용한 제품 개발에는 0.5개월에서 1개월째의 잎을 활용하는 것이 유리할 것으로 판단되었다.

***교신저자:** Tel. 064-741-2560, E-mail: kimsec@korea.kr

PC-0056

Identification of novel genetic resources regulating anthocyanin biosynthesis in pepper (*Capsicum annuum*)

Tae-Gun Kim[1], Jelli Venkatesh[2], Jinyoung Byun[2], Jin-Kyung Kwon[2], Byoung-Cheorl Kang[1,2*]

[1]Interdisciplinary Program in Agricultural Genomics, Department of Agriculture, Forestry, and Bioresources, Research Institute of Agriculture and Life Sciences, Plant Genomics Breeding Institute, College of Agriculture and Life Sciences, Seoul National University, Seoul, South Korea

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

Anthocyanins, which are important secondary metabolites in plants, play various roles such as enhancing survival against stresses, providing aesthetic value through antioxidant effects, and benefiting human health. The demand for purple peppers, which are rich in anthocyanins, is increasing in consumer markets. In the biosynthesis of anthocyanins, MYB transcription factors are crucial regulators. The gene *CaAN3*, encoding an R2R3 MYB transcription factor, has been identified as a key regulator of anthocyanin biosynthesis in pepper fruit (*Capsicum annuum*). However, there are certain pepper accessions that exhibit fruit-specific anthocyanin biosynthesis despite possessing a functional *CaAN3* allele, suggesting the involvement of other regulatory factors. To identify a novel locus responsible for fruit-specific regulation of anthocyanin biosynthesis, we conducted a cross between an accession with nonfunctional *CaAN2* and lacking *CaAN3* expression and an accession with green immature fruits. A phylogenetic tree was constructed using known R2R3 MYB transcription factors associated with anthocyanin biosynthesis in plants. Among the twelve MYB transcription factors clustered in the anthocyanin biosynthesis MYB transcription factors clade, including *CaAN2* and *CaAN3*, we focused on identifying the novel candidate gene responsible for purple immature fruits in the SNU_A cultivar with nonfunctional *CaAN2* and lacking *CaAN3* expression. Through quantitative PCR (qPCR), we analyzed the expression levels of the twelve MYB transcription factors in the fruit. Three transcription factors showed significant differences in expression levels, indicating their potential involvement in pepper fruit color variation. Further functional studies are necessary to elucidate the precise roles of these three MYB transcription factors in the variation of purple color in pepper fruits.

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

PC-0057

국내 국화 핵심 육성집단에 대한 주요 원예 형질의 유전력 검정

이향열[1], 김승영[1], 김경만[1], 김소현[1], 김대관[2], 정경진[3], 박하승[4], 정재아[5], 김태성[1*]

[1]서울시 종로구 대학로 86 한국방송통신대학교 농업생명과학과
[2]서울시 강남구 테헤란로 25길 디엔에이케어
[3]경상남도 창원시 의창구 대산면 진남로 149 경상남도농업기술원 화훼연구소
[4]충청남도 예산군 오가면 역탑리 충청남도농업기술원 화훼연구소
[5]전라북도 완주군 이서면 농생명로 100 농촌진흥청 국립원예특작과학원 원예작물부 화훼과

본 연구는 국내 국화 육종의 효율성을 제고시키고 국화 주요 원예 형질의 광의의 유전력 및 다양한 양적 형질의 지표를 산출하기 위하여 수행되었다. 사용된 국화 자원은 국화 육성 소재로써 국립원예특작과학원, 충남화훼연구소, 경남화훼연구소에서 각 32점씩 총 96점을 분양받았고, 유전력 계산 등을 위한 표현형 조사는 수원시 입북동에 소재한 비가림 하우스 내에서 실시되었다. 각 국화 자원은 피트모스와 펄라이트를 2:1(v/v)로 혼합한 토양에서 15cm x 15cm 간격으로 완전 임의 배치로 재식되었고, 5월에서 10월까지의 기간동안 관수와 관비는 자동 양액 공급장치로 일률적으로 제어되었다. 대상이 된 원예 형질은 초장, 줄기직경, 측지수, 착화수, 꽃목길이, 꽃목직경, 꽃직경, 통상화직경, 꽃볼륨, 꽃잎길이, 꽃잎너비 및 개화일수이었고 표현형 측정은 서로 다른 2개의 베드에서 각 자원 당 3 반복씩 2021년과 2022년, 총 2년간에 걸쳐 이루어졌다. 이를 바탕으로 광의의 유전력(Broad sense of heritability, H^2), 유전변이계수(genotypic coefficient of variation, GCV), 표현변이계수(phenothpic coefficient of variation, PCV), 유전적 진전(genetic advance, GA) 및 유전적 진전율(genetic advance as present of mean, GAM)이 R기반 Sommer package를 활용해 계산되었다. H^2는 각 국화 타입별로 표현형 간 큰 차이를 보였고 유용자원은 H^2이 80% 넘는 표현형 중에서 선발되었다. 스탠다드 타입에서는 초장과 꽃목길이, 꽃잎너비가 높은 유전력을 보였고, 조사가 된 스탠다드 국화 자원 중 용마와 단미가 가장 우수한 것으로 판명되었다. 겹꽃 스프레이 타입에서는 초장, 꽃목길이, 꽃볼륨이 높은 유전력을 보였으며 우수 자원으로 젬버라와 WR72가 선발되었다. 홑꽃 스프레이 타입에서는 초장과 줄기직경 및 꽃직경이 높은 유전력을 보였고, 예스루비와 러블리살몬이 선발되었으며 폼폰형 스프레이 타입에서는 초장과 꽃직경, 꽃목길이 중심으로 매직팝과 화이트팝이 선발되었다. 꽃직경을 중심으로 화단국에서는 다원볼과 다운볼, 소형분화국에서는 스노우빔과 핑크아이가 선발되었다.

***교신저자:** Tel. 02-3668-4638, E-mail: kts117@knou.ac.kr

PC-0058

국내 발생 상추 시들음병 균주(*Fusarium oxysporum* f.sp. *lactucae*)의 레이스 동정 체계화

김정분[1], 김소현[1], 김경만[1], 김대관[2], 김태성[1]*

[1]서울시 종로구 대학로 86 한국방송통신대학교 농업생명과학과
[2]서울시 강남구 테헤란로 25길 디엔에이케어

Fuusarium oxysporum f. sp. *Lactucae* (Fol) 은 상추의 시들음병(*Fusarium wilt*)의 병원균으로, 전 세계 토양에 분포하는 것으로 사료된다. 현재 4개의 race가 알려져 있는데 race 1은 1967년 일본에서 처음 보고된 이후 유럽, 중동 및 아메리카대륙에서도 발견되었으며, race 2는 일본에서만, race 3는 일본과 대만에서 발생한 것으로 보고되었으며, 최근 네덜란드에서 새로운 race가 창궐했다고 알려졌다. 국내에서도 시들음병은 하절기 상추 생산에 심각한 피해를 매년 끼치고 있지만, 국내에서 분화된 race에 대해서는 아직 보고된 사례가 없었다. 따라서 본 연구는 국내 발생 FOL 균주 15개를 대상으로 race 동정 및 체계화를 시도하였다. *F. oxysporum* genome 내에 존재하는 889개의 SNP로 15개 FOL에 대해 phylogenetic tree 분석을 한 결과 3개 이상의 group이 발견되었고, 그중 3개의 group은 race 1, race 2, race 3으로 사료 되었다. 특이하게 3개의 FOL 균주-16-086, 17-447 및 15-128은 race 1과 2와 비교하면 race 3과는 상대적으로 가깝지만 다른 clade에 속하는 것으로 관찰되었으며, 이들 균주가 race 3이 아님을 증명하기 위해 병원성 검정과 VCG (vegetative compatibility group) 검정을 수행하였다. 상추 시들음병 판별품종인 defender로 병원성 검정을 시도한 결과 16-086은 race 3인 09-192와 유의하게 다른 병 반응을 보였고, VCG 검정에서 09-192와 16-086은 compatible 하지 않는 것으로 관찰되어, 16-086은 race 3이 아닌 다른 새로운 race로 판명되었다. 또한, VCG test에서 16-086, 17-447 및 15-128은 각각의 조합에서 compatible 하지 않는 것으로 관찰되어, 16-086, 17-447 및 15-128은 서로 다른 race일 가능성이 크며, 이는 국내에 FOL race 1, 2, 3 외에 다양한 FOL race들이 존재할 것으로 예상할 수 있었다. 이 결과는 다른 나라에 비해 많은 FOL race가 국내에서 분화 되었다기보단 기존의 single locus 기반 FOL race 동정의 한계로 인한 false negative 결과로 판단되며, 좀 더 정확한 FOL race 진단을 위해 향후 SNP 등과 같은 multi-loci 기반으로 FOL race 진단이 국내뿐만 아니라 전 세계적으로 이루어져야 함을 시사해 주고 있다. 본 연구에서 활용한 SNP set은 향후 국 내외에 발생한 FOL의 race 체계화 확립에 유용하게 활용될 것으로 전망된다.

***교신저자:** Tel. 02-3668-4638, E-mail: kts117@knou.ac.kr

PC-0059

파파야 주요 유전자원의 국내 시설재배시 생육 특성 비교

김성철*, 이목희, 장연진, 한현희

제주특별자치도 제주시 애조로 1285 국립원예특작과학원 온난화대응농업연구소

파파야 디저트용 과실 신품종 육성을 위하여 2014년부터 2019년까지 해외에서 품종 및 유전자원 18계통을 수집하고 가온하우스 재배시 재배특성에 대하여 조사하였다. 2015년 11월부터 2019년까지 종자를 파종하여 제주지역 비닐하우스에 2.0m×2.5m 간격으로 정식하였으며 겨울철에 최저온도를 13℃로 유지하였다. 계통별로 잎에 대한 특성을 조사한 결과 엽장과 엽폭은 5차 Bolivia가 가장 길었으며 2차 잎은 ‘Callina’에서 만 나타났다. 과실 특성을 조사한 결과 종경과 횡경 및 과실의 크기는 ‘Australia’가 각각 138.9mm, 87.8mm, 그리고 441.0g으로 가장 작았으며 Bang Kok이 각각 323.1mm, 123.8mm, 그리고 1992.5.0g으로 가장 크게 나타났다. 당도는 Australia, 5차 볼리비아, 그리고 ‘Holland Gold’에서 각각 11.3°Brix, 10.2°Brix, 그리고 10.0°Brix로 높게 나타났으며 4차 DP 등이 낮았다. 경도는 ‘Calina’가 1.9N으로 가장 높았으며 4차 DP가 0.5N으로 가장 낮았따. 계통별 과피색을 조사한 결과 명도(L 값)는 ‘Holland Gold가 68.8로 나타났으며, a값은 2014 채종 왜성종이 24.9, b값은 Malaysia와 2014 Bolivia에서 높게 나타났다. 계통별로 질감과 향, 과즙 등 식미감을 평가한 결과 2014 Bolivia와 ‘Holand Gold’등이 양호한 것으로 나타났다.

***교신저자:** Tel. 064-741-2560, E-mail: kimsec@korea.kr

PC-0060

Establishment of Real-Time qPCR Primer Sets for Citrus Carotenogenesis-Related Genes and Their Applications During Fruit Development

Chang Jae Oh[1*], Eun-Sil Kim[1], Hye-Young Lee[1], Hee-Jung Jung[1], Cheol Woo Choi[2], Sukman Park[2], Su-Hyun Yun[2], Gun-Hyung Cho[1], Ho Bang Kim[3]

[1]Life Sciences Research Institute, Biomedic Co., Ltd., Bucheon 14548, Korea
[2]Citrus Research Institute, National Institute of Horticultural & Herbal Science, RDA, Jeju 63607, Korea
[3]Department of Equine Resources and Science, Cheju Halla University, Jeju 63092, Korea

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 64 isoforms for 16 enzymes and 30 putative transcription factors (TFs). We established real-time qPCR primer sets for those genes and tested their quality including PCR efficiency and specificity. Finally, during citrus fruit maturation, their temporal expression levels were analyzed in fruit peel/flesh of two representative citrus cultivars, *C. clementina* and *C. sinensis* and distinct characteristics of gene expression profiles between two cultivars will be discussed.

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

PC-0061

Identification of drought tolerant accessions and correlation analysis between morpho-physiological traits and drought tolerance in pepper

Kyu Kyu Thin, Je Min Lee*

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

Drought stress is one of the factors limiting pepper production in water-deficient regions. It affects growth and development by inducing morphological, biochemical, and physiological changes. Breeding drought-tolerant varieties is a sustainable strategy to mitigate drought, therefore reliable evaluation systems are essential to identify the drought-tolerant pepper accessions. In this study, 100 pepper accessions were screened for drought tolerance under highly controlled condition at the vegetative stage. Selected accessions exhibited a higher recovery rate after the drought stress and showed a durable tolerance at the flowering stage in greenhouse condition. Correlation analysis between morpho-physiological traits and drought tolerance indicated that the recovery rate was positively correlated with root length and relative water content, and negatively correlated with plant height, stem diameter, number of leaves, and stomatal density. Gene expression analysis showed that the drought-tolerant accession exhibited higher expression levels of ABA-related and drought-responsive genes under the drought stress at various time points. Drought-resilient accessions with favorable adaptive traits identified in this study will be valuable in breeding programs to generate new pepper cultivars to cope with climate change.

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

PC-0062

상추 핵심집단의 질산염 축적 관련 유용 자원 선발 및 관련 분자표지 동정

홍성이, 이향열, 김소현, 김경만, 김태성*

서울시 종로구 대학로 86 방송통신대학교 농업생명과학과

채소류의 질산염은 인체의 단백질 합성에 중요한 공급원으로, 전체 질산염 섭취량의 75~80%를 차지하며 소화과정을 통해 체내에 흡수되어 활용된다. 질산염은 자체의 독성은 없지만, 과도한 섭취는 영유아에게는 청색증을 유발하기도 하며 건강에 해로울 수 있으며, 아질산으로 환원된 상태에서 니트로사민(Nitrosamine)을 형성하면 발암물질로 인체에 유해할 수 있어서 미국 환경보호청은 질산염에 1일 섭취에 대한 독성 참고치를 정하고 있다. 주로 생채로 섭취하는 상추는 채소 중 질산염 함량이 높다고 보고되어 있고, 현재까지의 상추의 질산염 함량에 관한 연구는 특정 품종의 재배 환경적 영향에 대한 비교 연구가 대부분이나, 같은 재배환경에서 상추 자원에 따라 질산염 함량 범위가 매우 크므로, 그와 관련된 유전적 요인 발굴에 관한 연구가 필요하다고 사료된다. 따라서 본 연구는 KNOU 상추 핵심집단을 대상으로 Ion Chromatography를 기반 질산염 함량을 정량 평가하여, 질산염 축적 관련 유용 자원을 선발하고, GWAS(genome-wide association study)분석을 통해 관련 분자표지 동정을 목적으로 수행하였다. 핵심집단 내 상추 자원들 중 질산염 함량에 있어서 전체 평균을 유의하게 초과하는 자원들이 관찰되었고, 이들 자원은 특정 타입뿐만 아니라 주요 형질(추대일수, 비엽중, 시들음병 저항성, 조직감)간 상관관계는 연관성이 낮은 것으로 판명되었다. GBS(genotyping by sequencing)로 얻은 91,048개의 SNP(Single Nucleotide polymorphism)를 활용하여 GWAS를 분석한 결과 cut-off p-value 이상의 SNP들이 다수의 major peak뿐만 아니라 산재한 형태로 관찰된 것으로 보아, 질산염 체내 축적 정도는 다수의 유전자가 관여하는 complex trait로 사료되었다. 또한, 고 질산염 함량 자원, 저 질산염 함량 자원, 환경영향 질산염 함량 자원 그룹으로 분류하여, 재현성을 확인하여, 질산염 축적 관련 안정 자원들을 선발하였다. 본 연구를 통해 발굴된 후보 SNP들은 질산염 축적 안정 유용 후보자원을 효율적으로 선발하는 데 활용될 것으로 전망된다.

***교신저자:** Tel. 02-3668-4638, E-mail: kts117@knou.ac.kr

PC-0063

Knockout of the *SlSGR1* gene increases lycopene content and elucidates by transcriptomic and metabolome analysis

Jin Young Kim[1], Jong Hee Kim[1], Seong Yeon Sim[1], U Min Byeon[1], Yu Jin Jung[1,2], Kwon Kyoo Kang[1,2*]

[1]Division of Horticultural Biotechnology, School of Biotechnology, Hankyong National University, Anseong 17579, Korea
[2]Institute of Genetic Engineering, Hankyong National University, Anseong 17579, Korea

The SGR1 (STAYGREEN1) protein is a critical regulator of plant leaves in chlorophyll degradation and senescence. The functions and mechanisms of tomato *SGR1* action are poorly understood and worthy of further investigation. To investigate the function of the *SGR1* gene, we generated a *SGR1*-knockout (KO) null line via clustered regularly interspaced short palindromic repeats (CRISPR)/Cas9-mediated gene editing and conducted RNA sequencing and gas chromatography tandem mass spectrometry (GC-MS/MS) analysis to identify the differentially expressed genes. The *SlSGR1* (*Solanum lycopersicum SGR1*) knockout null line clearly showed a turbid brown color with significantly higher chlorophyll and carotenoid content compared to wild-type (WT) fruit. Differential gene expression analysis revealed 728 differentially expressed genes (DEGs) between WT and *sgr1* #1-6 line, including 263 and 465 downregulated and upregulated genes, respectively, for which fold change was >2, and the adjusted p-value was <0.05. Most of the DEGs were related to photosynthesis and chloroplast function. In addition, the pigment, carotenoid changes in *sgr1* #1-6 line was accumulated of key primary metabolites such as sucrose and its derivatives (fructose, galactinol, raffinose), glycolytic intermediates (glucose, G6P, Fru6P) and tricarboxylic acid cycle (TCA) intermediates (malate and fumarate). Taken together, the transcriptome and metabolite profiles of *SGR1*-KO lines presented here provide evidence for the mechanisms underlying the effects of *SGR1* and molecular pathways involved in chlorophyll degradation and carotenoid biosynthesis.

Keywords: lycopene, CRISPR/Cas9 system, genome editing, tomato fruits, carotenoid metabolic pathway

***Corresponding Author:** E-mail: zino@hku.ac.kr

PC-0064

Targeted mutant lines of *LsSOC1* gene greatly improves late-bolting in lettuce

Jin Young Kim[1], Jong Hee Kim[1], Young Hee Jang[1], Ye Ji Lee[1], Tae-Sung Kim[2], Yu Jin Jung[1,3], Kwon Kyoo Kang[1,3]*

[1]Division of Horticultural Biotechnology, School of Biotechnology, Hankyong National University, Anseong 17579, Korea
[2]Department of Agriculture and Life Sciences, Korea National Open University, Seoul, Korea
[3]Institute of Genetic Engineering, Hankyong National University, Anseong 17579, Korea

During high temperatures, floral transition reduces the productivity of lettuce, and changes in taste and texture cause lettuce to lose its economic value. *SOC1* (*SUPPRESSOR OF OVERREXPRESSION OF CONSTANS1*) is a gene expressed in the plant's main cortex that recognizes flowering signals and regulates flowering-related genes (*CO*; *CONSTANS, FLC; FLOWERING LOCUS C*). In this study, a knock-out editing system by the CRISPR/Cas9 system was fostered using the *SOC1* gene that encodes the MADS-box transcription factor. Of the 60 genetically modified plants, 34 gene editing systems were selected. Various variations have occurred in the form of bi-, hetero-, and homo-alleles, depending on the type of editing line. In addition, in the T1 generation, null lines from which transferred DNA (T-DNA) was removed were fostered, confirming that the conversion to growth phase was delayed at a high temperature of 35℃, resulting in a significant delay in bolting. Loss of function of *SOC1* through CRISPR/Cas9 mediated genome editing showed late-bolting in lettuce crops. These results are thought to be used to foster varieties for stable lettuce cultivation at high temperatures.

***Corresponding Author:** E-mail: zino@hku.ac.kr

PD-0001

Comparative transcriptome analysis shed light on *C. crenata* peelability by CcNST1 network and accumulation of condensed tannins

Jaewook Kim[1], Baeyoung Choi[1], Gyeong Tae Lee[2], Jeongwon Yoon[3], Yuree Lee[3*], Cheol-woo Kim[2*], Donghwan Shim[1*]

[1]Department of Biological sciences, Chungnam national university, Daejeon, 34134, Republic of Korea
[2]Forest Microbiology Division, National Institute of Forest Science, Suwon, 16631, Republic of Korea
[3]School of Biological Sciences, Seoul National University, Seoul, 08826, Republic of Korea.

Korean/Japanese chestnut, Castanea crenata is commonly used as food ingredient due to their nutritional value and sweet taste in Eastern Asia. However, C. crenata has hard shell tissue with pellicle tissue in outer layer which tastes bitter, protecting flesh and embryo tissues. Peelablity of shell and pellicle is one of the important traits determining market value and consumer preference of C. crenata cultivar. Breeding effort to develop an easy-peeling chestnut was performed and several cultivars were identified. To identify how outer-layer peelability is regulated, we performed mRNA-sequencing analysis on easy-peeling C. crenata cultivar Porotan and hard-peeling cultivar Tsukuba in outer tissues of early stage. We could identify cell wall related genes were up-regulated while cell division related genes and tannin biosynthetic genes were down-regulated in Porotan. Among those, we could identify expression level of NST1 (NAC SECONDARY WALL THICKENING PROMOTING FACTOR1), which is one of the key genes determining the thickness of the cell wall was up-regulated and several tannin biosynthetic genes were down-regulated in Porotan by in silico analysis and qPCR analysis. Moreover, we measured tannin amounts in 8 cultivars and found out hard-peeling cultivars tend to contain more condensed tannin. Thus, we found out outer-layer peelability is dependent on dual gene network which regulates condensed tannin amount and fruit dehiscence.

***Corresponding Author:** Tel. 02-880-2136, E-mail: yuree.lee@snu.ac.kr
Tel. 031-290-1153, E-mail: futuretree@korea.kr
Tel. 042-821-6279, E-mail: dshim104@cnu.ac.kr

PD-0002

The first genomic selection study of *Pinus Koraiensis* using GWAS marker information to improve prediction accuracy

Donghyun Jeon[1], Yuna Kang[2], Yoonho Lim[1], Donghwan Shim[3], Changsoo Kim[1,2*]

[1]Department of Science in Smart Agriculture System, Chungnam National University, Daejeon 34134, Republic of Korea
[2]Department of Crop Science, Chungnam National University, Daejeon 34134, Republic of Korea
[3]Department of Biological Sciences, Chungnam National University, Daejeon 34134, Republic of Korea

This study presents the first comprehensive genomic selection (GS) research on *Pinus koraiensis*, an economically and ecologically important tree species in South Korea. Due to the lack of a reference genome, research on *P. koraiensis* has been limited. In this study, we performed a genome-wide association study (GWAS) on five traits, including diameter at breast height (DBH), tree height (TH), crown area (CA), crown diameter (CD), and crown volume (CV) using 191 individuals from 23 full-sib families. Subsequently, we conducted genomic prediction (GP) to select the optimal prediction model by comparing 12 genomic statistical models among five genetic populations. We then evaluated the accuracy of GP by combining markers selected from GWAS with the prediction model and assessed the feasibility of GS in genetically distinct populations. We found that conducting separate GPs based on genetic subpopulations did not significantly influence the predictive accuracy for *P. koraiensis*. However, restricting the number of markers to 1.0 threshold markers using eight statistical models (GBLUP, EGBLUP, BRR, BL, BA, BB, BC, RKHS) improved the accuracy for all five traits, with the highest accuracy reaching 0.962 for CA using GBLUP. Moreover, our genomic estimated breeding values (GEBVs) showed a high correlation with the actual measured phenotypic values, indicating the practical applicability of our marker limitation and optimized statistical models in breeding selection. Remarkably, this approach was even applicable to genetically distinct subpopulations. In conclusion, this study demonstrates that marker limitation can lead to an improvement in GS accuracy, ultimately allowing for the shortening of breeding cycles, stabilizing forests, and increasing productivity.

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***Corresponding Author:** Tel. 042-821-7822, E-mail: changsookim@cnu.ac.kr

PD-0003

시비수준에 따른 편백 용기묘의 묘목품질 특성

김양수[1*], 양정모[2], 성환인[2], 김종진[2], 송기선[1], 이재선[1]

[1]국립백두대간수목원 산림생물자원본부 산림생태복원실
[2]건국대학교 산림조경학과

본 연구는 목재자원, 정유, 산림욕 및 치유의 숲 조성 등으로 이용되어 묘목 수요가 증가되고 있는 편백(*Chamaecyparis obtusa* Sieb. et Zucc.)의 효율적인 용기묘 생산을 위하여 적정 시비 수준에 대해 구명하고자 실시하였다. 이를 통하여 편백 용기묘의 최적 생육환경에 관한 기초자료를 확보하고자 하였다. 시비수준은 무시비구와 함께 수용성 복합비료인 Multifeed 19(N:P:K =19:19:19, v/v)를 500㎎・L^{-1}, 1,000㎎・L^{-1}, 1,500㎎・L^{-1}, 2,000㎎・L^{-1}로 조절하여 시비하였다. 실험은 2년간 수행되었다. 2년간 시비처리후 편백 용기묘의 간장과 근원경 생장 조사 결과는 1,500㎎・L^{-1}에서 각각 58.6cm, 5.97mm로 높게 조사되었다. 편백 용기묘의 2차년도 최종 H/D율을 보면 500㎎・L^{-1}에서 가장 높았으며 9.0~11.4로 조사되었다. T/R율의 경우 2차년도 최종 측정치를 보면 2,000㎎・L^{-1}에서 가장 높았으며 1.60~5.96로 조사되었다. 뿌리형태특성을 측정한 결과 1,500㎎・L^{-1}에서 뿌리 발달이 좋았다. 묘목의 품질을 나타내는 지수인 QI는 시비수준이 높아질수록 높아진 결과가 나타났다. 연구결과를 종합하여 정리하면, 편백 2년생 용기묘 생산의 적정 시비수준의 경우 1,500㎎・L^{-1} 범위 조건에서 좋은 생육상태를 보였다. 이러한 생육환경을 제공한다면 품질이 뛰어난 편백 용기묘 대량생산이 가능할 것이다.

주제어: 편백, 시비처리, 뿌리발달, 묘목품질지수

사사: 본 연구는 산림청(임업진흥원) "산림 내 재래원종 확보 및 활용지원의 지원으로 이루어진 것입니다.

***교신저자:** Tel. 054-679-0680, E-mail: kys7449@koagi.or.kr

PD-0004

Seed transfer zone delineation for *Pinus densiflora* using climate change senario

Yeongkon Woo[1,2], Kyungmi Lee[2], Kyu-suk Kang[1*]

[1]Department of Agriculture, Forestry and Bioresources, Seoul National University, Seoul 08826, Repulic of Korea

[2]Division of Forest Tree Improvement and Biotechnology, Department of Forest Bioresources, National Institute of Forest Science, Suwon 16631, Republic of Korea

A seed transfer zone is an area whre plants can be transferred with little risk to them adapting to a new location. The establishment of appropriate seed transfer zones plays an important role in increasing forest health and productivity. Howerver, climate change may result in the see transfer zone having a climate that is incompatible with the current vegetation, so it is necessary to set seed transfer zones that take account of climate change. The aim of this study was to define the seed transfer zone for *Pinus densiflora*, which is changing with climate change. Transfer functions were generated using growth data from 10 pine test sites and 36 seed sources, as well as six bioclimatic variables. Critical seed transfer distances for each climate variable were then calculated and used to create seed transfer zones by overlaying maps for all significant climate variables. Based on this, we wanted to apply how the seed transfer zone changes with climate change scenarios. As a result, the seed transfer zone under the climate change scenarios was considerably different from the current climate.

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***Corresponding Author:** Tel. 02-880-4753, E-mail: kangks84@snu.ac.kr

PD-0005

Selection of plus trees as breeding materials for tree improvement of *Tilia* amurensis Rupr

Kyungmi Lee*, In-Sik Kim

Division of Tree Improvement and Biotechnology, Department of Forest Bioresources, National Institute of Forest Science, Suwon 16631, Republic of Korea

This study aimed to select elite breeding materials of *Tilia amurensis* for tree improvement. A total of twenty sites in fifteen regions were identified as base populations with candidate superior trees. Base populations of *T. amurensis* were precedently investigated to assess site conditions, vegetation characteristics and growth characteristics of target species. The species composition of base populations was revealed to be varied by region and site with general dominancy of *Quercus mongolica*, *T. amurensis* and *Fraxinus rhynchophylla*. As the next phase, selection criteria for superior individuals of *T. amurensis* was established to consider growth and adaptation characteristics. Evaluation of candidate trees was performed based on the selection criteria, then the measurements were generalized to reduce bias that can be caused by age or environmental factors. The generalization was conducted by growth correction regarding age and weighting according to the selection criteria. After the selection process combined with optical and base line selection, 62 individuals were selected as plus trees out of the initial 176 candidates of *T. amurensis*. The selection scheme in this study can be useful to select plus trees in tree improvement especially for broad-leaved species with increasing demand in afforestation.

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***Corresponding Author:** Tel. 031-290-1123, E-mail: kmile@korea.kr

PD-0006

감나무 선발개체 및 재배종 건조감의 기능성 성분 분석과 관능평가

유희원, 박성인, 김철우*, 이욱

경기도 수원시 권선구 온정로 39 국립산림과학원 산림생명자원연구부

수요자 요구에 부합하는 품종 육성과 재배기술 개발 및 보급은 관련 산업의 기반을 마련하는데 매우 중요하다. 부가가치가 높은 건조감 가공에 적합한 감나무 신품종 육성을 위해 결실성과 내한성 등이 우수한 선발개체(대항1, 대항2, 영산1, 서하1, 황간1)와 국내 주요 재배종(청도반시, 상주둥시, 단성시, 고동시)을 대상으로 원료감과 건조감의 과실품질・기능성성분 분석과 관능평가를 실시하였다. 공시재료는 국립산림과학원 수원시험림에서 재배중인 감나무(13년생)로, 수확 직후 과실특성(과중, 크기, 색도, 당도, 경도)을 조사하였다. 또한, 건조감 가공을 위해 원료감을 자동박피기로 박피한 후 열풍건조기를 이용하여 13일간 건조하였다. 가공된 건조감은 품질특성(과중, 색도, 당도), 기능성 성분(총 폴리페놀・플라보노이드 함량) 및 항산화 활성(DPPH, ABTS)을 분석하였고, 전자혀(ASTREEⅡ, Alpha Mos, France)를 이용해 관능평가를 실시하였다. 원료감 과중은 서하1이 130.0g으로 가장 낮았고, 대항2가 294.0g으로 가장 높았다. 원료감 당도는 상주둥시가 20.5°Brix로 가장 높았고, 건조감 당도는 대항2가 53.7°Brix로 가장 높게 나타났다. 총 폴리페놀 및 플라보노이드 함량은 서하1이 각각 100.0mg/g, 0.763mg/g으로 가장 높게 나타났으며, 재배품종(각각 평균 53.6mg/g, 0.178mg/g) 대비 선발개체(각각 평균 81.7mg/g, 0.379mg/g)가 함량이 높은 경향을 보였다. DPPH와 ABTS를 이용하여 라디칼 소거활성능력을 측정한 결과, 각각 서하1, 황간1, 상주둥시(DPPH)와 서하1, 황간1(ABTS)에서 높게 나타났다. 시료의 맛을 패턴화하는 기기인 전자혀(ASTREEⅡ)는 AHS(신맛), CTS(짠맛), NMS(감칠맛), PKS, ANS, CPS, SCS 7개의 센서와 1개의 표준 전극을 사용하며, 측정한 센서값을 이용하여 PCA 분석결과 9개 개체가 모두 구분되었다. AHS(신맛) 스코어는 서하1이 가장 높았고, 영산1이 가장 낮게 나타났다. CTS(짠맛) 스코어는 단성시가 가장 높았고, 대항1이 가장 낮게 나타났다. NMS(감칠맛) 스코어는 상주둥시가 가장 높았고, 대항1이 가장 낮게 나타났다. 본 연구결과는 감나무 선발개체와 재배종의 원료감・건조감에 대한 이화학적 및 관능적 특성에 대한 기초 자료로 선발개체의 가공용 감나무 품종화에 활용이 가능할 것으로 사료된다.

사사: 본 연구는 국립산림과학원 연구과제 “건강증진 산림과수 품종 육성과 표준 재배기술 개발(과제번호: FP0802-2022-01-2023)”의 지원에 의해 이루어진 것임.

***교신저자:** Tel. 031-290-1153, E-mail: futuretree@korea.kr

PD-0007

밤나무 교잡종 내피박피성 검정

박성인, 김철우*, 이욱

경기도 수원시 권선구 온정로 39 국립산림과학원 산림생명자원연구부

밤은 가을과 겨울철 대표적인 먹거리로, 깐밤과 군밤, 통조림 및 제과・제빵 등의 원료로 이용되고 있어 과실 속껍질이 쉽게 벗겨지고 저장성이 우수하여 가공에 최적화된 밤나무 품종 개발이 시급하다. 국내에서 재배하고 있는 밤나무는 과실품질(크기, 맛 등)이 우수한 반면에 속껍질의 박피가 어려워 소비확대와 관련 산업활성화에 장애가 있다. 본 연구는 속껍질이 잘 까지는 밤나무 품종 육성을 위해 인공교배(2019년~2020년) 후 검정림에 식재한 교잡종(3~4년생)의 과실품질(과중, 경도, 당도)과 내피박피성을 분석하였다. 시험재료인 교잡종 밤나무는 DG×PRT-1, DG×HC12-5, DG×HC12-7, DG×SP-1, DB×HC12-15 등 총 34개체이며, 9월에 수확한 과실을 조사・분석에 사용하였다. 박피등급은 칼로 과피와 내피를 모두 제거하는데 소요되는 시간을 기준(과피, 내피 동시 제거:“0”, 1분 이내 내피 제거:“1”, 1~5분 이내 종피 제거:“2”, 5분 이상 소요:“3”)으로 하였고, 등급 조사를 위해 개체별 과실을 에어프라이어(DAP-I14DHB, CHINA)에서 220℃, 15분으로 구웠다. 조사결과, 과중은 MP×HC12-3 개체가 32.2 g으로 가장 높았고, 전체평균 17.8 g으로 나타났다. 경도는 MP×HC10-5 개체가 56.4 N 으로 가장 높았고, 전체평균 41.8 N으로 나타났다. 당도는 DG×HC10-15 개체가 22.6%으로 가장 높았고, 전체평균은 15.6%으로 나타났다. 박피등급은 DG×HC12-7(과중 12.7 g, 경도 37.9 N, 당도 17.3%)과 DB×PRT-10(과중 30.4 g, 경도 51.3 N, 당도 18.9%) 개체가 “0”으로 가장 우수하였다. 또한, DG×HC10-15(과중 20.7 g, 경도 34.5 N, 당도 17.4%), DB×PRT-9(과중 17.7 g, 경도 42.9 N, 당도 15.4%) 및 MP×HC12-1(과중 23.3 g, 경도 36.9 N, 당도 13.9%) 개체도 박피등급이 “1” 미만으로 분석되어 내피박피성이 우수한 것으로 나타났다. 본 연구결과는 가공에 특화된 밤나무 품종 육성을 위한 교잡종 우수개체 선발의 기초 자료로 과실품질과 내피박피성이 우수한 밤나무 품종화에 활용이 가능할 것으로 사료된다.

사사: 본 연구는 국립산림과학원 연구과제 “건강증진 산림과수 품종 육성과 표준 재배기술 개발(과제번호: FP0802-2022-01-2023)”의 지원에 의해 이루어진 것임.

***교신저자:** Tel. 031-290-1153, E-mail: futuretree@korea.kr

PD-0008

Functional study of *PagMYB15* in response to salt stress using hybrid poplar

Su Jin Park, Hyun-A Jang, Hyunmo Choi, Mi Young Son, Hyoshin Lee*

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

The R2R3-MYB transcription factor containing highly conserved DNA-binding domain, is known to be involved in the regulation of plant growth, development and stress response in various plant species. In this study, we investigated the function of MYB15 in hybrid poplar (*Populus alba*×*Populus glandulosa*). Transcript levels of *PagMYB15* increased under salt and drought conditions in wild-type plants. We generated *PagMYB15* knockout mutants using CRISPR/Cas9 genome editing. The CRISPR/Cas9 system has been used for genome editing in various plants due to its versatility and convenience. We examined the resulting mutations at the *MYB15* loci of the transgenic poplars. To investigate the role of *PagMYB15*, we exposed transgenic poplar plants to salt and drought stress. As a result, knockout of *PagMYB15* enhanced sensitivity to salt stress compared with wild-type plants; in contrast, phenotype of the mutants and wild-type plants were not significantly different under drought conditions. Changes in chlorophyll contents, transcript abundance of salt stress-responsive genes and activity of peroxidase (POD) also showed a consistent tendency to phenotypic changes. These results illustrated that *PagMYB15* negatively regulates salt stress resistant pathway and CRISPR/Cas9 genome editing would improve tree quality in hybrid poplars.

***Corresponding Author:** Tel. 031-290-1141, E-mail: hyoshinlee@korea.kr

PD-0009

Microsatellite Analysis in a Clonal Seed Orchard of *Abies koreana*

Sun-Cheon Hong*, Hye-Jin Lee, Yang-Gil Kim, Ye-Ji Kim, Chae-Bin Lee, Su-vi Kim, Tae-Lim Yeo, Yoon-Ji Hahn, Kyu-Suk Kang

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

Abies koreana is the threatened species for climate change and its popualation is decreasing as its habitat decreases. In 2007, the multi-purpose seed orchard was established in Jeju to protect endangered *A. koreana* in *ex situ* conservation forest. The purpose of this study was to evaluate the genetic diversity of seed orchard of *A. koreana* established in Donghong-dong, Seogwipo-si, Jeju. Among the 221 individuals planted, 125 individuals were changed into Abies holophylla due to failure graft and died, accounting for a high proportion of 56%. Therefore, leaves were collected from 96 individuals except 125 individuals to obtain microsatellite data using 6 highly polymorphic nSSR markers. When measured in genet units, the average number of different alleles was 11.5, the average number of effective alleles was 5.559, the fixation index was 0.057, the observed heterozygosity (H_O) was 0.770 and the expected heterozygosity (H_E) was 0.817. The number of clones was 53, and the polymorphism information content (PIC) values of each marker analyzed by cervus (version 3.0.7) were 0.748, 0.789, 0.840, 0.796, 0.761, and 0.810, showing high identifcation ability of markers. Considering that 30 clones were planted at the beginning of the orchard, the increase in the number of clones is presumed to be effect of supplemental planting. Based on the results, a clonal seed orchard of *A. koreana* will be able to function as an conservation forest of genetic resources. However, as the remaining population of *A. koreana* is small, a management plan for a clonal seed orchard of *A. koreana* is needed.

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

PD-0010

Pseudomolecule-level assembly of Korean oak (*Quercus acutissima*)

Kyeong-Seong Cheon*, Yongmin Kim, Kyungmi Lee, In Sik Kim

Division of Forest Tree Improvement and Biotechnology, Department of Forest Bioresources, National Institute of Forest Science, Suwon 16631, Republic of Korea

Quercus acutissima is an ecologically and economically important deciduous broadleaved tree species. In order to establish reference genome for *Q. acutissima* molecular breeding, we attempted to assemble pseudo-molecule level in *Q. acutissima.* After high-quality DNA extraction from young leaves of plus tree clone (Yeongam1ho), sequence productions were carried out by PacBio (HiFi) and Illumina (pair-end) sequencing methods. Long reads were assembled with Hifiasm program to total 1,169 contigs with N50 of 59.3Mb. Subsequently, polishing of contigs, which confirmed chromosome assignment with *Q. mongolica* genome (ASM1169623v1), were performed by trimmed short-reads, and 7 of 19 contigs were assembled to chromosome level. Moreover, five pseudo-molecules were assembled with remained 12 contigs after re-cofirmed ordering and orientation. Finally, 12 pseudo-molecules were conducted with 19 contigs. In the future, we will carry out gene annotation via transcriptome analysis and assembled genome of *Q. acutissima* will be utilized as reference genome for genotypic analysis and gene discovery in *Quercus* improvement.

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***Corresponding Author:** Tel. 031-290-1127, E-mail: kscheon16@korea.kr

PD-0011

Transcriptome analysis of *Pinus koraiensis* through artificial infection of Pine Wilt Nematode

Yongmin Kim[1], Kyeong-Seong Cheon[1*], Il-Hwan Lee[1], Chansik Jung[2], Heonil Kang[2]

[1]Division of Forest Tree Improvement and Biotechnology, Department of Forest Bioresources, National Institute of Forest Science, Suwon 16631, Republic of Korea

[2]Division of Forest Insect Pests & Diseases, National Institute of Forest Science, Suwon 16631, Republic of Korea

Pinus koraiensis, a forest tree distributed in East Asia including Korea, Japan, and China, has economically and ecologically important values. Nowadays, pine trees including *P. koraiensis* is threatened by pine wilt disease (PWD), but molecular research related to PWD-tolerance is still lacking. In order to discover PWD-responded genes from *P. koraiensis*, which were artificially inoculated with pine wood nematode (PWN, *Bursaphelenchus xylophilus*), cambiums were sampled according to time (0, 2, and 4 weeks) and total RNA extractions were performed for transcriptome analysis. In results, the candidates for PWD-responded genes from *P. koraiensis* were obtained by differentially expressed genes (DEGs) and gene ontology (GO) analysis. In future, gene selection based on expression level will be performed to utilize early diagnosis for PWD in *P. koraiensis*.

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***Corresponding Author:** Tel. 031-290-1127, E-mail: kscheon16@korea.kr

PD-0012

Tree Ring Growth of Clones in a Seed Orchard of *A. nephrolepis* during Drought Periods

Hye-Jin Lee[1*], Sang-Jin Yoon[1], Seonjeong Kim[1], Sun-Cheon Hong[1], Dayoung Lee[1], Tae-Lim Yeo[1], Yoonji Hahn[1], Gye-Hong Cho[1], Yang-Gil Kim[1], Kwang Hyun Nam[1], Hyunjoong Sung[1], En-Bi Choi[2], Jun-Hui Park[2], Jeong-Wook Seo[2], Kyu-Suk Kang[1]

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

[2]College of Agriculture, Life and Environment Sciences, Chungbuk National University, 1 Chungdae-ro, Seowon-gu, Cheongju-si, Chungcheongbuk-do 28644, Republic of Korea

Seed orchard of *A. nephrolepis* was established in 2005 with cuttings from Mt. Odaesan and Mt. Chiaksan. The average height of 91 trees (15 clones) is 5.5 m and the average DBH is 15.0 cm. In July 2022, 2 increment cores were collected from 84 trees of 8 clones (A to I). Tree rings from 2005 to 2021 were analyzed to investigate the correlation between climate factors and annual growth. The ring width was measured using LinTab dendrochronology measuring instrument and TSAP-Win program. The consistency of ring widths was statistically confirmed. Anomalies were calculated using the difference between monthly averages and the 50-year average of temperature and precipitation. Periods with a positive sum of temperature anomalies and a negative sum of precipitation anomalies were defined as drought periods. The ratio of growth during drought to pre-drought growth and the ratio of growth after drought to pre-drought growth were defined as drought resistance and drought resilience, respectively. As a result, it was observed that the growth of clones significantly declined during the years 2005, 2014-2015, 2017, and 2019 (t-value>3.7, G-value>68%). Except for the establishment year, these years coincided with drought periods. Among the total of 84 trees during drought periods, 77% (2014-15), 82% (2017), and 75% (2019) showed a decrease in growth (drought resistance<1), while 70% (2014-15), 35% (2017), and 69% (2019) of trees recovered their pre-drought growth (drought resilience>1). Significant differences in drought resistance were observed among clones during the 2014-15 drought period. In 2017 and 2019, ramets from clone G showed lower drought resistance compared to other clones and exhibited higher resilience after the drought, although this was not statistically significant.

***Corresponding Author:** Tel. 02-880-4762, E-mail: hyejinkr@snu.ac.kr

PD-0013

Optimization of tomato growth and harvest by editing *SlGA2ox7 and SlJUL*

Hye-Yeong Kang[1], Hong Kwan Beak[2], Hoyoung Nam[3], Ildoo Hwang[3], Soon Ju Park[1,2*]

[1]Division of Applied Life Science(BK21 four) and Plant Molecular Biology and Biotechnology Research Center(PMBBRC), Gyeongsang National University, Jinju 52828, Republic of Korea
[2]Division of Biological Sciences,Wonkwang University, Iksan 54538, Republic of Korea
[3]Department of Life Sciences, POSTECH Biotech Center, Pohang University of Science and Technology, Pohang, Republic of Korea

In agriculture, breeders have used various methods to increase crop yield and quality. Screening methods of genetic variants have been applied to optimize plant growth and increase tomato fruit yield and quality. Here, we screened mutations of *GA2-oxidase 7* (*GA2ox7*) and tomato *JULGI* (*SlJUL*) induced by genome editing technology to engineer genetically to increase tomato yield and quality. The *SlGA2ox7* editing mutants, CR-S*lga2ox7*, exhibited an enlarged plant size and significant tomato yield increase in micro-Tom. An optimal point between the height and yield of tomato was identified, and *GA2ox7* knock-out mutation was carried out with three types of tomato of different heights distributed by a seedling company.

CR-*Sljul* editing mutants increased the phloem size. RNA binding site mutations of SlJUL were induced by CRISPR-based adenine base edition (ABE) technology. Two ABE mutants (*SlJULCR-N147D*) showed significant enlargement of phloem size similar to CR-*Sljul*. To regulate phloem size by engineering *SlJUL* promoter, 3.5Kb *SlJUL* promoter was edited by eight sgRNAs with about 0.5kb intervals each other. Four types of promoter deletion mutants were selected by PCR and Sanger sequencing and crossed with *SlJULCR-N147D*. Hybrids showed relatively gradual short in stem lengths and gradually enlarged the phloem area associated with the phenotypic strength among biallelic of a genetic combination of promoter deletion alleles and ABE allele. Yield harvest and growth values were significantly enriched and scored top rank under *SlJULCR-N147D*/*SlJULCR-PRO*#4 and hybrids also increased the Brix value. By mutating plant stem growth and phloem control genes, we can optimize plant height and phloem size, leading to increased yield-related contents.

***Corresponding Author:** Tel. 055-772-1356, E-mail: sjpark75@gnu.ac.kr

PE-0001

Marker-assisted backcrossing (MABC) approach for introgression of high oleic acid content in peanut (*Arachis hypogaea* L.) cultivars

Rizwana Begum Syed Nabi, Sungup Kim, Jung In Kim, Min Young Kim, Sang Woo Kim, Jeongeun Lee, Eunsoo Lee, Kwang-Soo Cho, Myoung-Hee Lee, Eunyoung Oh*

Upland Crop Breeding Research Division, Department of Southern Area Crop Science, National Institute of Crop Science, RDA, Miryang, Gyeongnam, 50424, Republic of Korea

Marker-assisted backcrossing (MABC) is one of the most effective and widely used strategies for gene pyramiding or the introgression of the favorable trait from the donor to the elite line. The peanut (*Arachis hypogaea* L.) is an allopolyploid species mainly cultivated in tropical, subtropical, and warm temperate regions, and the fourth most important oilseed crop worldwide. The aim of this study is to increase the yield and oleic acid content of peanut in South Korean cultivars. Here we used the MABC and MAS approach to transfer two mutant alleles (*ahFAD2A* and *ahFAD2B*) from Hae-Ol that have high oleic acid (HOA) contents into the elite high-yielding genetic background namely Sewon and Sinpalkwang cultivars. Hae-Ol as a donor of HOA content was crossed with Sewon and Sinpalkwang according to the breeding objective. With the obtained F1 hybrids, backcross was conducted and selected individual BC_2F_2 seeds proceeded to BC_2F_3 by selfing in the greenhouse. The HOA introgression lines (ILs) were selected using MAS, whereas recurrent background was selected using 200 Kompetitive allele-specific PCR (KASP) markers. The KASP markers were designed based on 'Axiom Arachis' 48 K SNPs genotyping analysis, where we identified 2060 SNP's out of 47,837 SNPs based on the poly high resolution. Selected KASP markers showed polymorphism in parental screening and recurrent genetic background recovery in the BC_2F_2 generation was estimated to be 89.51%. In addition, populations of HOA, ILs with morphological features and agronomic traits similar to those of the recurrent parents will be evaluated in the field.

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***Corresponding Author:** Tel. 055-350-1225, E-mail: lavondy10@korea.kr, rizwananabi@korea.kr

PE-0002

RNA-Seq analysis of salt-tolerant soybean mutant induced by gamma irradiation

Byeong Hee Kang[1,2], Sreeparna Chowdhury[1], Sehee Kang[1,2], Seoyoung Shin[1,2], Won Ho Lee[1], Hyeon-Seok Lee[3], Bo-Keun Ha[1,2*]

[1]Department of Applied Plant Science, Chonnam National University, Gwangju, 61186, Republic of Korea
[2]BK21 FOUR Center for IT-Bio Convergence System Agriculture, Chonnam National University, Gwangju, 61186, Republic of Korea
[3]National Institute of Crop Science, RDA, Wanju, 55365, Korea

Soybean (*Glycine max* L.) is one of the most important multi-purpose legumes worldwide, used in a wide range of industries and products. However, soybean yields are often limited by various abiotic stresses. Salt stress is one of the abiotic stresses that reduce the potential yield and quality of crops, and soybeans are among the less tolerant groups to salt stress. In this study, we conducted RNA sequencing analysis using soybean mutants induced by gamma irradiation to understand the salt tolerance mechanism. The seedlings of two soybean genotypes, salt tolerant mutant, and salt susceptible wild type, were grown in Hoagland's solution and then treated with 200mM NaCl at V2 stages. For RNA sequencing, leaf and root were sampled at three-time points (0h, 24h, and 72h) after salt treatment with three biological replicates. A total of 36 libraries were constructed and sequenced using Illumina Novaseq 6000. As a result, 2132.9 million short reads were obtained, of which 94.48% were mapped to the soybean reference genome. Then, 296 and 170 differentially expressed genes (DEGs) were identified between the two genotypes at leaf and root, respectively. Based on the expression values of the identified DEGs, information on annotations, and mutations in the coding sequencing region, a total of 10 genes in leaves and roots were identified as the potential key to control salt tolerance in soybean mutants. These results will improve the understanding of the salt tolerance mechanism in soybeans.

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***Corresponding Author:** Tel. 062-530-2050, E-mail: bkha@jnu.ac.kr

PE-0003

Screening of soybean accessions lacking seed lipoxygenase in Korean soybean germplasm collection

Seo Young Shin[1], See Hee Kang[1], Byeong Hee Kang[1], Sree parna[1], Won Ho Lee[1], Yu Mi Choi[2], Bo-Keun Ha[1*]

[1]Department of Applied Plant Science, Chonnam National University, Gwangju, 61186, Korea
[2]National Agrobiodiversity Center, National Institute of Agricultural Sciences, RDA, Jeonju 54874, Korea

Lipoxygenase (LOX) is one of anti-nutritional factors that play a role in the development of unpleasant flavors in soybean seeds by oxidation of polyunsaturated fatty acids. Three lipoxygenase isozymes (LOX1, LOX2, and LOX3) are mainly expressed in mature soybean seeds and considered as the major contributor to beany flavor. The purpose of this study is to identify soybean accessions lacking LOX1, LOX2, or LOX3 in Korean soybean germplasm collection and develop KASP assay system for null lipoxygenase genes. Lipoxygenase enzymes were analyzed using colorimetric enzyme analysis based on pH. LOX1 and LOX2 use Methylene blue (blue), and LOX3 uses Beta-carotene (yellow) to confirm the photobleaching reaction. For the Lox1 assay, KASP marker was designed to flank the region containing the C2880A mutation and validated using F2 population. In the 908accessions, two null-LOX1 lines and three null-LOX2 lines were found based on colorimetric enzyme analysis. However, null-LOX3 line was not observed in 908 accessions. One null-LOX1 line contained a 74bp deletion in exon 8 of *Glyma.13G347600* gene and the other null-LOX1 line contained nonsense mutation, C2880A, in *Glyma.13G347600* gene. In this study, we developed KASP assay system for detecting SNP alleles of C2880A in *Glyma.13G347600* gene. As a result of validation using the 148 F2 plants, KASP assay showed 98% concordance with colorimetric enzyme analysis.

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

PE-0004

Identification of the candidate gene *CA10g01010* causing the ms_k genetic-male sterility in pepper (*Capsicum annuum* L.)

Donggyeom Kim, Soeun Lee, Jundae Lee*

Department of Horticulture, Institute of Agricultural Science and Technology, Jeonbuk National University, Jeonju 54896, Korea

F_1 hybrid pepper (*Capsicum annuum* L.) cultivars in Korea have been developed using the cytoplasmic-genic male sterility (CGMS) or genetic-male sterility (GMS) for economical seed production. In peppers, over 20 GMS genes have been reported, and naturally occurring ms_k gene has been widely used in Korean pepper breeding. In previous study, we developed 15 high-resolution melting (HRM) markers on pepper chromosome 10 by performing NGS resequencing of male-fertile (Ms_kMs_k) and male-sterile (ms_kms_k) individuals. A genetic map with 15 HRM markers closely linked to the ms_k locus was constructed to identify the physical location of the locus, and the 13-kb region with no recombination was identified. In this study, we identified 14 candidate genes (*CA01g00950* to *CA01g01080*) within the 13-kb region. In results, a candidate gene *CA10g01010* encodes transcription factor MYB80, which was reported to be required for pollen development and the regulation of tapetal programmed cell death in *Arabidopsis thaliana.* A comparison of sequences between the Ms_kMs_k and ms_kms_k individuals revealed a 163-bp sequence insertion in the third exon of the ms_k allele of *CA10g01010* gene, implying the insertion might cause male sterility. Based on the insertion, sequence characterized amplified region (SCAR) and HRM markers were developed to distinguish between Ms_k and ms_k alleles. The markers will be helpful for efficient pepper breeding using GMS, and the gene will contribute to further in-depth study of molecular mechanism of pollen development in pepper.

***Corresponding Author:** Tel. 063-270-2560, E-mail: ajfall@jbnu.edu

PE-0005

Gene editing of the *MTL/ZmPLA1/NLD*-like haploid inducer genes by CRISPR-Cas9 system in ginseng

Jae Hyun Lee[1,2], Jin Hoon Jang[1,2], Ok Ran Lee[1,2*]

[1]Department of Applied Plants Science, Chonnam National University, Gwangju 61186, Korea
[2]Interdisciplinary Program in IT-Bio Convergence System, Chonnam National University, Gwangju 61186, Republic of Korea

Doubled haploid technology accelerates crop breeding but lacks reliable *in vivo* haploid induction methods for many crops. Recently, the *MTL/NLD/ZmPLA1* gene was identified as a key gene for *in vivo* haploid induction in maize. This gene encodes a sperm-specific phospholipase A. Subsequent studies produced haploids in rice, wheat, and foxtail millet by editing orthologous genes of *MTL/NLD/ZmPLA1.* Moreover, knock-out of the gynoecium-expressed phospholipase A in *Arabidopsis* has induced maternal haploids. The use of phospholipase A method has demonstrated the broad applicability of haploid induction across monocots and dicots. *Panax ginseng*, being tetraploid (2n=4x=48) and requiring at least 3 years to reach the flowering stage, presents significant challenges. To address these challenges, this study focuses on identifing the phospholipase A gene responsible for haploid induction in ginseng and developing a reliable tool for ginseng breeding. To modify *MTL/NLD/ZmPLA1* homologs in *Panax ginseng*, we detected nine *PLA* genes of ginseng through a BLAST analysis on the Ginseng Genome Database. Based on the protein identity with MTL/NLD/ZmPLA1, two candidates (PgPLA1 and PgPLA2) were selected for further study. We designed two single guide RNAs to target *PgPLA1* and *PgPLA2*, respectively. These guides were then cloned into the pBAtC vector, and the resulting constructs were used to transform the *Panax ginseng* through *Agrobacterium*-mediated transformation. Finally, we confirmed that *PgPLA1* and *PgPLA2* were successfully edited by targeted deep sequencing. As a follow-up study to identify haploid induction function, this approach has the potential to be a powerful tool and open a new chapter in ginseng breeding.

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

PE-0006

Identification of transcription factors that regulate the biosynthetic pathway of ginsenosides through yeast one hybrid screening

Unenzaya Bayaraa[1,2,3], David Charles Simiyu[1,2], Ok Ran Lee[1,2*]

[1]Department of Applied Plant Science, College of Agriculture and Life Science, Chonnam National University, Gwangju 61186, Korea

[2]Interdisciplinary Program in IT-Bio Convergence System, Chonnam National University, Gwangju 61186, Korea

[3]Laboratory of Plant Biotechnology, Institute of Biology, Mongolian Academy of Sciences, Ulaanbaatar 13330, Mongolia

Panax ginseng Meyer, commonly known as Korean ginseng, is a highly valued medicinal plant renowned for its bioactive triterpene saponins called ginsenosides. With the increasing demand for ginsenosides and their potential therapeutic benefits, it is imperative to develop biotechnological approaches for enhancing their production. Transcriptional regulation plays a crucial role in controlling the expression of key genes involved in ginsenoside biosynthesis. However, the comprehensive understanding of the transcriptional regulation governing this pathway remains limited. This study aimed to investigate the transcriptional regulation of ginsenoside biosynthesis in *P. ginseng* by identifying putative transcription factors (TFs) that interact with the promoters of key genes in the pathway. Specifically, we focused on dammarenediol II synthase (DDS) and squalene epoxidase (SQE), essential enzymes in the biosynthetic pathway. Using the yeast one-hybrid system, we screened the promoter sequences of *DDS* and *SQE1*, resulting in the identification of 158 colonies for *pDDS* and 163 colonies for *pSQE1.* Subsequent analysis of the nucleotide sequences using Sanger sequencing allowed us to identify potential TFs that interact with promoters. The Basic Leucine Zipper (bZIP) TF emerged as a putative candidate for *pDDS*, while APETALA2/Ethylene Responsive Factor (AP2/ERF) was identified as a potential TF for *pSQE1.* This study provides valuable insights into the transcriptional regulation of ginsenoside biosynthesis in *P. ginseng*, shedding light on the intricate regulatory mechanisms involved.

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

PE-0007

Enhancing seed fatty acid content through CRISPR-Cas9-mediated *pPLAII* gene editing in *Arabidopsis* and camelina

Chae Ri Baek[1,2], Jin Hoon Jang[1,2], Ok Ran Lee[1,2*]

[1]Department of Applied Plant Science, College of Agriculture and Life Science, Chonnam National University, Gwangju 61186, Republic of Korea
[2]Interdisciplinary Program in IT-Bio Convergence System, Chonnam National University, Gwangju 61186, Republic of Korea

Plant fatty acids have a wide range of applications across various industries, including biofuel production, surfactant manufacturing, cosmetics, food, and pharmaceuticals, owing to their renewable and sustainable nature. *Camelina sativa*, an oil crop known for its unique fatty acid composition rich in polyunsaturated fatty acids, holds great potential. Utilizing camelina as an oil crop offers significant advantages, such as a short cultivation period, resistance to common pathogens and pests, and lower agricultural input requirements compared to other oil crops. Additionally, its genetic relationship with *Arabidopsis* suggests that genetic and genomic tools developed in *Arabidopsis* could be applied to camelina. Patatin-related phospholipase As (pPLAs) are a major family of plant lipid acyl hydrolases and involved in lipid metabolism. Specifically, studies conducted in *Arabidopsis* have demonstrated that loss-of-function mutations in the *pPLAII* gene result in a 20% reduction in seed weight, while simultaneously increasing the total fatty acid content by 30%. Our study builds upon the findings in *Arabidopsis* and aims to investigate the effects of manipulating the *pPLAII* gene in camelina. We aim to identify the *pPLAII* ortholog gene in camelina and explore its effect on the fatty acid composition of camelina seeds through gene editing.This investigation is of great significance as it will contribute to a deeper understanding of the genetic mechanisms involved in regulating fatty acid synthesis and accumulation in oil crops.

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

PE-0008

The Map-based cloning of the *Hairless on stems* involved in tomato trichome development

Jae-In Chun[1], Ga-Hae Han[2], Jin-Ho Kang[1,2,3*]

[1]Department of Agriculture, Forestry and Bioresources, College of Agriculture and Life Sciences, Seoul National University, Seoul 08826, Republic of Korea
[2]Graduate School of International Agricultural Technology, Seoul National University, PyeongChang 25354, Republic of Korea
[3]Institutes of Green-bio Science and Technology, Seoul National University, PyeongChang 25354, Republic of Korea

Trichomes, the hair-like structures formed by plant cells on their epidermis, exist in most plant species and can be classified into glandular and non-glandular types. These trichomes play a dual role, providing chemical and physical protection against herbivores and biotic and abiotic stresses. Our focus lies on a newly identified recessive mutation named *hairless on stems* (*host*), which exhibits an altered trichomes phenotype. In *host* plants, the density of trichomes on leaves, stems, and hypocotyls is lower than in wild-type (WT) plants. Notably, the absence of type I, III, and V trichomes on the stems of *host* plant is particularly prominent. Moreover, the length of type I trichomes is shorter in *host* plants compared to WT plants. To narrow down the location of the *Host* locus, we are currently developing new markers, as the mapping approach has positioned it between Sol280 and Sol360 on chromosome 9. Within this 1Mb interval containing 1967 putative genes, the identification of the *Host* gene will shed light on the development of multicellular trichomes while also providing potential for creating insect-resistant tomatoes.

***Corresponding Author:** Tel. 033-339-5841, E-mail: janechun@snu.ac.kr

PE-0009

Identification of genes involved in trichome development with the function of insect resistance in tomato

Seong-Min Kim[1], Jae-In Chun[1], Jin-Ho Kang[2,3*]

[1]Department of Agriculture, Forestry and Bioresources, College of Agriculture and Life Sciences, Seoul National University, Seoul 08826, Republic of Korea
[2]Graduate School of International Agricultural Technology, Seoul National University, Pyeongchang 25354, Republic of Korea
[3]Institute of Green-bio Science and Technology, Seoul National University, Pyeongchang 25354, Republic of Korea

Tomatoes are one of the most consumed vegetables worldwide. However, due to various biological stresses, tomato production is being reduced. Damage is mainly caused by feeding or sucking insects. Plants operate their defensive mechanism to counteract insects, and trichomes derived from epidermal cells also contribute to the plant's defense system. The trichomes hinder the access of insects and secrete chemical compounds with repellents or insecticidal effects. We intend to utilize trichomes as a genetic resource for increasing insect resistance. Two genes (*Tri-1* and *Tri-2*), expected to be involved in trichome development, were selected and knock-out (ko) mutants were generated using the CRISPR-Cas9 system. There was no difference between *Tri-1* single ko (sko), *Tri-2* sko mutants and WT plants in trichome number. However, The density of trichomes in *Tri-1*/*Tri-2* double ko (dko) mutants was significantly reduced compared to WT and sko plants. This implies that *Tri-1* and *Tri-2* genes had a functional redundancy. In the future, we plan to quantify the phenotypic changes in trichome development using ko T_1 plants. And transcriptome analysis will be conducted to investigate the molecular mechanism of trichome development by *Tri-1* and *Tri-2*. Through this study, it will be possible to confirm the feasibility of trichomes as a breeding material to develop insect-resistant tomato.

***Corresponding Author:** Tel. 033-339-5841, E-mail : poba7750@snu.ac.kr

PE-0010

Response to Bakanae Disease in major Korean rice varieties

Sais-Beul Lee[1], Ju-Won Kang[1], Ji-Yoon Lee[1], Gi-Un Seong[1], Yeong-Soo Park[1], Youngho Kwon[1], So-Myeong Lee[1], Nkulu Rolly Kabange[1], Jun-Hyeon Cho[2], Seong-Hwan Oh[1], Dongjin Shin[1], Jong-Hee Lee[1], Ki-Won Oh[1], Dong-Soo Park[1*]

[1]National Institute of Crop Science, Miryang 50424, Republic of Korea
[2]Sangju Sub-station, Sangju 37139, Republic of Korea

Bakanae disease, also known as foolish seedling disease, caused by *Gibberella fujikuroi*, is a serious issue in Korea. Since 2007, there has been a rapid increase in the occurrence of bakanae disease, which has caused severe damage to rice farmers every year. The most reliable and economical solution for bakanae disease is to cultivate resistant varieties, but currently there are not many rice varieties in Korea that can withstand this disease. Therefore, this study aimed to evaluate the resistance of 61 major rice varieties which accounts for 89% of the total rice cultivation area. Only six varieties, showed intermediate or higher resistance to bakanae disease including Anpyeong, Samkwang, and others. The genetic inconsistency between the results of the bioassay and the allele types of 12 molecular markers (associated with four QTLs) ranged from 4.7% to 48.7%. These findings indicate that more accurate markers, such as gene-based markers, may be required for their utilization in general breeding programs or gene pyramiding.

***Corresponding Author:** Tel. 055-350-1184, E-mail: parkds9709@korea.kr

PE-0011

Detection of viable transgenic plant cells in rice callus suspension cultures using PCR combined with Propidium Monoazide treatment

Yang Qin, Yang Ha Kim, Seonha Park, Mingwan Cheon, Areum Jeong, Bumkyu Lee*

Environment Safety & Biotechnology, Jeonju University, Jeonju 55069, Korea

In recent years, there has been a notable rise in the number of research studies and patents focusing on plant stem cell suspension cultures in large-scale bioreactors. Callus refers to an undifferentiated mass of totipotent cells. Due to high rates of cell multiplication, short life cycle and their ease of maintenance through sub-culturing into fresh medium, Callus suspension cultures offer experimental systems that are advantageous for productions of secondary metabolites or recombinant proteins. Transgenic plant cells are often preferred for achieving efficient production of specific compounds or proteins at an industrial scale. However, the use of transgenic cells raises concerns among the public regarding the environmental risks associated with the release of living modified organisms (LMOs) during the disposal of finely suspended cultures. One concern involves the presence of viable cells in the waste sub-culture medium and residual callus debris. Herein, we established cell suspension culture systems from friable embryogenic calli of a transgenic BT rice, which harbored an insect-resistant modified *Cry1Ac* (*mCry1Ac*) and a herbicide-resistant *bar* expression cassette. To detect viable cells in callus suspensions, we designed three specific primer sets targeting *mCry1Ac*, *bar*, and the rice endogenous gene sucrose phosphate synthase (*SPS*), and employed propidium monoazide (PMA) treatment in combination with cell-direct PCR. Our findings revealed a limitation in the direct PCR detection capability for eukaryotic organisms like rice and yeast cells when compared to prokaryotic bacterial cells. This limitation can be attributed to the presence of larger genome sizes and more complex membrane structures in eukaryotes.

***Corresponding Author:** Tel. 063-220-2227, E-mail: leebk@jj.ac.kr

PE-0012

QTL analysis for rice BLB disease resistance breeding by non-phenotypic trait data (HPLC data) (*Oryza sativa* L.)

Da-Hee Jeong[1], Xiao-Xuan Du[1,2], Kyung-Min Kim[2*], Gang-Seob Lee[1*]

[1]National Institute of Agricultural Science, Rural Development Administration, 370 Nongsaengmyeong-ro, Jeonju-si, 54874, Republic of Korea
[2]Coastal Agriculture Research Institute, Kyungpook National University, Daegu 41566, Republic of Korea

Bacterial leaf blight (BLB) caused by *Xanthomonas oryzae* pv. *oryzae* is a significant factor leading to yield reductions in rice crops worldwide. In response to infection, plants produce various metabolites to defend against pathogens. In this study, we employed high-performance liquid chromatography (HPLC) to quantify the levels of defense metabolites after *Xoo* inoculation in the Cheongcheong/Nagdong double haploid (CNDH) population of rice (*Oryza sativa* L.). By mapping quantitative trait loci (QTL), we aimed to identify genes associated with BLB resistance based on the concentrations of these plant defense metabolites. HPLC analysis allows for the measurement of metabolite concentrations, which correlate with the severity of disease symptoms. This approach proves to be highly effective in identifying candidate genes involved in BLB resistance, which can be directly linked to the causative pathogens. Through HPLC analysis, we detected a total of 17 metabolites in the CNDH population after *Xoo* inoculation. QTL mapping of the metabolite concentrations led to the identification of a candidate resistance gene for BLB, named *Os*WRKYq6, located at RM3343 on chromosome 6. *Os*WRKYq6 exhibits a high sequence homology with the WRKY transcription factor39. Traditionally, resistance genes have been identified solely based on phenotypic changes. However, in this study, we successfully detected resistance candidate genes by analyzing the concentrations of metabolites produced by plants after pathogen inoculation. This novel analysis method can effectively detect and identify genes directly involved in disease resistance, opening up new avenues for future studies in this field.

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

PE-0013

Development of Cleaved Amplified Polymorphic Sequence Markers for Classifying Ginger Based on Whole Genome Reference Sequencing

So-Hee Yang[1], Ji-Nam Kang[1], Gyeong-Hui Lee[2], Jin Yu[3], Simyung Lee[1*]

[1]Genomics Division, National Institute of Agricultural Sciences, 370 Nongsaengmyeong-ro, Jeonju-si, Jeollabuk-do, 54874, Republic of Korea
[2]Wanju-gun Agricultural Technology Center, 720-45 Gosancheonro, Gosan-myeon, Wanju-gun, Jeollabuk-do, 55310, Republic of Korea
[3]Ginseng Division, Department of Herbal Crop Research, 92 Bisanro, Eumseong, Chunbuk, 27709, Republic of Korea

Ginger (*Zingiber officinale*) is primarily used as a spice and medicinal plant in subtropical and tropical regions. Ginger is rich in secondary metabolites such as oleoresin and shogaol, which are the main substances responsible for the spiciness and flavor of ginger. Despite the economic importance of ginger, studies on its molecular work are limited. Moreover, since ginger grows vegetatively by the infertility of flowers, few molecular markers have been identified to distinguish cultivars. In present research, we developed five Cleaved Amplified Polymorphic Sequence (CAPS) markers based on whole genome reference sequencing. These markers can distinguish between the "Bongdong" ginger (Bg) cultivar, indigenous to South Korea, and the Chinese imported ginger (Cg) cultivar. Furthermore, the integrated application of these CAPS markers made it possible to distinguish between Bg, Cg, and Indonesian ginger cultivars. Among them, the *Cla*I-based CAPS marker was applied specifically to the Bg cultivars. Finally, we developed a TaqMan real-time PCR system for *Cla*I-based CAPS marker, which was effectively applied between Bg and Cg cultivars. This study is the first to report the development of whole genome-based single-nucleotide polymorphism markers in ginger and therefore provides important information for the breeding and conservation of ginger.

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

PE-0014

Genetic diversity and association analysis of Korean waxy maize inbred lines using SSR marker

Kyu Jin Sa[1], Hyeon Park[1,2], So Jung Jang[1,2], Ju Kyong Lee[1,2*]

[1]Department of Applied Plant Sciences, College of Agriculture and Life Sciences, Kangwon National University, Chuncheon 24341, Korea
[2]Interdisciplinary Program in Smart Agriculture, Kangwon National University, Chuncheon 24341, Korea

Compared with traditional quantitative trait locus (QTL) mapping, in recent years association analysis has become a more powerful tool for detecting molecular markers associated with specific morphological traits. This study aimed to evaluate the genetic diversity and association analysis for 100-kernel weight (100KW) and understand the population structure and genetic distance among Korean waxy maize inbred lines collected in South Korea. The average value of 100KW was 19.8 ± 4.7 g, with statistically significant differences between low and high groups based on the average value. Genetic diversity analysis using 150 simple sequence repeat (SSR) loci showed an average of 3.94 alleles and 4.32 genotypes per locus. The average genetic diversity was 0.581, and the average polymorphic information content was 0.522. A distance-based unweighted pair group method with arithmetic mean dendrogram showed all the inbred lines dividing into five subgroups at a genetic similarity of 35.1%. Group I consisted of 16 inbred lines, with nine low inbred lines and seven high inbred lines. Group II included 20 inbred lines, composed of 10 low inbred lines and 10 high inbred lines. Group III and V had each two high or low inbred lines, respectively. Group IV had only one high inbred line. The model-based population structure classified K=2 and K=4 based on delta K. Association analysis between 100KW and SSR markers identified five marker-trait associations involving four SSR markers. The information from this study may support opportunities for selecting inbred lines with desirable traits and for developing new waxy maize varieties in South Korea. This could enable maize breeders to improve crop yield and quality through marker-assisted selection.

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

PE-0015

Identification of the Role of *OsIAA17q5* in Rice Using CRISPR/Cas9

Do-Hyeong Gwon[1], Dan-Dan Zhao[1,2], Kyung-Min Kim[1,3*]

[1]Department of Applied Biosciences, Kyungpook National University, Daegu, 41566, Korea
[2]Crop Foundation Research Division, National Institute of Crop Science, Rural Development Administration, Wanju 55365, Korea
[3]Coastal Agriculture Research Institute, Kyungpook National University, Daegu 41566, Korea

Rice is one of the most important food crops and a source of nutrients worldwide. Various rice breeding studies are being conducted to increase food supply in response to population growth. Tiller number is among several of the most important traits that play an important role in rice growth and determine yield. *OsIAA17q5*, a gene in the RM18130-RM3381 region of chromosome 5, has been reported contributes to the regulation of rice tiller number in previous study. In this study, CRISPR/Cas9 was used for genome editing to the identification of the function of *OsIAA17q5.* Three sgRNAs were designed by CRISPR RGEN Tools. Three sgRNAs were ligated with pRGEB32, a CRISPR/Cas9 vector containing hygromycin and kanamycin resistance. The ligated plasmids were transformed into *Escherichia coli* competent cells to multiply and extracted. The plasmids were confirmed by Sanger sequencing. Confirmed plasmids were transformed into ilmi through inoculation of Agrobacterium tumefaciens EHA105 and co-cultured for 3 days. After co-culture, the inoculated calli were washed and transferred to regeneration medium containing antibiotics. The regenerated plants were transferred to soil for rooting and acclimatization after water culture. Regenerated plants from the inoculated calli were transplanted into the soil. Genome edited plants by using CRISPR/Cas9 may be used to identification of the function of *OsIAA17q5* gene. Identifying the function of OsIAA17q5 can be an important source of rice breeding and contribution to improving rice yield for food supply in response to population growth.

***Corresponding Author:** Tel. 053-950-5711, E-mail: kkm@knu.ac.kr

PE-0016

Exogenous GA and ABA Affects Rice Seed Germination under Low Temperature Stress

Nari Kim[1], Rahmatullah Jan[1,2], Saleem Asif[1], Jae-Ryoung Park[2,3], Eun-Gyeong Kim[2], Yoon-Hee Jang[2], Kyung-Min Kim[1,2*]

[1]Department of Applied Biosciences, Kyungpook National University, Daegu, 41566, Korea
[2]Coastal Agriculture Research Institute, Kyungpook National University, Daegu 41566, Korea
[3]Crop Breeding Division, National Institute of Crop Science, Rural Development Administration, Wanju, 55365, Republic of Korea

Rice seed germination is a crucial and complex process in entire rice life, including exogenous and endogenous factors. The impact of temperature on seed germination is associated with the biosynthesis and signaling of ABA and GA. ABA and GA are the major endogenous regulators that antagonistically control seed dormancy and germination in several plant species. A low temperature during seed development enhances the accumulation of ABA and reduces GA. Therefore, it is significant to figure out the effects of plant hormones in rice seed germination under low temperature conditions. To identify the effects of exogenous application in rice seed germination, we used Cheongcheong, Nagdong, CNDH 77 (resistant line), and CNDH 30 (susceptible line) as plant materials. Through the application of exogenous hormones, we checked the germination percentage (GP), coleoptile length, quantification of endogenous hormones, morphology, and phenotypes of rice seed germination response to control, 100 µM and 300 µM of GA_3 and ABA at 15°C. To summarize the results, mostly 300 µM of GA_3 expressed high GP. On the other hand, 300 µM of ABA suppressed seed germination more remarkably than other treatments. In the case of the coleoptile length, GA_3-treated seeds showed highly longer coleoptile length than the ABA-treated seeds. Through the quantification of endogenous GA_3 and ABA, it showed a highly significant increase under both concentrations of GA_3 treatment while a significant decrease was indicated in ABA treatment. Taken together, exogenous GA and ABA regulate antagonistically in rice seed germination under low temperature conditions.

***Corresponding Author:** Tel. 053-950-5711, E-mail: kkm@knu.ac.kr

PE-0017

Targeted Editing of *OsLA*q6 Using CRISPR/Cas9 Increases Grain Amylose Content in Rice

Eun-Gyeong Kim[1†], Jae-Ryoung Park[1,2†], Yoon-Hee Jang[1], Kyung-Min Kim[1,3*]

[1]Coastal Agriculture Research Institute, Kyungpook National University, Daegu 41566, Korea
[2]Crop Breeding Division, National Institute of Crop Science, Rural Development Administration, Wanju, 55365, Republic of Korea
[3]Department of Applied Biosciences, Kyungpook National University, Daegu, 41566, Korea

A crop grain with a high amylose content (AC) is a source of resistant starch (RS), which is not digested in the small intestines but passes to the large bowel for fermentation. The effects of RS in increasing faecal mass, protecting against colorectal cancer, and elevating large-bowel short-chain fatty acids (SCFA) have been reported in pigs, rats, and humans. And high-amylose starch assists in preventing the development of non-reversible insulin resistance and depresses plasma total lipid, cholesterol, and triacylglycerol concentrations. Therefore, among cereals, rice is a major food crop consumed as a staple food by more than half of the world's population, and increased RS levels in rice have the potential to improve human health. In this research, *OsLA*q6 genome-editing rice (*OsLA*q6-G) was bred by editing the function of *OsLA*q6 in Ilmi using the CRISPR/Cas9. After selecting lines in which the T-DNA region was segregated in *OsLA*q6-G lines by advanced generation, amylose, protein, and moisture content were analyzed to Ilmi and *OsLA*q6-G rice. And investigated the alkali digestion value, starch-iodine tests, and major agricultural traits. *OsLA*q6-G had higher amylose content than Ilmi. The content of protein was the equal or lower than Ilmi, and the content of moisture was the equal or higher than Ilmi. And the alkali digestion of *OsLA*q6-G lines was higher than Ilmi. *OsLA*q6-G lines were stained dark purple than Ilmi by starch-iodine test. As a result, *OsLA*q6-G can be used as a breeding resource for improving diabetes and cardiovascular disease.

[†] These authors contributed equally.

***Corresponding Author:** Tel. 053-950-5711, E-mail: kkm@knu.ac.kr

PE-0018

Find CNDH Grain Size Relate Gene, and Identification of Shape Based on QTL Mapping in Rice

Ji-Hun Kim[1], Jae-Ryoung Park[2,3], Yoon-Hee Jang[3], Eun-Gyeong Kim[3], Kyung-Min Kim[1,3]*

[1]Department of Applied Biosciences, Kyungpook National University, Daegu, 41566, Korea
[2]Crop Breeding Division, National Institue of Crop Science, Rural Development Administration, Wanju, 55365, Republic of Korea
[3]Coastal Agriculture Research Institute, Kyungpook National University, Daegu 41566, Korea

Rice is the world's top three crop and is eaten by 34% of the world's population. However, although the world's population is increasing, food security is not well protected. 800 millon people worldwide are starving and without food security. Quantitative trait locus (QTL) mapping is a statistical analysis using both phenotypic and genotypic dates. The purpose of QTL mapping is to determine a gene. Increasing grain size is a way to increase yield in rice. Grain size-related genes were mapped using CNDH population obtained by cross-breeding Cheongcheong (Indica) and Nagdong (Japonica) through anther culture. Grain harvested from experimental field of Kyungpook National University in Gunwi in 2021. The data were analyzed through QTL. Data analyzed through QTL used RiceXpro and RAP-DB to found candidate genes. Frequency distribution for grain length, grain width, and grain length&width ratio in CNDH lines. Because all traits showed a normal distribution. Genes related to grain length were detected between RM5964-RM12285 and RM20924-RM20967 in Chromosome 1,7. Genes related to grain width was detected between RM289-RM18130 in Chromosome. Genes related to grain length/width ratio were detected between RM5459-RM3482, RM5699-RM1211 and RM3838-RM3381 in Chromosome 1,2,5. Found the candidate gene *Os05g0232500*, *Os05g0235300* associated with the grain width. Though this, we will protect food security by looking for genes related to grain size.

***Corresponding Author:** Tel. 053-950-5711, E-mail: kkm@knu.ac.kr

PE-0019

OsCM Regulates Rice Defense System in Response to UV Light Supplemented with Drought Stress

Rahmatullah Jan[1,2], Nari Kim[1], Saleem Asif[1], Kyung-Min Kim[1,2*]

[1]Department of Applied Biosciences, Kyungpook National University, Daegu, 41566, Korea
[2]Coastal Agriculture Research Institute, Kyungpook National University, Daegu 41566, Korea

Study related to plant response to combined abiotic stress are very limited, especially in major crop plants. Current study was conducted to evaluate the response of chorismate mutase overexpressor (OxCM) rice line to UV light and drought combined stress. The result showed that, wild type rice reduced the growth vigor while transgenic rice plant maintain the growth vigor under UV light and drought combined stress compared with wild type. The reactive oxygen species (ROS) and lipid peroxidation analysis revealed that, chorismate mutase (*OsCM*) reduced oxidative stress mediated by ROS scavenging and reduced lipid peroxidation. Both the combined stress reduced the biosynthesis of total flavonoids, kaempferol and quercetin in wild treated plants, while increased significantly in OxCM treated plants compared with control plants. Phyto-hormonal analysis showed that salicylic acid (SA) was reduced 50 % and 73 % in wild type and transgenic treated plants respectively, while abscisic acid (ABA) was reduced 22 % in wild treated plants and increased 129 % in transgenic treated plants compare with control plants. Further, our results revealed that expression of *OsCM* gene regulates phenylalanine biosynthesis, UV light and drought stress responsive genes such as, phenylalanine ammonia lyase (*OsPAL*), dehydrin (*OsDHN*), dehydration responsive element-binding (*OsDREB*), ras-related protein 7 (*OsRab7*), ultraviolet-B resistance 8 (*OsUVR8*), WRKY transcriptional factor 89 (*OsWRKY89*) and tryptophan synthase alpha chain (*OsTSA*). Besides these, *OsCM* genes also increases the accumulation of free amino acids (aspartic acid, glutamic acid, leucine, tyrosine, phenylalanine and proline) and sodium (Na), potassium (K) and calcium (Ca) ions in response to both the combined stress. Taken together, all these results suggested that *OsCM* gene expression induce physiological, biochemical and molecular system to enhance tolerance in response to UV light and drought combined stress.

***Corresponding Author:** Tel. 053-950-5711, E-mail: kkm@knu.ac.kr

PE-0020

Enhancing Rice Crop Resistance to White-Backed Plant Hopper Infestation Through Foliar Application of Sodium Nitroprusside (SNP)

Muhammad Farooq[1], Yoon-Hee Jang[2], Eun-Gyeong Kim[2], Dan-Dan Zhao[3], Kyung-Min Kim[1,2*]

[1]Department of Applied Biosciences, Kyungpook National University, Daegu, 41566, Korea
[2]Coastal Agriculture Research Institute, Kyungpook National University, Daegu 41566, Korea
[3]Crop Foundation Research Division, National Institute of Crop Science, Rural Development Administration, Wanju, 55365, Korea

Plant hopper are the pest herbivores which significantly affect the growth and productivity of rice throughout the world. The study aims to investigate the role of two chemicals, sodium nitroprusside (SNO) as a nitric oxide inducer and Carboxy-PTIO potassium salt as a nitric oxide scavenger, in countering the infestation of white-backed plant hoppers (WBPH) in rice. We conducted a screening test of these chemicals to determine the appropriate concentrations that would be effective against WBPH infestation. We study various factors including agronomic traits, gene expression, nitric oxide concentration, mortality rate, relative water content, and electrolytic leakage. The findings showed that concentrations of 100 and 200 µM of cPTIO and SNP did not have a significant impact on the relative water content of both susceptible and resistant rice lines. However, electrolytic leakage was significantly higher in both susceptible and resistant rice lines. Specifically, the highest electrolytic leakage was observed under the 200 µM treatment of cPTIO in susceptible rice lines compared to the negative control. Furthermore, the gene expression of *OsNOA1*, and *OsEF-1α* was found significantly higher in resistance lines CNDH-78 and CNDH-87, whereas *OSNR* was up-regulated in susceptible rice line CNDH-48-3 after 12 and 24 h. The No contents was found significantly higher after 24 h in susceptible lines CNDH14-2 and CHND 48-3, whereas resistance lines show increase No contents after 6 to 24 h. Thus, the current study suggests that SNP application increases internal NO content, protecting rice from WBPH and improving agronomic traits.

***Corresponding Author:** Tel. +82-539505711, E-mail: kkm@knu.ac.kr

PE-0021

Halotolerant Edophytic Bacteria Alleviate Salinity Stress in Rice (*Oryza sativa* L.) by Modulating Ion Content, Endogenous Hormones, the Antioxidant System and Gene Expression

Saleem Asif[1], Rahmatullah Jan[1,2], Nari Kim[1], Kyung-Min Kim[1,2*]

[1]Department of Applied Biosciences, Kyungpook National University, Daegu, 41566, Korea
[2]Coastal Agriculture Research Institute, Kyungpook National University, Daegu 41566, Korea

Excessive salinity affects crop production and negatively impacts agriculture worldwide by reducing yield, plant growth, and seed germination. However, using Plant Growth Promoting Bacteria (PGPB) has the potential to mitigate salinity's negative effects on rice plants. We previously isolated endophytic bacterial strains from two halophytic species: *Artemisia princeps* and *Chenopodium ficifolium* from Pohang Beach South Korea and identified by phylogenetic analysis. We used three bacterial isolates: ART-1 (*Lysinibacillus fusiformis*), ART-10 (*Lysinibacillus sphaericus*), and CAL-8 (*Brevibacterium pityocampae*) to alleviate the impact of salinity stress on rice. The impact of 160 mM NaCl salinity on rice was significantly mitigated following inoculation with these bacterial strains, resulting in increased growth and chlorophyll content. Furthermore, *OsNHX1*, *OsAPX1*, *OsPIN1* and *OsCATA* expression was increased, but *OsSOS* expression was decreased. Inductively coupled plasma mass spectrometry (ICP-MS) revealed reduced K+ and Na+ levels in shoots of bacteria-inoculated plants, whereas that of Mg2+ was increased. Bacterial inoculation reduced the content of total flavonoids in rice leaves. Salinized plants inoculated with bacteria showed reduced levels of endogenous salicylic acid (SA) and abscisic acid (ABA) but increased levels of jasmonic acid (JA). Additionally, bacterial inoculation minimizes cell death and boosts the activity of enzymes which combat free radicals, such as superoxide dismutase (SOD). In conclusion, the bacterial isolates ART-1, ART-10, and CAL-8 alleviated the adverse effect of salinity on rice growth, which justifies their use as an eco-friendly agricultural practice.

***Corresponding Author:** Tel. 053-950-5711, E-mail: kkm@knu.ac.kr

PE-0022

Research on Function of *OsSFq3* Gene during High-Temperature Treatment in Grain Filling Stage of Rice Using Genome Editing

Seong-Beom Lee[1], Jae-Ryoung Park[2,3], Kyung-Min Kim[1,2*]

[1]Department of Applied Biosciences, Kyungpook National University, Daegu, 41566, Korea
[2]Coastal Agriculture Research Institute, Kyungpook National University, Daegu 41566, Korea
[3]Crop Breeding Division, National Institute of Crop Science, Rural Development Administration, Wanju, 55365, Republic of Korea

Rice is a staple crop of world's population. The high temperature during grain filling stage of rice decreases spikelet fertility and forms chalkiness grain. These affect rice yield and grain quality negatively. In particular, since the grain filling stage of early seasonal cultivation rice belongs to July to August, it is significant to prepare for high temperature for the early seasonal cultivation. The rice *OsSFq3* gene was identified as a gene that was reported to contribute to grain yield and quality for high temperature condition. In this research, the *OsSFq3* gene was selected as a target gene for genome editing. Guide RNAs were designed by the CRISPR RGEN Tools program. The pRGEB32 vector was utilized in the Cas9 vector. After the guide RNAs were integrated into the pRGEB32 vectors, the vectors were amplified through competent cells of *Escherichia coli.* The integrated pRGEB32 vectors were transformed into *Agrobacterium tumefaciens*. Using these transformed *Agrobacterium tumefaciens*, Ilmi calli were infected and co-cultured. After co-cultivation, the calli were inoculated on regeneration media. Green spots which indicate pre-stage of regenerated plants were formed from the calli. Regenerated plants were occurred from the green spots. The CRISPR/Cas9 can remove a gene function through targeted mutagenesis. This study suggests that CRISPR/Cas9 can be used to identify function of the *OsSFq3* gene through deletion of the gene function. The identification of the *OsSFq3* gene function can be the key of developing the rice breeding technology which improves grain yield and quality below high temperature during grain filling stage.

***Corresponding Author:** Tel. 053-950-5711, E-mail: kkm@knu.ac.kr

PE-0023

Exogenous Application of Gamma Aminobutyric Acid Increase Salt and Drought Resistance by Regulating ROS and Enhancing Antioxidants in Rice (*Oryza sativa* L.)

Zakir Ullah Khan[1], Rahmatullah Jan[1,2], Saleem Asif[1], Kyung-Min Kim[1,2*]

[1]Department of Applied Biosciences, Kyungpook National University, Daegu, 41566, Korea
[2]Costal Agriculture Research Institute, Kyungpook National University, Daegu 41566, Korea

Rice (*Oryza sativa* L.) is one of the major staple food and widely cultivated throughout the World, and about half of the World population depends upon rice. Soil salinity is an environmental factor growing in Magnitude in the rice growing areas due to the combine effects of high temperature, drought, sea level rising and inferior agriculture practices. Gamma-aminobutyric acid (GABA) is a ubiquitous four-carbon, non-protein amino acid. In plants, it is metabolized through the GABA shunt pathway, a bypass of the tricarboxylic acid (TCA) cycle. It is accumulated during plant responses to environmental stresses and pathogen and insect attacks. A high concentration of GABA elevates plant stress tolerance by improving photosynthesis, inhibiting reactive oxygen species (ROS) generation, activating antioxidant enzymes, and regulating stomatal opening in drought stress. Rice seeds of *Ilmi* cultivar were sterilized with 0.5% sodium hypochlorite for 10 min and then washed 3 time with distilled water. The seeds were soaked for 5 days and then transferred to plastic pots. After 2 weeks 1mM of GABA was applied to seedlings, and then 100mM of salt and 10% PEG were applied after 1 week of the treatment of GABA.A total of 8 samples were taken including control, GABA, salt, drought, salt+drought, salt+ GABA, drought+ GABA, and salt+drought+GABA. After one week of the treatments root, shoot length, biomass, chlorophyll contents, electrolyte leakage, antioxidants, and expression of different drought and salt genes were checked.

***Corresponding Author:** Tel. 053-950-5711, E-mail: kkm@knu.ac.kr

PE-0024

The Role of *Chorismate Mutase* in Regulating cq-9 Biosynthesis in Rice

Yoon-Hee Jang[1], Jae Ryoung Park[1,2], Eun Gyeong Kim[1], Kyung Min Kim[1,3*]

[1]Coastal Agriculture Research Institute, Kyungpook National University, Daegu 41566, Korea
[2]Crop Breeding Division, National Institute of Crop Science, Rural Development Administration, Wanju, 55365, Republic of Korea
[3]Department of Applied Biosciences, Kyungpook National University, Daegu, 41566, Korea

Rice is the main food source for the population, and its quantity must increase significantly to feed the growing population. Diseases and insects are major factor limiting rice yield, and host plant resistance is attracting attention as disease and insect management strategy in crops. In the past, traditional breeding methods have been used to introduce resistance to rice disease and pest, but increased pest diversity, lack of sources of cultivated rice gene pools, and a lack of understanding of complex resistance mechanisms need to be addressed. Therefore, advanced molecular biological approaches are being actively pursued and can provide a solid basis for cultivar breeding. *OsCM* identified on chromosome 8 based on QTL mapping encodes a *chorismate mutase* involved in prephenate synthesis in the shikimate pathway. The *OsCM* genome-editing lines (*OsCM*-G), edited using CRISPR/Cas9, showed that *OsCM* is involved in the biosynthesis of cochlioquinone-9 (cq-9) and control the damage of white backed planthopper. In addition, the major agricultural traits of *OsCM*-G showed a similar level of variation to that of the background cultivar Cheongcheong. Our results suggest that *OsCM* play an important role in rice disease and insect resistance by regulating in the shikimate pathway, and CRISPR/Cas9 technology can be effectively used to provide insight into the molecular basis of rice and biotic stress interactions. Understanding of rice defense mechanism promotes the breeding of disease and pest resistant rice cultivars, contributing to efficient, long-term pest management strategies.

***Corresponding Author:** Tel. 053-950-5711, E-mail: kkm@knu.ac.kr

PE-0025

Genome editing, Using CRISPR/Cas9 in Rice for Functional identification of *OsDGTq1*

Seung-Kyo Jeong[1], Jae-Ryoung Park[2,3], Kyung-Min Kim[1,2*]

[1]Department of Applied Biosciences, Kyungpook National University, Daegu, 41566, Korea
[2]Coastal Agriculture Research Institute, Kyungpook National University, Daegu 41566, Korea
[3]Crop Breeding Division, National Institute of Crop Science, Rural Development Administration, Wanju, 55365, Republic of Korea

As the world's population increase, the importance of rice will increase. However, due to the abnormal temperature, diseases of rice are getting worse, and the yield is decreasing. Among them damping-off is cause by fungus in the seedling stage, when the diurnal temperature difference is extreme. Thus reducing the yield. Therefore, research on creating resistant plants is needed. in this study will create resistance plants by using CRISPR/Cas9. And gene is *OsDGTq1* that is located between RM11849-RM212 on chromosome 1. cas9 vector is pRGEB32 vector that have Kanamycin and, Hygromycin site. When designing guide RNA, GC content was set to 50% to 60%, out-of-frame 65% or more, and mismatches to 1, 0, 0. restriction enzymes were used to cut the vector and ligate the guide RNA. *E.coli* transformate and, select, using Kanamycin contain LB media. When *E.coli* grows, plasmid is extracted and electrophoresis. With the current electrophoresis completed. Later, sequencing will be performed to check the guide RNA is inserted into the vector, and when the guide RNA is inserted, transformation of agrobacterium, infection of callus and plant regeneration experiments will be conducted. In this study, we will be able to create genome-editing plants. also use it check the function of the *OsDGTq1*. By checking the function of the *OsDGTq1*, it can be used as a genetic resource for related research. By reducing the number of dead plants due to damping-off, it can have a positive effect on increasing yield, which can contribute to global food problems.

***Corresponding Author:** Tel. 053-950-5711, E-mail: kkm@knu.ac.kr

PE-0026

Examining the transcriptome and the expression of heat-shock protein (HSP) families in the spikelets of hulless oat (*Avena sativa* L.) during heat stress

Woo Joo Jung[1], Chan Seop Ko[2], Yong Weon Seo[3*]

[1]Institute of Life Science and Natural Resources, Korea University, Seoul 02841, Korea
[2]Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, 29 Geumgu, Jeongeup, 56212, Republic of Korea
[3]Ojeong Plant Breeding Research Center, Korea University, Seoul 02841, Republic of Korea

Oats are an economically important cereal crop known for their unique nutritional profile, including β-glucan and avenin seed storage proteins. However, genomic research on oats has been hindered by their large and complex genome. Recently, the oat reference genome has been published, enabling studies on transcriptomes and genome-wide gene identification. Heat stress poses a growing threat to plant growth, worsened by climate change. Heat shock proteins (HSPs) are well-known for protecting plants from various stressors, but their role in oats remains unexplored. In this study, we conducted RNA-seq analysis on oat spikelets exposed to high temperatures. The results revealed the upregulation of glutathione and flavonoid pathways, while DNA replication and fatty acid elongation were downregulated. We also observed diverse expression patterns among cellulose synthase genes, and a significant downregulation of avenin genes under heat stress. Additionally, we identified and localized 823 *HSP* gene families in the oat genome, with different expression patterns at various temperatures. These findings provide insights into the complex mechanisms of heat tolerance in oats, and will contribute to future investigations in this area. Overall, the publication of the oat reference genome has opened doors for further genomic research on oats, allowing us to understand and address challenges such as heat stress in oat cultivation.

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

PE-0027

A zinc finger protein located on the short arm of chromosome 1 (1RS) in rye enhances resistance to cold temperatures and alter the timing of flowering in *Brachypodium distachyon*

Woo Joo Jung[1], Ji Hyeon Jeong[2], Jin Seok Yoon[3], Yong Weon Seo[2,3*]

[1]Institute of Life Science and Natural Resources, Korea University, Seoul 02841, Korea
[2]Department of Plant Biotechnology, Korea University, Seoul 02841, Korea
[3]Ojeong Plant Breeding Research Center, Korea University, Seoul, 02841, Korea

T1BL.1RS is a type of wheat-rye translocation lines that the short arm of wheat chromosome 1B (1BS) is switched to the short arm of rye chromosome 1 (1RS). It has superior biotic and abiotic tolerance and tend to flower late than common wheat. Zinc Finger Proteins comprise one of the largest transcription factor families and they are known to regulate plant growth, development, and stress signal transduction. In this study, we identified a novel zinc finger protein located on 1RS (ScZFP) and observed the phenotype of *ScZFP*-overexpressing *Brachypodium* (OE). The OE plants represented higher survival rate after freezing treatment and also higher proline and soluble sugar content whereas lower electrolyte leakage. The gene expression analysis revealed that in OE plants CBF-COR pathway was up-regulated. The OE plants also showed rapid flowering phenotype in both long-day and short-day conditions. The real-time PCR results indicated that vernalization pathway genes *VRN1* and *FT1* were up-regulated in the OE plants whereas photoperiod genes were not differentially expressed compared to the wild-type. The RNA-seq revealed that abiotic stress response genes such as dehydrin, LEA, and heat shock proteins, and a certain group of *MADSbox* genes were also highly expressed in the OE. Overall, the results of our study will help to investigate cold tolerance and flowering mechanism in cereal crops.

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

PE-0028

Wheat (*Triticum aestivum.* L) U-box E3 Ubiquitin Ligases *TaPUB2* and *TaPUB3* are involved in the positive regulation of ABA and salt stress response in *Arabidopsis*

Moon Seok Kim[1†], Jae Ho Kim[1,2†], Joseph Noble Amoah[1], Yong Weon Seo[1,3*]

[1]Department of Plant Biotechnology, Korea University, Seoul, Republic of Korea
[2]Institute of Animal Molecular Biotechnology, Korea University, Seoul, Republic of Korea
[3]Ojeong Plant Breeding Research Center, Korea University, Seoul, Republic of Korea

Plant U-box E3 ligases (PUBs) play a vital role in coordinating responses to various abiotic stress conditions. PUB genes have been found in a variety of plant species, but little is known about their possible roles in signaling crosstalk in wheat. In our research, we identified the physiological process of wheat PUB gene, *TaPUB2* and *TaPUB3*, in response to ABA and salt stress using overexpressed *Arabidopsis*. *TaPUB2* and *TaPUB3*-overexpressing *Arabidopsis* (OE) conferred ABA-hypersensitive primary root growth and reduced seed germination rate. Moreover, the OE plants showed improved salt tolerance. The results of real-time PCR exhibited highly enhanced transcript level of salt stress induced genes (A*tMYB2, AtCOR47, AtCOR15A, AtRD29A, AtRD29B, AtRAB18,* and *AtSOD4*) in transgenic *TaPUB2* and *TaPUB3* plants. Furthermore, chlorophyll, malondialdehyde (MDA) contents, and scavenging reactive oxygen species (ROS) were induced in *TaPUB2* and *TaPUB3*-overexpressing plants. These findings revealed the functions of PUBs in ABA and salinity stress conditions, providing valuable insights for improving the tolerance of crop species to salinity stress. (Published: *FEBS Letters* 596)

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

PE-0029

Genome-wide association study of strawberry fruit using image-based phenotype

Koeun Han[1*], Hong-Il Ahn[1], Jeong-Ho Baek[2], Seolah Kim[1], Ye-Rin Lee[1], Eun Su Lee[1], Do-Sun Kim[1]

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

[2]Department of Agricultural Biotechnology, National Institute of Agricultural Sciences, Rural Development Administration (RDA), Jeonju, 54874, Republic of Korea

To understand genetic diversity and identify genetic loci controlling fruit quality traits, we selected 160 strawberry (*Fragaria × ananassa*) germplasm and accumulated genotype and phenotype data. Genotyping was performed accurately using the FanaSNP 50K assay, resulting in 42,311 markers. The plants were cultivated over two growing seasons, and we evaluated 18 fruit-quality traits repeatedly, including fruit size, color, and total soluble sugar contents. We also used the image-based phenotyping method to increase phenotyping efficiency and accuracy. Eight image-based traits related to fruit size and included length, diameter, roundness, and area have been detected. Additionally, we manually characterized fruit color in stages from 1 to 4 and plan to develop an image analysis tool specifically for fruit flesh core color. Genetic loci controlling fruit quality were detected using genotypic data, conventionally investigated, and image-based phenotypes. Since most of these traits are quantitative, minor loci were identified across genetic regions. However, through comparison with previous and ongoing genetic studies, we will select major loci and develop molecular markers or genomic selection tools for breeding purposes.

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***Corresponding Author:** Tel. 063-238-6672, E-mail: hke1221@korea.kr

PE-0030

The effect of genetically modified (GM) crop on associated non-target insects and arachnids

Sung-Dug Oh[1], Doh-Won Yun[1], Seong-Kon Lee[1], Gang-Seob Lee[1], Sang Jae Suh[2*]

[1]Department of Agricultural Biotechnology, National Institute of Agricultural Sciences, Jeonju 54874, Republic of Korea

[2]School of Applied Biosciences, Kyungpook National University, Daegu, 41566, Republic of Korea

The evaluation of genetically modified (GM) crops regarding their effect on non-target organisms is necessary to safeguard ecosystem components. A field study was undertaken to examine whether GM soybean adversely affects the biodiversity of arthropods, by comparing with a non-genetically modified parental cultivar, Gwangan soybean. The GM soybean expresses bioactive human epidermal growth factor (EGF) and shows tolerance to the herbicide glufosinate. Surveys of soybean fields were conducted in 2016 and 2017, in Jeonju and Ochang, Korea. The number of captured arthropods increased over time in both soybean plants in both locations. Furthermore, the diversity and richness of insects and arachnids increased, whereas the dominance and evenness decreased and remained static, respectively. Of the identified insect pests, Hemiptera occurred the most frequently (25.4%); of the natural enemies, Hymenoptera occurred the most frequently (29.9%); and of the remaining insects, Diptera occurred frequently in both survey regions. Multidimensional scaling showed that the occurrence of insects and arachnids was distinct owing to cultivation regions and years, irrespective of the soybean genotype. Thus, no notable change occurred in the composition of arthropod communities in soybean agroecosystems owing to the genetic modification in soybean expressing EGF.

***Corresponding Author:** Tel. 053-950-7767, E-mail: sjsuh@knu.ac.kr

PE-0031

Analysis of weediness potential in β-carotene enhanced soybean and Hybrid soybean(LM x wild soybean)

JiEun Choi, Sung-Dug Oh, Seong-Kon Lee, Gang-Seob Lee, Doh-Won Yun*

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

Safety problems caused by environmental release from LM (Living Modified) crops are considered important. Among them, the possibility of weediness is constantly emerging. Accordingly, this study compared the growth characteristics and germination rate of hybrid soybean formed by hybridization with β-carotene enhanced soybean introduced with a gene that increases β-carotene content, and examined overwintering, survival and weed competitiveness to evaluate the impact on ecology in long-term unmanaged cultivation land. It was confirmed that the growth characteristics and germination rate of hybrid soybean exhibited intermediate traits between the β-carotene enhanced soybean and wild soybean, or were similar to those of the maternal. Overwintering experiments were conducted by landfill the seeds at depths of 0, 5, 10, and 20 cm for 3 and 5 months. As a result, after 5 months, when the depth was more than 5 cm, all seeds lost viability, and after 3 months, it was confirmed that seeds with the exception of wild soybean lost viability at depths of more than 5 cm. Survival and weed competitiveness were proceeded by sowing in 3 repetitions of 100 seeds each, and irrigation, pest and weed control were not performed. When the number of soybean individual that appeared in the experimental plot was investigated, all germinated after sowing, but plants except for wild soybean did not overwintering. Through this, it is thought that even if both LM soybeans and hybrid soybeans do environment release, they can’t settle in uncultivated land, so there will be little possibility of weediness.

***Corresponding Author:** Tel. 063-238-4713, E-mail: dwyun@korea.kr

PE-0032

수박 세균성과실썩음병 저항성 유전자원 수집 및 유전정보 탐색

Namsu Jo, Chnagguk Kim, Jin-hyuck Huh, Youn-Sung Kim*

Plant Biotechnology Institute, Jenong S&T Co. Ltd., Anseong-si, Gyeonggi-do, 17602, Korea

수박(*Citrullus lanatus*)은 남아프리카 원산인 한해살이 박과(Cucuebitaceae) 식물로 주로 고온지대에서 재배되는 주요한 작물 중 하나이다. 수박 육종은 1950년대 초에 일본에서 도입한 계통을 분리육종하여 1970년대 본격적으로 1대 잡종 품종이 육성되었다. 하지만 주요 병 저항성 품종 등 고품질 품종 개발을 위한 과제는 여전히 남아있다. 수박 재배에서 발생하고 있는 주요 병으로는 덩굴마름병, 탄저병, 역병, 흰가루병, 균핵병, 과실썩음병, 바이러스병 등이 있다. 특히 고온 다습한 조건에서 종자에 의해 전염되는 것으로 알려진 수박 세균성과실썩음병(Bacterial fruit blotch: BFB)은 현재까지도 저항성 유전자원에 대한 연구조차 미비한 실정이다. 따라서 본 연구에서는 수박 세균성과실썩음병 저항성 유전자원을 수집하고, 자원에 대한 유전적 분석을 통해 데이터를 확보하고자 하였다. BFB 저항성 유전자원 확보를 위해 국내・외에서 42개 유전자원을 수집하였고, 병원성 스크리닝 분석을 통해 성적이 우수한 2개의 저항성 자원(W402, W403)과 1개의 감수성 자원(W401)을 모계친, 부계친으로 확보하였다. 수집 자원 및 전개 세대에 대한 유전적 데이터 확보를 위해 병 저항성 검정을 통해 성적이 우수한 자원들에 대한 GBS(Genotyping by sequencing) 분석을 수행하였다. 우선 모・부계로 활용한 W401, W402, W403에서 S1 종자를 확보하여 총 10개 유전자원에 대한 GBS 분석을 수행하였다. 10개 유전자원의 SNP 탐색은 MAF(Minor allele frequency)가 5%보다 큰 SNP를 선발한 결과 60,930개의 SNP를 발굴하였다. 또한 수집된 42개 유전자원 및 S1 자원을 포함한 86개 유전자원에 대한 GBS 분석 수행을 통해 missing data가 30% 미만인 SNP를 선발, MAF가 5%보다 큰 SNP를 선발하여 총 118,352개의 SNP를 탐색할 수 있었고, 염색체별 분포도를 작성하였다. 본 연구를 통해 수집한 유전자원 및 유전정보를 활용한다면 BFB 저항성 판별이 가능한 마커 개발 및 품종 육성에 이바지할 것이라고 사료 된다.

***교신저자:** E-mail: kimys@jenong.co.kr

PE-0033

Assessing Genetic Diversity in Onion Germplasm Using a High-Throughput Marker Set

Ye-Rin Lee[1], JiWon Han[2], Koeun Han[1], Eun Su Lee[1], Hong-Il Ahn[1], Do-Sun Kim[1*]

[1]Vegetable Research Division, National Institute of Horticultural and Herbal Science, Rural Development Administration, RDA, Wanju, 55365, Republic of Korea
[2]Allium Vegetable Research Institute, National Institute of Horticultural and Herbal Science, RDA, 58545, Republic of Korea

Onion (*Allium cepa*) is a biennial, cross-pollinating crop that poses significant challenges in breeding due to its longer life cycle compared to other crops. However, considering the large economic scale and the growing demand for various new onion varieties, it is necessary to establish a core collection that includes the diversity of genetic resources for cultivating high-quality onion varieties. Additionally, the development of a marker set for genotyping analysis is required to commercialize advanced breeding technology. Therefore, to select core onion resources, we conducted a genotype analysis on 270 germplasms, including cultivars and genetic resources held by the Allium Vegetable Research Institute (RDA), using a previously reported high-throughput marker set. The data obtained from the analysis will be utilized to select core resources. Subsequently, these core resources will be used to develop a marker set for genotype analysis using onion genome information, thus establishing a precision molecular breeding-based technology.

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

PE-0034

무(*Raphanus sativus* L.)의 새로운 S haplotype 동정 및 유전적 유연관계 분석

김수연, 모숙연, 장재석, 박한용*

서울시 광진구 능동로 209 세종대학교 바이오산업자원공학과

무(*R. sativus* L.)를 포함한 배추과 작물은 타식성 작물로 유전적 다양성을 유지하기 위해 자가불화합성 현상을 나타낸다. 배추과의 자가불화합성은 포자체 자가불화합성으로 S locus는 암술머리(stigma)에서 발현되는 SRK, SLG 유전자와 화분(pollen)에서 발현되는 SCR/SP11 유전자로 구성되며, 3가지 유전자들은 함께 자손으로 유전되기 때문에 S haplotype이라 명명되었다. 배추과의 자가불화합성은 F_1 품종 육성을 위해 가장 많이 사용하는 특성으로 F_1 교배작성을 위해 양친 계통의 S haplotype의 동정과 식별은 필수적이다. 본 연구에선 SLG 유전자의 서열 분석을 통해 무 F_1 품종의 양친 계통으로 사용하는 ‘5065’ 계통이 새로운 종류의 S haplotype인 것으로 나타났다 (novel SLG로 명명). 이후 ‘5065’ 계통의 S haplotype과 무 class I의 15개 종류 S haplotype의 SLG 아미노산 서열, 무 class II의 2개 종류 S haplotype의 SLG 아미노산 서열, 9개의 다른 배추과 작물의 SLG 아미노산 서열을 이용하여 Neighbor-Joining Phylogenetic tree를 작성하였다(Bootstrap 1000). 작성 결과, 크게 class I와 class II의 2개 clade로 나뉘었고, Interspecific pair를 이루었다. class I SLG 아미노산 서열이 동일한 node에서 Group 1, 2와 Group 3으로 분기되었으며 novel SLG와 Br-SLG54가 Group 3에서 interspecific pair를 형성하였고 다른 Group을 포함하여 class I SLG는 총 4가지 그룹을 가지는 것을 확인했다(Group 1~4). 따라서 새롭게 동정한 SLG(novel SLG)는 기존에 보고된 S haplotype과 다르며 Class I 그룹에 속하지만, 기존에 보고된 무의 다른 class I SLG와 유전적으로 가깝지 않음을 알 수 있었다. 추후 연구에서 ‘5065’ 계통의 S locus 유전자의 서열 분석을 통해 새로운 S haplotype을 NCBI database에 등록할 예정이다. 최종적으로, 새로 동정한 S haplotype은 무 F_1 품종 육종을 위한 양친 계통 S haplotype 식별에 유용할 것으로 기대된다.

사사: 본 결과물은 농림축산식품부의 재원으로 농림수산식품기술기획평가원의 디지털육종전환기술개발사업의 지원을 받아 연구되었음(322063032SB010).

***교신저자:** Tel. 010-6746-7477, E-mail: hypark@sejong.ac.kr

PE-0035

무 SRK, SLG 유전자 염기서열을 이용한 S haplotype 분류 및 유전적 근연관계 분석

허성호[1,2], 박병준[1,2], 모숙연[1], 박한용[1*]

[1]서울특별시 광진구 능동로 209 세종대학교 바이오산업자원공학과
[2]경기도 평택시 이화로 251-29 농업회사법인 (주) 다산바이오

무(*R. sativus* L.)를 포함한 배추과 작물에서 자가불화합성 시스템은 F1 품종 육종에 광범위하게 사용되어왔으며 무 S haplotype 동정은 F1 품종 교배조합 작성 전에 가능한 반드시 해야되는 작업이기 때문에 무 S haplotype 동정에 관한 연구가 전세계에서 진행되었다. S haplotype에 대한 명명은 연구진에 따라 독립적으로 진행되어왔으며, 동일하거나 유사한 서열을 다른 S haplotype으로 명명하거나, 서로 다른 서열을 동일한 S haplotype으로 명명하고 데이터베이스에 등재하여 정확한 S haplotype 분류가 어렵다. 본 연구에서는 무 F_1 품종 육종에서 양친 계통으로 사용되는 22개 계통에서 동정한 9개 S haplotype의 SRK Kinase Domain과 SLG 유전자 염기서열을 이용하여 BLAST 검색, NCBI 에서 동일하거나 유사한 S haplotype을 분류하고 SRK와 SLG 유전자 염기서열을 이용하여 S haplotype 간 유전적 근연관계를 분석하였다. 실험 결과 유사한 서열 5개 이상 검색된 S haplotype은 S5, S10, S16, S21 총 4개이며 S5의 SLG5 서열은 97% 이상 유사한 서열이 6개가 검색, S10의 SRK10-KD 서열은 98% 이상 유사한 서열이 11개가 검색되었다. S16의 SRK16-KD 서열은 97% 이상 유사한 서열이 11개 검색, S21의 SLG21 서열은 98% 이상 유사한 서열이 5개 검색되었다. 이후 12개 S haplotype의 SRK S Domain, SLG 유전자를 이용하여 ML method로 phylogenetic tree를 작성했다. 크게 Class I, II 두 그룹으로 나뉘었으며, 대부분은 동일 S haplotype의 SLG와 SRK S Domain끼리 specific pair를 형성했다. 그러나 S1(Lim), S18(Lim), S1(Haseyama), S5(Lim), S21(Lim)은 다른 S haplotype의 SRK S Domain 또는 SLG와 specific pair를 형성하였다. 이를 통해 SRK S Domain과 SLG는 분화 이후 Gene conversion과 같은 event로 유사성을 유지한 것으로 추정, 반드시 동일한 S haplotype의 SRK S Domain과 SLG 염기서열이 가장 유사하지 않음을 보여주었다

사사: 본 결과물은 농림축산식품부의 재원으로 농림수산식품기술기획평가원의 디지털육종전환기술개발사업의 지원을 받아 연구되었음(322063032SB010).

***교신저자:** Tel. 010-6746-7477, E-mail: hypark@sejong.ac.kr

PE-0036

Genome-wide analysis of U-box E3 ubiquitin ligases in rye (*Secale cereale* L.)

Hyo Jeong Shin[1], Woo Joo Jung[2], Dae Yeon Kim[3], Yong Weon Seo[1,4*]

[1]Department of Plant Biotechnology, Korea University, Seoul 02841, Korea
[2]Institute of Life Science and Natural Resources, Korea University, Seoul 02841, Korea
[3]Department of Plant Resources, College of Industrial Science, Kongju National University, Yesan 32439, Korea
[4]Ojeong Plant Breeding Research Center, Korea University, Seoul 02841, Korea

Plant U-box (PUB) protein is one of the E3 ubiquitin ligases and has been known to be involved in plant biological processes including plant abiotic and biotic stress responses. Rye (*Secale cereale* L.) is an economically important crop which is used as food and forage, and is known as the most cold-resistant winter crop. In this study, a genome-wide investigation of rye *PUB* genes was conducted. A comprehensive computational analysis identified 100 *PUB* genes in rye, and the phylogenetic comparison was carried out with *PUB* genes of other winter crops and *Arabidopsis.* The rye *PUB* genes were spread across all seven chromosomes, and they were divided into seven groups according to their protein structures. The *cis*-acting regulatory elements in the promoters were analyzed to elucidate the potential regulating factors of rye *PUB* genes. The synteny analysis revealed that high synteny was conserved among those in rye, wheat, and barley, and it was consistent with evolutionary distance. Moreover, RNAseq analysis represented that more than half of rye *PUB* genes were most expressed in the root tissue and most of the genes were responsive to cold- and drought-treated conditions. The expressions of *PUB* orthologs in rye, wheat, and barley, which are all winter crops, were also compared plant tissue specifically. The results of our study would serve as a foundation for understanding PUBs in winter crops and their roles in plant cold resistance mechanisms.

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

PE-0037

Assessment of Drought Tolerance of Wild Soybean Accessions at Different Growth Stages

Thi Cuc Nguyen[1], Hyun Jo[1], Hai Anh Tran[1], Jinwon Lee[1], Jeong-Dong Lee[1], Jeong Hoe Kim[2], Hak Soo Seo[3], Jong Tae Song[1*]

[1]Department of Applied Biosciences, Kyungpook National University, Daegu 41566, Republic of Korea
[2]Department of Biology, Kyungpook National University, Daegu 41566, Republic of Korea
[3]Department of Agriculture, Forestry and Bioresources, Seoul National University, Seoul 08826, Republic of Korea

Drought is a significant abiotic stress that limits crop production. Soybeans [*Glycine max* (L.) Merr.] are regarded as drought-sensitive. In the present study, the drought responses of wild soybean accessions were evaluated at different growth stages. Based on the leaf wilting index at the vegetative stage, 7 very tolerant (VT) and 24 tolerant (T) accessions were identified, although most wild soybeans were classified as moderate (M), sensitive (S), and very sensitive (VS) genotypes. A total of 12 wild soybeans randomly selected from VT, T, S, and VS also showed consistent responses to drought stress with seed yield, root development, and water status at reproductive stages. However, the germination rate and root length at the germination stage under drought conditions were determined by soybean genotype, indicating that there may not be a robust correlation between phenotypic measurements at the germination stage and drought-related assessments at the two growth stages. With wild soybeans, stomatal density decreased in VT accessions but increased in VS accessions under drought conditions. The stomatal density of the cultivated soybeans was not significantly different between the two conditions. The expression levels of drought-related transcriptional factors were assessed in the leaf and root tissues of VT and VS accessions between the two conditions, resulting VT genotype may be correlated with the higher expression level of drought-related genes than that of the VS genotype. The information of this study can be used to identify candidate genes for drought stress and provide useful breeding materials for the development of drought-tolerant cultivars.

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

PE-0038

Comparison of flooding tolerance at germination and early vegetative stages of wild soybean accessions in a Korean core population

Hai Anh Tran[1], Cuc Thi Nguyen[1], Jeong-Dong Lee[1], Hak Soo Seo[2], Jong Tae Song[1*]

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

Flooding is one of the most serious abiotic stresses that reduce the productivity of crops in many important agricultural regions of the world. Soybean (*Glycine max* (L.) Merr.) is an important legume crop, which is generally sensitive to flooding stress. The present study is aimed to evaluate tolerance levels to flooding conditions at germination and early vegetative stages based on the variances in agronomic traits of accessions during stresses of 109 wild core soybean accessions. In Exp. 1, five-day-submergence stress reduced the germination rate, normal seedling rate, germination index, normal seedling index of soybean seeds significantly. However, four out of 109 accessions were determined as tolerant to submergence at this stage with the normal seedling index higher than 77%. In Exp. 2, foliar damage of soybean plants at vegetative stage (V2 stage) under conditions of submergence for 5-7 days, or waterlogging for 10-14 days was observed. Two wild soybean accessions were isolated as very tolerant to submergence, and 2 others were tolerant. Besides, in a waterlogged soil condition, 2 accessions and 7 others were very tolerant and tolerant, respectively. Furthermore, the injury levels of soybean seeds or plants during flooding stress was observed through the electric conductivity leaking from the submerged seeds or leaf/root samples collected after treatment. There was no association between tolerance levels of wild soybean to waterlogging and submergence. Similarly, tolerance levels to submergence between germination and early vegetative stage was not correlated. Further, the isolated tolerant lines will be utilized for the breeding program to identify the genetic background involved in the flooding tolerance and the nature of stress resistance.

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

PE-0039

Identification of *gibberellic acid sensitive dwarf* (*OsGASD*)gene, encoding an ARP subunit that mediates gibberellic acid biosynthesis and effects to grain yield in rice

Tae Young Um[1], Won Tae Yang[2], Doh Hoon Kim[2*]

[1]Agriculture and Life Science Research Institue, Kangwon National University, Chuncheon, 24341, Republic of Korea

[2]College of Life Science and Natural Resources, Dong-A University, Busan, 49315, Republic of Korea

The plant hormone gibberellic acid (GA) is important for plant growth and productivity. Actin-related proteins (ARPs) also play central roles in plant growth, including cell elongation and development. However, the relationships between ARPs and GA signaling and biosynthesis are not fully understood. Here, we isolated OsGASD, encoding an ARP subunit from rice (Oryza sativa), using the Ac/Ds knockout system. The osgasd knockout (Ko) mutation reduced GA3 content in shoots as well as plant growth and height. However, GA application restored the plant height of the osgasd Ko mutant to a height similar to that of the wild type (WT). Rice plants overexpressing OsGASD (Ox) showed increased plant height and grain yield compared to the WT. Transcriptome analysis of flag leaves of OsGASD Ox and osgasd Ko plants revealed that OsGASD regulates cell development and the expression of elongation-related genes. These observations suggest that OsGASD is involved in maintaining GA homeostasis to regulate plant development, thereby affecting rice growth and productivity.

***Corresponding Author:** Tel. 051-200-7500, E-mail: dhkim@dau.ac.kr

PE-0040

Genomic Insights into Plant Height and Growth Habits in Pepper (*Capsicum annuum*)

Abhinandan S. Patil, Geon Woo Kim, Min-Young Kang, Hea-Young Lee, Han Do Bae, Jelli Venkatesh, Jin-Kyung Kwon, Byoung-Cheorl Kang*

Department of Agriculture, Forestry and Bioresources, Research Institute, College of Agriculture and Life Sciences, Seoul National University, 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Republic of Korea

Plant height and growth habit are important traits that impact the overall performance and productivity of crops. In this study, we aimed to uncover the genetic basis of plant height and growth habit in pepper (*Capsicum* spp.) through quantitative trait locus (QTL) analysis and genome-wide association study (GWAS). To conduct the analysis, we used a mapping population consisting of 116 F2:3 plants obtained from crossing two pepper varieties, 'Jeju' and 'Micropep red,' which displayed contrasting plant height and growth habit phenotypes. Additionally, we utilized a core collection of diverse pepper accessions for GWAS. Genotyping was performed using 897 markers derived from genotyping-by-sequencing for QTL analysis, and 97,531 single nucleotide polymorphism markers for GWAS. Through composite interval mapping, we identified two QTLs associated with plant height located on chromosomes 4 and 7. For growth habit, we discovered eleven QTLs distributed across chromosomes 1, 2, 3, 6, 7, and 9. Furthermore, GWAS revealed 70 significant associations for both plant height and growth habit. While the QTLs and GWAS signals for plant height on chromosomes 4 and 7 were not co-localized, there were four growth habit GWAS signals on chromosomes 1 and 3 that co-localized with two QTLs for growth habit. Notably, a cluster of three significant markers on chromosome 6 in GWAS analysis coincided with the *fasciculate* gene, which is an ortholog of the *SP* gene found in tomato. The developed markers and novel candidate genes found in this study will be useful for understanding architectural traits and breeding for moderately compact cultivars.

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

PE-0041

Mutant based Quantitative trait loci (QTL) mapping analysis for fatty acid content in soybean

Ji Su Seo[1,2], Jung Min Kim[1,2], Jeong Woo Lee[1,2], Bo-Keun Ha[2*], Soon-Jae Kwon[1*]

[1]Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongeup, 580-185, Korea

[2]Division of Plant Biotechnology, Colleage of Agriculture and Life Sciences, Chonnam National University, Gwangju, Korea

Soybean (*Glycine max* L. Merr.) is one of the world's major resources for oil, accounting for about 56% of global oilseed production. Soybean has five major fatty acids such as palmitic acid (PA), stearic acid (SA), oleic acid (OA), linoleic acid (LA), and linolenic acid (LNA). In this study, we performed QTL mapping for fatty acids using a biparental population crossed between Danbaek and its mutant DB088 with different composition of fatty acids. Danbaek is a domestic excellent soybean variety, and DB088 is a mutant accession induced by gamma rays of 250 Gy. The F_2 population was measured for the contents of the five major fatty acids, ranging from PA (12.94 ~ 33.47%), SA (2.83 ~ 7.29%), OA (10.20 ~ 64.22%), LA (12.07 ~ 54.33%), and LNA (2.13 ~ 6.25%). The genetic linkage map consists of a total of 2,625 SNP markers by using Axiom® soya 180K array in 20 chromosomes, spanning a genetic distance of 2534.42 cM, with an average distance between neighboring markers of 0.90 cM. A QTL associated with OA was detected at GM13_31424193 on chromosome 13 (LOD: 6.15; R^2: 13.8%), and LA was detected in marker GM13_31736878 on chromosome 13 (LOD: 4.68, R^2: 10.7%). Based on this, 27 genes including RNA pseudouridylate synthase (Glyma.13G206600) and Triose-phosphate Transporter family (Glyma.13G206700) were identified in GM13_31424193, and Glyma.13G209400 (Serine incorporator) was identified in GM13_31736878. The causal QTL for fatty acids represents useful information for marker-assisted selection in soybean breeding programs.

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

PE-0042

Screening for *Broad bean wilt virus 2* Resistance Source and Mapping Resistance Gene Using BSR-seq

Jung-Min Kim[1], Joung-Ho Lee[2], Se-Ran Park[2], Na-Young Ro[3], Jin-Kyoung Kwon[2], Byoung-Cheorl Kang[2*]

[1]Interdisciplinary Program in Agricultural Biotechnology, College of Agriculture and Life Sciences, Seoul National University 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Republic of Korea
[2]Department of Plant Science and Plant Genomics and Breeding Institute, College of Agriculture and Life Sciences, Seoul National University 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Republic of Korea
[3]National Academy of Agricultural Science, Rural Development Administration, Jeonju, Korea

The *Broad bean wilt virus* (BBWV) belongs to the Fabavirus genus and is composed of two single-stranded RNAs. This virus poses a significant threat as it infects a wide range of hosts, including beans, spinach, grapes, and peppers. Six BBWV2 isolates and two BBWV1 isolates were previously reported in publications, and their host range is continuously expanding. In this study, we aimed to screen 1047 pepper genetic resource accessions (GRA) from the ‘Korean Gene Bank’ using the BBWV2-PAP1 strain. Through screening, we identified eight candidate accessions that exhibited resistance to BBWV2-PAP1. To confirm the resistance, we employed symptom index scoring and enzyme-linked immunosorbent assay (ELISA) methods, which cross-validated the putative resistant accessions. When we screened the F1 generation derived from a resistant accession (SNU-0) and a susceptible accession (ECW30R), we observed susceptible phenotypes. This indicates that the resistance gene in the resistant accession (SNU-0) is likely a recessive allele. To conduct further analysis, we utilized a recombinant inbred line (RIL) derived from a resistant accession (SNU-0) and a susceptible accession (ECW30R). The RILs were subjected to bulked segregant RNA sequencing (BSR-seq) analysis. By calculating the SNP index and △SNP values using the QTL-seq R package, we successfully identified a putative resistance gene region on chromosome 12. The findings of this study will contribute to the breeding of BBWV2-resistant pepper cultivars. The identification of resistant accessions and the mapping of a putative resistance gene region provide valuable insights for future breeding efforts aimed at developing resistant varieties to combat BBWV2 infection in pepper.

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

PE-0043

Selection of maize with high β-carotene content using molecular markers

MoonJong Kim*, SiHwan Ryu, JaeKeun Choi, HeeYeon Kim, JeongHeon Han, SeungHyun Wang, WooSik Yong, JaeNam Shim, KiSun Kim

Maize Research Institute, Gangwondo Agricultural Research & Extension Services, 26 Jangnam-gil, doochon-myeon, Hongcheon-gun, Gangwon-do, Korea

Carotenoids are mainly contained in red, yellow and orange fruits or vegetables, and are said to have medical effects on heart disease and cancer. β-carotene is a major component of carotenoids that can be converted into vitamin A through animal's metabolism, and plays a very important role in preventing vision-related retinal diseases and cataracts. Recently, studies have been conducted to utilize natural pigments, dietary fibers, and protein raw materials of these plants, and cultivation of varieties with high pigment content has become the main goal of breeders. In this study, we selected F_7 segregating generation(22Cr) corn using two molecular markers(5'TE, 3'TE) to select the hydroxylase 1(crtRB1) gene related to β-Carotene production developed by CIMMYT(International Maize and Wheat Improvement Center). In addition, high performance liquid chromatography(HPLC) analysis was performed to evaluate the β-Carotene content of the selected lines. In this study, 211 separate lines were evaluated, and each DNA was extracted from leaves and analyzed with two primers: crtRB1-3'TE, 5'TE. As a result of analyzing the β-carotene content of the selected lines, it was found to be 5.01mg/100g in 22Cr008. The results of this study are expected to save time and effort and enable accurate selection compared to visual selection by color for selection of high beta-carotene-containing maize lines using the crtRB1 molecular marker.

***Corresponding Author:** Tel. 033-248-6926, E-mail: mjkim7049@korea.kr

PE-0044

QTL-Seq Analysis for Marker Development Associated with Resistance to Powdery Mildew in a Korean Malting Barley

Jin-Cheon Park*, Young-Mi Yoon, Chang-Hyun Lee, Seul-Gi Park, On-Sook Hur, Kyong-Ho Kim

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

Powdery mildew(PM), caused by *Blumeria graminis* f. sp. *hordei*, is a serious fungal disease related to the yield loss of barley. Currently, many PM resistance genes have been identified, however, studies about barley PM resistance markers have not been conducted in Korea. In this study, we applied QTL-seq combined with bulked segregant analysis to identify QTL and development of marker for PM resistance using F_2 population derived from a cross between Korean malting barely 'Hopum' (susceptible) and 'Jeonju182' (resistant). Through PM resistance test of F_2 plants during the seedling stage, 20 resistant and 20 susceptable plants were selected respectively, whose genomic DNAs were extraced and pooled to prepare R bulk and S bulk DNA samples. Illumina whole genome sequencing (WGS) data of 106 - 110 Gb (~26X genome coverage) for each of two parents, S bulk and R bulk were generated and used for QTL-seq analysis. QTL-seq analysis is performed twice using WGS data of each of parents and then common QTLs and variants were investigated in order to increase the accuracy of the analysis. As a result, three significant QTL regions ($p<0.01$) located on 6.9-20.6 Mb in Chr1H, 331.2-331.3 Mb and 647.4-648.4 Mb in Chr2H were detected. Total 2,144 significant variant ($p<0.01$) were identified only in the QTL in Chr1H and consisted of 1,808 SNPs and 336 InDels. Through further selection of SNPs showing homozygous genotype in parents and uniqueness of flanking sequence, 21 non-synonymous SNPs causing missense mutations of 18 genes were identified and used to design CAPS markers. The CAPS markers developed in this study will be validated with parents and F_2 population for further analysis.

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***Corresponding Author:** Tel. 063-238-5226, E-mail: jinchun5214@korea.kr

PE-0045

Development of β-glucan dCAPs markers through GWAS for improving barley breeding efficiency

Sehyun Choi[1], Young-Mi Yoon[2], Seul-Gi Park[2], Jin-Cheon Park[2], Changsoo Kim[1,3*]

[1]Department of Crop Science, Chungnam National University, Daejeon 34134, Korea
[2]Crop Breeding Division, National Institute of Crop Science, Wanju-gun, 55365, Korea
[3]Department of Smart Agriculture Systems, Chungnam National University, Daejeon 34134, Korea

Barley is an important crop known for its nutritional properties, particularly its beta-glucan content, which has significant implications for human health. In this study, we aim to investigate the genetic factors associated with beta-glucan content in barley using a Genome-Wide Association Study (GWAS) approach.

We have identified a set of molecular marker candidates associated with barley beta-glucan content by utilizing the analysis data of barley germplasm with a score of 96 for beta-glucan and performing Genotype-by-Sequencing (GBS) for genomic sequence analysis. Subsequently, we applied the GWAS methodology to identify molecular marker candidates associated with barley beta-glucan content. Through exploring the genotype-phenotype relationship, we identified a single nucleotide polymorphism (SNP) that showed a significant correlation with beta-glucan levels. Through GWAS analysis, we discovered a single nucleotide polymorphism (SNP) with a high p-value on chromosome 1. We then designed 48 derived cleaved amplified polymorphic sequence (dCAPs) markers, including this SNP. These markers will provide a cost-effective and efficient means of detecting genetic variations associated with beta-glucan content in barley.

The findings of this study will shed light on the genetic architecture underlying beta-glucan content in barley and contribute to the understanding of its regulatory mechanisms. Furthermore, the molecular marker candidates identified through GWAS and the subsequent development of dCAPs markers will facilitate marker-assisted selection in breeding programs aiming to enhance beta-glucan content in barley varieties.

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***Corresponding Author:** Tel. 042-821-7822, E-mail: changsookim@cnu.ac.kr

PE-0046

Screening of Variations in Capsaicinoid Biosynthetic Genes using an EMS-induced Population and TILLING-by-Sequencing

Sang-Hyun Ahn, Seungki Back, Muhammad Irfan Siddique, Jin-Kyoung Kwon, Byoung-Cheorl Kang*

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

The capsaicinoids, which are responsible for the pungency of chili peppers, are specific secondary metabolites produced in *Capsicum* species. While several capsaicinoid biosynthetic genes (CBGs) have been identified, validating their functions poses challenges due to limited natural variation in peppers and complexities associated with genetic transformation. Therefore, inducing mutations in candidate genes becomes necessary to understand their roles in the capsaicinoid biosynthetic pathway. In this study, a high-throughput reverse genetics approach called TILLING (Targeting Induced Local Lesions in Genomes)-by-Sequencing (TbyS) was employed to screen mutations in four CBGs: *4C*L, *CSE*, *FatA*, and *Pun3*. The screening was conducted using an ethyl methanesulfonate (EMS)-induced population consisting of 1,400 M_2 mutant lines derived from *C. annuum* 'Micro-Pep Red'. To analyze the next-generation sequencing (NGS) data, the GATK Mutect2 tool, which detects short variations, was customized by modifying the settings. Results from customized GATK Mutect2 were cross-checked between all mutant pool samples. To reduce sequencing noise, only mutations with an allele frequency above 0.0125 were considered from the merged data. Furthermore, only mutations detected in a single pooled variant sample were selected for further analysis. Currently, a subset of the 57 obtained candidate mutations is being validated using Sanger sequencing, and four of them have been confirmed. Further study is required to test M_3 populations from the validated M_2 lines and screen for alleles of interest. In summary, this study utilized TILLING-by-Sequencing to screen mutations in capsaicinoid biosynthetic genes. The customized GATK Mutect2 tool was used for variant calling, and validated mutations are being further analyzed. The findings provide a foundation for exploring reverse genetic approaches and identifying crucial resources for future functional studies in pepper.

***Corresponding Author:** Tel. 010-8516-9362, E-mail: sd1892@snu.ac.kr

PE-0047

Elucidating the Genetic Mechanism Underlying Decreased Pungency in the EMS-induced Mutants (*Capsicum annuum* L.)

Seungki Back, Hayoung Choi, Joung-Ho Lee, Jung-Min Kim, Joohyun Lee, Jin-Kyoung Kwon, Byoung-Cheorl Kang*

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

The capsaicinoids are unique and pungent alkaloids found in *Capsicum.* They are synthesized through the condensation of byproducts from the phenylpropanoid and branched-chain fatty acid pathways and stored in glandular cells on the epidermal tissues of the placenta. While the functions of only a few structural and regulatory genes, including *Pun1*, *pAMT*, *Pun3*, and *CaKR1*, in the capsaicinoid biosynthetic pathway have been identified using loss-of-function variants, the functions of many other biosynthetic genes remain unknown. In this study, we utilized two different EMS-induced extremely low-pungent mutant lines, '221-2-1a' and '1559-1-2h', derived from the pungent Korean landrace 'Yuwolcho', to investigate a novel candidate locus, *Pun4*, which controls capsaicinoid biosynthesis. Since the pungency of the F_1 plants from the entire populations was similar to the pungent controls, we hypothesized that the target allele is recessive in controlling pungency. The segregation ratio of three F_2 populations resulting from crosses between mutants and pungent lines showed fluctuation, suggesting that the low-pungency of the *Pun4* mutants may be controlled by one or two genes with several minor factors. Expression analysis of putative capsaicinoid biosynthetic genes (CBGs) in placental tissues between 'Yuwolcho' and '221-2-1a' indicated that regulation of the branched-chain fatty acid pathway could be the primary factor for the low-pungency of the mutants. To identify the genetic loci involved, we performed genetic mapping using a combination of genome-wide SNP marker analysis, BSA-seq analysis, and BSR-seq analysis using the F_2 populations. As a result, one locus on chromosome 6 was identified. Using SNP markers, the *Pun4* region was delimited to a 0.66 Mbp region. Within this region, several candidate genes were identified through DEG detection and co-expression network analysis.

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

PE-0048

Characterization of the novel tomato mutants with orange color fruits and increased shelf-life

Seong-Yeop Kim[1], Jung-Won Jung[2], Jae-Kwang Kim[2], Jihye An[3], Donghwa Chung[3,4], Jin-Ho Kang[1,5*]

[1]Graduate School of International Agricultural Technology, Seoul National University, PyeongChang 25354, Republic of Korea
[2]Division of Life Sciences, Convergence Research Center for Insect Vectors, College of Life Sciences and Bioengineering, Incheon National University, Incheon 22012, Republic of Korea
[3]Department of Agricultural Biotechnology, College of Agriculture and Life Sciences, Seoul National University, Seoul 08826, Korea
[4]Center for Food and Bioconvergence, Seoul National University, Seoul 08826, Korea
[5]Institutes of Green-bio Science and Technology, Seoul National University, PyeongChang 25354, Republic of Korea

Carotenoids serve diverse functions in both plants and animals. In tomato (*Solanum lycopersicum*), the red color of fruits during fruit ripening is due to the accumulation of lycopene, one of the carotenoids. Here, we mutated wild-type tomato (cv. Micro-Tom) using the proton treatment at the Korea Atomic Energy Research Institute (Gyeongju-si, Gyeongsangbuk-do, Republic of Korea). During the mutant screening, we obtained a mutant with orange color fruit. So we named this mutant *juhwang* (*jh*). According to carotenoid analysis, the *jh* accumulated less lycopene and more β-carotene than wild-type fruit during ripening. In addition, *jh* had a more increased shelf-life than wild-type fruits. Therefore, *jh* may serve as an important genetic resource to study fruit ripening related to carotenoids and shelf-life. We are analyzing carotenoid biosynthesis, fruit ripening, and cell wall softening-related genes using qRT-PCR. We will identify the mutant gene using map-based cloning.

***Corresponding Author:** Tel. 033-339-5831, E-mail: philipbo66@snu.ac.kr

PE-0049

Functional analysis of *GmKIX9-1* mutants for the organ size regulation in soybean

Gyu Tae Park, Soo-Kwon Park, Yu-Na Kim, Dool-Yi Kim, Hyeon Jung Kang, Jung-Kyung Moon, Mi-Suk Seo*

Crop Foundation Research Division, National Institute of Crop Science, RDA, Wanju, 55365, Korea

The KIX domain, a conserved protein domain present in various nuclear transcription factors and co-activators, is reported to be involved in hormone signal transduction, stress regulation, cell cycle control, and differentiation in plants. This role suggests potential implications for enhancing plant productivity. In this study, we performed the functional analysis of *GmKIX9-1*, a member of the KIX domain family, in regulating cell proliferation in soybeans. We employed the CRISPR/Cas9 system to introduce targeted mutations into the *GmKIX9-1* gene of the soybean variety, Kwangan. Nine homozygous mutants were successfully isolated from the T_2 generation of the transgenic plants. Significant differences in leaf area at the V1 stage ($p < 0.01$) and the number of cells per unit area ($p < 0.01$) were observed between wild plant and the mutants. The average leaf area for wild plants was 22.07 cm^2 compared to 28.99 cm^2 for the T_2 homozygous mutants. Similarly, the average number of cells per unit area for wild plants were 90.4, compared to 105.3 for the mutants. These findings suggest that the loss of function in *GmKIX9-1* results in increased leaf size due to enhanced cell proliferation rather than cell expansion. Additionally, we plan to identify factors that interact with *GmKIX9-1* and conduct further investigations into traits closely associated with productivity, including 100-seed weight, chlorophyll content, and comprehensive growth assessment. This research will provide valuable insights into the role of KIX domain-containing proteins in soybean productivity and our better understanding of the mechanisms controlling plant organ size.

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

PE-0050

Identification and characterization of wheat lines missing omega-5 gliadins encoded by the 1D chromosome

Jae-Ryeong Sim, Sewon Kim, Yu-Jeong Yang, Eun Ji Park, Jong-Yeol Lee*

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

Efforts to reduce the levels of allergens in wheat flour that cause wheat-dependent exercise-induced anaphylaxis are complicated by the presence of genes encoding omega-5 gliadins on both chromosomes 1B and 1D of hexaploid wheat. In this study, we screened 665 wheat germplasm samples using gene specific DNA markers for omega-5 gliadins encoded by the 1D chromosome that were obtained from the reference wheat Chinese Spring. Eleven wheat lines missing the PCR product corresponding to 1D omega-5 gliadin gene sequences were identified. Two of the lines contained the 1BL.1RS translocation. Relative quantification of gene copy numbers by qPCR revealed that copy numbers of 1D omega-5 gliadins in the other nine lines were comparable to those in 1D null lines of Chinese Spring, while copy numbers of 1B omega-5 gliadins were like those of Chinese Spring. 2-D immunoblot analysis of total flour proteins from the selected lines using a specific monoclonal antibody against the N-terminal sequence of omega-5 gliadin showed no reactivity in regions of the blots containing previously identified 1D omega-5 gliadins. Interestingly, RP-UPLC analysis of the gliadin fractions of the selected lines indicated that the expression of omega-1,2 gliadins was also significantly reduced in five of the lines, implying that 1D omega-5 gliadin and 1D omega-1,2 gliadin genes are tightly linked on the *Gli-D1* loci of chromosome 1D. Wheat lines missing the omega-5 gliadins encoded by the 1D chromosome should be useful in future breeding efforts to reduce the immunogenic potential of wheat flour.

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

PE-0051

Analysis of Two Major Soybean Seed Storage Protein by RP-UPLC in Korean Soybean Core-collection

Yu-JeongYang, Sewon Kim, Jae-Ryeong Sim, Eun Ji Park, Jong-Yeol Lee*

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

Soybean protein 7S and 11S globulins are two major seed storage proteins, accounting for about 70% of total soybean protein. Two globulins show significant differences in nutritional and functional properties such as gel making ability, thermal stability and emulsifying capacity. 7S globulin (β-conglycinin) is one of the most allergenic proteins, 11S globulin (glycinin) is considered to play an important role in tofu gel formation. 7S globulin is composed of three kinds of polypeptides as α', α and β subunits, 11S globulin is formed by associating acidic, basic polypeptides. In this study, we established an optimized reverse-phase ultra-performance liquid chromatography (RP-UPLC) method for the identification of total soybean protein and two major seed storage proteins 7S and 11S globulins. A total of 12 soybean protein peaks were identified in the William 82 and also four 7S and eight 11S globulin fraction peaks were separated from total soybean proteins using soybean globulin fractionation method. Furthermore, major soybean globulins were analyzed by applying the optimized RP-UPLC method to Korean soybean core-collection. Various allelic variations of soybean globulin proteins in the core-collection were identified from chromatograms, and mutant lines with peak deletions were confirmed by Nu-PAGE. We found useful soybean resources with α and α′ -subunit null lines of the Korean soybean core-collection by RP-UPLC and Nu-PAGE. This study is expected to be useful as a high-throughput method for screening soybean globulin and can be applied to select breeding resources for highly functional soybean protein in various foods.

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

PE-0052

Identification of SNP markers for KASP assay related to heading date in oat (*Avena sativa* L.)

Keunha Kim[1,2*], Jisuk Kim[1], Kyungyoon Ra[1], Myoung Ryoul Park[1], Mi Jung Kim[1]

[1]Central Area Crop Breeding Division, Department of Central Area Crop Science, National Institute of Crop Science, Rural Development Administration, Suwon, 16429, Republic of Korea
[2]Department of Plant Biotechnology, Korea University, 145 Anam-ro, Seongbuk-gu, Seoul 02841, Republic of Korea

Heading date is one of the key agricultural traits for oat breeding research. With the release of oat reference (OT3098) whole-genome sequencing, molecular genetic studies for oats are actively being conducted. However, there have been few reports on molecular marker research related to the heading date. Therefore, we aimed to identify genes related to heading date and developed SNP makers for KASP assay. Based on the re-sequencing information of three Korean domestic oat varieties (Samhan, Daeyang, Highspeed), we selected six genes: early flowering 3-A1 (AVESA.00001b.r1.1Ag0002191, AVESA.00001b.r1.1Ag0003646), protein HEADING DATE 3A-like (AVESA.00001b.r1.3Dg0000173), early flowering 3-B1 (AVESA.00001b.r1.Ung0000166), flowering locus T protein (AVESA.00001b.r1.7Ag0000825, AVESA.00001b.r1.7Dg0003220), associated with the heading date. We analyzed single nucleotide polymorphisms (SNPs) from six genes. Among the analyzed SNPs, we selected eight SNPs (HD_SNP1~8) for Kompetitive Allele Specific PCR (KASP) assay. We confirmed the position of each SNP on the gene structures. The HD_SNP1 was located in the first intron of the AVESA.00001b.r1.1Ag0002191 on Chromosome (Chr) 1A, the HD_SNP2, and HD_SNP3 in the first intron and fourth exon, respectively, of the AVESA.00001b.r1.1Ag0003646 on Chr 1A, the HD_SNP4 in the second intron of the AVESA.00001b.r1.3Dg0000173 on Chr 3D, the HD_SNP5 and HD_SNP6 in the first intron of the AVESA.00001b.r1.Ung0000166 on Chr Un, the HD_SNP7 in the 3' UTR of the AVESA.00001b.r1.7Ag0000825 on Chr 7A, and the HD_SNP8 in the 5' UTR of AVESA.00001b.r1.7Dg0003220 on Chr 7D. These SNP markers for the KASP assay will be used for distinguishing various oat cultivars and genetic resources worldwide based on the heading date.

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***Corresponding Author:** Tel. 031-695-4053, E-mail: guna23@korea.kr

PE-0053

Analysis of genes related to soyasaponins biosynthesis pathway in soybean

Ji Hyun Bae, Gyu Tae Park, Soo-Kwon Park, Yu-Na Kim, Dool-Yi Kim, Hyeon Jung Kang, Jung-Kyung Moon, Mi-Suk Seo*

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

Soybeans are known as high-protein food and contain a large amount of secondary metabolites, including soyasaponins and isoflavones. Soyasaponins have physiological activities such as antioxidant activity and immune enhancement. There are several genes involved in soyasaponin biosynthetic pathway. We conducted an analysis of soyasaponin contents based on the germination period (1, 2, 4 days) and light/dark condition. In light condition, the soheung2 increased 83.45mg/100g, 94.49mg/100g and 204.96mg/100g with 1, 2, 4 days. Also, the PI9063 increased 354.67mg/100g, 384.88mg/100g and 406.41mg/100g, respectively. In dark condition, the soheung2 showed not significant difference and the PI9063 increased 328.28mg/100g, 357.29mg/100g and 374.60g/100g, respectively. Furthermore, we investigated the significance of the association between haplotypes of six *GmCYP* genes involved in soyasaponin biosynthesis and soyasaponin contents. The CYP72A69 was reported as gene related to biosynthetic pathway of soyasapogenol B, converting to soyasapogenol A. We used gene editing technology to reduce an unfavorable taste and elucidate its specific roles in soyasaponin biosynthesis in soybean. Four gRNA were analyzed the gene editing efficiency using a protoplast isolated from soybean hypocotyl. The JH3 showed the highest gene editing efficiency and selected as the final gRNA. We were currently performing *Agrobacterium*-mediated transformation using the selected gRNA of *GmCYP72A69.* The T_0 plants were validated for the presence of the transgene by bar-stripe and PCR analysis. Furthermore, deep-sequencing will be conducted to identify gene editing efficiency and homozygous plants will be separated. We will identify roles of genes in soybean mutant obtained by the gene-editing. The results of the present study improve our understanding of the soyasaponins biosynthesis pathway.

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

PE-0054

Development of molecular markers targeting the *Sdr4-k* allele derived from "Kasalath" for enhancing pre-harvest sprouting tolerance in early-maturing rice cultivars of Korea

So-Myeong Lee*, Jong-Hee Lee, Youngho Kwon, Hyeonjin Park, Jin-Kyung Cha, Ki-Won Oh

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

Pre-harvest sprouting (PHS) negatively impacts rice quality and yield, particularly in Korea due to prolonged periods of high temperature, humidity, heavy rain, and typhoons during the ripening stage of early-maturing rice cultivars. Our study focused on the *Sdr4* gene, associated with seed dormancy and PHS tolerance. Molecular markers targeting a 3bp deletion in the *Sdr4-k* allele from the aus rice cultivar "Kasalath" were developed to enhance PHS tolerance in early-maturing *japonica* rice.

The Sdr4-InDel marker, a gel-based dominant marker, distinguished PHS-tolerant and sensitive groups in the F_2 population derived from crossing the elite Korean *japonica* cultivar "Saeilmi" with the progeny line of the tongil-type cultivar "Milyang23". However, it could not differentiate heterozygous from *Sdr4-k* homozygous plants. To address this, the KASP marker Sdr4-IND was developed, targeting the same region as the Sdr4-InDel marker.

During our screening of genetic stocks and cross materials in Miryang in the summer of 2022, the Korean *japonica* cultivar "Nongan" was found to be the sole variety containing the *Sdr4-k* allele. Additionally, some tongil-type or indica cultivars and certain progeny lines of "Milyang23", "93-11" also possessed the *Sdr4-k* allele.

The findings indicate that both Sdr4-InDel and Sdr4-IND markers can facilitate selection of PHS-tolerant rice by targeting a specific deletion in the *Sdr4* gene. Notably, the Sdr4-IND marker, a KASP marker, offers the advantage of distinguishing heterozygous plants and exhibiting improved efficiency compared to the gel-based Sdr4-InDel marker. These insights are valuable for breeding PHS-tolerant rice cultivars, enhancing the accuracy of selection within rice cross populations.

***Corresponding Author:** Tel. 055-350-1173, E-mail: olivetti90@korea.kr

PE-0055

Assessing the genetic diversity of Korean maize (*Zea mays* L.) landraces having variations in the number of aleurone layers by using SSR and InDel markers

Jae-Hong Kim, Ji Won Kim, Eun Yeoung Kim, Jun IL Moon, Ji Hye Lee, Chae won Yoon, Min Jae Kim, Ja Young Kim, Seongmin Hong, Jinkwan Jo, Gibum Yi*

Department of Bio-Environmental Chemistry, College of Agriculture and Life Sciences, Chungnam National University, Daejoen, Republic of Korea

The aleurone layer of maize is an important tissue in endosperm related to grain quality and nutritional value. The increment of nutrient content in multi-aleurone layer lines have been proposed and shown in several studies. To investigate the properties of the aleurone layer, a total of 179 Korean maize landraces were evaluated. These Korean maize landraces exhibited a wide range of variation in the number of aleurone layers. Among the maize landraces, we assessed the genetic diversity of 75 maize germplasms with two or more aleurone layers and 8 germplasms with a single aleurone layer by using 16 SSR (Simple Sequence Repeat) and 60 InDel (Insertion/Deletion) markers. Through UPGMA (Unweighted Pair Group Method with Arithmetic Mean) cluster analysis, the 75 maize landraces were grouped into 8 clusters. These groups revealed a cluster of similar geographic origin. Interestingly, the single aleurone layer landraces clustered together indicating this character could be introduced later from a single genetic source. In this study, we showed phenotypic variation of aleurone layer number in Korean maize landraces and large genetic variation in the multi-aleurone layer germplasms. It suggests that there could be several different underlying genetic mechanism determining the multi-aleurone layer phenotype. This approach facilitates the identification and utilization of valuable genetic resources for crop improvement.

Keywords: maize, aleurone layer, SSR marker, InDel marker, genetic diversity

***Corresponding Author:** Tel. 042-821-6738, E-mail: gibumyi@gmail.com

PE-0056

CRISPR/Cas9-mediated knockout of transcription factor genes MS1-like and AMS-like can lead to male sterility in tomato due to their roles in anther and pollen development

Eunhee Kim, Jinjeong Lee, Il Pyung Ahn, Sung Mi Kim, Su Jung Ra, Seon-Hwa Bae, Hye-Jin Yoon, Young-Joo Seol, Jae-Hyeon Oh*

Gene Engineering Division, National institute of Agricultural Sciences, Rural Development Administration, 370, Jeonju-si, Jeollabuk-do 54874, Korea

Male sterility material is highly valuable for breeding F1 hybrids in terms of protecting superior male parent strains for seedling companies. Although efforts have been made to obtain male sterility materials in various crops, there are difficulties in making such materials with traditional breeding methods. Therefore, in this study, a gene editing technology was used to make male sterility materials. Candidate genes related to surgical development were identified and gRNAs were designed. A vector was constructed using the golden gate method and transformed into Agrobacterium. Each organism with a genotype suitable for adequate segregation was then selected through generation progress and the editing level of the editing site was confirmed. Organisms in which carrier DNA was removed and the targeted editing site was modified were obtained. Carrier DNA, on-target effect, and off-target effect were verified through WGS. In addition, male sterility phenotype was observed when genetic function was lost by editing MS1-like or AMS-like. Results of this study indicate that male sterility material can be used as an intermediate parent for breeding.

***Corresponding Author:** Tel. 063-238-4656, E-mail: jhoh8288@korea.kr

PE-0057

Identification of tomato yellow leaf curl virus KG1 and KG2 causing economic loss in tomatoes

Seon-Hwa Bae, Hong-Il Ahn, Jinjeong Lee, Sung Mi Kim, Eunhee Kim, Hye-Jin Yoon, Il-Pyung Ahn, Jae-Hyeon Oh, Young-Joo Seol*

Gene Engineering Division, National institute of Agricultural Sciences, Rural Development Administration, 370, Jeonju-si, Jeollabuk-do 54874, Korea

Tomato yellow leaf curl disease (TYLCD) is caused by tomato yellow leaf curl virus (TYLCV) known as the most serious virus affecting tomato production in many countries. TYLCV confirmed in Korea is divided into two groups, KG1 and KG2. The difference in whole genome of the two groups is about 2.8%, which is not very different. However, there is a difference in the pattern of symptoms caused by these two groups of TYLCV. As a result of this study, TY KG1 virus was detected by PCR from one week after inoculation into tomato individuals, but TY KG2 virus was detected at five weeks after inoculation. Regarding gene expression level, TYKG1 expression was increased rapidly from the 2nd week, but TYKG2 expression was increased slowly. In the case of KG1, the degree of yellowing and curling of shoots was severe, which affected photosynthesis, whereas in the case of KG2, the degree of yellowing and curling was weak, which did not significantly affect yield. As such, the 2.8% genomic difference showed a different tendency in disease symptoms. A specific DNA marker that can accurately distinguish KG1 and KG2 rather than existing TYLCV selection marker is needed. Therefore, in this study, we developed a marker that could easily and quickly discriminate KG1 and KG2 by PCR assay.

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

PE-0058

QTL Analysis of Resistance to Phytophthora Blight in Sesame

Jeongeun Lee*, Sungup Kim, Eunsoo Lee, Jung In Kim, Eunyoung Oh, Min Young Kim, Sang Woo Kim, An Yeon Ju, MyoungHee Lee, Kwang-Soo Cho

Upland Crop Breeding Research Division, Department of Southern Area Crop Science, National Institute of Crop Science, RDA, Miryang, Gyeongnam, 50424, Republic of Korea

Phytophthora blight (PB) caused by *Phytophthora nicotianae* is a major disease in sesame leading to yield losses. So, the development of PB resistant varieties is a crucial objective in sesame breeding. Evaluating PB resistance in the field presents challenge due to substantial yearly variation. In this study, We identified quantitative trait loci (QTLs) associated with resistance to PB in order to enhance breeding efficiency in sesame. A mapping population of recombinant inbred line (RIL) was derived from a cross between PB resistant 'Geonbeak' and PB susceptible 'Milsung'. We performed whole genome resequencing on two parents and 99 RILs. A total of 4,309 bin markers, developed from SNPs, were used to construct a genetic map of 13 linkage group. The significant major QTL was identified for PB resistance using the PB phenotype and markers derived from the genetic map. A major QTL was located on chromosome 10 with a marker interval spanning 0.51Mb and this QTL explained 69.35% of phenotypic variation. This QTL region contained several candidate R genes like NBS-LRR protein. Candidate genes were converted into Kompetitive allele specific PCR (KASP) markers, which were applied for genotyping the RILs. In the RILs, the concordance between phenotype and KASP assay was approximately 90%. This result will be useful in the marker-assisted selection for the breeding of PB resistance.

***Corresponding Author:** Tel. 055-350-1226, E-mail: jel6418@korea.kr

PE-0059

Inactivating transcription factor OsWRKY5 enhances drought tolerance through abscisic acid signaling pathways

Chaemyeong Lim, Nam-Chon Paek*

Department of Agriculture, Forestry and Bioresources, Plant Genomics and Breeding Institute, College of Agriculture and Life Sciences, Seoul National University, Seoul, Korea

During crop cultivation, water-deficit conditions retard growth, thus reducing crop productivity. Therefore, uncovering the mechanisms behind drought tolerance is a critical task for crop improvement. Here, we show that rice (Oryza sativa) WRKY transcription factor OsWRKY5 negatively regulates drought tolerance. We determined that OsWRKY5 was expressed in leaves, and that its expression was reduced by drought stress and abscisic acid (ABA). Notably, the genome-edited loss-of-function alleles oswrky5-2 and oswrky5-3 conferred enhanced drought tolerance. Loss of OsWRKY5 activity increased sensitivity to ABA, thus promoting ABA-dependent stomatal closure. Transcriptome deep sequencing analysis demonstrated that the expression of abiotic stress-related genes including OsMYB2 was upregulated in oswrky5 knockout mutants. Moreover, dual-luciferase, yeast one-hybrid, and ChIP assays showed that OsWRKY5 directly binds to the promoter of OsMYB2 and represses OsMYB2 expression. Our results demonstrate that OsWRKY5 functions as a negative regulator of ABA-induced drought stress tolerance, suggesting that inactivation of OsWRKY5 could be useful to improve drought tolerance in rice cultivars.

***Corresponding Author:** Tel. 010-6324-2302, E-mail: ncpaek@snu.ac.kr

PE-0060

Natural alleles of CIRCADIAN CLOCK ASSOCIATED1 contribute to rice cultivation by fine-tuning flowering time

Sang-Ji Lee, Nam-Chon Paek*

Department of Agriculture, Forestry and Bioresources, Plant Genomics and Breeding Institute, College of Agriculture and Life Sciences, Seoul National University, Seoul, Korea

Flowering with proper timing is a crucial for successful cultivation. Thus, during domestication, the rice genome has evolved natural alleles of flowering genes which allow rice to adapt to broader areas. Here, we found natural alleles of CIRCADIAN CLOCK ASSOCIATED 1 (OsCCA1) by analyzing SNPs from the International Rice Genebank Collection Information System database. Interestingly, rice varieties harboring japonica-type OsCCA1 flowered earlier than those harboring indica-type OsCCA1. Actually, japonica cultivar 'Dongjin' containing a T-DNA in OsCCA1 locus delayed flowering under both LD and SD. RT-qPCR analysis showed that mutation of OsCCA1 upregulates the expression of OsPRR37 or DTH8 by repressing Ehd1-Hd3a/RFT1 pathway. In addition, OsCCA1 directly bound to the OsPRR37 promoter. Further surveys showed that natural alleles of OsCCA1 are evolutionary conserved in O. rufipogon, a progenitor of cultivated rice. Or-I and Or-III type, the ancestors of O. sativa indica and japonica harbored indica- and japonica-type OsCCA1, respectively. Taken together, our results indicated that OsCCA1 could be a domestication locus contributing to the geographic adaptation of cultivated rice.

***Corresponding Author:** Tel. 010-6324-2302, E-mail: ncpaek@snu.ac.kr

PE-0061

Analysis of High Molecular Weight (HMW) and Low Molecular Weight (LMW) Glutenin subunits related to the seed quality traits of hard wheat (*Triticum aestivum* L.)

Ji Hyeon Jeong[1], Woo Joo Jung[2], Yong Weon Seo[1*]

[1]Department of plant biotechnology, Korea University, Seoul 02841, Korea
[2]Institute of Life Science and Natural Resources, Korea University, Seoul 02841, Korea

Wheat (*Triticum aestivum* L.) is one of the most important cereal crops in the world as a food resource. Wheat is used in the form of flour, and gluten protein in wheat grain is one of the most important factors affecting dough properties and bread quality. Gluten proteins consist of high molecular weight (HMW) and low molecular weight (LMW) subunits. In this study, a total of 156 hard wheat cultivars from 29 different countries including Mexico and China were analyzed. Polymerase Chain Reaction (PCR) of target genes was performed to evaluate the composition of HMW and LMW glutenin subunits, specifically *Bx7, Bx17, Dx2, Dx5, Dy10,* and *Dy12* were used for HMW, and *B3b* and *B3g* were used for LMW. The seed quality traits, such as protein content and SDS-sedimentation value, were determined using a Near Infrared Spectroscopy (NIRS). Furthermore, a genome-wide association (GWA) analysis was performed to find significant genomic regions regulating the both traits using the iSelect 90K genotyping array. Through combining the PCR results and the GWAS, we could suggest optimal combinations of the markers affecting bread quality. Our study will help to breed and develop wheat cultivars that suit each application.

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

PE-0062

Identification of SNPs Associated with Fruit Shape in Paprika Germplasms through Genome-wide Association Study Analysis

Eunji Hwang[1], Jong-Suk Park[2], Jin-Hee Kim[2], Jundae Lee[1*]

[1]Department of Horticulture, Institute of Agricultural Science and Technology, Jeonbuk National University, Jeonju 54896, Korea
[2]Jeollabuk-do Agricultural Research and Extension Services, Iksan 54591, Korea

Paprika (*Capsicum annuum* L.), also known as sweet pepper, is a high-value-added vegetable crop, which production and consumption are gradually increasing in Korea. Pepper and paprika belong to the same species, but they have different cultivation methods. In this study, we aimed to identify significant single nucleotide polymorphisms (SNPs) associated with fruit shape using 96 paprika germplasms through genome-wide association study (GWAS) analysis. We used the fruit shape index (length/width, fsi) as a criterion to distinguish between pepper and paprika. The fruit shape index of $0.8 \leq \text{fsi} \leq 1.2$ means the resemblance to paprika fruit shape. A total of 12,513 SNPs was identified through genotyping-by-sequencing (GBS) analysis. GWAS analysis was performed using GAPIT and TASSEL softwares with genotypic data of 12,513 SNPs and phenotypic data of fruit shape index. In results, GWAS analysis revealed two loci (*qFS1.1* and *qFS3.1*) associated with fruit shape on chromosomes 1 and 3, respectively. Two significant SNPs, C01_306308485 and C01_306488267, were associated with the QTL *qFS1.1* and five SNPs, C03_278409493, C03_278409468, C03_278408401, C03_278408579, and C03_278408321, were linked to *qFS3.1.* The identified SNPs will be used for developing molecular markers to distinguish between pepper and paprika.

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***Corresponding Author:** Tel. 063-270-2560, E-mail: ajfall@jbnu.edu

PE-0063

Association Mapping of Agro-Morphological Traits in Eggplant Core Collection

Mesfin Haile, Nayoung Ro*, Gyu-Taek Cho, Hee-Jong Woo, Pilmo Sung, Hocheol Ko, Jungro Lee, Bichsaem Kim

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

Eggplant is one of the most economically and nutritionally important vegetables worldwide. The study of the association between phenotypic traits and genetic factors is vital for the rapid and efficient identification and selection of eggplant genetic resources with desirable traits for breeding purposes. A total of 587 eggplant resources were collected from different countries, including Korea, to establish the core collection. From these resources, 288 accessions were selected based on 52 single nucleotide polymorphism (SNP) markers and 17 morphological traits. The core collection was then used to analyze the genetic associations of eggplant morphological variations. The evaluation of the eggplant accessions revealed significant variation in some agro-morphological traits. Stem prickles and leaf prickles showed a significant positive correlation (r = 0.83***), followed by days to flowering and days to maturity (r = 0.64***). A total of 114,981 SNPs were filtered and used for phylogenetic tree construction, population structure analysis, and genome-wide association studies (GWAS). Among the traits evaluated, significant SNPs associated with six agro-morphological traits were identified. In total, 377 significantly associated SNPs were identified for these six traits, namely: days to maturity (51), flower size (121), fruit width (20), harvest fruit color (42), leaf prickles (38), and stem prickles (105). The largest fraction of significant SNPs (11.94%) was found on chromosome Ch01, followed by Ch07 (11.67%) and Ch06 (10.08%). This study will facilitate the development of markers linked to the most important agro-morphological traits of eggplant genetic resources and support the selection of desirable traits for eggplant breeding programs.

***Corresponding Author:** Tel. 063-238-4943, E-mail: nonanona@korea.kr

PE-0064

Mapping of loci for drought tolerance derived from the soybean (*Glycine max* [L.]) cultivar SS2-2

Hakyung Kwon[1], Jae Ah Choi[1], Moon Young Kim[1,2], Suk-Ha Lee[1,2*]

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

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

Drought, a prominent environmental factor, significantly reduces soybean (*Glycine max* [L.]) yield. A promising approach to enhance the drought tolerance of soybeans involves leveraging the slow-wilting trait, which is characterized by limited transpiration under high vapor pressure deficit (VPD), thereby sustaining soil moisture during mild drought conditions. This study aimed to identify specific genomic regions (QTLs) controlling the slow-wilting in soybean. To achieve this, we employed a recombinant inbred line (RIL) population derived from a cross between two soybean cultivars: Taekwang (drought-susceptible) and SS2-2 (drought-tolerant). The RIL population was subjected to controlled drought stress by growing them in pots with a specified amount of topsoil. Drought tolerance was evaluated using two phenotypic indices: wilting scores obtained through visual inspection and moisture contents in the leaves. By employing the genotyping-by-sequencing method, a high-density genetic bin map was constructed using single nucleotide polymorphism markers. These comprehensive phenotyping approaches, in conjunction with the high-density genetic bin map, enabled the identification of multiple QTLs associated with drought tolerance in soybean, including a significant QTL on chromosome 10 with an LOD score of up to 18. Furthermore, the integration of multi-omics data facilitated a detailed examination of genetic candidates responsible for soybean's drought tolerance. Our findings provide essential insights into the mechanisms underlying drought tolerance in soybean and valuable resources for the development of drought-tolerant soybean varieties.

***Corresponding Author:** Tel. 02-880-4545, E-mail: sukhalee@snu.ac.kr

PE-0065

Chalcone Isomerase 1 Gene Is a Major Regulator Responsible for Seed Coloration in *Brachypodium*

Man Bo Lee, Jae Yoon Kim*

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

Brachypodium distachyon is a model plant for agriculturally important crops such as wheat, barley, and oat. *Brachypodium* has been widely utilized for gene function studies. Seed color is an attractive trait associated with seed quality, reflecting antioxidant materials. Seed color is one of the factors that can positively influence grower and customer preference. In our previous study, a yellow seed *Brachypodium* mutant induced by gamma radiation was detected. The anthocyanin content of the mutant seeds was significantly decreased compared to that of brown WT seeds. Also, homozygous 14 bp deletion was identified in the exon region of *chalcone isomerase 1.* In this study, *BdCHI1* was used for over-expression in *bdchi1* mutants to confirm the gene function of *BdCHI1.* Immature embryos were collected from *bdchi1* and used for callus induction. Subsequentially, embryogenic callus was transformed with *Agrobacterium* containing *BdCHI1.* The over-expression of *BdCHI1* complemented the loss function of *BdCHI1* observed in *bdchi1*, recovering the yellow seed color of *bdchi1* to brown. Here, we confirmed the gene function of *BdCHI1* using the transgenic plants. Further molecular studies using the transgenic plants will be performed to enrich our understanding of *BdCHI1* function.

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

PE-0066

High Throughput SNP Chip DNA Marker-Multiple GAPIT Models for Genome-Wide Association Study (GWAS) Revealed Genes Controlling Mesocotyl Elongation and Seedling Emergence in Rice (*Oryza sativa* L.)

Nkulu Rolly Kabange*, Youngho Kwon, So-Myeong Lee, Gi-Won Oh, Jong-Hee Lee*

Dep. of Southern Area Crop Science, National Institute of Crop Science, RDA, Miryang 50424, Korea

Introduction: The successful establishment of plants in the field largely depends on the ability of dry seeds to germinate, emerge, and fully differentiate. Failure in the emergence of seedlings may lead to crop failure and yield loss. Direct seeding is commonly used in many upland and lowland rice cultivation systems. Seeds are sown at 5-10 cm depth, and their emergence after germination could be affected by factors such as soil texture and moisture, seed vigor or genetic makeup, and physiological and biochemical properties of seeds. Advanced statistical tools applied in plant breeding and genome sequencing offered new possibilities to gain new insights into the genetic control of agronomically important traits at the whole genome level. This study aims at investigating novel genetic factors controlling the emergence of seedlings and mesocotyl elongation in rice, using GAPIT (Genome association and prediction integrated tool) models with enhanced statistical power for genome-wide associate study (GWAS).

Materials and Methods: A doubled haploid population (117 lines: 93-11 × Milyang352) and 230,526 SNP Chip DNA markers were used to investigate genetic factors controlling seedling emergence and mesocotyl elongation in rice. The phenotype (mesocotyl length, seedling emergence, and shoot length) was measured 14 days after sowing (6 cm depth). For genetic association analysis, GWAS with multiple GAPIT models (BLINK, FarmCPU, GLM, and MLM in R software) and genomic prediction (GP) were performed. The GP was done using the gBLUP(*), which estimates the genomic breeding value of lines.

Results and Discussion: Parental lines (93-11 and Milyang352) showed differential mesocotyl length, seedling emergence, and shoot length. Regression analysis showed that mesocotyl elongation positively correlated with emergence (R^2=0.246***) but not with shoot length (R^2=0.0674). In contrast, seedling emergence recorded a strong positive correlation with shoot length (R^2=0.3857***). Association between five (5) topmost significant SNP markers associated with variation in seedling emergence (Chr 1: AX-154356231, PVE 21.1% and Chr 9: AX-282097034, PVE 64.5%; AX-283652873, PVE 20.2%) and mesocotyl elongation (Chr 2: AX-155741269, PVE 37.5% and Chr 7: AX-155200917, PVE 13.8%) have been found. A high estimated heritability (Emergence: h^2=0.863; Mesocotyl length: h^2=0.955; seedling length: h^2=0.707) was found. GS/GP analysis suggested significant markers having a strong association with seedling emergence and mesocotyl elongation, useful targets for genomic selection and marker-assisted selection (MAS) and genomic selection.

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***Corresponding Author:** Tel. 010-5413-4881, 053-350-1168, Fax. 055-352-3059.
E-mail: rollykabange@korea.kr, ccriljh@korea.kr

PE-0067

High yield related QTL mapping and screening candidate genes for zero hunger in rice

Jae-Ryoung Park, Jeonghwan Seo, Songhee Park, Kyeong Min Kang, Mira Yoon, Mina Jin, O-Young Jeong, Hyun-Su Park*

Crop Breeding Division, National Institute of Crop Science, Rural Development Administration, Wanju, 55365, Republic of Korea

Rice is a major crop, providing calories and food for most of the world's population. Currently, the global population is rapidly increasing, and securing a yield of rice that can satisfy everyone is an ongoing challenge. To identify QTLs related to grain size, we screened 88 RIL individuals derived from a cross between JJ625LG, which has a long grain size, long spindle-shaped grains and low 1,000-grain weight, and Namchan, which has short grains with a round shape and heavy 1,000-grain weight, followed by their mapping. In 2021 and 2022, 511 SNP markers were used to map QTLs related to grain size to a physical map. The mapping results also show that the QTLs *qGl3-2*, *qRlw3*, and *qRlw3-2* of chromosome 3 and *qGt5* and *qRlw5* of chromosome 5 are, respectively, associated with *GS3* and *qSW5*, which are major genes previously cloned and found to be related to grain size. In addition, *qGw10* and *qGw10-1*, were found to be associated with *Os10g0525200* (*OsCPq10*), a potential candidate gene involved in controlling grain size. This gene codes for a cytochrome P450 family protein and is reported to have a positive effect on grain size by interacting with proteins related to mechanisms determining grain size. In particular, *OsCPq10* was screened in the same identified QTL region for 2 consecutive years, which is expected to have a positive effect on grain size. These results will be helpful for breeding elite rice cultivars with high yields through additional fine mapping related to grain size.

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

PE-0068

Breeding strategy by CRISPR/Cas9 for cold tolerance regulating cell wall component in rice

Jae-Ryoung Park[1], Eun-Gyeong Kim[2], Yoon-Hee Jang[2], Kyung-Min Kim[2,3*]

[1]Crop Breeding Division, National Institute of Crop Science, Rural Development Administration, Wanju, 55365, Republic of Korea
[2]Coastal Agriculture Research Institute, Kyungpook National University, Daegu 41566, Korea
[3]Department of Applied Biosciences, Kyungpook National University, Daegu, 41566, Korea

Globally, the frequency of climate change has increased and become difficult to predict. In particular, abnormally low temperatures in the rice seedling stage negatively affect rice yield. For rice breeders, breeding cold tolerance cultivars has become a constant requirement and is a major breeding goal. However, breeding a rice cultivar through cross-breeding requires an enormous investment of effort and time. Most cold stress-related researches were conducted at 4°C. However, the cold stress actually applied in the field is 18℃. Therefore, in this study, rice was breeding when subjected to cold stress at 18℃. Recently, improving the defects of elite cultivars by applying CRISPR/Cas9 has become a method of breeding cultivars that is more cost-effective and time-efficient than cross-breeding methods and can alleviate food insecurity. In this study, *OsCS511*, a gene involved in cold susceptible identified by QTL mapping, was genome-edited with CRISPR/Cas9 at Ilmi (*Oryza sativa* L. *spp. Japonica* cv. Ilmi). CRISPR/Cas9 edited Ilmi's *OsCS511* homozygous in G_0 and advanced generation in the field. And under normal condition and cold stress, agricultural traits, ROS scavenging level, and expression level of stress tolerance related genes were evaluated. Under normal conditions, the Ilmi and *OsCS511* genome-editing lines had the same level in all traits, but when subjected to cold stress, the cold tolerance was improved or the same level as that of Ilmi. From the perspective of breeding, we suggest that CRISPR/Cas9 can improve the defects of existing superior rice cultivars precisely with high efficiency and speed.

***Corresponding Author:** Tel. 053-950-5711, E-mail: kkm@knu.ac.kr

PE-0069

Unraveling the Roles of ARR13 and ARR21 in the Seed Cytokinin Signaling Pathway

Sujeong Jeong[1], Inyoung Kim[2], Hyun Uk Kim[1,2*]

[1]Department of Bioindustry and Bioresource Engineering, Graduate School, Sejong University, Seoul 05006, Republic of Korea

[2]Department of Molecular Biology, Graduate School, Sejong University, Seoul, 05006, Republic of Korea

Type-B ARABIDOPSIS RESPONSE REGULATORS 13 (ARR13) and ARR21 are transcription factors (TFs) that are highly expressed during seed development. They play a regulatory role in the cytokinin signaling pathway by controlling the expression of numerous cytokinin-responsive genes. Additionally, they have the ability to regulate the expression of Type-A ARRs. However, the specific roles of ARR13 and ARR21, as well as the upstream and downstream genes in the cytokinin signaling pathway, have not been fully elucidated. In this study, we hypothesize that the seed-expressed ARR13 and ARR21 can provide insights into the effects of the cytokinin signaling pathway in seed. Due to a high level of protein sequence redundancy between ARR13 and ARR21, we investigate these two TFs together. Using the clustered regularly interspaced short palindromic repeats-CRISPR-associated protein 9 (CRISPR-Cas9) system, we generated two mutants for each line: *arr13* single mutant, *arr21* single mutant, and *arr13arr21* double mutant, each exhibiting different variation patterns. Our final objective is to identify the upstream and downstream genes of ARR13 and ARR21 in the seed cytokinin signaling pathway.

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

PE-0070

Overexpression of McNADP-malic Enzyme 1 (*McNADP-ME1*) Confers Drought and High-light Stress Tolerance

Sang Hun Kim[1], Hong-Ju Lee[1], Yu Kyong Hu[1], John C. Cushman[2], Sung Don Lim[1*]

[1]Department of Applied Plant Sciences, Sangji University, 83 Sangjidae-gil, Wonju-si, Gangwon-do 26339, Republic of Korea

[2]Department of Biochemistry and Molecular Biology, University of Nevada, Reno, NV 89557-0330, USA

The global climate change is a pressing challenge for crop production to meet agricultural products of an increasing global population. Crassulacean acid metabolism (CAM) photosynthesis, which enables to grow well in arid or semi-arid environments, is an important biological mechanism for addressing the climate challenge by shifting the diel rhythm of CO_2 fixation from day to night. The facultative CAM model plant *Mesembryanthemum crystallinum* can transit from C_3 to CAM photosynthesis under unfavorable conditions. Our detailed time-resolved transcriptome profiling analysis in the *M. crystalinum* has revealed hundreds of genes are involved in CAM-associated functions. Among them, the cytosolic McNADP-dependent malic enzyme 1 (*McNADP-ME1*) in decarboxylation module increased transcription abundance dramatically in response to drought stress. Increased NADP-ME levels lead to supply reducing equivalent in the form of NADPH, which is the reductive power for the synthesis of defense compounds including flavonoids and maintenance of cell homeostasis. Overexpressing-*McNADP-ME1* lines displayed significant increases both drought tolerance and high-light tolerance in transgenic *Arabidopsis.* In this results, McNADP-ME1 might be a key C_4/CAM enzyme in decarboxylation module in a facultative *M. crystallinum* and overexpression of this enzyme confer ROS-mediated abiotic stress tolerance.

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***Corresponding Author:** Tel. 033-730-0513, E-mail: sdlim@sangji.ac.kr

PE-0071

Development of a Core Set of SNP Markers for DNA barcoding in Peach (*Prunus persica* L.)

Jaehun Heo[1], Jeyun Yeon[1], Sung-Chur Sim[1,2*]

[1]Department of Bioresources Engineering, Sejong University, Seoul 05006, Korea
[2]Plant Engineering Research Institute, Sejong University, Seoul 05006, Korea

Peach (*Prunus persica* L.) is a major crop species in the Rosaceae family that are widely cultivated in the world. With its economic importance, a large number of new varieties have been developed in breeding programs. Molecular marker is an effective tool for DNA fingerprinting and single nucleotide polymorphisms (SNPs) have been commonly used in crop species. In this study, we collected a total of 131 peach varieties that originated from the Republic of Korea (58), Japan (31), China (25), the United States (14), and The others (3). The 54,388 genome-wide SNPs were found using genotyping-by-sequencing(GBS) in a subset of 48 varieties. Of these, 384 SNPs were filtered based on polymorphic information content (PIC) and genome distribution for the Fluidigm assay in additional 83 varieties. The 240 SNPs showed reliable polymorphisms and were used to assess genetic variations between peach varieties. With the Euclidean genetic distance, the 131 peach varieties were separated into five groups and were also distinguished each other in the UPGMA dendrogram. In addition, three subsets of SNPs (192, 96, and 48) were also effective to differentiate all of the peach varieties including 13 bud mutants. These results suggest that the SNP markers will be useful to develop a DNA barcoding system for variety identification and protection of breeder’s rights in cultivated peaches.

***Corresponding Author:** Tel. 02-3408-4379, E-mail: sungchur@sejong.ac.kr

PE-0072

Development of DNA marker for seed coat pigmentation in soybean

Jinwon Lee, Junbeom Park, Jong Tae Song*

Department of Applied Biosciences, Kyungpook National University, Daegu, 41566, Republic of Korea

Seed coat color is determined by the *I* (*Inhibitor*) locus in soybean. Four alleles are known at the I locus. The dominant allele of *I* locus inhibits seed coat pigmentation (*I*: yellow seed coat), whereas the recessive *i* allele produce a pigmented seed coat (*i*: black or brown seed coat). Two other alleles, i^i and i^k, pigmented on the hilum (i^i: pigmented hilum and yellow seed coat) and the saddle-shaped region (i^k: pigmented saddle-shaped and yellow seed coat), respectively. The dominance relationships between the four alleles are $I > i^i > i^k > i$. Spontaneous mutations of $I \rightarrow i$ or $i^i \rightarrow i$ alleles confer the pigmented seed coat and the *I* locus was identified to be a region of repeated *chalcone synthase* (*CHS*) genes. Post-transcriptional gene silencing (PTGS) of *CHS* genes at the *I* locus, at least for the *I* and i^i alleles, controlled the soybean seed coat color pigmentation. In order to identify genes and markers related to the seed coat pigmentation, we used a 180K Axiom™ Soybean Genotyping Array and whole genome sequencing data from NCBI and SoyBase. Allele-specific DNA markers at the *I* locus are useful for genetic diversity study and multiple allele detection in soybean. In this study, we developed the SSR and CAPS markers and these DNA markers will facilitate marker-assisted breeding in soybean.

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

PE-0073

Functional analysis of Sorghum bicolor Heat-induced RING-type E3 Ligase 1 (HiREL1) in heat tolerance

Yu Kyong Hu[1], Min Seok Choi[2], Jong Ho Kim[2], Hyeon Ung Seo[2], Hong-Ju Lee[1], Sang Hun Kim[1], Cheol Seong Jang[2], Sung Don Lim[1*]

[1]Department of Applied Plant Sciences, Sangji University, 83 Sangjidae-gil, Wonju-si, Gangwon-do 26339, Republic of Korea

[2]Plant Genomics Laboratory, Interdisciplinary Program in Smart Agriculture, Kangwon National University, Chuncheon 200-713, Republic of Korea

The ongoing global climate change is pushing agricultural products to endure harsher environments. Historical adaptation of sorghum production to arid or semi-arid environments have considered to induce significant yield losses by heat stress. The average reduction across warming scenario in sorghum showed is 10% per degree Celsius. Here, we report that the Sorghum bicolor Heat-induced RING E3 Ligase 1 (*SbHiREL1*) plays an important role in regulating sorghum heat stress responses. SbHiREL1 has a RING-H2 type motif, which plays a role for attachment of ubiquitins to the target protein for posttranslational modification. The expression abundances of *SbHiREL1* are specifically up-regulated by heat stress treatment, suggesting its role in the response to heat stress. In addition, it plays *in vitro* E3 ubiquitin ligase activity, and the SbHiREL1-sGFP fusion protein was localized to the cytosol. In sorghum plants, virus-induced gene silencing of *SbHiREL1* resulted in enhanced sensitivity to heat stress. By contrast, overexpression of *SbHiREL1* in *Arabidopsis* confers enhanced resistance to heat stress during seed germination and vegetative stages. Taken together, these results suggest that *SbHiREL1* is involved in the thermotolerance mechanism with the potential to regulation of target proteins via Ub/26S proteasome pathway.

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***Corresponding Author:** Tel. 033-730-0513, E-mail: sdlim@sangji.ac.kr

PE-0074

Wheat seed coat color genome-wide association studies for identification of pre-harvest sprouting tolerance genes

Jun Yong Choi, Myoung Hui Lee, Chon-Sik Kang, Kyeong-Min Kim, Kyeong-Hoon Kim, Go Eun Lee, Ki-Chang Jang, Changhyun Choi*

Wheat Research Team, National Institute of crop Science, Rural Development Administration, Wanju, 55365, Republic of Korea

Wheat cultivation environment in Korea have frequent occurrences of pre-harvest sprouting due to heavy rainfall during grain filling. Therefore, development pre-harvest sprouting resistance wheat cultivars is one of the important goals in Korea wheat breeding. In this study, we evaluated the pre-harvest sprouting characteristics by constructed 614 wheat core-set and analyzing the seed coat color trait, which is closely related to pre-harvest sprouting, using a colorimeter. Furthermore, genome-wide association analysis (GWAS) was conducted using the genotypic information of the core-set obtained from a 35K SNP chip, along with the seed coat color phenotype. One of these SNPs was confirmed to be located in the exon of Cysteine proteinase (*CP1*) gene, which is associated with the pre-harvest sprouting tolerance locus, *Phs-A1*. Besides, the cysteine proteinase gene was known to play a crucial role in the degradation of gliadin at early times in seeds germination. To analyze the relationship between the expression of the CP1 gene and pre-harvest sprouting tolerance, the CP1 gene editing with CRISPR-Ca9 system is being performed by the particle delivery system with immature embryos of a pre-harvest sprouting susceptible wheat cultivar. Furthermore, GWAS was conducted using various approaches to investigate the seed coat color traits closely associated with pre-harvest sprouting in wheat. Consequently, novel candidate gene, *Myb1*, was discovered. Through this study, we expected to contribute to the enhancement of Korea wheat productivity and competitiveness by elucidate the underlying causes of the seed coat color difference between white and red wheat, and its impact on pre-harvest sprouting tolerance.

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***Corresponding Author:** Tel. 063-238-5454, E-mail: chchhy@korea.kr

PE-0075

Genetic Relationships of Garlic(*Allium sativum L.*) Genetic Resources Using Genotyping-by-Sequencing

Juhee Baek*, Jinseong Moon, Jiyoung Son, Byeonggyu Min, Mijin Lee, Jungho Shin, Jungmi Lee

Onion Research Institute, Gyeongsangnamdo Agricultural Research and Extension Services, Upo2-ro 1055, Changnyeong 50319, Republic of Korea

Garlic is a widely used seasoning vegetable in Korea, commonly used in dishes such as kimchi. As of 2022, the domestic cultivation area of garlic is 17,661 hectares, with a production volume of 273,000 tons. In the southern coastal region, NANJI-type garlic is cultivated, while in the central inland region, HANJI-type garlic is grown. NANJI-type garlic, which accounts for 80.5% of the national garlic cultivation area, is represented by introduced varieties, namely NAMDO and DAESEO. Garlic is generally classified based on its morphological and physiological characteristics, but little is known about their genetic differences. Therefore, this study aims to develop molecular markers for identifying NANJI-type garlic varieties mainly cultivated in Gyeongsangnam-do province. A total of 21 garlic genetic resources were collected for genetic variation analysis using Genotyping-by-sequencing (GBS) method. In the GBS analysis, DAESEO obtained a total of 30.668 million reads, NAMDO obtained 26.605 million reads, and UISEONG obtained 39.406 million raw reads, which were then subjected to trimming to obtain clean reads. These were mapped to the garlic reference genome, showing an average mapping region of approximately 0.42% genome coverage. Through filtering, a total of 2,899 SNPs were obtained, and the relationship between the genetic resources was examined using Principal Component Analysis (PCA). The genetic variation was found to be 18.6%, indicating that the genetic variation among the resources is relatively low compared to the size of the garlic chromosomes. These research findings will serve as fundamental data for future development of markers for identifying NANJI-type garlic varieties.

***Corresponding Author:** Tel. 055-254-1513, E-mail: juhee94@korea.kr

PE-0076

Molecular characterization of a low Ab-αg saponin mutant using CRISPR/Cas9 in soybean

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

[1]Department of Applied Biosciences, Kyungpook National University, Daegu 41566, Republic of Korea
[2]Department of Agriculture, Forestry and Bioresources, Seoul National University, Seoul 08826, Republic of Korea

Soybean saponins are classified into two main groups which are group A saponins and DDMP saponins. The group A saponins are known for causing a bitter and astringent taste. Therefore, the reduction of group A saponins has been considered a major goal in soybean breeding. In this study, PE1653, one of the ethyl methanesulfonate (EMS)-induced lines of soybean cultivar Pungsannamul, exhibits a low concentration of group A saponins. The phenotype of PE1653 shows a reduction of Ab-αg saponin in the hypocotyl, while no statistical difference is observed in DDMP saponins. The *Sg-10* locus was suggested and confirmed as a single recessive locus in segregation analysis. Through mapping analysis, the *Sg-10* locus was found to exist in 764-kb region on chromosome 6. The *Sg-10* gene, one of the candidate genes from NGS analysis, has an amino acid substitution, replacing serine with asparagine, caused by one single nucleotide polymorphism (SNP) in the seventh exon. Co-segregation analysis was conducted with F2 population using a derived cleaved amplified sequence (dCAPS) marker. To uncover the role of *Sg-10*, a mutant was developed through Agrobacterium-mediated soybean transformation using the CRISPR-Cas9 system.

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

PE-0077

Spatial and temporal transcription patterns of amaranth *DBEI*

Young-Jun Park*

Korea Rural Research Institute, Kores Rural Community Corporation, Asansi, Korea

We focused on patterns of DBEI transcription in relation to starch synthesis in developing amaranth storage tissues and in non-storage tissues. We evaluated the DBEI transcript levels in amaranth seeds at various developmental stages by qRT-PCR and RT-PCR analyses. There were low DBEI transcript levels in seeds at initial and early late developmental stages. In seeds, the DBEI transcript levels increased rapidly from the early late developmental stage, reached peak levels at the middle developmental stage, and then decreased thereafter. Previous report showed that starch granules in the perisperm were strongly stained during the middle and mid-late of seed development. Also, we quantified the transcript levels of DBEI in developing non-storage amaranth tissues. Amaranth DBEI mRNA was not detected in the stem, petiole, or root at the four-leaf stage. An expression analysis at the six- leaf stage showed that DBEI mRNA was present in all of the non-storage tissues. However, the transcript levels differed among the tissues. Moderate transcript levels were detected in leaves, petioles, and stems, but low levels were detected in roots. In another study, a similar pattern was observed in different tissues of tuberizing and non-tuberizing sweet potato.

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

PE-0078

Phylogenetic relationships among the GBSS enzymes of amaranth and various plant species

Young-Jun Park*

Korea Rural Research Institute, Kores Rural Community Corporation, Asansi, Korea

The relationships among the plant GBSS amino acid sequences were analyzed using the PAUP* 4.0 program, with the results presented in a neighbor-joining phylogenetic tree. The *E. coli* glycogen synthase sequence was used as an outgroup. The plant GBSSs were separated into two groups, with monocot GBSSI forming one group and dicot GBSSs with monocot GBSSII forming the other. Overall, the monocot GBSSII appears to be closely related to GBSSIs from several dicot plants, which is consistent with the results of an earlier study. The dicot GBSS could be grouped into three distinct clades, namely GBSSI, GBSSII, and amaranth GBSSs. Interestingly, the amaranth GBSSs form a sister group to the clade consisting of the rest of the dicot plants and are more closely related to GBSSIIs from monocot plants than to GBSSIIs from dicot plants. This tree implies that the amaranth GBSSIb pathway evolved differently than the pathways for the dicot GBSSIIs. Our results indicate that the amaranth *GBSSIb* isoform probably evolved independently from the *GBSSI* isoforms in this crop (i.e., intraspecies).

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

PE-0079

Development of a PCR-based DNA marker for distinguishing two HMW-GS *1Bx14* accession numbers

Myoung-Hui Lee, Kyeong-Min Kim, Chon-Sik Kang, Changhyun Choi*

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

In common wheat (*Triticum aestivum* L.), allelic variation in the high molecular weight glutenin subunit *Glu-B1* locus has important influences on grain end-use quality. The *Glu-B1* locus consists of two tightly linked genes encoding the x- and y-type subunits that exhibit high variable frequencies. Among them, the *1Bx14* allele has been reported with two accession numbers AY367771 and KF733216. These two showed 96% identity in nucleotide sequence and were distance in the phylogenetic tree. However, studies on the discriminating markers of these alleles that have not been reported yet. KF733216 sequence showed 15 bp deletion in coding sequence compared to the other *1Bx* alleles, but AY367771 was not. Here we compared the sequences of the two accession numbers of *1Bx14* and developed a discriminating allele specific polymerase chain reaction-based DNA marker. In addition, ultra-high performance liquid chromatography analysis and sodium dodecyl sulfate-polyacrylamide gel electrophoresis were performed to compare with two accessions. These results will contribute to reducing confusion in cultivar selection and providing accuracy in quality assessment by clarifying *1Bx14* allele selection.

***Corresponding Author:** Tel. 063-238-5454; E-mail: chchhy@korea.kr

PE-0080

AINTEGUMETA-LIKE 6 is a positive regulator for triacylglycerol biosynthesis in seed

Inyoung Kim[1], Hyun Uk Kim[1,2*]

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

Triacylglycerol (TAG), used as an energy source for seed germination, is accumulated during seed development. LEAFY COTYLEDON 2 (LEC2) controls various transcription factors (TFs) for TAG biosynthesis as a master regulator. However, the TFs regulated by LEC2 have been little studied. Here, we identified new seed-specific TFs upregulated by LEC2. Each 25 TFs overexpression in *Nicotiana benthamiana* leaves by Agrobacterium infiltration showed various changes in TAG accumulation. As a result, five TFs overexpression accumulated TAG contents as high as LEC2 overexpression. They were transactivated directly or indirectly by LEC2 in transcriptional activity assay. One of them is AINTEGUMENTA-LIKE 6 (AIL6), a member of APETALA2/ETHYLENE RESPONSE FACOTR (AP2/ERF) domain TF family. The overexpression of AIL6 in Arabidopsis increased total fatty acid (FA) content in seed compared to the WT. Their FA composition showed an increase of 16:0, 18:0, 18:1, and 18:2 FAs and decrease of 18:3 and 20:1 FAs compared to the WT. Furthermore, the various fatty acid and TAG biosynthesis genes were highly expressed in AIL6 overexpression line. Therefore, our results suggest that AIL6 may act as a positive regulator for TAG biosynthesis and this study will be very useful for improving seed oil content and specific fatty acid synthesis.

***Corresponding Author:** E-mail: hukim64@sejong.ac.kr

PE-0081

Antisense expression of apple *TERMINAL FLOWER 1*-like gene shortens the breeding time in Rice

Van Giap Do*, Youngsuk Lee, Seonae Kim, Sang-Jin Yang, Juhyeon Park

Apple Research Institute, National Institute of Horticultural and Herbal Science, Rural Development Administration, Gunwi, 39000, Republic of Korea

Rice is an important crop worldwide. It is one of the most widely consumed staple foods. Its breeding time depends on the heading date (flowering time) during the transition from the vegetative to the reproductive phase, which is controlled by the floral regulator *TERMINAL FLOWER 1 (TFL1)*. *TERMINAL FLOWER 1 (TFL1)* encodes a protein that controls meristem identity and participates in regulating flowering. In this study, we used a transgenic approach to promote the heading date in rice via antisense technology. Transgenic rice plants with antisense expression of *MdTFL1* promoted heading much earlier than wild-type plants by up to 20 days. Gene expression analysis suggested that antisense expression of *MdTFL1* upregulated multiple endogenous floral meristem identity genes, including the (early) *heading date gene* family, *FLOWERING LOCUS T*, and MADS-box transcription factors, thereby shortening the vegetative phase. Antisense expression of *MdTFL1* also produced high-throughput phenotyping, including a change in overall plant organelles that affected an array of traits, especially grain productivity. Transgenic rice exhibited a semi-draft phenotype, increased leaf inclination angle, restricted flag leaf length, reduced spikelet fertility, and fewer grains per panicle. *MdTFL1* plays a central role in regulating flowering and in various physiological aspects. These findings emphasize the role of *TFL1* in regulating flowering in shortened breeding and expanding its function to produce plants with high-throughput phenotypes.

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

PE-0082

Analysis of the expression level of *orf*s in the tomato (*Solanum lycopersicum* cv. Micro-Tom) mitochondrial genome and conservation of them in the Solanaceae

Chae Yun Jeong, Woo Hyuk Choi, Seong Hak Kim, Yeong Deuk Jo*

College of Agriculture and Life Sciences, Chungnam National University, 99 Daehak-ro, Yuseong-gu, Daejeon 34134, Republic of Korea

Currently, correlations between mitochondrial genomes and various phenotypes have been revealed in animals and related studies are being actively conducted. However, due to the complexity of mitochondrial genomes, as much extensive researches have not been conducted in plants. Besides known genes, long *orf*s that are often conserved in plant mitochondrial genomes may have specific roles, as seen in cases of cytoplasmic male sterility genes. Therefore, this study performed whole mitochondrial genome analysis using the tomato cultivar, Micro-Tom, and then screened *orf*s and analyzed their positional characteristics, expression level, and conservation in other plant species within the Solanaceae. As a result, *orf*s with high-expression levels were selected, and 8 of them were found to be conserved at least in 18 out of 20 different Solanaceae crops whose mitochondrial genomes have been reported so far. In particular, two of them were conserved in all 20 crops. However, these *orf*s were not conserved in other plant families. Therefore, the conserved *orf*s are likely to have specific roles within the Solanaceae. Further investigations are being conducted using several approaches to confirm this. Since mitochondrial genome editing has succeeded in plants recently, the information derived from this study is expected to be useful to determine targets for functional analysis and development of new breeding materials.

***Corresponding Author:** Tel. 042-821-5739, E-mail: ydjo@cnu.ac.kr

PE-0083

The AP2/ERF transcription factor ERF55 regulates seed triacylglycerol biosynthesis

Yuli Choe[1], Inyoung Kim[2], Hyun Uk Kim[1,2*]

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

Seed triacylglycerol (TAG) is a valuable resource used in food and industrial applications. Transcription factors that promote TAG synthesis are particularly important for improving oil crops. ERF55, a member of the ERF-group Ⅰ of the AP2/ERF family, is known to play a role in plant growth, development, responses to biotic and abiotic stresses, as well as hormone signal transduction. In this study, we examined the subcellular localization of ERF55 and observed that it localizes to the nucleus, as demonstrated by the colocalization of 326-ERF55-sGFP with DAPI staining. To further determine the tissue-specific expression pattern of *ERF55*, we conducted GUS staining. The *ERF55*-promoter-driven GUS activity was detected in the anthers of flowers and seed embryos. This observation was further validated through RT-qPCR analysis, which exhibited similar expression patterns to the GUS activity results across various tissues of Arabidopsis. Subsequently, to elucidate the role of ERF55 in TAG biosynthesis, we generated transgenic Arabidopsis lines using CRISPR/Cas9 technology to create knockout mutants for ERF55. Although the seed size of the *erf55* mutants resembled that of the wild type (WT), a slight reduction in seed weight was observed. Notably, the seed TAG content in the *erf55* mutants was significantly decreased compared to the WT. Furthermore, the TAG composition showed a decrease in 18:1 and 20:1 fatty acid, while 18:2 levels increased. These findings strongly indicate that ERF55 is involved in regulating TAG synthesis in seeds.

***Corresponding Author:** E-mail: hukim64@sejong.ac.kr

PE-0084

Identification of genetic loci associated with agronomic traits of bread wheat (*Triticum aestivum* L.) based on genome-wide association study

Ji Hyeon Jeong[1], Woo Joo Jung[2], Yong Weon Seo[1*]

[1]Department of plant biotechnology, Korea University, Seoul 02841, Korea
[2]Institute of Life Science and Natural Resources, Korea University, Seoul 02841, Korea

Bread wheat (*Triticum aestivum* L.) is one of the most productive and important crops in the world as a food resource that contributes about 20% of the calories consumed by humans, but genome analysis has been difficult due to the very large size and polyploid complexity of the wheat genome. Genome-wide association study (GWAS) is a useful method to identify the SNP loci associated with phenotypic traits. In this study, we observed total nine major quantitative agronomic traits of 288 wheat cultivars from diverse country origins including the winter survival rate, days to heading, days to maturity, number of spikes per square meter, spike length, stem length, yield, thousand kernel weight, and liter weight. The correlation between was detected between observed traits across all environments, and the wheat genotypes were divided into four subpopulations based on the population structural analysis. The best linear unbiased prediction (BLUP) value of the genotypic effect for the different environments was predicted, and a GWAS was conducted using the mixed linear model (MLM). A total of 30,235 single nucleotide polymorphism (SNP) markers from the wheat 90K array were selected for GWAS of agronomic traits. The region of potential candidate genes was determined according to the LD decay length, and genes were selected in the 200 kb region around SNPs for the whole genome. Significant marker-trait associations (MTAs) were selected, and candidate genes were identified according to annotation of genes and tissue-specific gene expression level.

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

PE-0085

Genetic mapping of a resistance locus to *Phytophthora sojae* in the soybean elite line CheonAl (a.k.a. 1000al)

Seo Yoon Yang, Hee Jin You, EunJee Kang, Yeong-ho Kim, Sungwoo Lee*

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

Phytophthora root and stem rot caused by *Phytophthora sojae* (*P. sojae*) reduce soybean yields worldwide. The use of resistance gene is effective to protect soybean from being damaged by *P. sojae.* The objective of this study was to identify loci associated with resistance to *P. sojae* isolate 40468 using a recombinant inbred line population derived from a cross of Daepung (susceptible) x CheonAl (resistance). Single-marker analysis of variance (ANOVA) for over 22K single nucleotide polymorphisms (SNPs) identified over 50 SNPs on chromosome 18 associated with resistance to the isolate, which explained 97% of phenotypic variance. Linkage analysis identified approx. 100-kb region on chromosome 18 with high significance (LOD =27.4). The identified interval of the locus remains wide due to the size of mapping population (*N*=38). The elite line CheonAl is the first Korean soybean genotype characterized for its resistance against the isolate 40468 of *P. soaje*. This region is well-known as a resistance gene locus to *P. sojae*, to which previous studies mapped the *R* genes from diverse genetic sources. Therefore, this genomic region can be used to improve for resistance to *P. sojae* in soybean breeding program.

***Corresponding Author:** Tel. 042-821-5727, E-mail: sungwoolee@cnu.ac.kr

PE-0086

FAD2 and *FATB* family gene editing by multi sgRNA-Cas9 system to produce high oleic/ low saturated fatty acid soybean and discovery of transcription factor to enhance oil production

Won Nyeong Kim, Hyun Uk Kim*

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

CRISPR/Cas9 is a general technique to knock out a gene of interest. However, when targeting a multi-gene family or multiple genes, it is necessary to construct a multiple single guide RNAs (sgRNAs) vector to knock out. In this research, the newly modified Golden Gate cloning method was used to generate multiple sgRNAs-Cas9 vector. Using this vector, *Fatty Acid Desaturase 2 (FAD2)* and *Fatty Acyl-ACP Thioesterase B (FATB)* in soybean were targeted for a simultaneous knockout. In each generation, Next-Generation Sequencing for indel investigation and gas chromatography for fatty acid analysis was done. The T1 seed showed maximum 84% increased oleic acid (18:1) and 11% decreased saturated fatty acid (SFA; 16:0, 18:0). However in T2 seed, the general amount of fatty acid has decreased including WT due to vegetation environment but most of T2 plant's indels were fixed. The last harvested seed was T3 and it showed maximum 87% increased oleic acid and 7% decreased saturated fatty acid. By comparing various indel type, we found that *FAD2s/FATBs* edited lines has larger oleic acid content about 6~10% and smaller SFA amount about 3~5% than *FAD2* edited lines. Additionally, in *Glycine max*, a candidate gene that homolog to *AtMYB89* which reported as negative regulator of fatty acid biosynthesis was found and planned for gene editing to enhance oil production. We will compare more indel types and investigate the detailed contribution of each gene.

***Corresponding Author:** E-mail: hukim64@sejong.ac.kr

PE-0087

Identification of candidate genes related to salt stress tolerance by GWAS in North Korea rice population

Chuluuntsetseg Jadamba, Je-Hyeong Hong, Soo-Cheul Yoo*

Crop Molecular Breeding Laboratory, Department of Plant Life and Environmental Science, Hankyong National University, 327, Jungangro, Anseong-si, Gyeonggi-do 17579, Korea

Salt stress is one of the most severe environmental stresses that cause plant growth retardation and significant crop loss. In this study, we evaluated three traits, including the standard evaluation score (SES), the shoot dry weight reduction rate (RDR), and the shoot dry weight (SDW), for salinity tolerance at the seedling stage using 190 varieties of the North Korean rice population. Two-week-old seedlings, grown hydroponically, were subjected to salt treatment with 150 mM NaCl. We conducted a genome-wide association study (GWAS) for the SES and SDW traits using trials from three years (2019, 2020, and 2021), with RDR being used in only two trial years, 2020 and 2021. In our study, total 2471649 SNPs with minor allele frequency (MAF) $\geq$ 0.05, missing data rate of $\leq$0.25, minimum genotype quality $\geq$30, and minimum depth $\geq$4 filtered by PLINK, were used for association analysis. GWAS analysis was performed using a mixed linear model (MLM) implemented in GAPIT packages in R. As a result, a total of 52 lead SNPs were identified, out of which 3 SNPs were included in 4 previously reported known candidate genes related to salt stress tolerance. The remaining 48 SNPs were located in unknown genes in terms of salt stress response. We found some known salt stress candidate genes, including *OsMAR1* and *OsMAPK4/OsMSRMK3*, in the 2020 SES, and *OsAPX2* and *OsSOS1* in the 2020 RDR. Additionally, we discovered eight new candidate genes for SES, 42 for RDR, and two for SDW. Finally, five lead SNPs were repeatedly found in both 2020 and 2021, and these were defined as valuable candidate genes.

***Corresponding Author:** Tel. 031-670-5082, E-mail: scyoo@hknu.ac.kr

PE-0088

BSA-seq analysis for alkaline stress candidate genes in rice seedling stage

HongJia Zhang[1], Seong-Gyu Jang[1,2], Ah-Rim Lee[1], Fang-Yuan Cao[1], Yuting Zeng[1], Da-Eun Im[1], So-Yeon Park[1], Emmanuel Galang[1], Sang-Cheol Kim[1], Backki Kim[1,2], Soon-Wook Kwon[1,2*]

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

In present study, we are using two opposite phenotype varieties, RWG-111 and RWG-045, as the alkaline-tolerance and alkaline-sensitive variety. A F2 population derived from cross of RWG-111 and RWG-045, a phenotype selection performed by testing of alkaline-tolerance score, Relative root length (RRL), relative shoot length (RSL). Two opposite pools, alkaline-tolerance and sensitive pools were scanned by phenotype of score, performed next-generation sequencing for bulked segregant analysis.

Over than 0.7 million Nucleotide variations were detected between two pools and parents, which include 79% SNP, 10% insertion and 10% deletion variations. Total two novel candidate regions were detected in chromosome 1 and 12, contained 2Mb and 200kb interval distance.

Using the linkage method, QTL *qALKS1.1* was narrow down to a 200kb region between the maker of RM5646 and RM8144 by SSR maker analysis. One gene of totally 11 candidate genes performed qRT-PCR test contained difference expression during the eight alkaline-tolerance and sensitive varieties. These results find a novel gene resource for alkaline-tolerance in rice seedling stage, it could be helpful for alkaline-related breeding in future.

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

PE-0089

Haplotype analysis of major QTLs attributed to grain size conducted in the population derived from a cross between japonica rice varieties

Da-Eun Im[1], Seong-Gyu Jang[1,2], Backki Kim[1,2], Fang-Yuan Cao[1], Yuting Zeng[1], Hongjia Zhang[1], Ah-Rim Lee[1], So-Yeon Park[1], Emmanuel Galang[1], Sang-Cheol Kim[1], Soon-Wook Kwon[1,2*]

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

Grain size and shape affects the grain quality and yield of rice. Also, with the internationalization of the rice market, various sizes of rice varieties are required. In a study, 149 F_2 plants resulting from a cross between ‘Hopum’ and ‘Basmati 370’ were utilized to analyze the quantitative trait loci (QTL) associated with grain length (GL), grain width (GW), grain thickness (GT), and the ratio of length to width (RLW). A Linkage map covering 1,116 cM of F_2 population was constructed using 89 fluidigm SNP markers. A total of nine QTLs for the four traits were identified on chromosomes 2, 3, 5, and 7. A major QTL for GL on chromosome 3 explained 43.2% of the phenotypic variation. Two QTLs, qGW2 and qGW5, were identified for GW on chromosomes 2, 5, explained 10.4% and 18.6% of the phenotypic variation, respectively. The three QTLs for GT detected on chromosomes 2, 5 and 7, explained 9.9%, 12.9%, 9.9% of phenotypic variation, respectively. Haplotype analysis was conducted on genes previously associated with grain size at each QTL site using 430 RWGs sequence data. *GS3* known as the main gene related to grain size was divided into five haploid types and *SW5* was divided into four haploid types. The QTLs identified in this study could be utilized in breeding programs to develop long and slender grain japonica rice varieties.

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

PE-0090

Molecular analysis and haplotype analysis of resistance to brown spot in rice (*Oryza sativa L.*)

Fang-Yuan Cao[1], Yuting Zeng[1], Hongjia Zhang[1], Ah-Rim Lee[1], Da-Eun Im[1], So-Yeon Park[1], Emmanuel Galang[1], Sang-Cheol Kim[1], Seong-Gyu Jang[1,2], Backki Kim[1,2], Soon-Wook Kwon[1,2*]

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

Rice brown spot caused by *Cochliobolus miyabeanus* affects both rain-fed and upland rice production, causing losses in yield and grain quality. The study utilized a genome-wide association study to analyze the resistance of 130 rice cultivars to brown spot disease. The analysis identified two quantitative trait loci regions on chromosome 4, and candidate genes were screened using RNA-seq and databases such as Gene Ontology and Kyoto Encyclopedia of Genes and Genomes (KEGG). To further understand the function of the candidate genes, reverse transcription-quantitative polymerase chain reaction (RT-qPCR) was conducted. The results revealed four genes associated with disease resistance. It play a role in abiotic stress responses in rice.

Haplotype analysis identified specific single nucleotide polymorphisms (SNPs) in the candidate genes. The key SNPs obtained based on the dominant haplotype provided a molecular basis for marker screening of brown spot-resistant varieties, facilitating their application in rice breeding efforts.

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

PE-0091

Quantitative Trait Locus(QTL) analysis on grain size in rice using RILs derived from a cross between japonica varieties

Sang-Cheol Kim[1], Seong-Gyu Jang[1], Fang-Yuan Cao[1], Yuting Zeng[1], JungHyun Gong[1], JinKyung Jeong[1], Han-Gyeol Kim[1], Soon-Wook Kwon[1,2*]

[1]Department of Plant Bioscience, College of Natural Resources and Life Science, Pusan National University, Miryang 50463, Republic of Korea

[2]Life and Industry Convergence Research Institute, Pusan National University, Miryang 50463, Republic of Korea

In rice, grain size is a significant trait that affects the quality and quantity of rice production. A population of 190 recombinant inbred lines (RILs) obtained from a cross between the rice varieties ‘Samnam’ and ‘Koshihikari’ was utilized to investigate quantitative trait loci (QTLs) associated with grain size traits. The grain size traits were analyzed using the ‘SmartGrain’ software, and genotyping of the RIL population was performed using 96 Fluidigm SNP markers. The QTL IciMapping 4.2 Program was employed to construct a linkage map and conduct QTL mapping. To examine variations between years and regions, the seed characteristics of the same RIL population were evaluated using seeds produced in Suwon in 2020 and seeds harvested in Suwon and Miryang in 2022. The three grain size traits analyzed were area size (AS), grain width (GW), and grain length (GL). A total of sixteen QTLs associated with six different traits across six chromosomes using the linkage map constructed with 74 SNP markers. These findings provide valuable genetic information that can be used to effectively manipulate rice grain size.

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

PE-0092

The Genome-wide Association Study for Ultraviolet-B Resistance in rice (*Oryza sativa* L.)

Yuting Zeng[1], HongJia Zhang[1], Ah-Rim Lee[1], Fang-Yuan Cao[1], Da-Eun Im[1], So-Yeon Park[1], Emmanuel Galang[1], Sang-Cheol Kim[1], Seong-Gyu Jang[1,2], Bakki Kim[1,2], Soon-Wook Kwon[1,2*]

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

Global warming accelerates the destruction of the ozone layer, increasing the amount of ultraviolet-B (UV-B) reaching the Earth's surface, which in turn alters plant growth and development. Organisms are negatively affected by enhanced UV-B radiation, and especially in crop plants this may lead to yield losses. Rice is one of the most important staple grains, grown worldwide in regions with different climates. In this study, we used a core collection of 137 rice cultivars which selected from potentially representing 25,604 rice germplasms in the Korean Genebank of the Rural Development Administration (RDA). These germplasms were collected from 28 countries and could be divided into 6 subgroups: tropical japonica (19 accessions), temperate japonica (62), indica (43), aus (8), aromatic (3), and admixture (2). Through this GWAS analysis, 3 lead SNPs in chromosome 2 and 8 were confirmed to be associated with UV-B tolerance, and a linkage disequilibrium (LD) decay analysis identified the 350 kb and 250 kb exploratory respectively in chr2 and chr8 for the detection of QTLs and candidate genes. Among the function annotated genes located in these three QTLs regions, four genes were selected as candidate genes for UV-B tolerance in rice seedlings.

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

PE-0093

Identification of PI88788-type and Peking-type genotypes of soybean cyst nematode (*Heterodera glycines*) resistance in Korean soybean germplasm

Jae Eun Jo[1], Soyeon Park[1], Hyoung-Rai Ko[2], Byeong-Yong Park[2], Kyung Do Kim[1*]

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

[2]Crop Protection Division, National Institute of Agricultural Sciences, Wanju 55365, Republic of Korea

Soybean cyst nematode (SCN, *Heterodera glycines*) is one of the most destructive pests in the world, affecting more than 90% of the soybean cultivating area. PI88788-type and Peking-type are two representative genotypes of *H. glycines* resistance, controlled by the *Rhg1* and *Rhg4* genes. These two genes are widely used in US breeding programs to select SCN-resistant varieties, while no varieties have yet been developed for SCN resistance in Korea. Here, we genotyped more than 800 soybean accessions, including both wild (*Glycine soja*) and cultivated (*G. max*) soybeans, for the *Rhg1* and *Rhg4* genes. We identified the PI88788-type and Peking-type genotypes and determined that those two genes were present in only a minority of soybean germplasm. Moreover, the frequency of PI88788-type and Peking-type genotypes varied among accessions derived from different geographical regions. We also found that nearly all Korean varieties lack *Rhg1* or *Rhg4* resistance. This suggests that these two genes have not been widely adopted in soybean breeding programs in Korea. Therefore, our genotyping results for the *Rhg1* and *Rhg4* genes will be useful for Korean breeding programs to develop SCN-resistant varieties.

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

PE-0094

Functional studies of chloroplast lipid associated protein FBN3 under abiotic stress

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

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

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. When seed germination rate was compared under various stress, seed germination of *fbn3a*, *fbn3b*, and CRISPR double K.O mutants exposed to ABA, NaCl, and mannitol were not significantly reduced compared to wild type. 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.

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

PE-0095

Novel alleles of *KASII-A* and *FAD2-1A* from EMS-induced mutant lines produces elevated level of palmitic and oleic acid in soybean

Hyun Jo, Jiyoung Park, Sooyeon Kim, Taemin Kim, Jong Tae Song, Jeong-Dong Lee*

Department of Applied Biosciences, Kyungpook National University, Daegu 41566, Republic of Korea

Soybean oils contain approximately 11% palmitic (16:0) and 23% oleic acid (18:1). Elevated 18:1 helps prevent cardiovascular diseases and improve quality of oil and elevated 16:0 can be used to shortening and margarine. In our previous study, a mutant population consisting of the M_4 generation was developed by EMS mutagenesis of the cultivar Pungsannamul. Based on fatty acid profiles of 2,281 mutant lines, two elevated 16:0 lines, PE1544 (~15.8%) and PE1604 (~16.2%), and an elevated 18:1 line, PE529 (~49.1%) were selected to identify novel alleles of the *KASII-A* for 16:0 and *FAD2-1A* genes for 18:1. This study identified two novel missense mutations of *KASII-A* from PE1544 and PE1604, respectively and a novel nonsense mutation of the *FAD2-1A* from PE529. The single nucleotide polymorphism (SNP) in PE529 had induced the conversion from tryptophan to a premature stop codon at position 293 in the amino acid sequence (W293STOP). In addition, we found SNPs leading to amino acid change (L712F) of the *KASII-A* gene for PE1604 and having amino acid change (G779D) of the *KASII-A* for PE1544. The amino acid position of two missense mutations for 16:0 was highly conserved. The inheritance analysis showed that the elevated 18:1 in PE529 were attributed to the *fad2-1a* W293STOP allele. Seeds capable of producing approximately 80.0% 18:1 were identified from F_2 populations where *fad2-1a* W293STOP and *fad2-1b* alleles were segregated. Hence, soybeans with novel alleles are useful genetic resources to improve soybean oil quality in breeding programs.

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

PE-0096

Identification of shattering gene loci of Japonica rice “Sailimi”

Jong-Hee Lee, Hyeonjin Park*, Jin-Kyung Cha, Youngho Kwon, So-Myeong Lee, Gi-Un Seong

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

Seed shattering is an important trait that wild rice uses to adapt to the natural environment and maintain population reproduction. The degree of shattering is not only one of the main reasons for rice yield reduction but also affects its adaptability to modern mechanical harvesting methods. Therefore, it is important to cultivate rice varieties with a moderate shattering degree. The cultivar ‘Saeilmi’ has an easy-shattering habit, such that up to 30 of grains were shattered after grasping a panicle by hand at the maturity stage. In contrast, almost no grains were shattered in ‘Koshihikari’, confirming that it is of non-shattering. To identify the gene controlling seed shattering gene of Saeilmi, we developed a F2 population derived from a cross between O. sativa cultivar “Saeilmi” and Koshihikari. The main QTL effect is detected between KASP marker KJ01-093 and KJ01-097 in the chromosome 1 which is alleles to qSH1 (a QTL of seed shattering on chromosome 1).

***Corresponding Author:** Tel. 055-350-1168, E-mail: ccriljh@korea.kr

PE-0097

Analysis of Sequence Variations in *SGR* and *CCS* to Develop Mature Green Pepper Cultivars

Jeongeun Kim, Joung-Ho Lee, Munseung Jung, Jin-Kyung Kwon, Byoung-Cheorl Kang*

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

Pepper fruit color usually transforms from green to red during ripening stage due to the conversion of the pigment contents, for example, chlorophylls to carotenoids. Previously, it was observed that the *stay green* (*sgr*) gene mutant in pepper inhibits chlorophyll degradation resulting in mature fruit color of brown or green, depending on *capsanthin-capsorubin synthase* (*CCS*) involved in the carotenoid biosynthesis. In this study, we aimed to gain a deeper understanding of the stay-green phenotype by conducting a genetic analysis of three fruit color-related genes: *phytoene synthase 1* (*PSY1*), *CCS*, and *SGR* in several pepper accessions with mature fruit color of yellow, brown or green. Based on the genotyping analysis of *PSY1*, all pepper accessions, except for 'Micro-Pep Yellow' and 'IT236421', exhibited the wild type (*PSY1*/*PSY1*) genotype. When analyzing *CCS*, we found two non-functional *ccs* alleles in two accessions, 'Micro-Pep Yellow' and 'Raymond, which likely affect carotenoid biosynthesis. The genotyping analysis of *SGR* revealed two single nucleotide polymorphisms (SNPs) in *sgr* allele, leading to missense and nonsense mutations, respectively. In one accession, both SNPs were observed as heterozygotes. To efficiently detect the *sgr* allele, we also developed Kompetitive Allele Specific PCR (KASP) markers using two SNPs in *sgr* allele, enabling marker-assisted selection. In the future, markers developed in the study will be valuable resources for further studies on the role of the SGR gene in pepper fruit color and its potential application in breeding programs.

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

PE-0098

A study on the vaccine of *Nicotiana benthamiana* based porcine circovirus 2

Seon-Kyeong Lee*, Jiseon Kim, Ju Ho Lee, Kyeong-Ryeol Lee

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

Plant-based vaccines have many advantages over conventional vaccine production methods such as eggs, animal cells, and microorganisms. In general, large-scale production is possible at a relatively low cost, and even if contamination occurs during the culture and production process, the biological system of plants and humans is far away, making it a safer platform than conventional vaccines. In this study, the most widely used *Nicotiana benthamiana* for plant-based recombinant protein production was used as a model system. Two methods were used to express foreign genes in *Nicotiana benthamiana*: stable transformation and transient expression. Porcine Circovirus 2 (PCV2) is a small single-stranded DNA virus that causes a porcine circovirus associated diseases (PCVAD). A transgenic plant was constructed to express the capsid gene of this virus in plants. In addition, the efficacy of foreign gene introduction using the green fluorescent protein (GFP) was evaluated to be used for agrobacterium-mediated transient expression. Generational progress is being made by identifying whether genes are introduced and patterns of gene expression. After that, the efficacy as a plant-based vaccine will also be evaluated by increasing protein expression. Through this, it is expected that it will be able to secure source technology for high-value recombinant protein production and contribute to increasing industrial production of plant-based vaccines.

***Corresponding Author:** Tel. 063-238-4623, E-mail: lsk220@korea.kr

PE-0099

Genomic Landscape of the *OSTPP7* Gene in Its Haplotype Diversity and Association with AG Tolerance in Korean Rice

Kyaw Myo Aung[1], Win Htet Oo[1], Thant Zin Maung[1], Myeong-Hyeon Min[1], Aueangporn Somsri[1], Jungrye Nam[2], Kyu-Won Kim[2], Bhagwat Nawade[2], Chang-Yong Lee[3], Sang-Ho Chu[2*], Yong-Jin Park[1,2*]

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

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

[3]Department of Industrial and Systems Engineering, College of Engineering, Kongju National University, Cheonan 31080, Republic of Korea

Early season flooding is a major constraint in direct-seeded rice, as rice genotypes vary in their coleoptile length during anoxia. *Trehalose-6-phosphate phosphatase 7* (*OsTPP7*, *Os09g0369400*) has been identified as the genetic determinant for anaerobic germination (AG) and coleoptile elongation during flooding. We evaluated the coleoptile length of a diverse rice panel under normal and flooded conditions and investigated the Korean rice collection of 475 accessions to understand its genetic variation, population genetics, evolutionary relationships, and haplotypes in the *OsTPP7* gene. Most accessions displayed enhanced flooded coleoptile lengths, with the temperate *japonica* ecotype exhibiting the highest average values for normal and flooded conditions. Positive Tajima's D values in *indica*, admixture, and tropical *japonica* ecotypes suggested balancing selection or population expansion. Haplotype analysis revealed 18 haplotypes, with three in cultivated accessions, 13 in the wild type, and two in both. HaP_1, Hap_2, and Hap_3 were major haplotypes found in 395 (300 *japonica*), 50 (44 *indica*), and ten (six *indica*) accessions, respectively. Further phenotypic performance of major haplotypes showed significant differences in flooded coleoptile length, flooding tolerance index, and shoot length between Hap_1 and Hap_2/3. These findings could be valuable for future selective rice breeding and the development of efficient haplotype-based breeding strategies for improving flood tolerance.

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

***Corresponding Author:** Tel: +82 41-330-1201, E-mail: yjpark@kongju.ac.kr
Tel: +82 41-330-1213, E-mail: sanghochu76@gmail.com

PE-0100

Genetic Characterization of the *gamma-Tocopherol Methyltransferase (γ-TMT)* Gene and Its Relationship with Tocopherol Content in the Korean Rice Collection

Aueangporn Somsri[1†], Sang-Ho Chu[2†], Bhagwat Nawade[2], Yong-Jin Park[1,2*]

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

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

Gamma-tocopherol methyltransferase (γ-TMT) is a key gene in the vitamin E biosynthesis pathway, regulating the accumulation of tocopherols and influencing rice nutritional quality. This study aimed to investigate the haplotype variations and evolutionary patterns of the γ-TMT gene in a collection of 475 Korean rice accessions. Our analysis revealed 19 nonsynonymous SNPs across the coding gene region, resulting in 16 distinct haplotypes. Interestingly, among the cultivated rice accessions, we found a major functional haplotype (Hap_18), while the remaining haplotypes were predominantly found in wild rice accessions. Hap_18, observed in 88 indica, four aus, and two admixture rice accessions, was characterized by two functional alleles, G/A and A/G SNPs, located in exons 2 and 4, respectively. These alleles appeared to play a crucial role in determining the vitamin E composition of japonica and indica rice accessions. Moreover, we observed higher nucleotide diversity in indica, followed by wild, tropical japonica, and temperate japonica, suggesting varying genetic variation and adaptation levels within these groups. The positive Tajima's D value (2.0985) observed in indica rice indicated a population contraction during the domestication of the γ-TMT gene, pointing towards the presence of balancing selection. Additionally, higher FST values demonstrated significant differentiation between indica and japonica groups, indicating limited genetic diversity shared between them. Overall, our study sheds light on the genetic diversity and evolutionary dynamics of the γ-TMT gene in Korean rice accessions, offering valuable information for rice nutritional improvement through haplotype-based breeding.

Keywords: Gamma-Tocopherol Methyl Transferase, Tocopherol, Vitamin E, Haplotype Analysis, Rice

†These authors contributed equally to this work.

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

PE-0101

Genome-wide Identification and Characterization of the *HIS1* Gene Family in Rice

May Htet Aung[1], Bhagwat Nawade[2], Sang-Ho Chu[2*], Yong-Jin Park[1,2*]

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

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

Herbicides play a crucial role in weed control, ensuring that rice plants have access to essential resources and optimizing crop yield and quality. Developing herbicide-tolerant crops is a significant research endeavor aimed at sustainable weed management and enhancing agricultural output. Recently, the *HIS1* (*HPPD INHIBITOR SENSITIVE 1*) gene was identified in Japonica rice, conferring resistance to benzobicyclon (BBC) and other β-triketone herbicides, providing a valuable tool for rice farmers. *HIS1* encodes Fe(II)/2-oxoglutarate-dependent oxygenase, enabling the detoxification of β-triketone herbicides through hydroxylation catalysis. However, the presence of orthologues of the His1 gene in other rice subspecies and crops remains unknown. This study aimed to elucidate the *HIS1* gene family through comprehensive genome-wide analyses of diverse cereal species. Among rice ecotypes, 11 *HIS1* genes were found in Japonica, 03 in Indica, and 05 in Aus. A phylogenetic analysis of 245 HIS1 orthologous genes from 17 cereal species revealed 10 main clades. Gene structure analysis showed variations in size and exon-intron arrangement of HIS1 orthologs among rice subspecies. Gene structure analysis demonstrated variations in gene size and exon-intron arrangement among the rice subspecies. Notably, *Os02g0280700* had the longest gene length (1727 bp) with four introns, while *Os06g0176850* had the shortest length (1062 bp) with three introns. Comprehensive bioinformatics analyses identified conserved sites, domains, motifs, physio-chemical properties, subcellular localization, and regulatory elements of the identified genes. This research provides valuable insights into the genetic makeup and features of the *HIS1* gene family, facilitating the improvement of herbicide tolerance in crops.

Keywords: HIS1, Herbicides, Rice, Gene family, HPPD

***Corresponding Author:** Tel: +82-41-330-1201, E-mail: yjpark@kongju.ac.kr
Tel: +82-41-330-1213, E-mail: sanghochu76@gmail.com

PE-0102

Unveiling the Genetic Architecture of HPPD Herbicide Tolerance in Rice: Insights from Nested Association Mapping

Bhagwat Nawade[1], May Htet Aung[2], Sang-Ho Chu[1*], Yong-Jin Park[1,2*]

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

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

HPPD (*4-Hydroxyphenylpyruvate Dioxygenase*) herbicides play a crucial role in weed management in rice cultivation. These herbicides offer effective and selective control of weeds, enabling rice plants to grow without competition for essential resources such as light, water, and nutrients. By suppressing weed growth, *HPPD* herbicides contribute to optimizing crop yield and quality. However, limited breeding efforts have focused on germplasm characterization and mapping candidate loci associated with *HPPD* herbicide tolerance. In this study, we employed Nested Association Mapping (NAM), which combines the benefits of linkage and association mapping to uncover the genetic architecture underlying *HPPD* herbicide tolerance in rice. Our investigation employed the Korice-NAM population, which consists of 1,100 recombinant inbred lines derived from 12 diverse Korean rice cultivars. Through screening, we evaluated the *HPPD* herbicide tolerance of these lines, and genotyping was performed using the '580 K _ KNU chip' array containing 580,000 single-nucleotide polymorphisms (SNPs). Leveraging genome-wide association studies (GWAS), we identified significant SNPs associated with HPPD herbicide tolerance located on chromosomes 2, 10, and 12. These SNPs demonstrated robust associations across various treatment durations (5, 10, 15, and 20 days). The identification of these significant SNPs provides valuable insights into the genetic basis of HPPD herbicide tolerance in rice. Understanding the underlying genetic mechanisms will facilitate the development of breeding strategies aimed at enhancing *HPPD* herbicide tolerance in rice varieties.

Keywords: HPPD, Nested Association Mapping, GWAS, Array, Mapping, Rice

***Corresponding Author:** Tel: +82-41-330-1201, E-mail: yjpark@kongju.ac.kr
Tel: +82-41-330-1213, E-mail: sanghochu76@gmail.com

PE-0103

Progress on Development of New Rice Varieties for Aroma and Medium-Amylose using CRISPR/Cas9 and Marker-Assisted Backcrossing (MABc)

Sang-Ho Chu[1]†, Thant Zin Maung[2]†, Bhagwat Nawade[1], Yong-Jin Park[1,2]*

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

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

Fragrance and amylose content (AC) are pivotal factors determining the premium cooking and eating quality (ECQ) of rice grains. In Korea, medium amylose content and fragrance are essential traits for the acceptability and marketability of rice varieties. This study aimed to enhance the ECQ traits of elite Korean rice cultivars, including Miho, Wolbaek, Samgwang, and Koshihikari. We utilized the CRISPR/Cas9 tool to create novel alleles of the *OsBADH2* gene, introducing fragrance into the targeted elite Korean rice cultivars. Furthermore, the edited *OsBADH2* mutant lines underwent a marker-assisted backcrossing program, targeting waxy genes to develop sticky rice varieties. Through Agrobacterium-mediated transformation, the CRISPR/Cas9-SgRNA complex effectively knocked out the BADH2 gene in the desired cultivars. Analysis of phenotypes and gene editing frequencies in the first generation of transformed plants revealed an approximate gene editing efficiency of 42.5% in the transformed plants. Homozygous edited lines were further utilized for intercrossing, and hybrid plants were selected for waxy genes using SNP markers. The generated introgression lines (ILs) will undergo comprehensive evaluations for phenotypic performance, including fragrance/2AP content, grain characteristics, and amylose content, to identify promising lines. This study demonstrates the effectiveness of marker-assisted backcrossing (MABc) using CRISPR-targeted OsBADH2 edited lines, enabling rapid and precise editing of desired traits. The generated lines hold significant potential as valuable parental resources for future breeding programs aimed at improving ECQ rice varieties.

Keywords: ECQ, BADH2, Rice, Fragrance, amylose, MABC

† These authors contributed equally to this work.

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

PE-0104

Revolutionizing Rice Improvement: CRISPR/Cas-Mediated Multiplex Editing Unleashes Potential

Gi Hwan Baek[1], Bhagwat Nawade[2], Sang-Ho Chu[2], Yong-Jin Park[1,2*]

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

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

The CRISPR/Cas (clustered regularly interspaced short palindromic repeats) system has revolutionized targeted genome editing in a wide range of crops. One of the powerful applications of CRISPR/Cas technology is multiplex genome editing (MGE), which enables the precise introduction of mutations at multiple loci in a single gene or multiple genes simultaneously. Several strategies have been developed to achieve MGE, including the co-delivery of multiple single-guide RNAs, dual sgRNA expression, multiplex oligonucleotide-mediated editing, and pooled CRISPR library screening. In the realm of rice improvement, MGE using CRISPR/Cas has shown remarkable success. For instance, mutant lines were generated in *O. alta* ecotypes using the MGE system, allowing the identification of lines with desirable agricultural traits. Furthermore, multiplex editing of the *OsGS3*, *OsGW2*, and *OsGn1a* genes led to improved grain shape in an *O. glaberrima* landrace. Moreover, MGE has been employed to modulate gene expression by targeting promoter regions of key genes involved in important traits. For example, transcription modulation of *OsWOX11* and *OsYUC1*, which play roles in crown root development and auxin biosynthesis in rice, was achieved using CRISPR/Cas-mediated MGE. Beyond these, CRISPR/Cas has been widely used in rice to improve traits such as herbicide resistance, disease resistance, stress tolerance, and domestication-related characteristics. The ability to perform multiplex gene editing using CRISPR/Cas technology holds immense potential for advancing rice functional genomics and breeding efforts.

Keywords: Rice, Cas9, Multiplex editing, Wild rice, domestication

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

PE-0105

Development of Nested Association mapping population (NAM): A Promising Tool for Integrating Genomics and Genetic Mapping in Rice Improvement

Sang-Ho Chu[1], Bhagwat Nawade[1], Yong-Jin Park[1,2*]

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

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

Understanding the genetic architecture of complex traits in rice poses a significant challenge for breeders. Traditional bi-parental populations with limited genetic diversity are often insufficient to explore the full extent of genetic variation underlying these traits. To overcome this limitation, Multi-parent populations (MPPs) such as Nested Association Mapping (NAM) and Multi-Parent Advanced Generation Inter-cross (MAGIC) populations have emerged as promising tools. These populations incorporate a diverse set of founder lines, allowing for increased genetic diversity and improved mapping accuracy using advancements in genomic technologies. In this study, we present the development of the first NAM population for Korean rice cultivars, named Korice-NAM. This population comprises 1,100 recombinant inbred lines derived from 12 diverse Korean rice cultivars, including 11 donors and a founder line. Korice-NAM exhibits broad phenotypic variation for various agronomical traits, making it an invaluable resource for genetic studies. To demonstrate the utility of Korice-NAM, we conducted genome-wide association studies (GWAS) to dissect the genetic control of panicle number per plant (PN) and stem thickness (ST). Using the Affymetrix GeneTitan platform, the NAM population was genotyped with the '580 K _ KNU chip' array containing 580,000 SNPs; we identified 11 and 35 highly significant SNP-trait associations (STAs) for PN and ST, respectively. The results highlight the power of Korice-NAM as a valuable tool for uncovering the underlying genetic mechanisms of complex traits in rice. When coupled with high-throughput phenotyping, genotyping, and advanced statistical models, Korice-NAM holds excellent potential for accelerating crop breeding efforts.

Keywords: Multi-parent populations, Nested Association Mapping, Rice, GWAS, Mapping

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

PE-0106

Leveraging GWAS to Decipher the Genomic Basis of Seed Dormancy and Pre-Harvest Sprouting in rice

Myeong-Hyeon Min[1†], Sang-Ho Chu[2†], Bhagwat Nawade[2], Yong-Jin Park[1,2*]

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

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

Seed dormancy plays a pivotal role in ensuring the survival of plants by preserving genetic information under adverse environmental conditions. However, the escalating threat of sudden climate change, exacerbated by global warming, poses significant challenges for less adapted plant varieties. Pre-harvest sprouting (PHS), characterized by premature seed germination triggered by typhoons and floods, can profoundly impact crop yield. In this study, we employed genome-wide association studies (GWAS) using diverse rice germplasm accessions and comprehensive genome-wide resequencing data to identify candidate genes associated with traits. Analysis of heritability indicated that 58% of the genetic variance in PHS and 91% of the genetic variance in dormancy were observed. In order to identify significant single-nucleotide polymorphisms (SNPs) associated with these phenotypes, a threshold level of 5 <-log10 (p-value) was set based on the Q-Q plot analysis. Our analysis confirmed the presence of previously identified PHS-associated genes and unveiled 16 novel candidate genes, which collectively encompassed 34 significantly associated single-nucleotide polymorphisms (SNPs) within coding regions. Furthermore, haplotype-based association analysis of candidate regions revealed their potential to enhance PHS tolerance. These findings contribute to a deeper understanding of the genetic underpinnings of seed dormancy and PHS in rice. By unraveling the genetic basis of PHS and seed dormancy, our research paves the way for the development of targeted strategies to enhance crop resilience and mitigate the detrimental effects of global warming on agricultural productivity.

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

[†] These authors contributed equally to this work.

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

PE-0107

Profiling Haplotype Diversity and Evolutionary Signatures of the SSIII-1 Gene in Rice for Improved Resistant Starch Traits

Bhagwat Nawade[1], Yong-Jin Park[1,2*]

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

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

Soluble starch synthases (SSs) play a vital role in the synthesis of resistant starch in rice by elongating α-glucans. This study focused on profiling the genetic diversity of the SSIII-1 gene, which is involved in amylopectin metabolism and less understood compared to other SS isoforms. A total of 10 SS isoforms have been reported in rice, including SSIIIb (SSIII-1). We investigated the genetic diversity of the SSIII-1 gene in 374 rice accessions, comprising 54 wild-type accessions and 320 bred cultivars of various ecotypes (temperate japonica, indica, tropical japonica, aus, aromatic, and admixture). In the SSIII-1 coding region, 17 haplotypes were identified in the bred cultivars, while 44 haplotypes were detected in the wild-type accessions. Tajima's D values indicated balancing selection in most ecotypes, except for a negative value in the temperate japonica, suggesting purifying selection. Nucleotide diversity was highest in the wild group, indicating a greater variation, while the temperate japonica exhibited lower nucleotide diversity due to purifying selection. The fixation index (F_{ST}) analysis revealed high gene flow between the tropical japonica and admixture groups (F_{ST}=-0.21), followed by the admixture and wild groups. Lower gene flow was observed between the temperate japonica and aus groups (F_{ST}=0.72), tropical japonica and aromatic groups (F_{ST}=0.71), and temperate japonica and admixture groups (F_{ST}=0.52). Understanding the genetic diversity and evolutionary dynamics of SSIII-1 contributes to the broader goal of enhancing the nutritional quality of rice through targeted breeding strategies.

Keywords: Starch synthases, Korean rice, Diversity, Haplotypes, Evolution

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

PE-0108

Transcriptogenomic convergence reveals a regulatory network of rice-eating and cooking quality

Weiguo Zhao[1,2†], Qiang He[1,3†], Kyu-Won Kim[4†], Sang-Ho Chu[4†], Sang-Kyu Lee[5†], Feifei Xu[1,6], Rungnapa Phitaktansakul[1,7], Kyaw Myo Aung[1], Myeong-Hyeon Min[1], Thant Zin Maung[1], Aueangporn Somsri[1], Min-Young Yoon[1], Sang-Beom Lee[8], Seung-Hyun Kim[9], Joohyun Lee[9], Soon-Wook Kwon[10], Gang-Seob Lee[11], Jungrye Nam[4], Sang-Won Park[12], Yoo-Hyun Cho[13], Bhagwat Nawade[4], Chang-Yong Lee[14], Ill-Min Chung[9*], Jong-Seong Jeon[15*], Yong-Jin Park[1,4*]

[1]Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 32439, Korea
[2]Jiangsu Key Laboratory of Sericultural Biology and Biotechnology, School of Biotechnology, Jiangsu University of Science and Technology, Zhenjiang 212100, China
[3]Institute of Crop Science, Chinese Academy of Agricultural Sciences, Beijing 100081, China
[4]Center for Crop Breeding on Omics and Artificial Intelligence, Kongju National University, Yesan 32439, Korea
[5]Division of Life Science, Plant Molecular Biology and Biotechnology Research Center, Gyeongsang NationalUniversity, Jinju 52828, Republic of Korea
[6]Institute of Nuclear Agricultural Sciences, Key Laboratory of Nuclear Agricultural Sciences of Ministry of Agriculture and Zhejiang Province, College of Agriculture and Biotechnology, Zhejiang University, Zijingang Campus, Hangzhou 310058, China
[7]Biotechnology Research and Development Office, Department of Agriculture, Bangkok 10900, Thailand
[8]National Institute of Crop Science, Rural Development Administration, Wanju 55365, Korea
[9]Department of Applied Bioscience, Konkuk University, Seoul 05029, Korea
[10]Department of Plant Bioscience, College of Natural Resources and Life Science, Pusan National University, Miryang 50463, Korea
[11]National Institute of Agricultural Sciences, Rural Development Administration, Jeonju 54874, Korea
[12]R&D Cooperation Division, Rural Development Administration, Jeonju 54875, Korea
[13]Seedpia, 85 Maesil-ro, Kwonsun-ku, Suwon 16395, Korea
[14]Department of Industrial and Systems Engineering, College of Engineering, Kongju National University, Cheonan 31080, Korea
[15]Graduate School of Biotechnology & Crop Biotech Institute, Kyung Hee University, Yongin 17104, Korea

Eating and cooking quality (ECQ) is rice's most complex quantitative trait. Understanding the genetic regulation of ECQ traits is essential for rice breeding programs. A transcriptome-wide association study (TWAS) was conducted, and a regulatory network was built using the whole-genome resequencing, transcriptomic, and phenotypic data from 84 Japonica accessions. Further, we validated the implications of our findings through genome editing. ECQ traits displayed considerable variation and significant phenotypic correlations among the traits. The TWAS identified 285 transcripts significantly associated with six ECQ traits. Genome-wide mapping of these transcripts revealed 66,905 expression quantitative trait loci (eQTLs), which included 21,747 local eQTLs and 45,158 trans-eQTLs. These eQTLs were found to regulate the expression of 43 genes, including starch synthesis-related genes, *starch synthase IV-1* (*SSIV-1*), *starch branching enzyme 1* (*SBE1*), *granule-bound starch synthase 2* (*GBSS2*), and *ADP-glucose pyrophosphorylase small subunit 2a* (*OsAGPS2a*), as well as regulators such as *basic helix-loop-helix* (*bHLH*), *pyrophosphatase/ phosphodiesterases* (*NPP1*), and *ethylene response 3* (*ETR3*). Genome-wide co-expression analysis of 285 guide genes revealed 130 genes forming at least one network, and 22 master regulators were discovered. Furthermore, to validate the TWAS analysis implications, we selected alpha-globulin (glb1), which was co-expressed with *GBSS1*, and analysis of CRISPR/Cas9 edited glb1 mutant lines confirmed its role in starch synthesis. By integrating genomic, gene expression, and phenotype data, our transcriptogenomic convergence approach provides new insights into the genetic regulation of ECQ traits. This demonstrates the effectiveness of such an integrative approach in uncovering the genetic basis of complex traits, which can facilitate rice breeding efforts.

Keywords: ECQ, TWAS, GWAS, editing, co-expression, network

[†] These authors contributed equally to this work.

***Corresponding Author:** Yong-Jin Park (E-mail: yjpark@kongju.ac.kr)
Ill-Min Chung (E-mail: imcim@konkuk.ac.kr)
Jong-Seong Jeon (E-mail: jjeon@khu.ac.kr)

PE-0109

Genetic Variability and Haplotype Analysis of *Xa39* Gene for Bacterial Leaf Blight Resistance in Korean Rice Accessions

Kyaw Myo Aung[1†], Kyu-Won Kim[2†], Jee-Su Kang[1], Bhagwat Nawade[2], Sang-Ho Chu[2*], Yong-Jin Park[1,2*]

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

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

Bacterial Leaf Blight (BLB), caused by *Xanthomonas oryzae* pv. oryzae (Xoo) is a major disease affecting rice cultivation worldwide. Particularly prevalent during the monsoon season, BLB poses a significant threat to high-yielding rice varieties, especially in irrigated and rainfed lowland ecosystems. With substantial yield losses ranging from 20% to 80%, developing BLB-resistant rice varieties is crucial for mitigating the impact of this devastating disease. The Xa39 gene, encoded by the *Os11g0588600*, is considered a key genetic determinant for BLB resistance in rice. This study employed a collection of 475 core Korean rice accessions representing seven distinct ecotypes for dissecting evolutionary aspects of the *XA39* gene. A total of 171 haplotypes with 133 polymorphic sites (24 InDels and 109 SNPs) were identified in the coding region *Xa39*. Hap_1 is the largest haplotype with 206 accessions, including *japonica* (184 accessions), *indica* (5 accessions), and wild (17 accessions). Principal component analysis (PCA) and phylogenetic tree analysis clearly separated wild types and other groups, indicating a unique Xa39 mutation in wild types. Furthermore, FST analysis of the Xa39 gene revealed the highest mean weighted value between japonica and aus ecotypes, while the lowest value was observed between indica and admixture ecotypes. By understanding the genetic variability and haplotype patterns of the Xa39 gene, this study contributes to the development of effective strategies for combatting BLB and safeguarding rice production.

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

[†] These authors contributed equally to this work.

***Corresponding Author:** Tel. +82-41-330-1201, E-mail: yjpark@kongju.ac.kr
Tel. +82-41-330-1213, E-mail: sanghochu76@gmail.com

PE-0110

Identification of QTLs for heading date in rice using a RIL population derived from two *japonica* cultivars

Jeonghwan Seo[1*], So-Myeong Lee[2], Hyun-Su Park[1], Jae-Ryoung Park[1], Songhee Park[1], Kyeong Min Kang[1], Mira Yoon[1], Mina Jin[1], O-Young Jeong[1], Hee-Jong Koh[3]

[1]Crop Breeding Division, National Institute of Crop Science, Rural Development Administration, Wanju, 55365, Republic of Korea
[2]Department of Southern Area Crop Science, National Institute of Crop Science, Rural Development Administration, Miryang, 50424, Republic of Korea
[3]Department of Agriculture, Forestry and Bioresources, Plant Genomics and Breeding Institute, Research Institute for Agriculture and Life Sciences, Seoul National University, Seoul, Korea

Heading date exerts a significant influence on the agronomic performance of rice. In this study, a recombinant inbred line (RIL) population consisting of 94 lines derived from two temperate *japonica* varieties, the high-quality Japanese cultivar Koshihikari and the high-yielding Korean cultivar Samnam, was employed to identify the quantitative trait loci (QTLs) responsible for controlling heading date. The heading dates of the two parental cultivars and the 94 RILs were evaluated at Suwon in 2018 and 2020, as well as at Wanju in 2022. The heading date distribution of the RIL population displayed transgressive characteristics when compared to the two parental lines. Through Target Capture Sequencing, we obtained 427 polymorphic and clear SNP data points, which were utilized to construct a linkage map. The total size of the linkage map across 12 chromosomes was determined to be 1830.3cM, with an average interval of 3.9cM between adjacent markers. Three QTLs associated with heading date were identified on chromosomes 3, 6, and 7. Among these, *qDTH3* exhibited the highest LOD score and phenotypic variation explained (PVE), resulting in an average advancement of heading date by 9 days when the Koshihikari allele was present. In contrast, *qDTH6* and *qDTH7* demonstrated relatively lower LOD scores and PVE, leading to a delay in heading date by approximately 2.5 and 4.8 days, respectively, when the Koshihikari allele was present. Collectively, these three QTLs accounted for over 70% of the phenotypic variation observed across the three years. Notably, all QTLs were identified at the same marker interval and exhibited similar LOD scores, PVE, and additive effects across the three years. The QTLs discovered in this study hold promise for their application in heading date control within breeding programs utilizing *japonica* cultivars.

***Corresponding Author:** Tel. 063-238-5217, E-mail: rightseo@korea.kr

PE-0111

Anti-nutritional factors of soybean [*Glycine max* (L.)]: A review

Yeong-ho Kim, Sungwoo Lee*

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

The soybean [*Glycine max* (L.) Merr.] is worldwide used legume renowned for their high oil and protein content. They serve as the foundational ingredients in various products, including soybean meal and various soy foods. However, anti-nutritional factors (ANFs) in soybean can limit nutrient availability and absorption, also necessitating labor-intensive and time-consuming post-processing treatments like heat treatment, fermentation, soaking, and enzymatic applications. This review presents a comprehensive investigation of four most significant ANFs in soybean; trypsin inhibitors, phytic acid, saponins, and lipoxygenase. This presentation will summarize up-to-date research status of them, including genes associated with each ANF. (*Tia*, *Tib* for trypsin inhibitors; *MIPS*, *IPK1* for phytic acid; *Sg-1*, *Sg-2* and *Sg-3* for saponin; *Lox1*, *Lox2* and *Lox3* for lipoxygenase.) Biosynthesis pathways, and regulation of the ANFs Such comprehensive information will provide a robust foundation for future research on ANFs in soybeanss.

***Corresponding Author:** Tel. +82-42-821-5727, E-mail: sungwoolee@cnu.ac.kr

PE-0112

Phenotypic and genetic analysis of seedling height in a rice RIL Population for Image-Based Phenotyping Development

Jeonghwan Seo*, Hyun-Su Park, Jae-Ryoung Park, Songhee Park, Kyeong Min Kang, Mira Yoon, Mina Jin, O-Young Jeong

Crop Breeding Division, National Institute of Crop Science, Rural Development Administration, Wanju, 55365, Republic of Korea

Image-based phenotyping is an emerging tool in crop breeding that offers valuable insights into plant development. In rice, seedling height plays a crucial role in determining early growth and development. This study aims to collect basic phenotypic and genetic information on rice seedlings to further develop image-based phenotyping techniques during the seedling stage. A recombinant inbred line (RIL) population consisting of 88 lines derived from a cross between JJ625LG and Namchan was used. Seedling height at 15 days after sowing was manually measured for the two parents and 88 RILs. Additionally, seedling images were collected using three cameras for future applications of image-based phenotyping. The average seedling height was 14.0cm for JJ625LG, 13.0cm for Namchan, and 15.5cm for the RILs. The minimum and maximum seedling heights among the RILs were 12.3cm and 18.4cm, respectively. The RIL population exhibited a transgressive and wide distribution compared to the two parents. By utilizing Target Capture Sequencing, we obtained 511 polymorphic and clear SNP data points, which were employed for constructing a linkage map. Three quantitative trait loci (QTLs) associated with seedling height were identified on chromosomes 1 and 3. Among these, *qSH3-2* displayed the highest LOD score, phenotypic variation explained (PVE), and additive effect. The JJ625LG allele on *qSH1* increased seedling height, while the Namchan allele of *qSH3-1* and *qSH3-2* also contributed to increased seedling height. The seedling height data and QTL information obtained in this study will serve as valuable control data for the development of image-based phenotype analysis in future studies.

***Corresponding Author:** Tel. 063-238-5217, E-mail: rightseo@korea.kr

PE-0113

A multiplex panel for marker-assisted backcrossing (MABC) in tomato cultivars and its application

Jin Jeon[1], Su-Ryun Choi[1], Jae-Eun Oh[2], Young Seo Ji[1], Da Young Jeon[2], Da Yeong Son[1], Sung-Hwan Jo[1,2*]

[1]XENOTYPE Inc., 118 Jungang-ro, Jung-gu, Daejeon, 34912, Republic of Korea
[2]Seeders Inc., 118 Jungang-ro, Jung-gu, Daejeon, 34912, Republic of Korea

Marker-assisted backcrossing (MABC) is a breeding strategy that combines traditional backcrossing with the use of genetic markers to improve specific traits in crops. Conventional backcrossing requires at least 6-7 generations to recover the genomic background of the recurrent parent, while MABC represents several advantages over conventional backcrossing, including increased efficiency, accuracy, and precision in trait selection. To facilitate MABC in tomato, we developed a multiplex panel using tag-single nucleotide polymorphisms (tag-SNP). In this study, we selected a total of 313 tag-SNPs evenly distributed on each chromosome and primers were designed for high throughput multiplex panel. This marker set was tested for its polymorphism in each pairwise cross combination constructed with 124 of the 234 tomato accessions, and a relatively high number of SNP markers polymorphic for the cross combination was observed. The reliability of the MABC SNP set was assessed by converting 18 SNPs into Luna probe-based high-resolution melting (HRM) markers and genotyping nine tomato accessions. The results show that the SNP information and HRM marker genotype matched in 98.6% of the experiment data points, indicating that our sequence analysis pipeline for SNP mining worked successfully. We have also developed a genome graphic viewer for MAB (Marker-Assisted Breeding) applications in intergeneric hybridization of tomatoes. These results suggest that the SNP multiplex panel developed in this study will be valuable for MABC, cultivar identification, and comparative genome analysis in tomatoes.

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***Corresponding Author:** Tel. 010-6417-0614, E-mail: shjo@seeders.co.kr

PE-0114

Development of genome-edited Korean wheat variety through the application of *in planta* bombardment

Geon Hee Lee, Tae Kyeom Kim, Jae Yoon Kim*

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

The genome editing technology using CRISPR/Cas9 has been applied to various major crops because of the convenience of inducing editing to the desired target DNA in a simple way. The *in planta* bombardment (iPB) technique, recently developed by Japanese researchers, was successfully applied to wheat genome editing, bypassing tissue culture. The iPB technology made gene editing technology, which was only applicable to a limited number of wheat varieties with good tissue culture response, possible in a wide range of wheat varieties. To briefly summarize the application process of the iPB method, after exposing the shoot apical meristem (SAM) region of mature embryos, particle bombardment was performed targeting the L2 cell layer and growth into regular plants. Genome editing was confirmed by the high-resolution melting (HRM) analysis using gDNA extracted from the flag leaf of each tiller and leaves of T_1 plants. As a result of HRM analysis in T_1 plants, three melting curve patterns different from the wild type were detected in five plants. This study can be applied to CRISPR/Cas9 gene editing of Korean wheat varieties, bypassing tissue culture.

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

PE-0115

Guide sequence validation for CRISPR/Cas9 gene editing in wheat protoplasts

Deok Ryong Koo, Tae Kyeom Kim, Jae Yoon Kim*

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

Wheat accounts for the second-largest portion of global grain production after corn. Transformant construction using protoplasts requires less sample preparation time than tissue culture-based plant transformation. Therefore, the gRNAs efficiency can be rapidly tested in large quantities via protoplast transformation. This experiment was conducted to confirm the efficiency of guide sequences for CRISPR/Cas9 gene editing in wheat protoplasts. Protoplasts were isolated using 1% cellulose + 0.25% macerozyme solution from the first leaf of “Chinese spring”. Three gRNAs were designed by targeting genes(TraesCS5A02G193700.1) related to pre-harvest sprouting resistance. Protoplasts were transformed with Lipofectamine + PEG-mediated method and transferred to regeneration medium. After two days of culture, gDNA was extracted from the transformed protoplast and HRM was performed to confirm gene editing. For each gRNA, peaks different from the wild type appeared. With this, we can confirm that protoplast gene editing has occurred through gRNA and Cas9.

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

PE-0116

Identification of Genes associated with resistance to Aflatoxin B_1 Accumulation in Peanut (*Arachis hypogaea* L.) via a genome-wide association study

Seungah Han[1], Byeong-Cheol Kim[2], Kunyan Zou[1], Min-Jae Choi[1], Jungmin Ha[2], Tae-Hwan Jun[1*]

[1]Department of Plant Bioscience, Pusan National University, Miryang-si, Gyeongsangnam-do 50463, Republic of Korea

[2]Department of Plant Bioscience, Gangenung-Wonju National University, Gangeung 25457, Korea

Since 1960, when it was identified as "Turkey X Disease" in the UK, Aflatoxin (AF) has been the subject of research. As a member of the group I, the International Agency for Research on Cancer (IARC) of the World Health Organization (WHO) has classified AFB_1 as having the highest hepatocellular carcinoma-causing toxicity. This study used 223 peanut accessions harvested in 2021 and 2022 to evaluate aflatoxin resistance and identify resistance genes related to aflatoxin accumulation. The quantitative analysis of aflatoxin B_1 content in peanut accessions inoculated with *Aspergillus flavus*, which primarily produces aflatoxin B_1 and B_2, was performed using UPLC-PDA in accordance with the protocol of the Korean Food Standards Codex. A genome-wide association study (GWAS) was conducted using the peanut 58K Axiom_Arachis array chip to identify the genes associated with aflatoxin B_1 content in 223 peanut accessions. Using FarmCPU model of the GAPIT package, two putative SNPs were identified on chromosomes Araip.B04 and Araip.B09 that were significantly associated with Aflatoxin B_1 levels. Based on the reference genome, sixty-eight annotated genes flanked by significant SNPs were identified within an estimated ±250 kb window. Two candidate genes encoding pathogenesis-related thaumatin protein from the PR-5 (Pathogenesis-Related-5) protein family and a leucine-rich repeat receptor-like kinase (LRR-RLK) for disease resistance indicating apoptosis and immune responses may be involved in the peanut response to aflatoxin production. To develop resistant varieties, it is anticipated that the outcomes of this study will be useful for evaluating aflatoxin B_1 resistance and identifying genomic regions associated with aflatoxin B_1 contents.

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

PE-0117

The rate of stem maturation affects gravity sensing time and the plant architecture in Solanaceae species

Jun-Woo Lee[1], Seung Han Son[2], Jung Heo[1], Soon Ju Park[1,2*]

[1]Division of Applied Life Science, and Plant Molecular Biology and Biotechnology Research Center (PMBBRC), Gyeongsang National University, Jinju 52828, Republic of Korea
[2]Division of Biological Sciences, Wonkwang University, Iksan 54538, Republic of Korea

In plant developmental stages, there are crucial time points to react to the gravity vector. Sensing and response to gravity in plants have evolved differently among species and tissues. In Solanaceae, shoot architecture has been remarkably diverged, developing sympodial (inflorescence) shoot carrying single flower to both sympodial shoot and inflorescence-producing compound flowers. To understand this divergence, we hypothesize that sympodial growths were differently decided by maturation status and potential response of lateral meristem to gravity after a floral transition of the central meristem. Here, we show that tomato inflorescence could be shifted to sympodial shoot growth in mutants having inflorescence meristems in the delayed maturation state at the molecular level. Tomato inflorescence grows horizontally. However, *mc sp* double and *s* single mutant developed inflorescence growing up-right direction, which is similar to that of *S. peruvianum*. Erect type and inflorescences reverted to the vegetative state were developed in *sft*, *mc*, and *j* background. Moreover, *sft*, *j* double produced only sympodial shoots carrying a single flower, which is similar to the sympodial shoot of *N. benthamiana*. Interestingly, the molecular state of inflorescence meristems indicated delayed maturation of the meristems in *s* mutant and *sft* mutant. Therefore, we suggest that sympodial shoot meristem and sympodial inflorescence meristem might have evolved by the difference in maturation state and activity of response to gravity on each young stem in Solanaceae.

***Corresponding Author:** E-mail: ljw5451@gnu.ac.kr

PF-0001

Development of Polymorphic Microsatellite Markers for Genetic Diversity Analysis in the genus *Polygonatum* spp.

Sebastin Raveendar, HyeRan Shin, Jong-Wook Chung*

Department of Industrial Plant Science and Technology, Chungbuk National University, Cheongju 28644, Republic of Korea

Polygonatum is an important genus with many medicinal and edible plants. There are about 60 species in the genus that are widely distributed in the boreal zones of the northern hemisphere and with about 50 species, East Asia is the diversification center of this genus. The genetic diversity of *Polygonatum* germplasm resources has been assessed by using three *Polygonatum* species, which includes cultivar varieties and landraces. We have used 100 pairs of SSRs primers and selected 54 polymorphic SSRs markers. The results showed that the number of alleles (N_A) ranged from 2 to 11, with a mean alleles number of 5.2. The major allele frequency (M_{AF}) ranged from 0.15 to 0.80, observed heterozygosity (Ho) ranged from 0 to 0.80, and the polymorphic information content (PIC) ranged from 0.27 to 0.89. The unweighted pair group mean algorithm (UPGMA) dendrograms with all 54 SSR markers revealed that three groups among the *Polygonatum* populations. Furthermore, minimum markers set (combination of 6 markers) combinations was identified and proved to be useful for variety identification. Therefore, the six SSR markers as a core set will be a valuable tool for several applications, including cultivar identification and seed purity tests in *Polygonatum* populations. The SSR markers developed will contribute to applications such as varietal identification, genetic diversity analysis, and population structure analysis of *Polygonatum* germplasm.

***Corresponding Author:** Tel. 043-261-2518, E-mail: jwchung73@chungbuk.ac.kr

PF-0002

Development of SSR marker for genetic diversity and variety discrimination in *Fallopia multiflora*

Sebastin Raveendar, HyeRan Shin, Jong-Wook Chung*

Department of Industrial Plant Science and Technology, Chungbuk National University, Cheongju 28644, Republic of Korea

Fallopia multiflora, as a perennial herb in the *Polygonaceae* family belonging to the genus *Fallopia* Adanson, is used as traditional Chinese herbal medicine. However, there is still confusion about the botanical origin of the herbal and the phylogenetic relationship between the cultivars and the wild relatives. To develop an efficient method for identification, a molecular analysis was performed based on SSRs markers. The genetic diversity of *F. multiflora* germplasm resources has been assessed by using 10 locally collected accessions, which includes cultivar varieties and landraces. We have screened 100 pairs of SSRs primers and selected 71 successfully amplified SSR markers, in which one SSR found to be monomorphic marker. The results showed that the number of alleles (N_A) ranged from 2 to 10, with a mean alleles number of 4.1. The major allele frequency (M_{AF}) ranged from 0.20 to 0.90, observed heterozygosity (Ho) ranged from 0 to 0.80, and the polymorphic information content (PIC) ranged from 0.16 to 0.86. The unweighted pair group mean algorithm (UPGMA) dendrograms with all 70 SSRs markers revealed that three clusters among the *F. multiflora* accessions. Furthermore, minimum markers set (combination of 7 markers) combinations was identified and proved to be useful for variety identification. Therefore, the SSR markers set will be a valuable tool for several applications, including cultivar identification and seed purity tests in the *F. multiflora* populations. Levels of genetic differentiation among the three groups were close to that between different accessions within the species. Thus, the three genetic groups of *F. multiflora* should be considered as independent units for conservation and breeding management of the species.

***Corresponding Author:** Tel. 043-261-2518, E-mail: jwchung73@chungbuk.ac.kr

PF-0003

Identify volatile compounds contained in three different types of *Perilla* crop leaves collected from South Korea

So Jung Jang[1,2], Kyu Jin Sa[1], Sookyeong Lee[3], Hyeon Park[1,2], Jungeun Cho[1,2], Jungsook Sung[3], Ju Kyong Lee[1,2*]

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

[2]Interdisciplinary Program in Smart Agriculture, Kangwon National University, Chuncheon 24341, Korea

[3]National Agrobiodiversity Center, National Institute of Agricultural Sciences, RDA, Jeonju 54874, South Korea

To develop new *Perilla* varieties with high levels of useful volatile compounds for health, it is essential to conduct research on the content and composition of the volatile compounds in breeding materials. Therefore, this study was performed to identify and profile the volatile compounds present in three different types of *Perilla* leaves collected from South Korea. Volatile compounds were analyzed by gas-chromatograph-mass spectrometry. In total, 41 volatile compounds were identified belonging to 10 chemical classes (six alcohols, seven aldehydes, two benzodioxoles, two esters, three ethers, four ketones, five monoterpenes, one phenylpropanoid, eight sesquiterpenes, and three terpenes). In cultivated var. *frutescens* (CF), weedy var. *frutescens* (WF), and weedy var. *crispa* (WC), a total of 34, 39, and 41 volatile compounds, respectively, were identified. The predominant compound in CF and WF was perilla ketone (PK; 87.2% and 64.5%, respectively) and in WC was perilla aldehyde (PA; 26.4%). There were 29 and 27 volatile compounds that showed significant differences of content between WC and CF or WF, respectively. In terms of chemotype based on the volatile compounds, CF and WC were PK type and PA or phenylpropanoid (PP) types, respectively. WF accessions, which were PK and PP types in chemical composition, showed intermediate characteristics in the composition of volatile compounds compared with CF and WC. The results obtained in this study identified successfully the composition and content of volatile compounds in *Perilla* crop in South Korea. These results will provide useful information for industries and research related to *Perilla* crop.

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

PF-0004

Comparative Analysis of Chemical Compounds for Bio-based plastic in Kenaf (*Hibiscus cannabinus* L.) Mutant Cultivars

Jaihyunk Ryu, Woon Ji Kim, Baul Yang, Ye-Jin Lee, Sang Hoon Kim, Seung Hyeon Lee, Jae Hoon Kim, Joon-Woo Ahn*

Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongup, Jeonbuk 56212, Korea

Kenaf is one of the most important industrial crops, and their fiber and biomass have been used for new biodegradable plastic production. Terpenes, ketones, acetate and esters are molecules of natural origin whose multifunctional nature renders them into great candidates to be used as bio-plastics and packaging films. We investigated the chemical compound compositions of three mutant cultivars and their original cultivars. Three kenaf mutant genotypes were developed by treatment with 300 Gy of ^{60}Co gamma irradiation. Chemical compounds from the bark and leaf of the kenaf genotypes were analyzed by gas chromatography-mass spectrometry. The terpene (21.7 to 35.3%), fatty acid ester (30.6 to 55.5%), ketone (5.8 to 14.0%) and aliphatic alcohol (0.6 to 6.8%) compounds were abundant categories in all kenaf leaves. Fatty acid ester (63.6 to 81.4%), terpene (8.6 to 24.9%), aliphatic acetate (7.8 to 9.6%) and ketone (1.0 to 1.9%) were major categories in all kenaf bark. Wandae mutant cultivar showed higher terpene and acetate composition in the bark than other cultivars. Jeokong mutant cultivar had highest fatty acid ester composition in all parts. These findings will be useful for the selection of kenaf cultivars with improving bioplastics manufacturing efficiency.

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***Corresponding Author:** Tel. 063-570-3314, E-mail: joon@kaeri.re.kr

PF-0005

Genome-wide association study of agronomic traits in kenaf (*Hibiscus cannabinus* L.)

Woon Ji Kim[1], Baul Yang[1,2], Ye-Jin Lee[1,2], Sang Hoon Kim[1], Jin-Baek Kim[1], Joon-Woo Ahn[1], Jaihyunk Ryu[1*]

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

[2]Department of Plant Production Sciences, Graduate School, Sunchon National University, Suncheon 57922, Republic of Korea

A species in the Malvaceae family, kenaf (*Hibiscus cannabinus* L.) is one of the third largest fiber crop after cotton and jute. Kenaf fiber is highly valuable as a breeding material because it can be used as a raw material in a variety of industries, including wood, pulp, and plastic materials. Mutagenesis is gaining traction in crop breeding as an alternative to the limitations of conventional breeding and the controversial food and environmental risks of transgenic organisms. In this study, we conducted a genome-wide association study (GWAS) analysis of agronomic traits using total 96 kenaf genetic resources and varieties developed by irradiation. Genotypes were assigned by the genotyping-by-sequencing, and GWAS analysis for flower color (FC), stem color (SC), and bloom date (BD) were performed using a mixed linear model. GWAS identified 14 SNPs linked to FC, 10 SNPs to SC, and 2 SNPs to BD at thresholds $-\log_{10}(P) = 3$. 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 kenaf breeding.

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***Corresponding Author:** Tel. 063-570-3311, E-mail: jhryu@kaeri.re.kr

PF-0006

A Sesame variety ‘SuperHani’ with non-shattering capsule and high lignan content

Sung-Up Kim*, Jeongeun Lee, Min Young Kim, Eunyoung Oh, Jung In Kim, Sang Woo Kim, Eunsoo Lee, Kwang-Soo Cho, Myoung Hee Lee, Choon-song Kim

Upland Crop Breeding Research Division, Department of Southern Area Crop Science, National Institute of Crop Science, RDA, Miryang, Gyeongnam, 50424, Republic of Korea

Sesame(*Sesamum indicum* L.) is cultivated worldwide, mainly in Asia and Africa. However, sesame is harvested manually due to the seed shattering at maturity in most countries. Non-shattering capsule is the most important trait for harvesting sesame by machinery combine. A sesame variety ‘SuperHani’(*Sesamum indicum* L.) with non-dehiscent capsule and high lignan content was developed in 2022. It was crossed between ‘Suwon 195’ and ‘YCS71’ in 2016. After acceleration of generation in the greenhouse up to F_4 and analyzed lignan content in the F_6 in 2018. It has many branch and triple capsule per node and white seed coat color. And maturing date of it is 18 August. Its height is 155cm and capsule number of it is 117. Especially it showed non-shattering capsule trait. And the yield of it was about 1.20ton per hectare, 10% lower than ‘Goenbaek’. It showed crude fat content with 53.0% and crude protein content with 25.3% and lignan content with 14.8mg/g 3.4 times higher than Goenbaek.

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

PF-0007

Comparison of Growth Characteristics according to Branch Number, Flower Color, Spinous Phyllary, and Days to Flowering of Safflower Genetic Resources

Young Min Choi[1*], Jeong Seop Mun[1], Dong Chun Cheong[2], Hee Kyung Song[1], Seung Yoon Lee[1], Jin Jae Lee[1], So Ra Choi[1], Eun Ae Yoo[3]

[1]Medicinal Resource Research Institute, Jeollabuk-do Agricultural Research & Extension Services, Namwon 55720, Republic of Korea
[2]Horticulture Division, Jeollabuk-do Agricultural Research & Extension Services, Iksan 54591, Republic of Korea
[3]National Agrobiodiversity Center, NIAS, RDA, Jeonju 54874, Republic of Korea

This study was conducted to compare the growth characteristics according to the branch number, flower color, spinous phyllary, and days to flowering of safflower 852 genetic resources (*Carthamus tinctorius*). In statistical analysis, coded numbers were used for the branch number, plant length, flower color, spinous phyllary, leaf margins, and leaf length, leaf width, and 100 seed weight were measured. In addition, the number of days required for each growth stage was calculated after observing the flowering, ripening, and harvesting periods of genetic resources. Resources with more than 5 branches had shorter days to flowering than those with less than 5 branches, but the days from flowering to ripening and harvesting were longer. When classified based on flower color (yellow, purple, red, white, etc.), purple flower resources tended no spine of phyllary. Red flower resources had shorter days from sowing to ripening and harvest stage than yellow, red, and white flower resources. When classified based on spine of phyllary (without spines, less than 2 mm, more than 2 mm), those with short or no spines tended to have rounded leaf margins, and although the days to flowering were longer, statistically significant there was no difference. There was no difference in the qualitative characteristics of the number of days from sowing to flowering (less than 80, from 80 to 89, and more than 90 days), but the shorter days to flowering, ripening and harvesting tended to be. The classified growth characteristics are expected to provide information to improve the breeding efficiency of safflower.

***Corresponding Author:** Tel. 063-290-6304, E-mail: cym9288@korea.kr

PF-0008

Comparison of Growth Characteristics according to Utilization Method of Safflower Genetic Resources

Young Min Choi[1*], Jeong Seop Mun[1], Dong Chun Cheong[2], Hee Kyung Song[1], Seung Yoon Lee[1], Jin Jae Lee[1], So Ra Choi[1], Eun Ae Yoo[3]

[1]Medicinal Resource Research Institute, Jeollabuk-do Agricultural Research & Extension Services, Namwon 55720, Republic of Korea

[2]Horticulture Division, Jeollabuk-do Agricultural Research & Extension Services, Iksan 54591, Republic of Korea

[3]National Agrobiodiversity Center, NIAS, RDA, Jeonju 54874, Republic of Korea

This study was conducted to compare the growth characteristics after classifying 850 safflower resources (*Carthamus tinctorius*) according to the utilization method. The utilization method is classified as follows: 1) vegetable (more than 400 kg of vegetable yield per 1,000 m^{-2}), 2) landscape (phyllary without spines, plant length less than 100 cm, and flower color change type), and 3) resources for seed production (more than 6 g in 100 seeds weight). In statistical analysis, coded numbers were used for the branch number, plant length, flower color, spinous phyllary, and leaf margins, leaf length, width, and 100 seed weight were measured. In addition, the number of days required for each growth stage was calculated after observing the flowering, ripening, and harvesting period of genetic resource. The yield per 1,000 m^{-2} of vegetable resources was 455.4±34.4 kg. Among the growth characteristics, spinous phyllary of vegetable resources was less than 2 mm, and the landscape resources was spineless. The 100 seeds weight of seed production resources was 6.7±0.7 g, which was about 2.2 g heavier than the average of 850 genetic resources (4.5±1.4 g). Among the differences in growth period, the days to flowering were 2.3 to 8.3 days shorter in seed production resources (78.8±8.6) than in the average of all resources (85.4±8.9), vegetable (81.1±8.1), and landscape (87.1±7.9) resources. Additionally, there was no statistical difference in the number of days from sowing to ripening and harvesting.

***Corresponding Author:** Tel. 063-296-6304, E-mail: cym9288@korea.kr

PF-0009

Development of Doubled Haploid Lines using Shed-Microspore Culture in *Platycodon grandiflorum*

Woo Seok Ahn, Tae Il Kim, Mok Hur, Jang Hoon Kim, Sung Cheol Koo, Woo Tae Park, Youn-Ho Moon, Yun Chan Huh*

Department of Herbal Crop Research, NIHHS, RDA, Eumseong 27709, Republic of Korea

The production of haploid plants through anther or microspore culture enables the development of homozygous lines followed by chromosome doubling in a relatively shorter period compared to the production of inbred lines through traditional method involving repeated selfing. Therefore, this study aimed to develop homozygous doubled haploid (DH) through shed-microspore culture in *P. grandiflorum.* We utilized a shed-microspore culture protocol developed by Supena et al. (2005). Previous reseach has shown that microspore embryogenesis can be influenced by the bellflower genotype, type of medium, bud size, and microspore developmental stage. Haploids were induced approximately 70 days after culture initiation in the shed-microspore culture, resulting in the induction of 89 haploids in 2021. Flow cytometry analysis of the microspore-derived plants revealed that a low percentage (10~15%) of the plants underwent spontaneous diploidization during the in vitro culture, although this varied depending on the cultivar. To obtain DH plants, haploids were subjected to chromosome doubling treatment using oryzalin. As a result, we obtained 46 haploid lines and 43 DH lines, which were subsequently cultivated in the greenhouse. Seeds from 39 DH lines were harvested in 2021. Haploid plant of bellflower generally exhibit poor growth, with smaller leaves, flowers, and root lengths compared to DH plants. we evaluated the horticultural characteristics of these 39 DH lines. The root fresh weight of the tested DH lines ranged from 6.6 to 213.3 g per plant, while the root length varied from 15.3 to 27.0 cm. Some DH lines exhibited reduced fertility and a decreased seed number compared to the original diploid cultivars. Future breeding programs will focus on the development of excellent cultivars by utilizing DH lines with desirable traits, such as high yields and highly useful ingredients.

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***Corresponding Author:** Tel. 043-871-5662, E-mail: wmelon@korea.kr

PF-0010

Developing elite line of ‘Eumseong14ho’ showing tolerance for Alternaria blight in Korean ginseng

Jang Uk Kim*, Jung Woo Lee, Na Young Kwon, Sung Min Jung, Sung Woo Lee

National Institute of Horticultural & Herbal Science(NIHHS), RDA, Eumseong 27709, Korea

Alternaria blight(AB) is the most common disease occurring in ginseng cultivation, causing significant damage primarily on stems and leaves due to the pathogen *Alternaria panax.* Therefore, the development of ginseng cultivars resistant to AB and high-yielding is essential for stable production of ginseng.

A new ginseng elite line ‘Eumseong14ho(ES14)’ with AB tolerance was developed in the NIHHS. In 1999, genetically diverse plant materials exhibiting excellent growth and resistance to diseases were collected from farms. These collected plant materials were multiplied and harvested for seeds in 2003. In 2004, mature leaves of one-year-old plant materials were selected, and they were inoculated with *Alternaria panax* at a concentration of 1.0×10^6 spores/ml. The plants were maintained at a relative humidity of 100% and a temperature of 25℃ for 72 hours to induce the occurrence of AB. From this screening, G04076-9, exhibiting a high level of tolerance, was selected. Physiological investigation and propagation were conducted from 2006 to 2009. It was given the name ES14 through the observed yield trial from 2010 to 2014 and local adaptability was carried out from 2015 to 2021.

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***Corresponding Author:** Tel. 043-871-5617, E-mail: k2korea@korea.kr

PF-0011

A Peanut Variety, 'K-Ol 2' with High Oleic Acid and Oil Content

Eunyoung Oh*, Sungup Kim, Jung In Kim, Min Young Kim, Sang Woo Kim, Jeongeun Lee, Eunsoo Lee, Rizwana Begum Syed Nabi, Kwang-Soo Cho, Myoung-Hee Lee

Upland Crop Breeding Research Division, Department of Southern Area Crop Science, National Institute of Crop Science, RDA, Miryang, Gyeongnam, 50424, Republic of Korea

'K-Ol 2' is a new peanut (*Arachis hypogaea* L.) variety that has high oil content and high-oleic acid composition. This variety has developed to improve low productivity of 'K-Ol', which has released in 2013, yet keeping the high properties for the processing and oil stability of seed. 'K-Ol 2' was developed at the Department of Southern Area Crop Science in Miryang, NICS, and approved to be released in 2022. This variety was developed by pedigree method from the single cross between short-stem variety 'Jaseon' and high-oleic elite line 'YG377'. From the regional adaptation trial at four locations in three years (2020-2022), 'K-Ol 2' showed 29 cm and 36 cm in the main stem and branch length, respectively, which were 28% and 26% shorter than a check variety 'Ahkwang'. This comparably shorter length showed the higher tolerance to lodging in mature stage. The 100-seed weight of 'K-Ol 2' was 87 g and the seed contained 54.5% of oil content and 82.8% of oleic acid composition. The average seed yield of 'K-Ol 2' was 4.6 MT · ha^{-1}, which was 10% higher than a check variety. It also showed higher resistance to web-blotch disease compared to the reference at the trials.

***Corresponding Author:** Tel. 055-350-1232, E-mail: lavondy10@korea.kr

PF-0012

Variation in Germination during the Acceleration of Breeding Cycle in Peanut (*Arachis hypogaea* L.)

Eunyoung Oh*, Sungup Kim, Jung In Kim, Min Young Kim, Sang Woo Kim, Jeongeun Lee, Eunsoo Lee, Rizwana Begum Syed Nabi, Kwang-Soo Cho, Myoung-Hee Lee

Upland Crop Breeding Research Division, Department of Southern Area Crop Science, National Institute of Crop Science, RDA, Miryang, Gyeongnam, 50424, Republic of Korea

For reducing the breeding cycle in peanut, we checked the germination properties from 10 peanut varieties which were harvested in indoor environment and grown in minimized plant cycle. The sample were grown on Φ15 pot filled with horticulture soil, and kept on 26 ℃±2 and 14/10 hours of light/dark cycle, and all plant were harvested 85 days after sowing regardless of maturity. Among 10 varieties, flowering day varied from 29 to 32 days after sowing, and number of harvested pods per plant varied from 3 to 39. On the germination test, we classified seeds into four maturity grades after shelling the dried pods, and germinated them in 28℃ incubator. Most of variety except 'Da-an', showed positive correlation between seed maturity and average germination ratio. Ratio of seed decay was highest in the least matured seed group (No.4) showing 66% of seed decayed during germination on average. In contrast, the two highly matured seed groups (No.1 and 2) which were closed to the well-matured seed, showed no decayed seed during germination in all tested groups. We obtained normally germinating seeds from the cultivation in short period (85 days after sowing) which is 35 to 65 days reduced than cycle (120-150 days) in field. However, some varieties failed to germinate although seeds were fully matured. We need further investigation of additional treatment for breaking the dormancy, and detailed adjustment of light and temperature for minimizing the flowering days.

***Corresponding Author:** Tel. 055-350-1232, E-mail: lavondy10@korea.kr

PF-0013

Effect of harvesting time on the fresh weight and components of triticale (× *Triticosecale* Wittmack)

Jisuk Kim*, Keunha Kim, Kyungyoon Ra, Myoung Ryoul Park, Mi Jung Kim

Central Area Crop Breeding Division, Department of Central Area Crop Science, National Institute of Crop Science, Rural Development Administration, Suwon, 16429, Republic of Korea

Triticale is an anthropogenic hybrid crop with high yield and functionality as a livestock feed. However, few studies have been conducted to analyze variation of components in triticale harvested at different growth stages. This study was aimed to investigate the differences in yield and functionality composition in triticale haylage. Triticale haylage which was contained about 60% moisture were harvested at five growth stages: seedling stage (SS), booting stage (BS), heading stage (HS), 10 days after heading (10 DAH), and 20 days after heading (20 DAH). The triticale were measured the fresh weights by harvesting stages, and analyzed contents of mineral and octacosanol in each haylage. The fresh weight of triticale by growth stages, SS, BS, HS, 10 DAH, and 20 DAH, were 50.8, 148.2, 167.8, 190.6, and 265.4 kg/10a, respectively, meaningful that were increased towards the latter stages. The range of Mg, Mn, and Zn in the haylage were 3.83-3.33 mg/L, 0.67-0.60 mg/L, and 0.33-0.18 mg/L, respectively. The potassium contents were decreased from 31.03 to 2.57 mg/mL as the triticale was grown up. The contents of octacosanol showed a range of from 0.28 to 0.09 mg/ml with the tendency for a decrease as the harvesting time was delayed ($p < 0.05$). These results demonstrated that contents of mineral and octacosanol were decreased towards the latter stages, although the fresh weight was showed an increasing tendency.

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***Corresponding Author:** Tel. 031-695-4054, E-mail: jisuk105@korea.kr

PF-0014

Anaerobic Fermentation Quality of Triticale (x Triticosecale Wittmack) Haylage

Jisuk Kim*, Keunha Kim, Kyungyoon Ra, Myoung Ryoul Park, Mi Jung Kim

Central Area Crop Breeding Division, Department of Central Area Crop Science, National Institute of Crop Science, Rural Development Administration, Suwon, 16429, Republic of Korea

Triticale as livestock feed has the advantage for fermentation due to the high proportion of plant leaves. A fermented feed has the potential to produce metabolites and organic acid to be used for animal nutrition, converting into nutraceutical sources. This study was aimed to investigate the composition of lactic acid bacteria in triticale haylage fermented under anaerobic condition. Triticale were harvested at five growth stages (SS; seedling stage, BS; booting stage, HS; heading stage, 10 DAH; 10 days after heading, 20 DAH; 20 days after heading), and then fermented for 40 days under room temperature. The fermentation quality was analyzed based on pH and microbial composition. The pH value was decreased from 6.6 to 5.7 as the triticale was grown up, while the microbial composition value increased from 5.89 to 7.85 log CFU/ml ($P < 0.05$). Using the 16S rRNA gene sequence of lactic acid bacteria in each haylage, it was determined that the DSM 36 isolate identified from the SS haylage had 98.54% similarity with *Paeibacillus polymyxa*, the NBRC 15891 from the BS and HS had 100% similarity with *Lactobacillus Plantarum*, and the ATCC14869 from the 10 and 20 DAH had 99.7% similarity with *Lactobacillus brevis.* These results demonstrated that the pH and microbial composition which affected to fermentation quality of the triticale haylage were varied depending on the growth stages.

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***Corresponding Author:** Tel. 031-695-4054, E-mail: jisuk105@korea.kr

PF-0015

Mass propagation of ginseng by temperature-treated somatic embryo

Nayeong Kwon*, Jung Woo Lee, Sung Min Jung, Jang Uk Kim, Ick Hyun Jo, Sung Woo Lee, Dong Hwi Kim

Department of Herbal Crop Research, NIHHS, RDA, 92 Bisan-ro, Eumseong, Chung-cheong bukdo, 27709, Republic of Korea

Ginseng (*Panax ginseng* C. A. Meyer) is valuable medicinal plant. However, due to the juvenile period and low seed production, it takes a long time to harvest seeds and propagation efficiency is very low. It is obstacle to distribution of new cultivars. Thus development of tissue culture technology is important for mass propagation of ginseng. For somatic embryogenesis, zygotic embryos dissected from seed were excised aseptically and placed on Murashige and Skoog(MS) medium including 5% sucrose. During induction of somatic embryos(SE), temperature were treated with 10℃, 18℃, 23℃(control), 28℃ respectively. After SE induction, the rate of SE formation, the number of SE formed, and the embryo forming capacity(EFC) were investigated. EFC was multiplied by the SE formation rate and the number of SE formed and then divided by 100. Shoots were generated from matured SE in 1/2 MS medium containing 10 mgL^{-1} gibberellic acid. As a result, SE were not produced at 10℃. There was no significant difference in the number of SE and EFC by temperature. As inducing shoots from temperature-treated SE, in 18℃ treatment, the number of shoots was the highest and increased by 40% compared to the control. The number of shoots in 28℃ treatment was similar to that of the control.

Therefore, SE induction of ginseng is possible at 18℃ to 28℃, and the number of shoots could changed depending on the SE induction temperature

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***Corresponding Author:** Tel. 043-871-5611, E-mail: skdud1699@korea.kr

PF-0016

Functional Components and Antioxidant Activities of Perilla Leaf Genetic Resource

Yeon Ju An*, Min Young Kim, Sungup Kim, Jung In Kim, Eunyoung Oh, Jeongeun Lee, Sang Woo Kim, Eunsoo Lee, Kwang-Soo Cho, Myoung Hee Lee, Choon-Song Kim

Upland Crop Breeding Research Division, Department of Sourthern Area Crop Science, National Institute of Crop Science, RDA, Miryang, Gyeongnam, 50424, Republic of Korea

The objective of this study was to investigate the distribution of functional compounds in the perilla leaves of various genetic resource, as well as their antioxidant activities. A comprehensive analysis of functional compounds was conducted on 100 genetic resources, focusing on total polyphenol content(TPC), total flavonoid content(TFC), individual phenolic content(IPC), and lutein. And then, their antioxidant activities analyzed radical scavenging capacity using ABTS and DPPH. The TPC content exhibited a range of 13.19 to 35.85 mg gallic acid equivalent/g, whereas the TFC content varied from 11.74 mg catechin equivalent/g. The individual phenolic profile revealed the presence of four pehnolics - caffeic acid, rosmarinic acid, apigenin, and luteolin comprising the standard using UHPLC (STD; 280 nm). Total IPC revealed a range of 6310.98 to 40491.82 μg/g, with lutein detected at levels between 70.97 and 597.97 μg/g. ABTS and DPPH radical scavenging activities of perilla leaves ranged from 30.39 to 58.58 mg trolox equivalent(TE)/g and from 7.74 to 46.56 TE/g, respectively. Furthermore, the correlation analysis demonstrated that phenolic acids, rosmarinic acid, exhibited a significantly positive correlation with antioxidant activity when compared to luteolin, which is a type of flavone. These findings suggest that the various genetic resource of perilla leaves could effectively mediate antioxidant capacity and provide valuable information for use of perilla leaves in Korea as functional food materials.

***Corresponding Author:** Tel. 055-350-1239, E-mail: ayj3043@korea.kr

PF-0017

Comparison of Morphological Characteristics of Major Domestic Wild Vegetable Cultivation Resources (*Ligularia stenocephala*, *Ligularia fischeri*, and *Aster scaber*)

Seung Yoon Lee[1*], Dong Chun Cheong[2], Young Min Choi[1], Hee Kyung Song[1], Jin Jae Lee[1], So Ra Choi[1]

[1]Medicinal Resource Research Institute, Jeollabuk-do Agricultural Research & Extension Services, Namwon 55720, Korea

[2]Horticulture Division, Jeollabuk-do Agricultural Research & Extension Services, Iksan 54591, Korea

This study was conducted to evaluate the excellence among native resources through the collection of genetic resources and characteristic investigation of wild vegetables and to use it as basic data for rasing varieties. Genetic resources of wild vegetables were assembled, and the external morphological and flowering characteristics were investigated for three resources of *Ligularia stenocephala* (native resources of Hoengseong, Gyeongju, and Namwon regions), six resources of *Ligularia fischeri* (native resources of Jiri Mountain, Handaeri, Taebaek, Jeju, 'Dumehyang', and 'Jamani') and four resources of *Aster scaber* (native resources of Namwon, Wanju, Jinan, and Jangsu regions). In comparison three resources of *Ligularia stenocephala*, Namwon resources were characterized by a large leaf area, an individual tillering conformation and leaf emergence in the center. Hoengseong and Gyeongju resources were characterized by a pile of tillering conformation. Leaves of *Ligularia stenocephala* (3 resources) had a cardiac polar shape and a V-shaped flexure. The leaf stalk did not have hair and grooves and the leaf margin was in the form of an acute serrate. The number of ray flower ranged from 2 to 5. *Ligularia fischeri* (6 resources) were characterized by an individual tillering conformation and leaf emergence in the center. In comparison the six resources of *Ligularia fischeri*, most of the leaves had a heart-shaped and U-shaped flexure. The leaf stalk had hair and grooves and the leaf margin was in the form of an dentate. The number of ray flower ranged from 7 to 10. In comparison four resources of *Aster scaber*, the leaf shape was divided into heart shape and ovalness. The leaf apex was acuminate and the leaf base shape was some differences among native resources. The flowering time of *Aster scaber* was in mid-July and the number of ray flower ranged from 6 to 11. These results can be used as basic data for rasing varieties on future research.

***Corresponding Author:** Tel. 063-290-6306, E-mail: yoona921@korea.kr

PF-0018

CRISPR/Cas9-mediated genome editing of DDS (dammarenediol-II synthase) in *Panax ginseng*

Ju Young Ahn, Seon Heui Jeong, Padmanaban Mohanan, Hyeonah Shim, Tae-Jin Yang*

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

Panax ginseng is a representative traditional medicinal plant in Korea. It is a perennial shade plant and produces ginsenosides that have pharmacological effects on the human body. In *P. ginseng*, dammarane-type ginsenosides are produced by dammarenediol-II synthase (DDS), which catalyzes the cyclization of 2,3-oxidosqualene to dammarendiol metabolites. *PgDDS* has been reported to consist of four paralogous genes (*PgDDS1*, *PgDDS1a*, *PgDDS1b*, *PgDDS2*). *PgDDS* paralogous gene sequences were first extracted from the *P. ginseng* genome database and characterized. Then, sgRNAs targeting the *PgDDS1* and *pgDDS1b*, *pgDDS1a* and *pgDDS2* sequences simultaneously were designed and ligated into the pBAtC vector. *Agrobacterium*-mediated transformation was performed on ginseng adventitious roots. Each transformed line was selected using phosphinothricin. *PgDDS* genes had 16 exons and 15 introns, with sizes ranging from 4,165 to 80,917 bp. The coding regions of *pgDDS1* and *pgDDS1a* showed high sequence similarity, with a 99.4% match. Targeted deep sequencing of the mutation lines showed InDel frequencies ranging from 25.3 to 100% in *PgDDS*. Further validation will be done by analyzing ginsenoside metabolites using Ultra-High Performance Liquid Chromatography (UHPLC) and *PgDDS* expression levels. The molecular characterization of *PgDDS* and knock-out lines from ginseng using the CRISPR-CAS9 system targeting *PgDDS* will provide a broader understanding of the function of *PgDDS* in the ginsenoside biosynthesis mechanism.

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

PF-0019

분자마커 기술을 활용한 홉(*Humulus lupulus* L.)의 암수구별

하태현[1], 유재일[2], 이준형[1], 이소영[2], 강시용[1,2]*

[1]충청남도 예산군 예산읍 대학로54 공주대학교 산업과학대학 원예학과
[2]충청남도 예산군 예산읍 대학로54 공주대학교 작물오믹스지능육종연구센터

홉은 자웅이주이며 홉의 주요 성분인 루풀린은 암그루의 꽃에서 많이 생산된다. 루풀린은 맥주의 풍미와 쓴 맛을 제공하며, xanthohumol과 같은 페놀성분을 함유하여 항암, 항산화, 항염증 등 인체에 유익한 활성을 가져오기 때문에 산업적으로 암그루가 많이 재배된다. 또한, 홉의 연구적인 측면에서도 종자를 통해 세대를 진전하거나 교잡을 통해 신품종을 육성하는 경우 암수 개체를 확인해야 할 필요가 있다. 하지만 종자가 발아하여 개화하기 전까지 암그루인지 수그루인지 외형적으로는 차이가 없어, 성염색체를 찾아 확인하는 것으로 홉의 암수를 판별하는 방법을 이용해왔다. 본 연구는 PCR을 기반으로 하여 신속하게 암수를 판별할 수 있는 분자마커를 제작하여 다양한 홉 품종을 대상으로 검증 실험을 수행하였다. 분자마커 제작을 위해 hopbase DB에 등록된 USDA 21422M 계통에서 추출된 male specific region(MSR) 염기서열 정보를 바탕으로 분자마커(MSR-88, MSR-150, MSR-216, MSR-334)를 제작하였고, 추가적으로 기존에 보고된 홉 암수구별 마커 hPb-CONT(GenBank MG744433), hPb-719005(GenBank MG744432)를 대조구로 하여 실험하였다. 홉 5개 품종(Calypso, El Dorado, Cluster, German magnum, Saaz)을 대상으로 암수구별 연구를 수행한 결과 홉 5개 품종 모두 암그루와 수그루를 밴드형성 유무와 밴드형성 위치로 암수구별이 가능하였다. 이를 토대로 본 실험에 사용된 홉 품종 이외의 다른 품종에서도 암수구별이 가능할 것이라 사료된다.

***교신저자:** Tel. 041-330-1226, E-mail: sykang@kongju.ac.kr

PF-0020

Boosting camelina seed oil with castor *WRI1A* and *MYB96* transcription factors

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

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

Triacylglycerol (TAG) is abundant in vegetable oil in the form of glycerol-3-phosphate esterified with three fatty acids. Vegetable oil is used for industrial applications and edible oil. Because the demand for plant oils is increasing due to population growth, enhancing the oil content in seeds is important. In this study, castor WRINKLED1 (RcWRI1), which regulates genes involved in fatty acid synthesis, and castor MYB DOMAIN PROTEIN 96 (RcMYB96), which regulates the TAG synthesis, were overexpressed respectively or together under the control of seed-specific promoters in camelina (*Camelina Sativa*). The total oil content was increased in seeds of three different transgenic plants. The expression of *RcWRI1* has an effect to increase the oil content compared to the expression of *RcMYB96.* However, the co-expression of *RcWRI1* and *RcMYB96* showed a similar effect to that of expression of *RcWRI1* alone. *RcWRI1* OX lines resulted in an increase in the order of 18:2, 16:0 18:3, but did not significantly affect fatty acid composition in *RcMYB96* OX lines. Changes in fatty acid composition showed a combined effect of two transcription factors. In summary, we suggest that the co-expression of *RcWRI1* and *RcMYB96* can increase the seed oil content of various oil crops.

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

PF-0021

Agronomic Traits and Soluble Solid Content in Sugar Beet (*Beta vulgaris* L.) at Different Developmental Stages

Baul Yang[1,2], Ye-Jin Lee[1,2], Woon Ji Kim[1], Seung Hyeon Lee[1], Dong-Gun Kim[1], Sang Hoon Kim[1], Joon-Woo Ahn[1], Jae Hoon Kim[1], Chang-Hyu Bae[2*], Jaihyunk Ryu[1*]

[1]Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongeup 56212, Korea

[2]Department of Plant Production Sciences, Graduate School of Sunchon National University, Suncheon 57922, Korea

Sugar beet (*Beta vulgaris* L.) plays a crucial role in global sugar production, contributing up to 30% of the total output, and serves as a valuable raw material for bioplastic. This study investigated the agronomic traits and soluble solid content (SSC) of sugar beet at different developmental stages. Based on the developmental stages of sugar beet, we determined four stages such as 50, 90, 160, and 330 days after seeding (DAS) with distinct differences in taproot weight, taproot length, taproot width and soluble solid content. Of the four stages, stage 1~3 were not bolted, while stage 4 was bolted. Among these stages, the taproot weight increased significantly from S1 (50 DAS) to S2 (90 DAS). Similarly, taproot length showed a notable increase from S1 to S2, and another increase from S3 (160 DAS) to S4 (330 DAS). Taproot width demonstrated continuous growth with significant differences across developmental stages. The SSC exhibited a significant increase until S3, reaching its highest value (17.0 brix°), and then decreased at S4. High-performance liquid chromatography (HPLC) analysis of the sugar composition at S3 and S4 revealed a sucrose content of 98%, and subsequent quantitative analysis showed that it had a concentration of 50 g/kg. These findings provide valuable insights into determining the optimal timing for high SSC and taproot yield, provides baseline data for future comparisons with gamma-ray derived mutants.

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***Corresponding Author:** Tel. 061-750-5183, 063-570-3311, E-mail: chbae@scnu.ac.kr, jhryu@kaeri.re.kr

PF-0022

Evaluation of agriculture traits, total oil content and fatty acid composition in seeds of 278 sesame genotypes

Weilan Li, Jungsook Sung, Eunae Yoo, Sojeong Hwang, Sookyeong Lee*

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

Sesame is one of the oldest oilseed crops cultivated primarily for its seeds, which is a food source with various health benefits. To explore the potential benefits, 278 sesame accessions were cultivated, and their agricultural traits, total oil content, and ten fatty acids including palmitoleic acid, oleic acid, linoleic acid, linolenic acid, palmitic acid, stearic acid, arachidic acid, behenic acid, lignoceric acid, and tetradecanoic acid were investigated. Soxhlet method and gas chromatography mass spectrometry were applied for the oil extraction and fatty acid analysis. Wide variations in agricultural traits, total oil contents, and fatty acid profile were observed among the accessions. The association between agriculture traits, total oil content, and fatty acid composition were studied, and the results indicated that seed coat color differently affect the total oil content and fatty acid composition. The entire dataset was subjected to principal component analysis, and distinctive aggregation was observed between genetic resources with different seed coat colors. Moreover, 278 genotypes were clustered into three groups. Our findings could provide useful data for evaluating sesame seed quality and developing new varieties with health benefits.

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***Corresponding Author:** Tel. 063-238-4873, E-mail: xsanta7@korea.kr

PF-0023

택사 돌연변이체 유기를 위한 적정 감마선 처리 선량

박신영*, 김동관

전라남도 나주시 산포면 세남로 1508 전라남도 농업기술원

택사(*Alisma canaliculatum*)는 논이나, 습지에서 자라는 택사과의 다년생 식물로 덩이줄기를 이뇨, 소염, 고지혈증 치료 한약재로 이용한다. 본 연구는 감마선 조사를 통해 택사 돌연변이체를 유기하여 유전자원 pool을 확대하고 신품종 육성을 위한 우수 돌연변이체를 선발하기 위하여 수행하였다.
시험에 사용된 종자는 2021년 전남 순천 해룡면 농가에서 수집한 종자를 이용하였다. 2022년 한국원자력연구원 첨단방사선 연구소에서 저준위 감마선 (^{60}Co)을 선량별(0, 50, 75, 100, 125, 150, 175Gy)로 24시간 동안 종자에 조사하였다. 감마선 처리 후 처리 종자를 수도용 상토를 이용하여 50공 플러그트레이에 파종 후 40일 동안 육묘하고 생존한 유묘를 개체별로 포트(직경15cm)에 이식하여 처리 선량별 생존율과 생육특성을 조사하였다. 감마선 처리 선량별 유묘기 생존율을 조사한 결과 100Gy 95%, 125Gy 85%, 150Gy 70%, 175Gy 25%로 150Gy 이상의 선량에서 생존율이 감소하는 경향을 보였다. 반면 0~75Gy 선량 범위에서는 무처리 98%, 75Gy 98%로 생존율의 차이를 보이지 않았다. 유묘기 생육을 조사한 결과 0~75Gy 선량 범위에서는 초장이 10~12cm로 무처리구와 동일하였고, 100Gy~125Gy 처리구에서는 초장이 2~5cm로 생육이 저하되는 경향을 보였다. 파종 70일 후 지상부 생육을 조사한 결과 초장 48~50cm, 엽장 15~17cm로 감마선 처리구와 무처리구 간의 생육의 차이를 보이지 않았다. 택사 종자 돌연변이 유기를 위한 감마선 처리 결과 유묘기의 생존률과 생육에 영향을 미쳤으며, 반수치사(LD_{50})선량은 150Gy~170Gy, 생육반감(RD_{50})선량은 100Gy~125Gy로 조사되었다.
이상의 결과 택사 돌연변이 유기를 위한 적정 감마선 조사 선량은 100~125Gy 처리가 적당한 것으로 사료되며 돌연변이체 유기를 통해 유전자원 pool을 확대하고 신품종 육종 연한을 단축할 수 있을 것으로 보인다.

***교신저자:** Tel. 061-330-2531, E-mail: sinyoung7449@korea.kr

PG-0001

QTL analysis by rice BLB (bacterial leaf blight) micro-trait data with using Optical Coherence Tomography technology (*Oryza sativa* L.)

Xiao-Xuan Du[1,2], Kyung-Min Kim[2*], Gang-Seob Lee[1*]

[1]National Institute of Agricultural Science, Rural Development Administration, 370 Nongsaengmyeong-ro, Jeonju-si, 54874, Republic of Korea
[2]Coastal Agriculture Research Institute, Kyungpook National University, Daegu 41566, Republic of Korea

With the increasing global population and concerns about food security, the efficiency and accuracy of traditional manual screening methods in breeding face significant challenges. To address this, non-invasive investigation of rice leaf specimens using swept source optical coherence tomography (SS-OCT), a low coherence interferometric method, was demonstrated to characterize morphological formation and provide valuable structural information from an agricultural perspective. By comparing healthy and abnormal leaf specimens, which can exhibit enlarged leaf angles due to increased cell division in the adaxial epidermis, a morphological and quantitative comparison was conducted. The results obtained from this method hold significant potential in agriculture. SS-OCT demonstrates its effectiveness as a non-destructive and rapid investigation method for the selection of mutant-infected rice leaf specimens, providing a superior alternative to the destructive and time-consuming gold-standard methods that often lack precision. Overall, the application of micro-trait data and SS-OCT technology in QTL analysis for rice BLB offers a promising approach to improve the efficiency and accuracy of breeding programs. This method allows for non-invasive characterization of morphological and structural traits, enabling the rapid and precise identification of disease-resistant mutants, which is crucial for addressing the challenges posed by the growing global population and food security concerns.

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

PG-0002

Genotype and Phenotype Interaction between *OsWKRYq6* and BLB after *Xanthomonas oryzae* pv. *Oryzae* Inoculation in the Field

Hyoun-Woo Lee[1], Xiao-Xuan Du[1,2], Kyung-Min Kim[2*], Gang-Seob Lee[1*]

[1]National Institute of Agricultural Science, Rural Development Administration, 370 Nongsaengmyeong-ro, Jeonju-si, 54874, Republic of Korea

[2]Coastal Agriculture Research Institute, Kyungpook National University, Daegu 41566, Republic of Korea

In particular, in recent years, the occurrence of abnormal climate and warming phenomena has produced a good environment for the occurrence of BLB, and the rice yield due to the occurrence of BLB continues to decrease. Due to recent rapid climate change, BLB is a major problem that has a more serious negative effect on rice yield. Therefore, we suggest OsWRKYq6 to be effectively used for breeding BLB-resistant cultivars by screening BLB-resistant genes. In this study, the BLB-resistant gene was screened using the lesion length, which most definitely changes to the phenotype when *Xoo* is infected. OsWRKYq6 was finally selected as a BLB resistance gene by analyzing the phenotype and genotype after inoculating *Xoo* in 120 Cheongcheong/Nagdong double haploid (CNDH) lines in the field. After Xoo inoculation, lesion length and yield were investigated, and 120 CNDH lines were divided from BLB-resistant and susceptible lines. Moreover, when the transcription level of OsWRKYq6 was analyzed in the resistant and susceptible lines after *Xoo* inoculation in the field, the expression level was regulated to a high level in the resistant line. In this study, we propose OsWRKYq6 as a transcription factor involved in BLB resistance. Currently, the differentiation of various races is proceeding rapidly due to rapid climate change. In addition, screening of transcription factor genes involved in BLB resistance in the field can be effectively applied to molecular breeding to develop resistant cultivars in preparation for rapid climate change.

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

PG-0003

Rice seed setting rate analysis algorithm improvement using digital image processing method

Woo-Jin Im, Wan-Gyu Sang*, Hyeok-Jin Bak, Dong-Won Kwon, Sung-Yul Chang, Ji-Hyeon Lee, Jung-Il Cho

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

Introduction: Rice is the most important food crop in South Korea. In order to stably supply food, it is crucial to predict the crop's growth status and productivity accurately and early through crop condition surveys. In this regard, this study aims to utilize digital image analysis technology to early and accurately determine grain setting rate, while enhancing the convenience of the survey method.

Materials and Method: In this study, we performed algorithm development using the OpenCV package, one of the prominent image analysis modules. Seeds harvested on the 21th day after heading were selected as the image analysis, and a light exposure-based image acquisition platform was established to capture a large quantity of RGB images. The grain fertilized status was determined by assessing the shade level transmitted through the seeds using the image acquisition platform. The most noticeable improvement compared to the previous algorithm is significantly reducing errors in detecting filling areas. The developed algorithm quantized the continuous color values of the seeds, with a fertile grain threshold set at a shade level of 35% or higher. Additionally, the ratio between the area of each seed and the shaded area was calculated to evaluate the grain filling degrees. The developed algorithm demonstrated results of RMSE=4.45 and rRMSE=4.41.

Results and Discussion: This study proposed a method for investigating the grain setting ratio in rice using image analysis. The developed technique has the potential to advance the survey timing, increase accuracy, and enhance convenience compared to existing methods. As a result, it is expected to find applications in various fields of agriculture.

***Corresponding Author:** Tel. 063-238-5255, E-mail: wg_sang@korea.kr

PG-0004

Estimation of rice panicle area from top-view image using deep learning-based segmentation model

Hyeok-jin Bak[1,2], Sungyul Chang[1], Dongwon Kwon[1], Jae-Kyeong Baek[1], Woo-jin Im[1], Jung-Il Cho[1], Wan-Gyu Sang[1*]

[1]National Institute of Crop Science, RDA, Wanju 55365, Republic of Korea
[2]Crop Science and Biotechnology, Jeonbuk National University, Jeonju 54896, Republic of Korea

Rice yield is known to increase as the number of panicles and grains increases. However, the current methods of measuring this information rely on laborious and inefficient manual counting. Therefore, there is a need for an automated method to acquire data on rice panicles and grains. In this study, we propose a deep learning-based segmentation model to quantify the panicle area in top-view images of paddy rice. The training dataset consists of images taken at different stages, from heading to harvest. Each image is cropped to 512x512 pixels to enhance learning efficiency, and LabelMe is used to create binary images of the panicle area and non-panicle area. Furthermore, image augmentation techniques are employed to improve segmentation accuracy for panicles photographed at various heights. We evaluate four deep learning networks: DeepLabV3+, U-net, Linknet, and FPN, for image segmentation. The trained model performs well even in environments not included in the training data, such as 1/5000 Wagner pots and $1m^2$ pots. To validate the applicability of our approach in breeding programs, we map the panicle area of a segregating F2 population using images captured by an unmanned aerial vehicle (UAV). Additionally, we track the panicle area of a rice field over time, starting from the heading stage. Our study demonstrates that estimating the panicle area through image analysis can automate the rice breeding selection process. Moreover, it can serve as an effective method for estimating rice yield based on panicle area estimation.

***Corresponding Author:** Tel. 063-238-5285, E-mail: wg_sang@korea.kr

PG-0005

영상 기반 콩잎 표현형 데이터 추출 및 분석 기술 개발

장윤호[1], 김진수[1], 김영욱[2], 김재영[2], 백정호[2], 김송림[2], 이홍로[1*]

[1]전라북도 군산시 대학로 558, 군산대학교 소프트웨어학부 컴퓨터정보공학과
[2]전라북도 완주군 이서면 농생명로 166 국립농업과학원 유전자공학과

전 세계적으로 농업의 다양한 분야에 걸쳐 빅데이터 기반의 육종연구가 진행되고 있으며, 빅데이터 활용 역량이 미래의 종자산업에 큰 영향을 미치고 있다. 두과작물 중 하나인 콩은 식용, 접착제, 페인트와 사료 등 다양한 용도로 재배 및 소비되어 왔으며 이러한 작물들을 더 우수한 품종으로 육성하기 위한 기술이 존재해 왔다. 기존의 육종 기술은 대상의 생육, 질, 생산성 정보 등을 사람의 눈으로 계측했지만, 디지털 육종은 최적의 종자를 선별하기 위해 빅데이터 기술과 컴퓨터 비전 기술을 활용하여 세분화된 정보를 수집 및 분석한다. 이를 통해 대량의 종자를 정밀하고 신속하게 처리하여 기존의 육종방법을 보완할 수 있다고 본다. 이 연구에서는 작물의 표현형 정보 데이터베이스 구축을 위한 영상 기반 표현형 추출 프로그램을 개발하고자 한다. OpenCV를 활용하여 콩잎의 면적(area), 둘레(perimeter), 장축(major axis), 단축(minor axis) 원형율(roundness), 원형 정도(circularity), 조밀한 정도(solidity)와 종횡비(aspect ratio) 등의 표현형 정보를 계산하여 콩 육종을 보조하는 기술을 개발했다. 이 표현형 속성 정보를 계산하기 위해서 lab 색 공간을 채널 분리 후 임곗값을 적용하여 이진화하고 개체 후보 영역을 구했다. 개체 후보 영역 중에서 노이즈를 제거하기 위해 개체 후보 영역의 크기가 일정값 미만인 개체를 제거한 후 남은 개체에서 여러 표현형 지표를 구했다. 또한, 콩잎의 형태는 종실의 무게와 밀접한 관계가 있기 때문에 향후 콩잎의 형태 분석으로 발전하고자 한다. 이러한 기술을 작물 육종에 활용하여 디지털 표현형 데이터 수집 기술로 활용이 가능할 것으로 기대된다.

***교신저자:** Tel. 063-469-4558, E-mail: boiselee@kunsan.ac.kr

PG-0006

Application of hyperspectral imaging to identify haploid and diaploid maize seeds

Yeongtae Kim[1], Minji Kim[1], Younguk Kim[1], Jaeyoung Kim[1], Nyunhee Kim[1], Eunsook An[1], JeongHo Baek[1], Hwang Weon Jeong[1], Hyenso Ji[1], Jaeil Ryu[1], Seung Hyun Wang[2], Si Hwan Ryu[2], Song Lim Kim[1*]

[1]Gene engineering Division, National Institute of Agricultural Sciences, RDA, Jeonju 54874, Republic of Korea

[2]Maize Research Institute, Gangwon-do Agricultural Research and Extension Service, Hongcheon 25160, Republic of Korea

Maize(*Zea may*), an important crop cultivated extensively worldwide, serves as a significant grain for food, industrial materials, feed, and energy sources. Advanced maize breeding techniques employ doubled haploid(DH) technology, which effectively accelerate the process of maize breeding. However, accurate selection of haploids remains a major challenge, as conventional selection methods based on experience are subjective. R1-navajo (R1-nj) gene is commonly used to efficiently select haploid. The anthocyanin produced by R1-nj marker accumulates in diploid embryos but not in haploid embryos. Recently, the hyperspectral imaging technology is emerging as a powerful tool for investigating the components of substances, and its utility is progressively increasing in agricultural research. This study explored the applicability of visible and near-infrared(VNIR, 400 - 1000nm) hyperspectral imaging (HSI) to identify the maize haploid and diploid of seeds. We obtained the hyperspectral images of 700 seeds, comprising 50 seeds each from seven haploid and diploid lines, and performed spectral analysis of the embryo region. In the spectral plot of the point scanning, the reflectance value of the haploids at a wavelength of 550nm was approximately 2.8 times higher than that of the diploids. However, in the average spectral plot obtained through line scanning, the difference was not significant. Furthermore, the reflectance values of diploids and haploids showed the most difference at approximately 623nm. Anthocyanin reflectance index (ARI) values were 2.5 for diploids and 0.4 for haploids. By applying hyperspectral imaging to discriminate haploids and diploids in maize seeds, we obtained positive results and established a valuable and effective method.

***Corresponding Author:** Tel. 031-296-6898, E-mail: greenksl5405@korea.kr

PG-0007

Development of high-throughput phenotyping system for selecting drought-tolerant lines in gene-edited rice

Min Ji Kim, Nyunhee Kim, Eunsook An, Yeongtae Kim, Dong-Kyung Yoon, Hyeonso Ji, Mi Hyun Cho, Jiseon Song, In Sun Yoon, Sang Ryeol Park, Song Lim Kim*

National Institute of Agricultural Sciences, RDA, Wanju 55365, Republic of Korea

Water shortage due to climate change is causing agricultural productivity problems such as reduction of arable land and yield of crops. The National Institute of Agricultural Sciences operates a center for transformation of rice, corn, and cabbage, and through this, 315 gene-edited homozygous rice lines were produced targeting transcription factor genes. Among them, 186 gene-edited lines (T1/T2, 43 genes) were tested for drought tolerance through image analysis, and 43 lines (13 genes) were selected in the first year (2022). In the second year (2023), more precise tests for drought tolerance are being carried out with the seven gene-edited lines of the six genes including bHLH, bZIP, MyB, and so on which were selected in the first year. First, photosynthetic efficiency (Fv/Fm) was measured by acquiring fluorescence images of seedlings during normal growing, drought treatment, and recovery period. In the normal growing period, the gene-edited lines and Samgwang variety plants (control) showed Fv/Fm values between 0.7 and 0.8 which were usual values from healthy plants, but in the recovery period after drought treatment, all of the gene-edited lines showed more than 15% higher photosynthetic efficiency than Samgwang. In the top-view RGB image, the plant area of Samgwang was about 24,000 pixels, whereas the gene-edited lines of genes such as bHLH and bZIP showed plant area of about 100,000 pixels, which were about 4 times larger plant area than control. It seems that these gene-edited lines underwent less growth inhibition than the control, showing higher photosynthetic efficiency and growth. Currently, we are testing yield of these drought tolerant gene-edited lines according to soil moisture content.

***Corresponding Author:** Tel. 063-238-4663, E-mail: greenksl5405@korea.kr

PG-0008

Development of a physiological disorder app for crop disease detection and identification using smartphone

HwangWeon Jeong, Seon-Hwa Bae, Jinjeong Lee, Sung Mi Kim, Eunhee Kim, Hye-Jin Yoon, Il-Pyung Ahn, Jae-Hyeon Oh, Young-Joo Seol*

Gene Engineering Division, National institute of Agricultural Sciences, Rural Development Administration, 370, Jeonju-si, Jeollabuk-do 54874, Korea

Big data and artificial intelligence (AI) are being actively used not only in bioinformatics, which manages and analyzes large amounts of information, but also in various fields of academia such as meteorology, geography, and various industries such as medicine and finance. In particular, in the agricultural sector, various technologies are being developed to promote digital agriculture based on AI and big data. Research is underway to minimize damage to physiological disorders by establishing a growth management system and crop management, such as measuring environmental information, crop growth, and predicting diseases in real time. However, collected crop growth information are insufficient for accurate and rapid evaluation of physiological disorders. Therefore, growth information of various crops should be collected and managed with big data. Currently, the developed web has functions such as crop physiological disorder information, image, various physiological disorder searches, and experimental management. We developed an app that could systematically and easily collect cultivation environment information such as images of crop physiological disorders in laboratories, fields, and facilities using smartphones. Furthermore, a large amount of physiological disorder image information stored in the database can be extracted and used as a dataset for AI learning. Currently, 47,000 images of physiological disorders such as salt damage, bacterial wilt, and tomato yellow leaf curl virus have been produced for seven tomato varieties. We plan to upgrade the evaluation of physiological disorders on smartphones through AI learning in the future.

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

PG-0009

Image-based seed classification among crop species via deep learning model

JaeYoung Kim, Younguk Kim, Joon Ki Hong, Alebel Mekuriaw Abebe, Jae Il Lyu, Hwangweon Jeong, Song Lim Kim, Hyenso Ji, JeongHo Baek*

Gene Engineering Division, National Institute of Agricultural Science, RDA, Jeonju, 54874, Republic of Korea

Since current global warming and rapid population increase, agricultural industries have been forced to meet increased food demand. As a result, the importance of germplasms has significantly increased. Germplasm exchange for plant breeding varies among countries, regions, and individuals. This process demands thorough management because intermixing is detrimental to breeding process. To prevent intermixing of germplasms with high-similarity in seed morphology, we conducted a preliminary study on seed classification. The ambiguous discrimination of their species from seeds by bare eyes and conventional image-based analysis methods were caused by high similarities in color, size, shape, and other characteristics. Therefore, our experiment was based on deep learning methods. We trained a classification model consisted of input/output layers and 5 hidden layers using Keras, a deep learning application programming interface. A total of 3000 images, with 1000 images per species of soybean, mung bean, and red bean varieties, were used. The validation loss and accuracy results ended up at 0.0474 and 0.9917, respectively, when using 25% of the training set. The test sets were divided into two different datasets. The first test set, which composed by 360 seeds per species in various colors, showed an accuracy of 0.9917 and a loss of 0.0172. The second test set composed by yellow-colored seed images (100 seeds per species), showed an accuracy of 0.9759 and a loss of 0.0372 from the trained model. The results showed the possibility of more accurate image-based classification. Our further studies aim to classify more various species using deep learning techniques.

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

PG-0010

Real-time mushroom morphological trait analysis web system based on deep learning

Younguk Kim[1], JaeYoung Kim[1], JiHoon Im[2], Joon Ki Hong[1], Alebel Mekuriaw Abebe[1], Jae Il Lyu[1], Hwangweon Jeong[1], Song Lim Kim[1], Hyenso Ji[1], Hongro Lee[3], JeongHo Baek[1*]

[1]Gene Engineering Division, National Institute of Agricultural Science, RDA, Jeonju, 54874, Republic of Korea

[2]Mushroom Research Division, National Institute of Horticultural and Herbal Science, RDA, Eumseong, 27709, Republic of Korea

[3]Computer Information Engineering, Kunsan National University, Gunsan, Republic of Korea

Recent increase in the awareness of the nutritional benefits and functional properties led to a rise in the demand for mushroom. Sequentially, breeding programs for mushroom varieties with various desirable traits are being conducted. Cap size is one of the traits used for mushroom quality evaluation. Evaluation of mushroom cap size is mainly based on internationally standardized by UPOV as large, small, and medium conventionally measured by experienced person. The results of such evaluation methods are error prone and subjective. Therefore, we aimed to develop a web-based system that utilizes real-time images- to analyze morphological traits of mushrooms including area, length, and width The model was generated using YOLOv8, which is specialized in predicting the locations of objects in an image. The web client was implemented using HTML5, JQuery, and WebRTC techniques, while the web server was implemented using Python's aiohttp and ultralytics. The training dataset consisted of 16,000 individual mushroom objects, and training images were multiplied by data augmentation techniques. The results showed a loss of 0.64 in bounding box and 0.99 in segmentation, accuracy of 93% in mAP@.5 and 77% in mAP@[.5:.95]. Compared to conventional methods, analysis based on our deep learning models has significantly reduced the time required for measurements, especially with the use of real-time imaging and web systems. Our deep learning model showed intense potential for extracting highly reliable morphological traits of mushrooms and will greatly facilitate the mushroom breeding with better quality.

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

PG-0011

High-Throughput Phenotyping of Milk Thistle (*Silybum Marianum*) Seed Using Image Analysis and Deep Learning

Alebel Mekuriaw Abebe[1], Younguk Kim[1], Jaeyoung Kim[1], Suyoung Hong[2], Kwanghoon An[3], Jeehyoung Shim[3], JeongHo Baek[1*]

[1]Gene Engineering Division, National Institute of Agricultural Science, RDA, Jeonju, 54874, Republic of Korea
[2]Genomics Division, National Institute of Agricultural Science, RDA, Jeonju, 54874, Republic of Korea
[3]EL & I Co, Ltd., 17, Jangdoek-ri, Namyang-eup, Gyeonggi-do, Hwaseong, 18281, Republic of Korea

Milk thistle (*Silybum marianum*) is a member of *Asteraceae* family, and well-known for its medicinal value due to high content of silymarin. Conventional seed phenotyping using manual measurement of morphological traits is time consuming and labor intensive as they are irregularly shape and small size. Here, we developed a method for image acquisition and analysis to enable high-throughput phenotyping of milk thistle seed using image analysis. The method allowed rapid and accurate quantification of seed morphological traits such as area, perimeter, length, width, circularity, roundness, and solidity in 397 milk thistle lines (100 seeds each). Furthermore, we developed a deep-learning based approach to detect milk thistle seed elaiosome using Detectron2. For model training, a total of 3000 images were used, and data were augmented by rotation and resizing methods to increase the recognition rate of manifold data. The error rate and accuracy of deep learning results were tested using loss and accuracy, and class loss 0.001, mask loss 0.107, and box loss 0.057 were obtained with 95.29% accuracy in prediction result. Detection of elaiosome from the digital images of milk thistle seed enabled rapid and reliable quantitative measurement of its phenotypic traits. Efficient, accurate, and non-destructive evaluation of seed morphological traits will greatly benefit seed industries and crop breeding programs to develop cultivars with desirable seed traits.

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

PG-0012

Characterization of diverse pepper (*Capsicum* spp.) germplasm based on agro-morphological traits and phytochemical contents

Suyun Moon[1], Ho-cheol Ko[1], Nayoung Ro[1], SuKyeung Lee[2], Hyeonseok Oh[1], Bichsaem Kim[1], Ho-Sun Lee[1], Gi-An Lee[1*]

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

[2]International Technology Cooperation Center, Rural Development Administration, Jeonju 54875, Republic of Korea

Pepper (*Capsicum* spp.), one of the most important crops in the Solanaceae family, is cultivated and consumed worldwide. The fruits of *Capsicum* species are known to contain high vitamins and carotenoids, and they have health beneficial properties such as stress relief and fat breakdown. In this study, a total of 796 pepper accessions (4 *Capsicum* species), conserved in National Agrobiodiversity Center(NAC), were investigated for their morphological characters and phytochemical contents including capsaicinoids, sugars, carotenoids and vitamins. The results revealed wide variations in the morphological traits and phytochemical contents amongst accessions. Among morphological traits, fruit lengths ranged from 0.8 to 34.4 cm (mean = 7.7 cm), fruit widths ranged from 0.4 to 9.4 cm (mean = 2.1 cm), fruit weights ranged from 0.2 g to 218.4 g (mean = 17.2 g), fruit wall thicknesses ranged from 0.1 mm to 9.0 mm (mean = 2.0 mm), and the number of days to flowering and fruiting ranged from 59 days to 129 days and 110 days to 191 days, respectively. Some pairs of quantitative descriptors showed a strong correlation. Especially, vitamin C contents were positively correlated with fruit widths, weights, and wall thicknesses, and showed negative correlation with sugar contents and the number of days to flowering and fruiting. Our findings revealed morphological and phytochemical diversities and these could be useful information for the breeding program.

***Corresponding Author:** Tel. 063-238-4813, E-mail: gkntl1@korea.kr

PG-0013

Analysis of Rice Leaf Spectral Reflectance Response by Nitrogen Fertilization Level of Paddy Field

Dongwon Kwon, Wangyu Sang, Sungyul Chang, Woojin Im, Hyeokjin Bak, Ji-Hyeon Lee, Jung-Il Cho*

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

This study aimed to analyze the growth response of rice to different nitrogen fertilization levels using spectral reflectance measurements. The recommended nitrogen fertilization rate of 9 kg/10a, as specified in the standard rice cultivation method, was set as the control, and four levels of treatments were applied: 0, 0.5, 1.5, 2 times the control rate. Shindongjin was used, and the transplanting date is June 10th. Spectral reflectance measurements of the upper fully expanded leaves' reflectance were taken at intervals of 1-2 weeks, starting from 30 days after transplanting, using a leaf spectrometer(CI-710s, CID Bio Science). The measured data were interpolated using a third-order interpolation method to extract reflectance values at 1 nm intervals within the wavelength range of 380-949 nm. The correlation between spectral reflectance and treatments was analyzed. In all treatments, reflectance values were low in the blue range(380-500 nm) and the red range, including yellow(600-700 nm). Differences in reflectance were observed in the green range(500-600 nm), and a high correlation was found between the 550 nm wavelength and the treatments(R^2=0.7). Reflectance values decreased as the nitrogen fertilization levels increased, indicating an increase in chlorophyll content due to nitrogen fertilization. In future studies focusing on environmental stresses such as drought and flood, spectral reflectance values may be utilized for crop growth diagnosis.

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***Corresponding Author:** Tel. 063-238-5286, E-mail: jungilcho@korea.kr

PG-0014

Optimal vegetative index combination analysis and validation using machine learning for nutrient stress diagnosis

Ji-Hyeon Lee, Hyeokjin Bak, Dongwon Kwon, Woojin Im, Wan-Gyu Sang, Jung-Il Cho, Sungyul Chang*

Crop Physiology and Production Div, National Institute of Crop Science, Rural Development Administration, 181, Wanju 55365, Republic of Korea

Crop stress diagnosis is an important technology in agricultural as it enables early intervention to mitigate damage. However, traditional methods have limitations, such as being destructive and labor-intensive. Thus, non-contact diagnosis methods and technologies are needed. With an anticipated increase in demand for large-scale imagery-based crop growth diagnosis, research utilizing phenomics for crop health detection is necessary. In 2022 experiment, five nutrient stress treatments (Control, N0, P0, K0, NPK0) were applied. A drone captured aerial images with 10-day interval at 80m altitude. Image processing pipeline implemented in Python, RGB and NIR-based spectral reflectance values were extracted, resulting in total of 13 vegetative indices (VI) such as NDVI and GNDVI. Machine learning algorithms were employed to evaluate classification models using the extracted VIs as input data. A model was created to identify the VI that best represents nutrient stress. The Random Forest (RF) model was utilized as the classification model and a time-series-based model was constructed. Furthermore, to evaluate the VI that represents crop nutrient status more effectively, recursive feature elimination (RFE) and was applied and select 8 VIs out of 13 VIs with feature importance. The time-series-based model showed overall improvement in accuracy compared to the non time-series model. Each treatment group exhibited an accuracy of over 90%, with the NPK0 treatment group achieving 100% accuracy. As a result, selecting a representative index proved more effective than using all VIs for nutrient stress diagnosis. And this study suggests that image-based models offer potential for field-level nutrient stress diagnosis in rice.

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***Corresponding Author:** Tel. 063-238-5279, E-mail: schang8@korea.kr

PG-0015

Genome-wide association study of soybean canopy wilting under drought stress

Hyeon Jun Cho[1], Sang Yeab Lee[1], Seung Min Choi[1], Hyun Jo[1], Yoon Ha Kim[1], Jong Tae Song[1], Jeong-dong Lee[1,2*]

[1]Department of Applied Biosciences, Kyungpook National University, Daegu, 41566 Republic of Korea
[2]Department of Integrative Biology, Kyungpook National University, Daegu, 41566, Republic of Korea

Climate change increases the frequency of extreme weather conditions in global agricultural areas. Plant growth and productivity are adversely affected by abiotic stress factors. Among abiotic factors, drought is a significant environmental stress that exerts influences on plant metabolism and growth. Soybean (*Glycine max*) is generally sensitive to drought stress. Drought stress significantly causes soybean yield losses by more than 40%. In addition, several studies indicated a decline of 73-82% in yield when drought stress is imposed during the flowering and seed filling stages. It is necessary to develop drought stress-tolerant cultivars to prevent yield losses in drought conditions worldwide. The objective of this study was to identify the genomic regions associated with canopy wilting under rainout shelter for drought stress by genome wide association study (GWAS). After two-year evaluations under drought conditions of 1000 soybean germplasm from the National Agrobiodiversity Center of Rural Development Administration, 300 accessions were selected for further research. Three hundred accessions were grown for two years to determine canopy wilting phenotype under drought conditions. A total of 1000 soybean accessions were genotyped using the Affymetrix Axiom® 180k SoyaSNP array. Through this study, the selected soybean accessions will be suitable as breeding materials for the development of stress tolerant-soybean cultivars under drought conditions. In further research, bi-parental mapping populations can be used for the detection of QTL regions for drought stress.

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

PG-0016

Variation of vegetation indices from hyperspectral imagery in cultivated and wild soybean of Korean core collections

Sang Yeab Lee, Hyeon Jun Cho, Seung Min Choi, Hyun Jo, Yoon Ha Kim, Jong Tae Song, Jeong-Dong Lee*

Department of Applied Biosciences, Kyungpook National University, Daegu, 41566 Republic of Korea

High-throughput phenotyping is utilized as a method in phenomics to obtain phenotypic measurements non-invasively and accurately in both field and controlled environments using advanced tools. Vegetation indices (VI) can be calculated based on the wavelength-specific reflectance values obtained from hyperspectral imagery. VI can be divided into structural vegetation indices (related to morphological characteristics), and biochemical compound-related indices, measuring physiological responses or metabolic products of plants. The range of VI values showed differences based on crops, species, and plant genotypes. The objective of this study was to evaluate natural variation of VI values from hyperspectral reflectance images with wild soybean (*Glycine soja*) and cultivated soybean (*Glycine max*) and relationship between genotype and phenotype to understand the measured VI in soybean through genome-wide association mapping (GWAS). A total of six VI have been selected: Normalized Difference Vegetation Index and Simple Ratio related to chlorophyll content, Photochemical Reflectance Index and Structure Independent Pigment Index related to photosynthesis efficiency, Anthocyanin Reflectance Index and Chlorophyll Reflectance Index related to leaf pigment. Hyperspectral images were obtained using a Korean soybean core collection consisting of 430 accessions of *G. max* and 408 accessions of *G. soja* during the early vegetative stages. GWAS will be conducted to identify genomic regions for measured VI values in *G. soja* and *G. max* with Affymetrix Axiom® 180k SoyaSNP array data. This study will provide information for the range of VI values in soybeans and will be useful not only in breeding programs but also in precision agriculture.

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

PG-0017

다분광 영상데이터를 이용한 배추 내건성 평가

이준호*, 이상덕, 김진희, 정화현, 장윤아

전라북도 완주군 이서면 농생명로100 국립원예특작과학원

배추는 우리나라 주요 채소 작물로 연중생산되고 있다. 배추의 생육은 기상환경에 많은 영향을 받아 가격변동성이 커서 안정생산에 어려움이 있다. 최근 기후변화로 인해 안정생산이 더욱 어려워져 가뭄, 고온 등 환경에 강한 적응력을 갖는 품종의 개발이 요구되고 있다. 따라서 환경저항성 유전자원 소재를 빠르게 선발하여 환경저항성 배추를 개발 할 필요가 있다. 최근 영상기술을 활용한 표현체 연구가 늘어나고 있는데 영상기술을 이용하면 식물의 표현형 형질을 객관적이고 빠르게 분석 할 수 있다. 본 연구에서는 다분광 영상데이터를 이용하여 배추의 내건성 평가 가능성을 검토하였다. 국립원예특작과학원 표현체 연구온실의 인공환경에서 배추를 트레이와 화분에 나눠심어 재배하였다. 품종은 내건성이 강한 품종 3종과 약한 품종3종을 심었다. 발아 후 내건성 평가 종료시까지 매일 같은 시간 다분광 영상을 촬영하였다. 내건성은 본엽이 3~4매 나왔을 때 일주일간 단수처리를 한 후 평가하였다. 내건성을 평가하는 건조지수는 0(정상) ~5(고사)의 척도로 나누어 조사하였다. 다분광 영상 데이터로는 형태 관련 지표(area, convex hull area 등), 색상지표(RGB, NIR)를 분석하였다. 형태관련 지표는 단수 처리 기간에 따라 변화하는 양상을 보여 배추의 생육을 측정하는 지표로 사용할 수 있을 것으로 생각된다. 영상 데이터 지표와 건조지수의 상관관계를 분석하였고 영상 데이터 지표 중 높은 상관관계를 보인 지표들은 건조지수를 대체할 수 있을 것으로 생각된다. 추후 추가적인 연구를 통해 초분광 카메라 등의 영상 데이터를 활용한다면 육안으로 조사하는 건조지수를 영상으로 대체할 수 있을 것으로 보인다.

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***교신저자:** Tel. 063-237-6622, E-mail: skyjh07@korea.kr

PH-0001

Development of Useful Perilla Traits Using CRISPR/Cas9 system

Jee Hye Kim, Jae Bok Heo*

Department of Molecular Genetic Engineering, Dong-A University, Busan, 49315, Korea

Perilla (*Perilla frutescens*) is an annual plant and grown in Asian countries including Korea, Japan, China. Perilla seeds contain approximately 45% oil, which is composed of over 90% unsaturated fatty acids such as oleic acid (18:1), linoleic acid (18:2), and linolenic acid (18:3). Its leaves contain various functional compounds, including caffeic, rosmarinic, and γ-aminobutyric acids, as well as luteolin. We are focusing on developing new perilla traits, pathogen resistant and increased leaf production using CRISPR/CAS9 system. To develop the pathogen resistant and increased leaf production perillas, we chose s-gene to the downy mildew pathogen, PfDMR6 and several perilla flowering activating genes, PfHd3a and PfGI. All constructs were transformed through Agrobacterium-mediated tissue culture method. Positive perilla transformants were selected on SIM media containing phosphinothricin (PPT) and by genomic PCR. Next, deep sequencing was performed with all T0 transformants to check whether gene editing was achieved in each perilla transformant. After confirming gene editing ratio, we will investigate the pathogen resistant and increased leaf production in perilla transformants. The CRISPR/Cas9-generated *Perilla*-mutation approach have never reported before, this study will provide insight to many researchers who study for crop productivity and pathogenesis.

Keywords: Perilla, PfDMR6, PfHd3a, Leaf productivity

***Corresponding Author:** E-mail: jbheo72@dau.ac.kr

PH-0002

BrHSBP1 significantly influences abiotic stress response genes and confers drought tolerance in *Brassica rapa*

Muthusamy Muthusamy, Sang Ryeol Park, Eun Jung Suh, Soo In Lee*

Department of Agricultural Biotechnology, National Institute of Agricultural Sciences (NAS), RDA, Jeonju 54874, Republic of Korea

Plant heat shock factor binding proteins (HSBPs) are majorly pronounced for their implications in the negative regulation of heat stress responses. Herein, we study the hitherto unknown functions of the BrHSBP1 gene in *Brassica rapa. BrHSBPs* were responsive to heat stress and other stress conditions and the activity of BrHSBP1-GFP fusion proteins was found to be localized to both nuclei and cytosols at cellular levels. *BrHSBP1* overexpression improved the pod and seed sizes whereas loss of function mutants (*Brhsbp1*) created with gene-specific sgRNAs as part of CRISPR-cas tools resulted in seedless phenotypes. The RNA-seq-based comparative transcriptomic approaches between wild and *Brhsbp1-KO*/BrHSBP1^{OX} showed several differentially expressed genes that were known to influence flower or seed development were regulated by BrHSBP1. The application of yeast two-hybrid approaches confirmed that BrHSBP1 can bind and interact with reproduction-associated genes a part from HSR genes. BrHSBP1 can also interact with itself and with its segmental duplicate gene designated as BrHSBP1-like. Our findings add a new regulatory player of pod and seed development in *Brassica rapa.*

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

PH-0003

Breeding of multi-viral resistance tomato by CRISPR/Cas9 genome-editing technology

Yujin Kweon[1,2], Sang-Yoon Shin[2,3], Minsu Park[1,4], Minsun Oh[1,2], Chanseok Shin[1,2,3,4,5*]

[1]Department of Agricultural Biotechnology, Seoul National University, Seoul 08826, Republic of Korea
[2]Research Center for Plant Plasticity, Seoul National University, Seoul 08826, Republic of Korea
[3]Interdisciplinary Program in Agricultural genomics, Seoul National University, Seoul 08826, Republic of Korea
[4]Research Institute of Agriculture and Life Sciences, Seoul National University, Seoul 08826, Republic of Korea
[5]Plant Genomics and Breeding Institute, Seoul National University, Seoul 08826, Republic of Korea

Tomato Spotted Wilt Virus (TSWV), a member of the *Bunyaviridae*, is a plant viral pathogen that affects over 900 species of crops and weeds, including *Solanaceae.* TSWV infection results in significant economic losses. Although several TSWV-resistance alleles had been discovered, resistance-breaking TSWV strains have been recently reported. Management strategies for TSWV mainly focus on preventing the virus from spreading by weed control and reducing thrips populations. Therefore, the improvement of TSWV resistant tomato lines has become increasingly important. In this study, we aim to develop the multi-viral resistant tomato by CRISPR/Cas9 system. We selected four disease-resisting candidate genes and two miRNAs that are related to the salicylic acid-mediated resistance and recessive resistance. In collaboration with KRIBB and CNU, we successfully regenerated *Solanum lycopersicum* cv. Micro-tom. To confirm knock-out transformants, regenerated Micro-tom were genotyped using Illmina miniseq. 220 T0 Micro-tom transformants were obtained and their seeds were harvested to raise the T1 generation. At first, screening of the TSWV resistance of Micro-tom transformants was conducted. Assessment of TSWV were conducted through phenotype observation and DAS-ELISA test on TSWV-treated plants. If TSWV resistance is observed from tested mutant lines, these plants will be tested for evaluation of resistance on other plant viruses such as CMV and PepMoV.

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***Corresponding Author:** Tel. 02-880-4643, E-mail: cshin@snu.ac.kr

PH-0004

Suppression of *Phytophthora infestans* via exogenous dsRNA-induced gene silencing

Yujin Kweon[1,2], Dowhan Lee[1], Chanseok Shin[1,2,3,4,5*]

[1]Department of Agricultural Biotechnology, Seoul National University, Seoul 08826, Republic of Korea
[2]Research Center for Plant Plasticity, Seoul National University, Seoul 08826, Republic of Korea
[3]Interdisciplinary Program in Agricultural genomics, Seoul National University, Seoul 08826, Republic of Korea
[4]Research Institute of Agriculture and Life Sciences, Seoul National University, Seoul 08826, Republic of Korea
[5]Plant Genomics and Breeding Institute, Seoul National University, Seoul 08826, Republic of Korea

Potato late blight, infected by *Phytophthora infestans* (*P. infestans*), mainly affects *Solanaceae* crops such as potato, tomato, and pepper. After the Irish potato famine, continuous studies were conducted to control the infection of *P. infestans*. However, *P. infestans* still remains the costliest potato pathogen to manage worldwide. In this study, we aim to suppress *P. infestans* infection by regulating the expression level of pathogen effectors via RNA interference (RNAi). *P. infestans* carries various effector proteins that modulate plant innate immunity to enable infection. Therefore, we designed three kinds of exogenous dsRNAs that are targeting *P. infestans* effector proteins. By applying dsRNAs to *Nicotiana benthamiana*, we investigated their disease control ability against the *P. infestans.* As a result, we identified that the exogenous dsRNAs we designed could successfully suppress the pathogenesis of *P. infestans.* Our study suggest that RNAi could be an effective tool for crop protection and crop quality improvement. In addition, research on these dsRNAs can contribute to the RNAi-based disease control.

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***Corresponding Author:** Tel. 02-880-4643, E-mail: cshin@snu.ac.kr

PH-0005

Plant Regeneration using Nanoparticles based on Microspore Regeneration System in Pepper (*Capsicum annuum L.*)

Hye-Eun Lee*, Hwa Hyun Jeong, Jinhee Kim, Hyo-Bong Jeong, Oak-Jin Lee, Na-Ree Yu, Woo-Moon Lee

Vegetable Research Division, National Institute of Horticultural and Herbal Science, RDA, Wanju 55365, Republic of Korea

It is very important to have genetic resources with excellent traits for each target market in order to expand seed export market and volume. Genetic resources utilized in pepper breeding program in Korea have a limited range of variation and, therefore, a variety of useful traits must be incorporated in breeding program for the diversification of export markets. Haploid/double haploid production techniques offer a valuable means to rapidly generate superior homozygous lines, significantly reducing the time required for developing new cultivars. In this study, we explored new breeding technology by combining microspore culture technology and CRISPR/Cas9 RNP (Ribonucleoprotein) gene editing methods. To deliver the gene editing components efficiently, we used carbon nanoparticles (CNPs). This is the first attempt to use carbon nanotubes in microspore embryogenesis.

To optimize regeneration efficiency, we investigated suitable culture medium conditions, carbon nanoparticle treatment concentration, and time. RNP-carbon nanoparticle treatments were conducted under two conditions, namely RNP : carbon nanoparticle ratios of 5:1 and 1:1 (w/w). Microspore-derived embryos were observed under all conditions, irrespective of guide RNA, carbon nanoparticle type, or processing ratio. Efficient introduction of nanoparticles into pepper microspores was confirmed, and several plantlets were obtained through this gene editing procedure. The results of this study can be extended to develop a potential CRISPR/Cas9 system for horticultural crops and create new varieties using genome editing techniques.

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***Corresponding Author:** Tel. 063-238-6640, E-mail: helee72@korea.kr

PH-0006

iBreeder: Data archiving system for digital breeding

Jeonmo Kang[1], Kyooyeol Lee[1], Yu-jin Lim[1], Junseok Lee[1], Byung-jun Lee[1], Sungjin Kim[1], Sung-min Kim[1], Sathiyamoorthy Subramaniyam[1], Myunghee Jung[1], Seowoo Park[1], Yongchin Kim[2], Junhwa Choi[3], Youn-Sung Kim[4], Younhee Shin[1*]

[1]Research and Development Center, Insilicogen Inc., 13, Yongin-si, Gyeonggi-do, 16954, Republic of Korea
[2]Institute of Breeding Research, Dana Co. Ltd, Yongin-si, Gyeonggi-do, 16949, Republic of Korea
[3]Institute of Breeding Research, MIRACLE Co.Ltd, Jeju 63022, Republic of Korea
[4]Institute of Plant Biotechnology, Jenong S&T Anseong-si, Gyeonggi-do, 17602, Republic of Korea

In the agricultural sector, digital breeding is a key technology, which is emerging from the benefits of big data and artificial intelligence (AI). The major challenge in agriculture is global warming and its subsequent production losses in various crops worldwide. Scientist around the world working together to identify the key solution by integrating genotype and phenotypes from multiple traits for same plant, explaining us the importance of systematic digital breeding archiving system powered by AI with the principles of genetics. In research perspective, communication between breeders and researcher is the biggest hurdle. Here, we developed iBreeder digital archiving system to easily integrate new genetic resources and upgrade the existing resources in plug and play style and can easily connect researcher and breeders in real time. Currently, iBreeder is supporting to collect and manage the genetic resources such as genotype, phenotype and pedigree from multiple users around the world. The facility management functions, i.e., phenotype management function manages plantation, storage, and cultivation environmental information and the genotype management function manages the complete genotype information from genome annotation, variant calls and genome wide association study (GWAS) for all available traits. Furthermore, through the lineage management function, we can prioritize the plant from wild to elite lines. In, iBreeder, the core function is phenotype management function which collects images as per plant life cycle and integrate with plant ontology (PO) schema to improve the plant characteristics. The incorporation PO along with genotype, phenotype and images, which collectively assist breeders/researcher to interpret the trait in more precisely. Mainly, the user can customize the phenotype template as per plant and breeding scheme. Moreover, the data security is high, which can also prioritize and grand the permission by the administrator. Finally, the iBreeder is good partner for breeders and researcher to effectively utilize the large data.

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***Corresponding Author:** Tel. 031-278-0061, E-mail: yhshin@insilicogen.com

PH-0007

Agrobacterium-Mediated Transformation and Characterization of Beta-Amyrin Synthase Genes in *Platycodon grandiflorum*

Mi-Hwa Choi, Ji-Nam Kang, Chang-Kug Kim, Si-Myung Lee*

Genomics Division, National Institute of Agricultural Sciences, 370 Nongsaengmyeong-ro, Jeonju-si, Jeollabuk-do, 54874, Republic of Korea

Bellflower (*Platycodon grandiflorum*) is a perennial plant belonging to the Campanulaceae family, and is mainly used as a medicinal herb in East Asia, including Korea, China, and Japan. The root of this plant is used as a medicinal part and has been reported to relieve hypotension, arteriosclerosis, inflammation, cough, and phlegm. Platycodin D, a type of triterpenoid saponin, is a major compound in bellflower. This compound is abundant in bellflower root, and pharmacological effects of anti-tussive, anti-obesity, anti-fibrosis, anti-inflammatory, and anti-tumor effects have been reported. Despite its pharmacological importance, little research has been done to enhance Platycodin D from this plant to date. Beta amyrin synthase (BAS) is a key gene in the triterpenoid saponin pathway including platycodin D. In this study, we generated BAS gene overexpressing plants using *Agrobacterium*-mediated transformation for the characterization of BAS genes in bellflower. Integration of the 35S promoter-BAS recombinant DNA was confirmed via PCR. The bellflower tissue culture system was well established in this process, which will be useful for genetic manipulation using transformation in the future. This study is the first step of research to enhance the production of Platycodin D in bellflower.

***Corresponding Author:** Tel. 063-238-4555, E-mail: chang@korea.kr

PH-0008

Machine Learning and Genomic Selection powered digital breeding method to predict weight of Onion

Sunghyun Cho[1], Junhwa Choi[2], Subin Choi[3], Han Yong Park[3], Sathiyamoorty Subramaniyam[1], Myunghee Jung[1], Hyojung Son[1], Yu-jin Lim[1], Jaewon Lim[1], Younhee Shin[1*]

[1]Research and Development Center, Insilicogen Inc., 13, Yongin-si, Gyeonggi-do, 16954, Republic of Korea
[2]Institute of Breeding Research, MIRACLE Co.Ltd, Jeju 63022, Republic of Korea
[3]Department of Bioresource Engineering, Sejong University, Seoul 05006, Korea

Worldwide, onion is second largest vegetable crop, which is widely cultivated and consumed after tomatoes with largest genome. The factors pushed us to develop the digital breeding (GB) framework for onion, with basic GB tools such as 1) Genomic Estimated Breeding Values (GEBVs) that estimates BV and phenotype from genotype information; 2) A machine learning (ML) model that classifies groups according to the onion weight information; 3) Generation of *in-silico* offspring based on parental phased haplotype information; 4) Estimation of the BV and phenotype of *in-silico* offspring using the previous statistical models and classification analysis of elite offspring. Currently, we included 98 lines for weight trait, from data repository and called 51,499 high-quality SNPs were cataloged in our DB framework. A case study performed to select the elite onion weight trait individuals from the high-quality SNPs has resulted in 39 SNP markers, which can classify elite individuals through ML models with an accuracy of 0.87. Similarly, this method is not limited to weight traits, but it can be extended to various traits. This readily available genotype and phenotype information can feed to different ML models to prioritize the elite models as per the given phenotypes. Finally, we expect this framework will be readily applicable to various phenotype- and genotype-based assessments.

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***Corresponding Author:** Tel. 031-278-0061, E-mail: yhshin@insilicogen.com

PH-0009

Development of Marker-free TuMV Resistance in Chinese cabbage Using the CRISPR/Cas9 Gene Editing System

Hong-Il Ahn, Ye-Rin Lee, Eun Su Lee, Hye-Eun Lee, Koeun Han, Do-Sun Kim*

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

The presence of plant viruses as pathogens poses a significant threat to agricultural production, leading to the deterioration of both crop yield and quality. In recent years, with the rise of climate change and the expansion of international trade, there has been a gradual increase in the damage inflicted by viruses that were not previously prevalent domestically. The most common virus in Chinese cabbage is the *turnip mosaic virus* (TuMV) of the potyvirus genus, which causes significant damage not only in Korea but also worldwide. Host factors such as *eIF4E* and *eIF(iso)4E* exhibit recessive resistance against potyviruses. In the case of Chinese cabbage, researchers have identified *eIF(iso)4E*-related genes and conducted transformation experiments to investigate the mechanism of resistance against TuMV. Therefore, the objective of this study was to develop a new breeding material by creating marker-free Chinese cabbage varieties resistant to TuMV. To achieve this, we employed *Agrobacterium*-mediated transformation on both the F_1 cultivar and an inbred line. As a result, we obtained T_0 plants that contained both Cas9 and selection markers. Among the T_0 plants obtained, individuals exhibiting a high rate of editing at the target locus were chosen for further generational progress. At the same time, we performed deep-sequence analysis to select an individual with a high editing rate at the target locus among marker-free individuals, in which both Cas9 and selection markers were removed by PCR analysis. Finally, we selected marker-free individuals with TuMV resistance and high rates of editing, and obtained T_2 seeds through generational progress.

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

PH-0010

The breeding methods of medical Cannabis in U.S.A and suggestion for breeding program of Korean medical Cannabis

Youn-Ho Moon, Mok Hur, Jang Hoon Kim, Yun Chan Huh, Tae Il Kim, Woo Tae Park*

Department of Herbal Crop Research, NIHHS, RDA, Eumseong 27709, Korea

In hemp plant (*Cannabis sativa* L.), sinsemilla, a non-pollinated female flowers, contains a lot of cannabinoids. Among the compounds, THC (Tetrahydrocannabinol) is a major component of drug hemp causing ‘high effect’, but CBD (Cannabidiol) is used to cure intractable diseases including epilepsy. In U.S.A, hemp plant with below 0.3% of THC were permitted to grow for industrial and medical purpose by legislation of ‘Agriculture Improvement Act of 2018’. Many commercial cultivars were released on on-line or off-line seed market but there were inferior cultivar which were not uniform and exceeded 0.3% of THC threshold. In hemp breeding program, developing pure line by self-pollination were difficult because of dioeciousness and wind-pollination. Plant cuttings ensures that plants are identical to the mother stock, which offers more consistency and uniformity of yield and cannabinoid content than many current seed cultivar. Thus many clone cultivar including ‘Abacus’ are on the market. With development of inducing male flowers on female plants by sex-reversion, self-pollenation can be practiced to obtain pure lines of medical hemp. That process are: selection of superior female plants → propagation by cutting → inducing male flowers by partial sex-reversion → self-pollination by isolation → seed harvest. In Korea, effective sex-reversion method were developed for female seed production in 1991. With the method and improving self-pollination process, superior medical cultivar can be bred as soon as possible.

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***Corresponding Author:** Tel. 043-871-5686, E-mail: harusarinamu@korea.kr

PH-0011

Machine learning powered digital breeding method to predict the pungency of *Capsicum annuum*

Sanghyeob Lee[1,2], Yu-jin Lim[3], Younhee Shin[3], Sathiyamoorthy Subramaniyam[3], Eunae Lee[4], Myunghee Jung[3*]

[1]Bioindustry and Bioresource Engineering Major, Sejong University, Seoul 05006, Republic of Korea
[2]Plant Engineering Research Institute, Sejong University, Seoul 05006, Republic of Korea
[3]Research and Development Center, Insilicogen Inc., Yongin 16954, Republic of Korea
[4]Breeding Institute, Asiaseed CO.,LTD., 109-35, Gyeongchung-daero 518beon-gil, Janghowon-eup, Icheon-si, Gyeonggi-do 17414, South Korea

Capsicum spp., commonly known as chili peppers, are widely cultivated and economically important horticultural crops. With numerous varieties of peppers existing worldwide, each possessing a unique taste and preferred by indigenous populations, selecting a specific pepper variety for breeding and cultivation based on pungency characteristics has been challenging. Although various molecular markers have been proposed for assessing pungency, many lack specificity. Moreover, environmental stress factors such as temperature, moisture, and nutrient levels can also influence changes in pungency characteristics. To address these challenges, this study utilized RNA-Seq-based genotyping and phenotypic data combined with machine learning techniques to predict pungency characteristics. A set of 23 single nucleotide polymorphisms (SNPs) showed strong associations with pungency and exhibited high classification potential, achieving an accuracy of 95%. Additionally, the association of capsaicin biosynthesis, particularly with the *Pun1* gene, was validated using novel non-polymorphic primer regions. This machine learning model, utilizing only 23 SNPs, can effectively predict pungency characteristics in new samples, aiding breeders in trait selection. Furthermore, this approach can be extended to other breeding objectives and traits beyond pungency.

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***Corresponding Author:** Tel. 031-278-0061, E-mail: mhjung@insilicogen.com

PH-0012

고온 스트레스 저항성 상추 개발

Eun-Ji Jo, Bo-Ram Baek, Youn-Sung Kim*

Plant Biotechnology Institute, Jenong S&T Co. Ltd., Anseong-si, Gyeonggi-do, 17602, Korea

상추는 국화과에 속하는 대표적인 잎채소 작물로서 세계적으로 샐러드용 채소로서 많이 소비되고 있다. 상추는 고온 스트레스에 의한 추대, 발아불량 그로 인해 발생하는 상품성 저하 등의 문제가 발생하기 때문에 여름철에는 상추 가격이 폭등하는 때도 있다. 이처럼 고온기 재배 시에 안정성이 높은 품종이 필요하지만, 전통육종 방식으로 원하는 형질을 갖는 신품종을 개발하는 데는 한계가 있다. 따라서 본 연구에서는 유전자교정기술을 이용하여 고온에서도 추대, 발아 등에 안정적인 새로운 육종소재를 개발하고자 하였다. 본 연구를 위해서는 상추 떡잎을 재료로 하였으며, CRISPR/Cas9 시스템 적용을 위해 만추대 타겟 유전자인 GI 및 SOC1와 고온 발아 타겟 유전자인 NCED4의 sgRNA 및 *SpCas9*과 선발마커 *npt*Ⅱ를 암호화하고 있는 염기서열을 삽입한 pECO301 재조합 벡터를 제작하였다. 이를 *Agrobacterium tumefaciens* LBA4404에 도입하였다. 조직배양을 통해 확보한 유식물체는 *Cas9*과 *npt*Ⅱ에 특이적인 프라이머 세트를 이용한 PCR 분석 진행하였으며, 일부 개체에서 예상했던 밴드(*Cas9*; 590bp, *npt*Ⅱ;710bp)를 확인하였다. 이를 통해 상추 형질전환체에 CRISPR/Cas9 시스템이 제대로 도입되었음을 확인할 수 있었다. 이후 유전자교정 여부를 확인하기 위해 확보된 형질전환체의 deep-sequencing 분석을 진행하였다. 그 결과 GI 유전자교정체(T0 세대)는 20~100% indel을 갖는 16개체가 선발되었고 현재 46~100% indel을 갖는 T1 세대 4개체를 확보하였다. SOC1 유전자교정체(T0 세대)는 6~100% indel을 갖는 9개체가 선발되었고 현재 75~100% indel을 갖는 T1 세대 4개체를 확보하였다. 마지막으로 NCED4 유전자교정체(T0 세대)는 38~100% indel을 갖는 5개체가 선발되었고 현재 99~100% indel을 갖는 T1 세대 2개체를 확보하였다. 기확보한 상추 유전자교정체의 자가교배를 통한 세대진전을 진행하고 개화시기 및 고온발아 분석을 통해 고온기에도 안정적으로 재배할 수 있는 상추 유전자교정체를 개발하고자 한다.

***교신저자:** E-mail: kimys@jenong.co.kr

PH-0013

Virus-mediated Genome Editing in Solanaceous Crops

Bomi Kang[1], Seo-Young Lee[2], Jelli Venkatesh[2], Dahyeon Ko[2], So-Hee Lee[1], Seyoung Lee[2], Byoung-Cheorl Kang[1,2*]

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

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

Genome editing (GE) using CRISPR/Cas enables rapid induction of genetic variations for desired traits in a short time. However, conventional transgene-mediated GE methods have limitations due to the time-consuming generation of stable transgenic lines expressing Cas9/single guide RNA (sgRNA) module through tissue culture. Virus-induced genome editing (VIGE) systems have been successfully employed in model plants, such as *Arabidopsis thaliana* and *Nicotiana* spp. In this study, we developed two VIGE methods for Solanaceous crops. The first method is delivering sgRNA into *Cas9* transgenic plants using *tobacco rattle virus* (TRV). Second, we devised a transgene-free GE method based on *potato virus X* (PVX) vector to deliver *Cas9* and sgRNAs. We have set up the VIGE systems in *N. benthamiana.* Based on these studies, VIGE in *Solanum lycopersicum* (tomato) was optimized. The editing efficiency of the virus-inoculated leaves was 40.3% and 36.5% for TRV- and PVX-mediated GE, respectively. To further improve the editing efficiency, we conducted 37°C heat treatment (HT), which increased the editing efficiency by 33-46% and 56-76% for TRV- and PVX-mediated VIGE, respectively. To obtain edited plants, we subjected inoculated cotyledons to tissue culture, yielding successful editing events. In addition, these VIGE systems are being applied to pepper (*Capsicum annuum*), and conditions are being optimized in pepper. These simple and highly efficient VIGE methods have great potential for generating genome-edited plants in Solanaceous crops.

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

PH-0014

Change of fatty acid composition in the seed oil of *diacylglycerol acyltransferase 1* and *2* knockout camelina by CRISPR-Cas9 system

Kyeong-Ryeol Lee[1*], Yumi Yeo[1], Jihyea Lee[1], Semi Kim[2], Chorong Im[1], Inyoung Kim[3], Juho Lee[1], Seon-Kyeong Lee[1], Hyun Uk Kim[3], Mi Chung Suh[2]

[1]Department of Agricultural Biotechnology, National Institute of Agricultural Sciences, Rural Development Administration, Jeonju 54875, Republic of Korea
[2]Department of Life Science, Sogang University, Seoul 04107, Republic of Korea
[3]Department of Bioindustry and Bioresource Engineering, Plant Engineering Research Institute, Sejong University, Seoul 05006, Republic of Korea

Triacylglycerol (TAG) is the storage oil of plant seeds or fruits for providing energy for seed germination. It has been reported that TAG is synthesized by three different diacylglycerol acyltransferases through the endoplasmic reticulum-dependent pathway by DGAT1 and DGAT2, and the cytosol-dependent pathway by DGAT3. Previously, we confirmed that camelina DGAT3 was involved in the seed oil content and the accumulation of α-linolenic acid (C18:3). In this study, we confirmed molecular and functional characterization of *CsDGAT1* and *CsDGAT2* using CRISPR/Cas-mediated *csdgat1* or *csdgat2* KO camelina. Camelina plants were transformed with a binary vector carrying two guide RNA cassettes for the editing of *CsDGAT1* and *CsDGAT2* genes, respectively, *Cas9* gene under the control of the egg cell-specific EC1.2 promoter, and *DsRed* gene for efficient selection. As a result, 5 *csdgat1* (EDD1) and 12 *csdgat2* (EDD2) camelina lines with an indel frequency over 15% were selected, respectively. The seed fatty acid composition of the complete *csdgat1* KO camelina lines showed decreased C18:1 and C18:2 contents and increased C18:3 content compared to that of WT. The seed fatty acid composition of most of the complete *csdgat2* KO camelina lines was similar to that of WT, however, EDD2#9-2 and EDD2#30-5 showed increased C18:1 and C18:2 content and decreased C18:3 content. In conclusion, we found that CsDGAT1 prefers C18:1 and C18:2 rather than C18:3, meanwhile, CsDGAT2 prefers C18:3 rather than C18:1 and C18:2. This can be helpful to generate camelina varieties with a different fatty acid composition tailored to the purpose of uses.

***Corresponding Author:** Tel. 063-238-4608, E-mail: realdanny@korea.kr

PH-0015

Development of soybean seeds with low storage proteins using RNAi and CRISPR/Cas9 systems

Hye Jeong Kim[1], Wan Woo Yeom[2], Hyemin Park[2], Ye Won Kim[2], Young-Soo Chung[1*]

[1]Department of Molecular Genetics, College of National Resources and Life Science, Dong-A University, Busan 49315, Republic of Korea

[2]Department of Applied Bioscience, College of National Resources and Life Science, Dong-A University, Busan 49315, Republic of Korea

Soybean (Glycine max), one of the major crops in the worldwide, is composed of 40% protein, of which 70% is the storage proteins including β-conglycinin (7S) and glycinin (11S). The storage proteins prevent the accumulation of the useful external proteins. Therefore, we tried to produce soybean transgenic plants with low storage proteins using RNA interference (RNAi) and CRISPR/Cas9 systems. In this study, transgenic soybean seeds with low storage proteins were produce by introducing 7S and 11S coding sequences within RNAi inducing hairpin construct via *Agrobacterium*-mediated transformation. Three plasmids, including pCKLSL_RNAi:7S, pCKLSL_RNAi:11S, and pCKLSL_RNAi:7S+11S, were transformed into the soybean, and a total of 10, 17, and 18 soybean plants were produced, respectively. The protein contents were analyzed with the sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) in T_1 soybean seeds, and it was confirmed that the storage proteins were reduced in the line #4 of pCKLSL_RNAi:7S and the line #2 of pCKLSL_RNAi:11S. For developing low storage proteins in soybean, we also attempted to perform the 7S and 11S gene editing using the CRISPR/Cas9 system to introduce mutations into the 7S and 11S genes with guide RNAs in soybean. Two plasmids, including pECO201:7S and pECO201:11S were also transformed into the soybean, and a total of 34 and 27 soybean plants were produced, respectively. As a result of performing the SDS-PAGE with T_2 soybean seeds, it was confirmed that the β-conglycinin protein was knocked out in the line #19-8 of pECO201:7S.

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***Corresponding Author:** Tel. 051-200-7510, E-mail: chungys@dau.ac.kr

PH-0016

Allergy-reducing wheat production using genome editing technology

Sewon Kim, Jae-Ryeong Sim, Eun Ji Park, Yu-Jeong Yang, Jong-Yeol Lee*

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

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. Celiac disease (CD), an autoimmune disease that affects 1-2% of the world's population, inhibits gluten absorption in the small intestine, causing inflammation and villus damage, leading to indigestion and abdominal pain. The omega-1,2 gliadins are a group of wheat gluten proteins that contain immunodominant epitopes for CD and also have been associated with food allergies. In this study, a Korean commercial wheat (cv. *Keumkang*) was transformed with gold particle bombardment and *Agrobacterium*-mediated using the CRISPR/Cas9 genome editing system. First, an omega gliadin gRNA was designed, inserted into a GE vector containing the CRISPR/Cas9, and transformed by gold particle bombardment. The fraction of omega-1,2 gliadin protein in half of the seeds of regenerated transformants (T_1) was analyzed by RP-UPLC. In the T_2 generation, 4 individuals lacking the omega-1,2 gliadin fraction were selected and the loss of the *omega-1,2* gliadin gene was confirmed by PCR. In addition, *omega-1,2* gliadin deficiency has been confirmed by copy number variation (CNV) analysis and NuPAGE. In the T_2 generation, it was confirmed that they were transgene-free using the structural gene of the GE vector. Next, *omega-1,2* gliadin gRNAs were designed and inserted into multiple vectors, pGoldenGreenGate-MoClo (pGGG-M), and transformation was performed through *Agrobacterium*. In the T_0 generation, four regenerative transformants were obtained. And among those lines, one transformant was observed which the *hyg* gene was inserted.

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

PH-0017

Genomic Selection Using Deep Learning for *Triticum aestivum* L. Traits

Yoon Ho Lim, Changsoo Kim*

Department of Smart Agriculture Systems, Chungnam National University, Daejeon 34134, Republic of Korea

Genomic selection (GS) is a method of predicting and calculating the complex traits of a crop capturing all variants affecting traits as a genomic estimated breeding value (GEBV). The complex traits we are interested in are determined by an infinite number of unlinked and additive loci each with an infinitesimally small effect. So, GS has become a popular way to predict these traits. Wheat (*Triticum aestivum* L.) has a genome size estimated at ~ 17 Gb, making it difficult to determine which parts affect the trait. Therefore, we applied Deep Learning (DL) to solve complex genome data of wheat. We applied two DL models, multilayer perceptron (MLP) and convolutional neural network (CNN). A total of 17,978 markers for genotype data and 28 traits in wheat grown in 2018 and 2019 for phenotype data were subjected to GS using DL. We used a total of 566 wheat samples, of which 20%, or 114 samples, were isolated as the test set. The remaining 452 samples were used to train the DL model and 5-fold cross validation was performed to improve the prediction accuracy of the DL model results. As a result, the prediction accuracy of the results varied by trait. The reason for this is expected to be the phenotypic distribution of the trait. Therefore, we elucidate that GS using DL works well, and we suggest that accurate phenotyping is essential to improve the prediction accuracy of the trait. Solving these problems will help advance the breeding of crops with complex genomes.

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

PH-0018

Development of PCR primer sets for screening of green mold-free mushrooms

Ji Weon Choi[1*], Sooyeon Lim[1], Han Ryul Choi[1], Hyang Lan Eum[1], Yeo Eun Yun[1], Hye Sung Park[2], Jae Han Cho[1]

[1]Postharvest Technology Division, National Institute of Horticultural and Herbal Science, RDA, Wanju 55365, Korea
[2]Mushroom Research Division, Institute of Horticultural and Herbal Science, RDA, Eumseong 27709, Korea

Species of *Trichoderma* and *Penicillium* are the main pathogens of mushroom, causing the most common green mold diseases. We developed molecular markers for rapid diagnosis of the green mold pathogens occurring in mushrooms. *Trichoderma harzianum* (KACC 40549, 40787), *Trichoderma koningii* (40779), *Trichoderma atroviride* (42248), *Trichoderma longibrachiatum* (44701), and *Penicillium brevicompactum* (45899) obtained from Korean Agricultural Collection Center were used as strains for the experiment, and DNA extraction was performed after culturing the strains. For adapting the PCR method for quick and specific detection of green mold fungi, and designed four pairs of PCR primers by analyzing the nucleotide sequence. The amplification product band size of *Trichoderma* spp., *T. longibrachiatum*, *T. harzianum*, and *Penicillium brevicompactum* were 498, 339, 529, and 402 bp, respectively. Result could be useful for diagnosing green mold fungi contamination in mushrooms by the application electrophoresis or real time PCR and screening of green mold-free mushrooms.

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***Corresponding Author:** Tel. 063-238-6521, E-mail: jwcnpri@korea.kr

PH-0019

Transgenic chili peppers overexpressing Cas9

Je Wook Woo, Eun Ji Sung, Yun Ji Park, Chee Hark Harn*

Dept. of Seed R&BD, ToolGen Inc., Seoul, 08501, Korea

Chili pepper is one of the most important vegetables globally. Many varieties have been developed through conventional and molecular breeding tools in the last 50 years. Still, breeders and scientists pursue new breeding technologies to develop new varieties that adapt to environmental changes and biotic stresses and have value-added traits. Genome editing technology emerged in 2012 as a fascinating tool to induce precision mutation to target an exact gene sequence site to get traits of interest. To obtain genome-edited pepper, an *Agrobacterium*-mediated transformation system is required, and chili pepper's transformation itself is a considerable challenge due to many obstacles, such as vector transformation to the nucleus and recalcitrant characteristics against organogenesis, including regeneration.

We have established a pepper transformation system with GFP expression. From the callus development stage, we can monitor GFP expression to ensure the pepper was transformed. Finally, we selected Cas9 GM peppers, and T1 seeds will be obtained this spring. The GM peppers will be used for the functional analysis of pepper genes by inoculating the viral vector composed of genome-edited components such as sgRNA. If viral vectors transfect the Cas9 GM pepper, the pepper genome of inoculated tissue can be edited. If pollen and egg carry the edited cells and fertilization occurs, targeted traits will appear in the next generation.

In the poster, we will mention the pepper transformation conditions, transformation efficiency, and monitoring system of transformation using GFP expression.

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***Corresponding Author:** Tel. 02-3660-1341, E-mail: chharn@hanmail.net

PH-0020

Development of early maturating soybean by using genome editing technology

Su Jin Lee[1], Hyeong Kyu Kim[1], Hyun Jin Chun[2], Mi Suk Park[3], Chun Hee Chung[3], Byung Jun Jin[2], Min Chul Kim[1,2,3*]

[1]Division of Applied Life Science (BK21 Four), Gyeongsang National University, Jinju 52828, Republic of Korea
[2]Institute of Agriculture & Life Science, Gyeongsang National University, Jinju 52828, Republic of Korea
[3]Plant Molecular Biology and Biotechnology Research Center, Gyeongsang National University, Jinju 52828, Republic of Korea

The proper timing of flowering in response to environmental changes is critical for ensuring crop yields. Modulation of the period required for flowering and maturation of soybean is important to maximize yield under current climate change conditions. To date, 11 major genes, *E1* through *E10* and *J*, have been identified as being involved in the control of flowering and maturity in soybean. To develop early flowering and maturating soybean, we generated CRISPR/Cas9 constructs targeting *E1* and *E2* gene, which suppress the flowering and maturation of soybean under long-day conditions. First, we generated CRISPR/Cas9 vector targeting both *E2* (*GmGIa*) and its close homolog (*GmGIb*) genes, simultaneously, and transformed it into Williams 82 cultivar. We confirmed gene editing (GE) of *GmGIa* and *GmGIb* by InDel PCR and targeted deep sequencing. The T2 plants of *GmGIa*/*GmGIb* GE lines showed early flowering and promoted maturation phenotypes compared to Williams 82 cultivar. And also, we generated GE soybean targeting *E1* gene, which has the biggest effect on soybean flowering time. So far, we obtained 20 T1 lines for *E1* GE and analyzed T-DNA insertion and genome editing in T1 plants by using *Bar* PCR, InDel PCR, and targeted deep-sequencing. Deletion of *E1* gene significantly shortened reproductive period. Genome editing of *E1* and *E2* genes can be applied to expand cultivating region of soybean.

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***Corresponding Author:** mckim@gnu.ac.kr

PH-0021

Molecular breeding of genome editing soybean lines with reduced anti-nutritional factors

Tae Hee Han[1], Dongwon Baek[2], Hyun Jin Chun[3], Mi Suk Park[2], Chun Hee Chung[2], Ye Jin Cha[1], Hae Rang Seo[1], Min Chul Kim[1,2,3*]

[1]Division of Applied Life Science (BK21 Four), Gyeongsang National University, Jinju 52828, Republic of Korea

[2]Plant Molecular Biology and Biotechnology Research Center, Gyeongsang National University, Jinju 52828, Republic of Korea

[3]Institute of Agriculture & Life Science, Gyeongsang National University, Jinju 52828, Republic of Korea

Soybean is a major source of oil and protein for human and animal nutrients. However, anti-nutrition factors included in soybean seed, such as allergenic proteins and phytic acid, limit the extensive use of soybean in the food and feed industry. P34 is a papain superfamily cysteine proteinase occupying <1% of the total seed proteins and regarded as a major soybean allergen to which more than 65% of soy-sensitive patients react. Phytic acid is the major storage form of phosphorus (P) in crops accounting for about 75% of total P in mature seeds. Phytate can chelate cationic metal micronutrients, such as iron and zinc, and may interact with proteins making them nutritionally unavailable. Here, we present the development of genome editing (GE) soybean lines exhibiting low allergen and phytic acid, respectively, by using CRISPR/Cas9 system. First, we developed three soybean GE lines, including simultaneously edited lines for both *P34* and *P34 homolog* genes, and specifically edited lines for each *P34* and *P34 homolog* gene. Then, we confirmed the reduction of P34 protein levels in these lines by using P34 antibody. To develop low phytate soybean, we generated CRISPR/Cas9 construct targeting both *GmMIPS1* gene, which functions at the first step in phytate biosynthesis, and its close homolog gene. Simultaneous deletion of both genes reduced phytate contents by about 40% in seeds compared to wild-type soybean seeds. These approaches would provide useful soybean germplasms to expand soybean utilization in the food and feed industry.

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***Corresponding Author:** mckim@gnu.ac.kr

PH-0022

반수체 배가에 활용하는 colchicine 대체용 자연배가 옥수수 계통선발

류시환*, 최재근, 김희연, 김문종, 한정헌, 왕승현, 김기선

강원도 홍천군 두촌면 장남길 26, 강원특별자치도농업기술원 옥수수연구소

옥수수에서 99% 이상의 순도를 가진 계통을 육종하기 위해서는 전통적인 방법에 의해 7회 이상의 인공교배(selfing)를 실시하여야 한다. 많은 노동력과 시간이 소요되는 전통육종의 이러한 단점을 보완하고자 선진국을 중심으로 배가 반수체(Doubled Haploid) 방법에 의한 계통육종이 실용화되고 있다. 배가 반수체 방법에 의하면 2~3작기에 순도 100%의 계통을 육성할 수 있다. 선진기술인 배가반수체 기술을 도입하여 국내 옥수수 계통육종의 효율성을 향상시키고자 강원특별자치도농업기술원 옥수수연구소에서는 국제옥수수・밀연구소(CIMMYT)와 협력하여 배가반수체 기술 이용에 필수적인 반수체 유기체의 사용 권리를 확보하였고, 2014년부터 이 기술을 국내 환경에 맞게 정착시켜 활용하고 있다. 국내에서 배가반수체 기술을 활용한 계통육성은 반수체 유기 및 종자선별, 염색체 배가 및 인공교배를 통한 계통 육성, 그리고 육성 계통의 특성평가 및 종자증식 등 3단계로 진행되고 있다. 이 중에서 두 번째 단계인 염색체 배가는 colchicine을 이용하는 것이 배가효율이 가장 좋다. 그러나 colchicine은 독성이 강하여 취급에 주의가 필요하므로 안전한 사용에 장해요인으로 알려져 있다. 이를 극복하고자 최근 자연배가를 이용하는 방법이 대두되었다. 아직 실용화 단계는 아니지만 향후 옥수수 계통육종에 활용도가 높을 것으로 기대되어 자연배가에 적합한 계통을 선발하고자 하였다. 옥수수연구소에서 육성한 26계통을 반수체 유기체와 교배하여 반수체를 생산하였고, 계통당 6~192주의 반수체 식물체를 확보하였다. 반수체 옥수수는 꽃가루 생산이 저해되는 것이 일반적이다. 총 868주의 반수체 식물체에서 단 10주만 인공교배를 통한 종자생산이 가능하였다. 이 중 19DHF158과 19DHF258은 각각 2주에서 종자생산이 가능하였고, 종자량도 10~260립을 확보하여 자연배가를 위한 중요한 자원으로 활용가치가 높을 것으로 기대된다.

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

PH-0023

Phenotype evaluation of a large-scale CRISPR/Cas9-mediated gene-edited rice population

Yurim Kim[1], Sieun Choi[1], Song Lim Kim[2], Sang Ryeol Park[2], In Sun Yoon[2], Jiheon Han[1], Hayeong Lee[1], Yeeun Jun[1], Soonhwa Kwak[1], Hosun Cheon[1], Youngjun Mo[1*]

[1]Department of Crop Science and Biotechnology, Jeonbuk National University, Jeonju 54896, Republic of Korea

[2]Gene Engineering Division, National Institute of Agricultural Sciences, Rural Development Administration, Jeonju 54874, Republic of Korea

CRISPR/Cas9 technology is being actively used to enhance various breeding traits such as biotic and abiotic stress tolerance and yield in rice. As part of the New Breeding Technologies Development Program, approximately 3,600 independent transgenic lines were generated in the Samkwang background, targeting transcription factors associated with biotic and abiotic stress responses and key agricultural traits. Among these, 235 lines with homozygous mutations in target genes were selected, including the T_2 (55 genes, 128 lines) and the T_3 (18 genes, 107 lines) generations. We visually evaluated major phenotypic variations compared to Samkwang and measured key agricultural traits including days to heading (DTH), culm length (CL), panicle length, and panicle number in 194 lines with at least five plants. Compared to Samkwang (DTH: 80 days, CL: 88 cm), the edited lines showed wide variations in DTH (67-86 days) and CL (64-100 cm), with phenotypic variations including early/late maturing, dwarfism, as well as leaf rolling and large grain size. Using the Cas9-free plants screened by PCRs, we are performing more precise evaluations of agricultural traits and productivity, especially focusing on lines exhibiting early maturity, dwarfism, and leaf rolling. Disease resistance and drought tolerance tests will be also conducted along with the relevant transcriptome analyses.

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***Corresponding Author:** Tel. 063-270-2530, E-mail: yjmo@jbnu.edu

PH-0024

Development and application of genome editing technology for peppers

Jae-Hyeong Park[1], Hyun Cho[2], Hyeran Kim[1,2*]

[1]Interdisciplinary Graduate Program in BIT Medical Convergence
[2]Department of Biological Sciences, College of Natural Sciences, Kangwon National University, Chuncheon, 24341, Republic of Korea

Rapid climate change is causing significant impacts on crop productivity and leading to the emergence of new plant-microbe interactions. Developing disease-resistant crops has become a crucial agricultural objective in light of these challenges. The utilization of CRISPR/Cas9-based genome editing plays a vital role in enhancing disease resistance in cultivated crops. Among the diverse species in the Solanaceae family, pepper (Capsicum annuum L.) stands out as one of the most extensively grown and cultivated varieties. In this study, we focused on editing the CaMLO2 gene using a highly efficient CRISPR/Cas9 RNP complex to confer disease-resistant traits in bell pepper Dempsey and six commercially important pepper cultivars. Currently, we are cultivating CRISPR/Cas9-RNP-delivered protoplasts under various culture conditions and optimizing the culture parameters to select the most promising cultivars. Moreover, we aimed to develop an improved binary vector for gene editing in pepper by introducing Cas9 protein and a guide RNA expression cassette using CRISPR/Cas9 technology. Considering the low gene editing efficiency observed in pepper cultivars, we designed binary vectors with enhanced promoters to facilitate efficient Cas9 expression. Four binary vectors were successfully constructed, and their editing efficiency was verified through next-generation sequencing in pepper protoplasts.

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

PH-0025

Development of infrastructure technologies for multipurpose farmland of reclaimed tidelands

Young-Jun Park[1*], Hyun-Tai Kim[2], Geon-Heo[1]

[1]Korea Rural Research Institute, Kores Rural Community Corporation, Asansi, Korea
[2]Mirae Rural Technology Institute, Uiwangsi, Korea

This study is aims to develop infrastructure technologies for multipurpose farmland of reclaimed tidelands for food security. The main contents is evaluate the irrigation method, the drainage management method and the optimal cultivation management model. In this study, we developed the technology of high value added agricultural land based on Hwa-Hong reclaimed tidelands through exploration and demonstration of optimal environmental condition.

Major results in this study were as follows:

1. (Surface drainage) The pavement slope was planned as a natural slope, 0.2~0.4% before reclaimed land was reclaimed in consideration of drainage efficiency.
2. (Irrigation) Underground irrigation (optimized soil moisture measurement system and algorithm) at reclaimed tidelands was developed using the non-excavation culvert installed in Hwa-Hong reclaimed tideland.
3. (Cultivation) Crop management system was developed for high value crops in Hwa-Hong reclaimed tideland.
   wheat: 390kg/10a, 93% yield compared to normal field (400kg/10a)
   soybean: 170kg/10a, 84% yield compared to general field (203kg/10a)
   maize: 490kg/10a, 85% yield compared to general field (580kg/10a)

These results will provide the standardization of a high value crop cultivation system at reclaimed tidelands.

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

PH-0026

Development and confirmation of Cas9-expressing soybean for efficient mutagenesis

Hyeon Do Lim[1], Jaehwan Kim[1], Jae Eun Jo[1], Myung-Shin Kim[1], Hyunwoo Park[2], Kyung Do Kim[1*]

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

[2]Future Technology Center, LG Chem, LG Science Park, 30 Magokjungang 10-ro, Gangseo-gu, Seoul 07796, Republic of Korea

The CRISPR/Cas9 system has been widely used for genome engineering in various organisms. However, soybeans have relatively few results compared with other plant species due to their low transformation rate. The size of the plasmid is one of the factors that affects transformation efficiency. Smaller plasmids generally have higher transformation rates than larger plasmids. Hence, higher transformation and editing efficiency might be accomplished by introducing the guide RNA portion of the CRISPR/Cas9 component to soybean plants that endogenously express the Cas9 gene. Here, we generated soybean transgenic plants expressing *Streptococcus pyogenes* Cas9 (SpCas9) under the constitutive 35S promoter. Soybean transformation was conducted using the Agrobacterium-mediated half-seed method. Transgenic plants with BASTA resistance were selected at T0 generation. Homozygous lines carrying the Cas9 insertion were selected by genotyping the T1 and T2 populations, and RT-PCR results confirmed Cas9 gene expression in transgenic plants. To confirm the presence of the Cas9 insertion, Illumina sequencing was used instead of the Southern blot experiment. De novo assembly of a 20-fold sequence identified the T-DNA insertion and the location of the insertion in the soybean genome. Together, we successfully developed Cas9-expressing soybeans for efficient and multiplex mutagenesis.

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

PH-0027

상추핵심집단 내 양상추 자원의 기내 재분화 체계 검정

조미현, 김정분, 김소현, 김경만, 김태성*

서울시 종로구 대학로 86 한국방송통신대학교 농업생명과학과

상추(*Lactuca sativa L.*)는 대표적 호냉성 작물로 고온, 장일 조건의 추대로 인해 여름철 생산량 저하로 연중 공급에 매년 차질을 생기고 있다. 최근 국내 소비자의 다양한 기호, 서구화된 식습관 등으로 잎상추보다 결구상추의 수입이 매년 큰 폭으로 증가하고 있는 가운데, 잎상추는 만추대에 대해 다양한 품종이 국내에서 개발되어 있으나, 양상추는 이에 대한 개선이 시급히 요구되고 있다. 또한, 만추대 형질은 전통육종에 의한 교배육종의 한계에 다다랐기 때문에 잎상추 및 양상추의 만추대 형질을 획기적으로 개선하기 위해 CRISPR/Cas9 등 생명공학적인 새로운 기술 도입이 필요한 시점이다. 따라서 본 연구는 KNOU 상추핵심집단 내 결구상추 대표자원(Butterhead 5점, Crisphead 5점, Romaine 5점)을 선발하여 효율적인 조직배양 Protocol을 확립하여, 다양한 head type에 적용할 수 있는 재분화 조건을 규명하고자 연구를 수행하였다. 무균 식물체를 얻기 위해 종자 소독용액의 침지 시간을 조절하였고, 표면 살균된 종자들은 1/2 MS 배지에 파종하여 온도20℃±1, 습도 50%±5 그리고 12시간 광조건에서 발아시켰다. 소식물체의 각1엽당 1개의 절편을 이용하여 Auxin 및 cytokinin계 호르몬 농도를 최적화하여 캘러스 유기 및 재분화 조건을 확립하였다. 마지막으로 기내 배양된 소식물체가 자연조건에 활착할 수 있도록 순화조건을 확립하였다. 본 연구를 통해 확립된 기내 재분화 체계는 다양한 양상추 자원을 대상으로 추대 등의 특성 등을 New breeding technique으로 효율적으로 개선하는 데 유용하게 활용될 것으로 전망된다.

***Corresponding Author:** Tel. 02-3668-4638, E-mail: kts117@knou.ac.kr

PH-0028

Developing rice mutants having superior quality through gene editing technology

Ah-Rim Lee[1], Backki Kim[1,2], Hyunjin Park[3], Tae-ho Ham[3], Joohyun Lee[4], Soon-Wook Kwon[1,2*]

[1]Department of Plant Bioscience, Pusan National University, Miryang, 50463, Republic of Korea
[2]Life and Industry Convergence Research Institute, Pusan National University, Miryang, 50463, Republic of Korea
[3]Department of Agricultural Science, Korea National Open University, Seoul, 03087, Republic of Korea
[4]Department of Crop science, Konkuk University, Seoul, 05029, Republic of Korea

Rice quality is mainly determined by starch characteristics such as variations in amylose content. In addition, the aroma components and lipid content of rice are also equally important. In this project, Gene-editing technology is being used to introduce variations in the fragrance characteristics and fatty acid composition of rice by targeting specific genes. The final goal of this project is to develop aromatic rice varieties with superior agricultural traits, and variations related to aroma components and fatty acid content. In this study, using the allele information of betaine aldehyde dehydrogenase (*badh2*) which leads to the accumulation of a fragrant compound in rice, We developed new variants (MS11_*badh2.2*, MS11_*badh2.3*, MS11_*badh2.7*) which introduce fragrance characteristics targeting tropical japonica with excellent global scalability. We are currently searching for new trait-related genes for 51 fragrance components found in rice and developing gene-edited variants. Also, two genes have been selected to improve fatty acid characteristics, and their variants are being developed. In addition, these variants are being developed using traditional breeding methods such as backcross breeding with a wild type rice variety or elite rice variety. Major agricultural genetic information is used to improve efficiency by simultaneously selecting and quickly purifying useful agricultural traits. The fragrance characteristic is a trait with high global consumer demand, and it is expected to contribute to securing competitiveness in domestic and global markets and in the agricultural industry by developing various aromatic rice varieties.

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

PH-0029

Comparison of Untargeted Metabolite Profiling of Low Phytic acid Soybean Mutants Mediated by CRISPR/Cas9

Eun-Ha Kim, Jeong Won Jeong, Myeong Ji Kim, Oh Suk Yu, Sang-Gu Lee, Hyoun-Min Park, Soo-Yun Park, Seon-Woo Oh*

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

Reduction of phytic acid (PA) in Soybean (*Glycine* max [L.] Merr.) seeds has the potential to improve food and feed nutritional value and decrease PA related environment pollution. Recently, the GmIPK1 (myo-inositol pentakisphosphate kinase 2) gene edited mutants (*GmIPK1* sgRNA-4 lines) by the CRISPR/Cas9 system were developed, yielding low phytic acid (LPA) in soybean seeds. In this study, untargeted metabolite profiling studies based on LC-MS on the two *GmIPK1* sgRNA-4 lines were conducted to assess the gene editing and environmental impact on the metabolite levels. Two *GmIPK1* sgRNA-4 (G4#21-10, G4#21-15) mutants were grown with the parental variety (Kwangan) and six commercial varieties in Gunwi and Jeonju during 2022. G4#21-10 and G4#21-15 showed about 20% decrease in phytic acid contents. The PLS-DA analysis by variety at each location revealed that G4#21-10 and G4#21-15 were tightly clustered with Kwangan, indicating their metabolite profiles were very similar to those of Kwangan. In addition, the PLS-DA analysis by location showed clear separation of two locations, demonstrating significant metabolite changes by environments. A number of EMRT (exact mass at retention time) ranged from 30 to 50 were statistically significant different in G4#21-10 and G4#21-15 compared to Kwangan. However, their differences were relatively small and mean of EMRT were in the range of conventional varieties. The majority of these differences were observed in metabolites related to environmental impact, including isoflavones. Our results suggested that untargeted metabolite profiles of G4#21-10 and G4#21-15 were equivalent to Kwangan and conventional varieties.

***Corresponding Author:** Tel. 063-238-4708, E-mail: ohsw0507@korea.kr

PI-0001

Identification of *TaF-box3*, post translation modification participant, confers regulation of *Arabidopsis* growth

Jae Ho Kim[1,2], Woo Joo Jung[3], Moon Seok Kim[1], Yong Weon Seo[1,4*]

[1]Department of Plant Biotechnology, Korea University, Seongbuk-Gu, Seoul, Republic of Korea
[2]Institute of Animal Molecular Biotechnology, Korea University, Seoul, Republic of Korea
[3]Institute of Life Science and Natural Resources, Korea University, Seoul, Korea
[4]Ojeong Plant Breeding Research Center, Korea University, Seoul, Republic of Korea

Histone methylation affects plant growth and is controlled by an array of genetic pathways that combine endogenous and external signals. In this study, we identified the involvement of TaF-box3, a member of the SCF (Skp1-Cul1-Rbx1-TaF-box3) ubiquitin ligase complex, in reproductive development of wheat. In addition, *in vitro* ubiquitination assays demonstrated that the $\text{SCF}^{\text{TaF-box3}}$ complex possessed a F-box domain that confers ligase functionality. *TaF-box3*-overexpressing *Arabidopsis* plants (OE) constitutively respresented early flowering as well as more differentiated cell size phenotype than wild-type. Moreover, in the OE plants, the transcript level of an *FLC* gene was considerably induced, which was connected to histone H3 Lys4 trimethylation (H3K4me3) and H3 Lys36 trimethylation (H3K36me3), according to chromatin-immunoprecipitation (ChIP) assay. Proteomic analysis confirmed that the methylation enzyme TaMETS1 was significantly degraded in the OE plant. Our study will help to improve physiological process of developmental study including flowering and cell growth in wheat. (Published: *Plant Science* **331**)

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

PI-0002

Allele Mining of Novel Loci and Expression Analysis of Candidate Genes for Fusarium Root Rot Resistance in Sweetpotato

Tae Hwa Kim[1,2*], Won Park[1], Mi Nam Chung[1], Koan Sik Woo[1], Hyeong-Un Lee[1], Kyo Hwui Lee[1], Jae-Myung Kim[1], Sang-Sik Nam[1]

[1]Bioenergy Crop Research Institute, National Institute of Crop Science, Rural Development Administration, Muan, Republic of Korea

[2]Department of Applied Biosciences, Kyungpook National University, Daegu, Republic of Korea

Fusarium root rot, caused by *Fusarium solani*, is one of the major postharvest diseases in sweetpotato (*Ipomoea batatas* (L.) Lam.). Developing resistant varieties is a sustainable way to control the disease. However, there are few studies on fusarium root rot resistance in sweetpotato. In this study, allele mining of significant SNPs and the expression analysis of candidate genes were conducted based on the results of previous GWAS for fusarium root rot resistance. The lesion length of 96 genotypes was evaluated in 2021, 2022, and combined years, and phenotypic variation was analyzed according to alleles of significant SNPs (LG3_22903756, LG4_2449919). In addition, qRT-PCR of 11 candidate genes, located within 100 kb flanking regions of the significant SNPs, was conducted for Geonhwangmi (resistant) and Beniharuka (susceptible) cultivars at 0, 1, 3, 6, 12, and 24 h post-inoculation with the isolate SPL21019. The frequencies of genotypes showed normal distribution in two and combined years. The genotypes carrying the SNP LG3_22903756-A allele exhibited significantly higher lesion length than those carrying the G allele in two and combined years, indicating that a molecular marker may be developed to select resistant lines based on the SNP information. The expression analysis of candidate genes showed up- (g12492, g12493, and g12495) and down- (g12494, g12497, g13128, and g13136) regulation, indicating that these genes may be involved in fusarium root rot resistance of sweetpotato. The results of this study will be helpful in marker-assisted selection (MAS) in breeding programs and mechanism studies for fusarium root rot resistance in sweetpotato.

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***Corresponding Author:** Tel. 061-450-0143, E-mail: taehwa123@korea.kr

PI-0003

Growth Characteristics of Sweetpotato Seedlings According to Cultivars and Sowing times

Kyo Hwui Lee*, Won Park, Tae Hwa Kim, Sang-Sik Nam, Hyeong-Un Lee, Mi-Nam Chung, Koan Sik Woo

Bioenergy Crop Research Institute, National Institute of Crop Science, Rural Development Administration, Muan 58545, Republic of Korea

In Korea, due to the low temperatures in early spring, the cultivation of sweetpotato(Ipomoea batatas(L.) Lam.) seedlings in green houses is essential. This study aimed to evaluate seedling growth characteristics according to sweetpotato cultivars and sowing times. Three cultivars, Hopungmi, Sodammi, and Jinyulmi, were buried in a double-layered green house on February 8, February 17, and February 27. The seedlings were harvested five times at one-week intervals, and measurements were taken for the number of nodes, internode length, etc. The results of the investigation into the characteristics based on sowing times and cultivars revealed significant differences in growth traits. Among the cultivars, Sodammi, sown on February 8th, exhibited the highest number of nodes with an average of 8.57, while Hopungmi, sown on February 27th, had the lowest number of nodes with an average of 6.1. Moreover, regarding internode length, Hopungmi sown on February 17th had the longest average length of 4.5 cm, whereas Sodammi sown on February 8th had the shortest internode length of 2.88 cm. In terms of the growth characteristics trend based on sowing times, the seedlings sown in February 8th showed the shortest internode length of 3.4 cm. However, they showed the thickest diameter of 4.29 mm. It is speculated that the seedlings sown in early February, being exposed to lower temperatures, experienced slower internode elongation. These research findings are anticipated to serve as fundamental data for the production of high-quality seedlings by considering the characteristics of different cultivars and sowing times.

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***Corresponding Author:** Tel. 061-450-0145, E-mail: leegh1131@korea.kr

PI-0004

Assessment Sweetpotato (*Ipomea batatas* L.) Cultivars for Adaptability in High-altitude Region of South Korea

Won Park*, Sujung Kim, Mi-Nam Chung, Koan Sik Woo, Hyeong-Un Lee, Tae Hwa Kim, Kyo Hwui Lee, Sang Sik Nam

Bioenergy Crop Research Institute, National Institute of Crop Science, Rural Development Administration, Muan, South Korea

In order to select sweetpotato cultivars adapted to high-latitude regions with cool climate, growth and yield characteristics of 20 sweetpotato cultivars (Domestically bred cultivars such as Sodammi, Hogammi, etc) were assessed in three different field during 2021~2022: Pyeongchang, Daegwallyeong (37° north latitude, 770m above sea level), Namwon, Unbong (35° north latitude, 500 m above sea level), and Muan, Cheonggye (35° north latitude, 14m above sea level). As for aboveground growth characteristics, the number of branches and nodes showed similar trends in all three regions during both years. The two-year average of data relating to number and weight of storage roots per plant, yield of total storage root and marketable storage root were recorded. Among the sweetpotato varieties for table use, Dahomi (5.5 tons/10a) and Pungwonmi (4.6 tons/10a) showed the high yield of marketable storage root in Pyeongchang regions with cool climate during both years. In the Namwon region, these two varieties also showed the highest yield. In case of sweetpotato varieties for starch processing, high yields of Jinhongmi (4.2 tons/10a) and Jeungmi(4.6 tons/10a) were observed in Pyeongchang and Namwon. Danjami showed the highest yield with (4.4 tons/10a) among the flesh colored cultivars. On the other hand, Shincheonmi variety seems to have low adaptability in high latitudes due to the low yield of marketable storage root. The results of this study will contribute to securing the foundation for sweetpotato cultivation in various regions and increasing productivity through the selection of varieties adapted to high latitude regions.

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***Corresponding Author:** Tel. 061-450-0142, E-mail: midaswon@korea.kr

PI-0005

Molecular characterization of novel sucrose transporters in wheat (*Triticum aestivum* L.)

Depika Prasad[1], Woo Joo Jung[1], Yong Weon Seo[1,2*]

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

Common wheat (*Triticum aestivum*. L) is one of the major cereal crops grown and consumed globally. Exploring its large and repetitive genome is now possible owing to recent developments in sequencing technology. Plant sucrose transporter (*SUT*) genes are a vital component of the energy transport system. These transporter genes have also been found to play important roles in a number of plant processes, including signaling and stress control. The purpose of this study was to identify and analyze five novel sucrose transporter genes in wheat. On the basis of their evolutionary relationships, the wheat sucrose transporter genes were subsequently split into five clades. Synteny analysis of the sucrose transporter genes revealed that the genome synteny between wheat and each of rye, barley, and *Brachypodium* is largely conserved. Additionally, cis-element analysis revealed that several phytohormones and light may operate as transcriptional regulators of the sucrose transporter genes. The transporter genes were generally expressed more in the root and stem of the plant, whereas they were differentially expressed in response to the abiotic stress treatments (cold, heat, NaCl, PEG-6000, and sugar). This was indicated by plant tissue-specific gene expression. This finding suggests that each *TaSUT* gene may be crucial in stabilizing the plant under stress by actively controlling the energy requirements of cells. The results of this study could serve as a foundation for future studies on sucrose transporters and their vital functions in plants' energy metabolism, as well as in their reaction to abiotic stress and in signaling and regulation.

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

PI-0006

LM 유채의 현장 검출을 위한 RPA(recombinase polymerase amplification)기반 진단 기술 개발

박선하, 친양, 천민관, 김양하, 정아름, 이범규*

전주대학교 환경생명식품과학학과

유전자변형생물체(GMO, Genetically Modified Organism)의 계속된 국내사용 증가에 따라, GM 작물 또한 의도적·비의도적으로 환경방출이 증가하고 있다. GM 작물의 환경방출이 증가하면서 정부 기관과 시민단체에서는 정기적으로 환경모니터링을 수행하고 있으며, GMO 이용 증가에 따라 모니터링의 중요성과 필요성이 강조되고 있다. 본 연구는 GM 유채의 야외환경 모니터링에서 현장 검출에 적용할 수 있는 재조합 효소-중합효소 증폭법(RPA, Recombinase Polymerase Amplification) 기술을 이용한 검출법을 개발하였다. GM유채 event T45, MON88302의 gDNA를 추출하여, 유채 event gDNA에 대한 염기서열을 이용 확보하였다. 확보한 서열로 primer designing software를 이용하여 유채 event에 대한 RPA primer 후보를 선별한 후, PCR 증폭과 qPCR에서의 RFU 값으로 최적의 primer와 probe를 결정하였다. 유채 event를 판별하기위해서 PCR(Portable Real-time PCR System, Gentier Mini)기기를 사용하였으며 Lid Heating 체크 해제하고 3step Amplication 20cycle과 39℃에서 20초씩의 PCR조건을 설정하였다. 마지막 step에만 flour선택하여 1분마다 한번씩 형광값을 측정하도록 하였고 Flourescence Setting에서 FAM만 선택하여서 최적의 측정 조건을 구성하였다. Positive Control은 TwistAMP exo kit에서 제공되는 것을 사용하였다. GM유채 event T45, MON88302에 대한 결과는 실험결과에서 나온 Amplication curve의 Ct값에 따라 결정하였다. 임계값(Threshold)의 경우 Positive Control RFU 값의 1/10로 설정하였으며, 임계값보다 낮은 결과값은 유전자 변형이 일어나지 않았다고 판정하였다. GM유채 event T45, MON88302 결과는 Ct값이 약 4.84와 6.56으로 각 event에대해 검출이 되었다 판정할 수 있다. 본 연구에서 개발된 기술을 사용하면 현장에서 20분이내에 신속한 검출이 가능하고, 등온PCR 기기 또한 3.2 kg의 작은 크기로 휴대가 간편하다는 장점이 있다. 등온PCR 기기를 사용하여 RPA 기반 진단 기술은 LM유채 환경 방출 모니터링에도 유용하게 적용될 수 있을 것이다.

***교신저자:** Tel: 063-220-2227, E-mail: leebk@jj.ac.kr

PJ-0001

Draft genomes of two morphologically similar mushrooms endemic in Korea; *Ganoderma lingzhi* and *Perenniporia fraxinea*

Hyun Jo Koo, Eun-Kyung Kim, Hwa-Yong An, Soyeon Kang, Gyoungju Nah*

Genome Analysis Center at National Instrumentation Center for Environmental Management, Seoul National University, 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Republic of Korea

Both *Ganoderma lingzhi* (Yeongji-beoseot in Korean) *Perenniporia fraxinea* (Acaseehwingoomeong-beosot in Korean) are large mushrooms, and they have been used as traditional medicine. Ganoderic acids, which belong to a group of highly oxygenated lanostane-type triterpenoids, are known as the major pharmacologically active compounds of *Ganoderma* species. The genomes of *Ganoderma lingzhi* and *Perenniporia fraxinea* wee sequenced using both PacBio Sequel IIe and Illumina short read platforms. We generated 1.32 Gb (~29X coverage) and 1.60 Gb (~44X coverage) of PacBio HiFi data for *Ganoderma lingzhi* and *Perenniporia fraxinea*, respectively, and 7.68 Gb and 7.99 Gb of Illumina short read data for *Ganoderma lingzhi* and *Perenniporia fraxinea*, respectively. To estimate the genome size, k-mer analysis was performed, resulting in genome size of 45.5 Mb and 36.7 Mb for *Ganoderma lingzhi* and *Perenniporia fraxinea*, respectively. Through *de novo* genome assembly using Nextdenovo followed by polishing and Purge Haplotigs process, we obtained 45.9 Mb and 36.5 Mb of genome sequences consisted of 36 and 38 contigs with N50 of 2.93 Mb and 2.31 Mb for *Ganoderma lingzhi* and *Perenniporia fraxinea*, respectively. We also tried Flye for genome assembly. Through *de novo* genome assembly using Flye followed by polishing and Purge Haplotigs process, we obtained 46.2 Mb and 36.3 Mb of genome sequences consisted of 21 and 46 contigs with N50 of 3.63 Mb and 1.68 Mb for *Ganoderma lingzhi* and *Perenniporia fraxinea*, respectively. Based on *ab initio* annotation, a total of 16,024 genes and 9,720 genes were predicted for *Ganoderma lingzhi* and *Perenniporia fraxinea*, respectively.

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***Corresponding Author:** Tel. 02-880-4974, E-mail: gnah.nicem@snu.ac.kr

PJ-0002

Pseudo-chromosomal genome assembly of salt marsh turfgrass *Zoysia sinica*

Hyeonseon Park[1†], Eunji Bae[2†], Kyuchan Kim[1], Jaekyung Jung[1], Jaewook Kim[1], Bae Young Choi[1], Chetan Kaur[3], Geungjoo Lee[3,4], Changsoo Kim[5], Donghwan Shim[1,6*]

[1]Department of Biological Science, Chungnam National University, Daejeon 34134, Republic of Korea
[2]Forest Biomaterials Research Center, National Institute of Forest Science, Jinju 52817, Republic of Korea
[3]Department of Horticulture, Chungnam National University, Daejeon 34134, Republic of Korea
[4]Department of Smart Agriculture Systems, Chungnam National University, Daejeon 34134, Republic of Korea
[5]Department of Crop Science, College of Life Sciences, Chungnam National University, Daejeon 34134, Republic of Korea
[6]Center for Genome Engineering, Institute for Basic Science, Daejeon 34126, Republic of Korea

Zoysia species have been commonly used in golf courses, gardens, and parks and tolerate various abiotic stresses. Salt marsh plants face multiple environmental stresses such as high soil salinity and low oxygen concentration. *Zoysia sinica* is a salt marsh grass that is capable of thriving in such a stressful environment. However, the genetic mechanisms behind its adaptation to such conditions and its genome information have been unveiled till date. In this study, we assembled a pseudo-chromosomal genome of allotetraploid grass, *Z. sinica* using Nanopore sequencing and Illumina sequencing. The genome had 20 pseudo-molecules with a total length of 313.7 Mb and a high contiguity with the scaffolds N50 value of 18.9Mb. We predicted 30,476 protein-coding genes based on full-length transcripts using PacBio long-read isoform sequencing (Iso-Seq) and 41.64 % of repeat sequences in the *Z. sinica* genome. The comparative genomic analysis identified orthologous genes in seven species and provided Copy number variants of genes involved in salt stress and waterlogging responses. A high-quality genome coupled with genomic architecture analysis could provide insights into understanding of plant adaptation to these harsh environments in *Z. sinica.* Investigating these genetic factors provides new insights into the development of stress-tolerant crops for agriculture and to identify potential targets for genetic engineering.

†Co-first authors: Hyeonseon Park, Eunji Bae.

***Corresponding Author:** Tel. 042-821-6279, E-mail: dshim104@cnu.ac.kr

PJ-0003

Characterization of complete mitochondrial genomes of *Ganoderma lingzhi* and *Perenniporia fraxinea*

Jiran Jeong, Sanghee Um, Eunkyung Chun, Eunbyeol Ko, Gyoungju Nah*

Genome Analysis Center at National Instrumentation Center for Environmental Management, Seoul National University, Seoul, Korea

We have generated complete mitochondrial genome sequence of *Ganoderma lingzhi* in the *Ganodermataceae* family and *Perenniporia fraxinea* in the *Polyporaceae* family, featuring de novo assembly of Illumina NovaSeq paired-end sequencing data. Although they belong to different families, they are easy to mix and difficult to distinguish due to their similar appearance. So, the analysis was conducted with the aim of developing markers that can be distinguished. The mitochondrial genome size of *Ganoderma lingzhi* was 115,192 bp and *Perenniporia fraxinea* was 60,459 bp. As a result of annotation, a total of 50 genes in the mitochondrial genome of *Ganoderma lingzhi*, including 24 protein-coding genes and 26 transfer RNA (tRNA), and a total of 79 genes in the mitochondrial genome of *Perenniporia fraxinea*, including 53 protein-coding genes, 24 transfer RNA (tRNA) genes and 2 ribosomal RNA (rRNA) genes. Among the annotation results, we will develop markers in the gene sequence regions found together in two mitochondrial genome sequences.

Keywords: Mitochondrial genome, authentication, *Ganoderma lingzhi*, *Perenniporia fraxinea*

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

PJ-0004

Development of PCR-based markers for discrimination of *Solanum iopetalum* from other *Solanum* species

Ju-Ryeon Jo, Tae-Ho Park*

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

The hexaploid *Solanum iopetalum* is a wild potato species that forms tubers and originates from Mexico. Because of its diverse useful traits, such as resistance to late blight, potato wart, root-knot nematode, potato virus X, and potato virus Y, as well as some degree of tolerance to drought and heat, it can be used as an important material for developing new potato varieties. *S. iopetalum* has the same EBN value as cultivated potatoes, and can be used for breeding purposes through direct crosses with potatoes. In this study, the chloroplast genome of *S. iopetalum* was completely sequenced using next-generation sequencing technology, and specific markers for *S. iopetalum* were developed by comparing its chloroplast genome with those of other *Solanum* species. The total length of the chloroplast genome of *S. iopetalum* was 155,625 bp, and its structure, length, gene number, and composition were highly similar to those of other *Solanum* species. In addition, phylogenetic analysis using coding sequences of chloroplast genomes of *S. iopetalum* and 18 other species belonging to the Solanaceae family revealed that *S. iopetalum* was closely grouped with *S. stoloniferum*, *S. verrucosum*, *S. hougasii*, *S. hjertingii*, and *S. demissum*. Sequence alignment of chloroplast genomes of *S. iopetalum* and 10 other *Solanum* species identified four InDels and nine SNPs specific to *S. iopetalum*, and a total of five PCR-based *S. iopetalum*-specific markers were developed. The results obtained in this study will contribute to understand the evolutionary aspects of *Solanum* species and to breed new potato varieties using *S. iopetalum*.

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***Corresponding Author:** E-mail: thzoo@daegu.ac.kr

PJ-0005

Development of PCR-based markers to select plastome genotypes of *Solanum mochiquense* using complete chloroplast genome sequences

Ju-Ryeon Jo, Tae-Ho Park*

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

The diploid *Solanum mochiquense* originates from Peru and is one of the tuber-bearing wild potato species. It can be useful for potato breeding due to its resistance to late blight, alfalfa mosaic virus, potato leafroll virus and potato virus X. However, it is not possible to introduce these useful traits into cultivated potatoes through sexual hybridization between them, because its Endosperm Balanced Number (EBN) value differs from those of cultivated potatoes. Somatic fusion can overcome these sexual reproduction barriers, but the process requires the confirmation of hybrid genotypes using molecular markers. In this study, we reported the complete chloroplast genome of *S. mochiquense* sequenced using next-generation sequencing technology and compared it with those of other *Solanum* species to develop *S. mochiquense*-specific markers. The total length of the chloroplast genome of *S. mochiquense* was 155,547 bp and composed of 158 genes with a circular molecular structure. The structure and gene composition were very similar to those of other *Solanum* species, and maximum likelihood phylogenetic analysis comparing *S. mochiquense* with 19 other species belonging to Solanaceae family revealed that *S. mochiquense* was closely related to other *Solanum* species. Sequence alignment of chloroplast genomes of *S. mochiquense* and 10 other *Solanum* species identified 7 InDels and 113 SNPs specific to *S. mochiquense*, and developed PCR-based specific markers targeting the 2 InDels and 3 SNPs of them. These results will provide an opportunity to understand the evolution of *Solanum* species and to breed new potato varieties using *S. mochiquense.*

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***Corresponding Author:** E-mail: thzoo@daegu.ac.kr

PJ-0006

Development of *Solanum vernei*-specific markers using the complete chloroplast genome sequences of *Solanum* species

Seoyeon Son, Tae-Ho Park*

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

Solanum vernei, originating from Argentina, is being utilized as an important material for developing new potato varieties due to its resistance to Potato wart, Potato cyst nematodes, and Potato virus X. However, *S. vernei* used in this study has an EBN (Endosperm Balanced Number) value of two, which is different from that of cultivated potatoes (*S. tuberosum*) and it causes sexual reproduction barriers between them. To overcome this problem and to introgress the novel traits from *S. vernei* into cultivated potatoes, cell fusion can be performed. In this study, the chloroplast genome sequence of *S. vernei* was obtained by next-generation sequencing technology (NGS) and was compared with those of eleven other *Solanum* species to identify *S. vernei*-specific molecular markers. The total length of the chloroplast genome of *S. vernei* is 155,591 bp and its structure and gene composition are similar to those of other *Solanum* species. Phylogenetic analysis with the chloroplast genome of *S. vernei* and those of 21 other Solanaceae family members revealed that *S. vernei* was most closely related to *S. kurtzianum.* Sequence alignment with the chloroplast genomes of *S. vernei* and ten other *Solanum* species revealed 30 SNPs specific to *S. vernei.* Based on these, five PCR-based markers for distinguishing *S. vernei* from other *Solanum* species were developed. The results obtained in this study will aid in exploring evolutionary aspects of *Solanum* species and accelerating potato breeding using *S. vernei.*

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***Corresponding Author:** E-mail: thzoo@daegu.ac.kr

PJ-0007

Development of molecular markers for selection of plastid genotypes of *Solanum kurtzianum*

Seoyeon Son, Tae-Ho Park*

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

Solanum kurtzianum is one of the wild potato species originating from Argentina, and exhibits resistance to abiotic factors such as heat, drought, and salinity, as well as biotic factors such as blackleg, Potato wart, and potato leafroll virus. These useful traits make it a valuable resource for potato breeding. Due to different EBN values of two and four between *S. kurtzianum* and *S. tuberosum*, respectively, direct cross between them is not possible, and somatic cell fusion can be utilized to overcome this limitation. In this study, we report chloroplast genome of *S. kurtzianum* completed using next generation sequencing technology and *S. kurtzianum*-specific markers based on the comparison of *S. kurtzianum* cpDNA with those of other *Solanum* species. The total length of the *S. kurtzianum* cpDNA was 155,522 bp, and its length and structure were similar to those of other *Solanum* species. Phylogenetic analysis with cpDNAs of *S. kurtzianum* and 21 other species belonging to the Solanaceae family revealed that *S. kurtzianum* is most closely related to *S. vernei.* After multiple alignment of the complete cpDNA sequences of *S. kurtzianum* and ten other *Solanum* species, 26 SNPs specific to *S. kurtzianum* and one InDel specific to both *S. kurtzianum* and *S. hougasii* were identified. Based on these, one Indel and four SNP-based PCR markers specific to *S. kurtzianum* were developed. The results of this study will contribute to understand more comprehensive, and evolutionary aspects of *Solanum* species and to breed new potato varieties using *S. kurtzianum.*

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***Corresponding Author:** E-mail: thzoo@daegu.ac.kr

PJ-0008

EXTRA-LARGE G-PROTEIN2 (XLG2) interacts with RTV1 to regulate flowering in Arabidopsis

Jae Bok Heo*

Department of Molecular Genetic Engineering, Dong-A University, Busan, 49315, Korea

Heterotrimeric G proteins, consisting of Ga, Gb and Gg subunits, play important roles in plant development and cell signaling. In Arabidopsis, in addition to one prototypical G protein a subunit, GPA1, there are three extra-large G proteins, XLG1, XLG2, and XLG3 of largely unknown function. Each XLG has a C-terminal Ga-like region and a ~400 amino acid N-terminal extension. Here we show that the three XLG proteins specifically bind and hydrolyze GTP, despite the fact that these plant-specific proteins lack key conserved amino acid residues important for GTP binding and hydrolysis of GTP in mammalian Gas. Moreover, unlike other known Ga proteins, these activities require Ca^{2+} instead of Mg^{2+} as a cofactor. XLG2 interacts with nuclear protein RELATED TO VERNALIZATION1 (RTV1). Electrophoretic mobility shift assays show that RTV1 binds to DNA *in vitro* in a non-sequence specific manner and that GTP-bound XLG2 promotes the DNA binding activity of RTV1. Taken together, a Ca^{2+}-dependent G protein, XLG2, may play a role in promoting RTV1 DNA binding activity.

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Keywords: XLG2, G protein, RTV1, Protein-protein interaction

***Corresponding Author:** E-mail: jbheo72@dau.ac.kr

PJ-0009

Syntenic relationship analysis between *c. transvaalensis*, rice, and sorghum

Sol Ji Lee, Chang Soo Kim*

Department of Crop Science, Chungnam National University, Daejeon 34134, Korea

Cynodon transvaalensis is a perennial grass species that belongs to the Chloridoideae subfamily. It is a warm-season grass with a global distribution. This species is of significant economic and ecological importance due to its notable characteristics, including excellent resistance to abiotic stress and the ability to recover rapidly. As a result, it is now utilized for various purposes. In a previous study, we successfully completed the genome assembly of *C. transvaalensis.* In the current study, we conducted a genome synteny analysis to explore the evolutionary relationship between rice and sorghum, using the assembled genome of *C. transvaalensis.* We found that *C. transvaalensis* exhibited a high level of collinearity with rice and sorghum, two plants closely related to the Chloridoideae subfamily. This limited genomic information is anticipated to contribute to our understanding of grass species genome evolution and serve as a valuable resource for investigating the complex genome composition of Bermuda grass.

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***Corresponding Author:** Tel. +82-10-3021-1559, E-mail: changsookim@cnu.ac.kr

PJ-0010

A gap filled reference genome sequence for Korean native radish (*Raphanus sativus L. Bakdal*)

Han Yong Park[1], Yu-jin Lim[2], Myunghee Jung[2], Hyojung Son[2], Sathiyamoorthy Subramaniyam[2], Seong Ho Heo[1,3], Byeong Jun Park[1,3], Younhee Shin[2*]

[1]Department of Bioresource Engineering, Sejong University, Seoul 05006, Korea
[2]Research and Development Center, Insilicogen Inc., 13, Yongin-si, Gyeonggi-do, 16954, Republic of Korea
[3]Institute of Breeding Research, DASAN Co.Ltd, Pyeongtaek 17864, Korea

Radish is a food vegetable, widely exists in the cultivation process. Continuous growth in global population and global warming pressuring the scientific community to ensure the food sustainability. Thus, promote crop scientist to uncover the hidden nature of individual traits in each and every crop to enhance the productivity through identifying the various stress resistance trait. In genomic era, due to cost reduction in sequencing procedures keep promoting the pan-genome and multiple genome reference for individual crops to understand the genetic diversity. In this study, we generated the genome sequences from Korean breeding line *Raphanus sativus* with Illumina, PacBio Sequel and Omni-C sequencing technologies. The sequenced genome estimated to be 427.71 MB and assembled into 398.01 MB (N50: 40.3 MB), with 9 chromosomes. We achieved the chromosomal level assembly with 0.76 MB (0.19%) of gaps, while the pan-genome reference (RS00) has 34.08 MB (7.41%) of gaps and RS1.0 had a gap of 54.6 MB (12.8%). In the case of BUSCO, an core gene index, RS00 has 4,534 (98.6%) and RS1.0 has 4,484 (97.5%), whereas *L. Bakdal* has 4,537 (98.7%), which was the most complete. Finally, we uncovered the improved genome for Korean native *Raphanus sativus L. Bakdal*, with less gaps, which is a good addition to the Raphanus family genus genetic resource.

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***Corresponding Author:** Tel. 031-278-0061, E-mail: yhshin@insilicogen.com

PJ-0011

Exploring SNP variations in β-conglycinin: Enhancing soybean protein quality and allergenicity assessment

Soo-Kwon Park[1], Sang-Beom Lee[2], Gyu-Tae Park[1], Dool-Yi Kim[1], Mi-Suk Seo[1], Yu-Na Kim[1], Joo-Mi Jun[1], Sun-Kyung Jung[1], Hee-Ju Jeong[1], Jung-Kyung Moon[1], June-Yeol Choi[1], Hyeon-Jung Kang[1*]

[1]National Institute of Crop Science, RDA, Wanju 55365, Republic of Korea
[2]National Institute of Crop Science, RDA, Suwon 16429, Republic of Korea

β-conglycinin is a glycosylated protein consisting of trimers, with a molecular weight ranging from 150 to 200 kDa. It is rich in aspartic acid, glutamic acid, leucine, and arginine, and constitutes approximately 34% of the total protein content in soybeans. The protein composition, such as the presence of 7S and 11S fractions, can affect the nutritional quality and functional properties of soy protein products. Notably, several cupin proteins, including soybean 7S globulin (β-conglycinin), are recognized as major plant food allergens. Hence, genetic studies focusing on storage proteins like β-conglycinin are crucial for reducing soybean allergens and developing improved-quality functional varieties. In this study, SNP variations in the soybean core collection were identified through functional haplotype analysis of the cupin 7S vicilin-like N domains of the β-conglycinin subunit genes (α’ and β). The α’ subunit gene of β-conglycinin, Glyma.10g246300, exhibited a substitution of Arg^{427} to His^{427} at position 47.4 Mb in the coding sequence. On the other hand, the β subunit gene, Glyma.20g146200, showed five distinct groups, with the identification of seven non-synonymous and one synonymous SNPs at position 38.4 Mb. Based on the information on SNP variations, soybean varieties with major or minor alleles for both the α’ and β subunit genes were selected. The genetic information regarding storage proteins in soybeans can be valuable for selecting suitable varieties for food production and utilizing protein components in various applications.

***Corresponding Author:** Tel. 063-238-5321, E-mail: happykorean@korea.kr

PJ-0012

Genetic analysis and database construction of new domestic and imported rice varieties

Myoung-Jin Kim[1], SooMin Park[1], Young-Joon Choi[1], Hee-Chang Shin[2], Mi-Ri Hong[2], Min-Hee Jeong[1], Woo-In Choi[1], Eun-Joo Moon[1], Ju-Seon Ahn[1], Hye-Yeong Jin[1], Hyun-Young Lee[1], Ki-Chul Jung[2*]

[1]Gyeonggi Provincial Office of National Agricultural Products Quality Management Service, 114, Anyang-ro, Manan-gu, Anyang-si, Gyeonggi-do, 14035, Republic of Korea
[2]Experiment Research Institute of National Agricultural Products Quality Management Service, 141, Yongjeon-ro, Gimcheon-si, Gyeongsangbuk-do, 740-220, Republic of Korea

New domestic rice varieties are cultivated and distributed every year in Korea. Also, due to the expansion of tariff rate quotas(TRQ) importing countries, continuous management through the establishment of a database of genetic information on new domestic and imported rice varieties is required. In addition, it is necessary to prepare in advance whether the current genetic analysis method (Identification of rice variety and country of origin with 22 SNP markers) can be applied to new varieties of public stockpiled rice that are selected every year. Therefore, To cope with the above situation, this study conducted sample collections and genotype anlaysis of new domestic and foreign rice varieties and research on re-sequenced rice genome information. First, standard samples of 16 new domestic varieties and 22 foreign varieties were collected, and genotypes were analyzed using the 22 SNP marker set. As a result of genotype analysis, 11 out of 16 domestic varieties could be distinguished by 22SNP gene markers. 59 genotypes were identified by analyzing 22 foreign species(rice samples) and 9 of which will be listed in the manual as new TRQ genotypes and used for country of origin management. In addition, 2 SNP markers were selected to distinguish 22SNP pattern overlap (4 varieties) with existing varieties listed in the manual, and an average of 8,013Mbp sequences including 416,953 SNPs and 64,919 Indels were obtained through next generation sequencing(NGS) and bioinformatic analysis in 17 domestic varieties. The information on DNA polymorphisms was registered in NAQS server. Therefore, it is judged that it is possible to preemptively deal with illegal distribution of new varieties through genome analysis and database establishment of new rice varieties, and it can be used for grain management and country of origin analysis.

***Corresponding Author:** Tel. 031-470-2981, E-mail: gumdung3@korea.kr

PJ-0013

Phylogeny and comparative mitochondrial genomes, a medicinal and vegetable plant of the Campanulaceae family

Hoy-Jin Choi, Mi-Hwa Choi, Ji-Nam Kang, Si-Myung Lee, Chang-Kug Kim*

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

Campanulaceae family is medicinal plants which have the application of oriental medicine, food fields, herb tea, ornamental flower and health products. We compared the complete mitochondrial genomes between Korean balloon flower (Platycodon grandiflorus) and bonnet bellflower (Codonopsis lanceolata)

Assembled mitochondrial genome of P. grandiflorus consists of two circular chromosomes and master circle contained 56 genes, whereas the minor circle contained 42 genes. The C. lanceolata comprised a single circle harboring 54 genes. Using the comparative genome structure and repeat pattern, we revealed that P. grandifloras minor circle was resulted by recombination of the direct repeats of the master circle. Phylogenetic relationship of 16 asterids determined using 14 conserved mitochondrial protein-coding sequences.

Our dataset can be useful as a comparative genome for evolution studies and will facilitate characterizations for biological research in the Campanulaceae family.

***Corresponding Author:** Tel. 063-238-4555, E-mail: chang@korea.kr

PJ-0014

Chromosome-scale genome assembly of *Codonopsis lanceolata* provides insights into its genome evolution

Chang-Kug Kim*, Hoy-Jin Choi, Mi-Hwa Choi, Ji-Nam Kang, Si-Myung Lee

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

The lance asiabell (Codonopsis *lanceolate*) belonging to the Campanulaceae family is a valuable medicinal and vegetable plant distributed mainly in East Asia. Here, we present a high-quality chromosome-scale genome assembly of *C. lanceolata* based on hybrid method using Nanopore long-read, Illumina short-read, and Hi-C data. The assembled genome was completed as 1,273 Mb containing eight pseudo-chromosomes. The genome comprised 71.3 % of repeat sequences and 46,005 protein-coding genes, of which 85.7 % genes were functionally annotated. Completeness of the assembled genome and gene was assessed 97.5 and 90.4 %, respectively by BUSCOs analysis. Phylogenetic and synteny analysis showed that *C. lanceolata* was closely related to *Platycodon grandiflorus* in the Campanulaceae family. Gene family evolution revealed significantly expansion of related genes involved in saponin biosynthesis in the *C. lanceolata* genome. The genome resources for various studies to improve this medicinal plant and will broaden the understanding for the Campanulaceae family

***Corresponding Author:** Tel. 063-238-4555, E-mail: chang@korea.kr

PJ-0015

Two rice genes encoding cyclic nucleotide-gated channel are redundantly required for pollen germination and tube growth

Eun Young Kim[1], Myung-Hee Kim[1,2], Sang Dae Yun[1], Su-Kyoung Lee[3], Sung-Aeong Oh[1], Yu-Jin Kim[4], Ki-Hong Jung[3*], Soon Ki Park[1*]

[1]School of Applied Biosciences, Kyungpook National University, Daegu 41566, Republic of Korea
[2]Genomics Division, Department of Agricultural Bio-Resources, National Institute of Agricultural Sciences, Rural Development Administration, Wansan-gu, Jeonju 54874, Republic of Korea
[3]Graduate School of Green Bio-Science & Crop Biotech Institute, Kyung Hee University, Yongin, 17104, Republic of Korea
[4]Department of Life Science and Environmental Biochemistry, Pusan National University, Miryang, 50463, Korea

Pollen is crucial for seed production in the staple crops. However, the molecular mechanisms of pollen germination and tube growth in rice (*Oryza sativa L.*) have been little revealed. Recently, we identified that two rice genes encoding cyclic-nucleotide-gated channels, *OsCNGC4* and *OsCNGC5* are redundantly expressed in mature pollen and interact mutually. To overcome the functional redundancy, we produced the gene edited rice plants which have mutations in both genes. The homozygous *OsCNGC4* and *OsCNGC5* gene-edited mutants (*oscngc4/5*) using the CRISPR-Cas9 system showed significantly low pollen germination rate compared to wild type. Transcriptome analysis displayed that receptor kinase, transporter, and cell wall metabolism related genes were downregulated in double *oscngc4/5* mutant. To know the direct regulators of OsCNGC4 which form a heterodimer with OsCNGC5, we screened a yeast two hybrid library having rice cDNAs from mature anther. Subsequently, we identified two CaM, NETWORKED 2A (NET2A), and Proline-rich extension-like receptor kinases 13 (PERK13) proteins as interactors of OsCNGC4, suggesting its roles in regulating Ca^{2+} channel activity, F-actin organization and ROS homeostasis. Our results suggest that *OsCNGC4* with *OsCNGC5* may play critical roles on pollen germination and elongation by regulation of Ca^{2+} gradient in growing pollen tube.

***Corresponding Author:** Tel. 053-950-7751 E-mail: psk@knu.ac.kr, khjung2010@khu.ac.kr

PJ-0016

Alternative splicing affects the tolerance under salt stress in sorghum

Ha Jeong Lee[1], Yuna Kang[1], Changsoo Kim[1,2*]

[1]College of Agriculture and Life Sciences, Chungnam National University 99 Daehak-ro, Yuseong-gu, Daejeon 34134, Republic of Korea

[2]Department of Smart Agriculture Systems, Chungnam National University, Daejeon 34134, Korea

In crop cultivation, external environmental factors, including abiotic stress, can have negative implications for productivity and economic viability. Among these stressors, salt stress can trigger oxidative stress, osmotic stress, and ion toxicity, and this association impacting the growth and development of crops. Due to their immobility, plants arise various mechanisms to endure and adapt to adverse conditions. Notably, alternative splicing (AS) contributes to the generation of diverse transcript isoforms, resulting in variations in gene expression and protein diversity. This capability enables plants to withstand extreme environments and external stimuli.

In this study, we conducted RNA-seq analysis using three sorghum varieties: “Sodam-chal” (sensitive response to salt), “Nampung-chal” (resistant response to salt), and “Hwanggeum-chal” (intermediate respone sensitivity and resistance to salt). The experiments were conducted by subjecting the plants to untreated control conditions and treatment with 150 mM NaCl for 3 and 6 days, respectively, followed by leaf sampling after a total of three biological replicates. To identify significantly differentially expressed genes (DEGs) within and between varieties under salt stress, comparative transcriptome analysis was performed. The comparison between Sodam-chal and Hwanggeum-chal revealed the highest number of DEGs, indicating substantial differential gene expression. Moreover, through alternative splicing analysis, we investigated the occurrence and event types of AS within and between varieties in each comparison group. Based on the AS list overlapping with DEGs, we conducted a protein domain search to identify protein domains related to salt tolerance, and AS event types and transcript isoform changes occurring in the corresponding genes were confirmed.

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

PJ-0017

Genetic diversity of *Glycyrrhiza uralensis* and its closely related species based on plastid genome and nrDNA sequences

Daewon Kang[1], Jong-Soo Kang[1], Hyeonah Shim[1], Sae Hyun Lee[1], Jin Tae Kim[1], Jungeun Kim[2], Jeonghoon Lee[3], Tae-Jin Yang[1*]

[1]Department of Agriculture, Forestry and Bioresources, Plant Genomics & Breeding Institute, Research Institute of Agriculture and Life Sciences, College of Agriculture & Life Sciences, Seoul National University, 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Korea
[2]Personal Genomics Institute, Genome Research Foundation, Cheongju, 28190, Korea
[3]National Institute of Horticultural and Herbal Science, RDA, Eumseong 27709, Korea

Glycyrrhiza L. (Fabaceae), commonly known as licorice, is an economically important genus in pharmacology. Some *Glycyrrhiza* species contain glycyrrhizin, which is a compound having pharmacological properties. The glycyrrhizin-containing species, such as *G. aspera*, *G. glabra*, *G. inflata*, and *G. uralensis*, belong to the GAU clade within the IR-lacking clade. The glycyrrhizin-containing species are mainly distributed in Central Asia, exhibiting morphological variations in their leaves, inflorescences, and pods. Their intermediate forms are commonly observed and have emerged as problems in species identification and delimitation. To examine the species delimitation between the glycyrrhizin-containing species, an extensive dataset comprising 115 plastid genome sequences and 111 nrDNA sequences was utilized in this study. We newly assembled plastid genome and nrDNA sequences of 29 accessions, which were mainly collected from central Asia including China, Mongolia, Uzbekistan, Kazakhstan, Kyrgyzstan, and Russia by the Rural Development Administration (RDA). The assembled plastid genomes of 29 *Glycyrrhiza* accessions were consistent with the previously reported genomes of the IR-lacking clade in genome structure, and the assembled 45S nrDNA sequences were highly conserved in the genus *Glycyrrhiza*. The phylogenetic analyses based on plastid genome and nrDNA sequences supported the monophyly of most species, but those two glycyrrhizin-containing species, *G. glabra*, *G. uralensis*, and their hybrid *G. korshinskyi* were unclear. This study will be helpful for understanding the genus *Glycyrrhiza*, especially the glycyrrhizin-containing species, and facilitates the utilization of this valuable plant for medical and industrial purposes.

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

PJ-0018

Development and application of novel gDNA-SSR Markers in *Salvia miltiorrhiza.* in Korea

Eihyun Kim[1,2], Jong-Wook Chung[1], Kyung Ho Ma[2], Jeong Hoon Lee[2], Jin Tae Jeong[2], Jong Won Han[2*]

[1]Department of Industrial Plant Science and Technology, Chungbuk National University, Cheongju 28644, Republic of Korea

[2]Department of Herbal Crop Research, National Institute of Horticultural and Herbal Science, Rural Development Administation, Eumseong 27709, Republic of Korea

Molecular markers are very useful tool for genetic studies and used for crop breeding. Simple sequence repeat (SSR) marker has various uses including genetic diversity analysis, variety discrimination, population structure analysis, marker assisted selection (MAS). This study was conducted to assess *S. miltiorrhiza* accessions and to provide basic data for efficient breeding. 50 SSR markers were designed using whole genome resequencing data of *S. miltiorrhiza* and 41 polymorphic markers were selected. 44 *S. miltiorrhiza* accessions were assessed by 41 SSR markers. A total of 346 alleles were detected ranging from 2 to 17 with an average of 8.4 alleles per locus. The major allele frequency (MAF) was 0.19 to 0.83 with an average 0.47. The observed heterozygosity (HO) were 0 to 0.60 with an average 0.22 and polymorphic information content (PIC) were 0.29 to 0.87 with an average 0.64. UPGMA clustering showed that 44 *S. miltiorrhiza* accessions were classified into three groups and each accession was differentiated by 41 SSR markers. Population structure analysis suggested that all accessions were divided into two subpopulations and one admixed group at K=2. 17 SSR markers out of 41 SSR markers were selected as a marker for variety discrimination. Three cultivars that *S. miltiorrhiza* 'Dasan', *S. miltiorrhiza* 'Gosan' and *S. miltiorrhiza* 'Hongdan' were discriminated using each marker. These SSR markers developed in this study could be effectively used for variety discrimination, genetic diversity and population structure analysis for crop breeding program.

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***Corresponding Author:** Tel. 043-871-5673, E-mail: pvphan@korea.kr

PJ-0019

국내 무화과 유전자원의 전장유전체 연관분석 및 품종군 분류

이소미[1*], 윤창용[1], 조윤섭[1], 박수현[2], 김대관[2], 유의수[2], 한범수[3]

[1]전라남도 해남군 옥천면 용정리길 20 전라남도농업기술원 과수연구소
[2]서울특별시 강남구 역삼1동 628-58 DNACARE
[3]전라북도 전주시 덕진구 농생명로 370 국립농업과학원 농업유전자원센터

본 연구는 국내에 도입 무화과 유전자원 30자원을 대상으로 품종분류체계 확립에 필요한 정보 제공을 위해 수행되었다. 전장유전체염기서열(WGS: whole-genome sequences)데이터와 17개의 양적 형질에 대한 수치형, 범주형 데이터를 사용하여 무화과 유전자원의 유전적 차이와 계통 유연관계를 구명하기 위해 260만 여개의 SNP데이터를 사용하여 계통 분석하였다. 승정도우핀(IT no.233550)을 제외한 29개의 자원이 크게 Group1, Group2로 분류되었고 Group2의 경우 4개의 subgroup으로 분류되었다. 양적 형질에 대한 수치형 데이터와 범주형 데이터의 상관 분석에서는 과실의 종경과 횡경, 과중과 종경, 과중과 횡경이 서로 양의 상관관계를 나타내었다. 수확일은 subgroup2에 브라운 터키(IT no.233553)를 제외하고 브룬스윅(IT no.233552), 바나네(IT no.233557)가 8월 달로 대체로 빠른 편이었고 과실의 횡경과 종경이 긴 편으로 과중도 높았다.

***교신저자:** Tel. 061-880-8013, E-mail: iamsom@korea.kr

PJ-0020

Extensive mitochondrial plastid DNA (MTPT) transferred sequences in plastomes of Asclepiadoideae revealed by *de novo* mitochondrial genome assembly pipeline utilizing long HiFi sequence read

Jeongjin Choi, Sae Hyun Lee, Minjeong Kang, Jee Young Park, Tae-Jin Yang*

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

The mitochondrial genome (mitogenome) has been extensively studied for breeding purposes, particularly for cytoplasmic male sterility (CMS) and marker-assisted selection. Despite its importance, the assembly of the complete mitogenome remains challenging due to its complex structure, which comprises repetitive sequences and intracellular transferred sequences. Especially mitochondrial plastid DNA (MTPT) regions can result in misassembly due to the sequence homology within the plastid genome (plastome) and mitogenome. To overcome this hurdle, we developed a *de novo* assembly pipeline for the mitogenome utilizing HiFi long-read sequencing data. This pipeline computes the mitogenome composition from HiFi data through read mapping on the conserved mitogenome-specific genes from allied species. Based on the mitogenome read composition of the HiFi data, organelle genomes are assembled with optimally scaled-down sequencing data. Subsequently, the chimerically assembled sequences caused by MTPT are removed, and overlapping assembled sequences with each other complete the assembly. The mitogenomes of three *Cynanchum* species (*C. auriculatum*, *C. rostellatum*, and *C. wilfordii*) were assembled, and 38 protein-coding genes were annotated with GeSeq and Artemis programs in their mitogenomes. Including newly assembled species, the subfamily Asclepiadoideae showed a higher proportion of MTPT and tandem repeat contents in the plastome than other Gentianales taxa. The Asclepiadoideae have 24,674 bp of the commonly transferred sequences with 48 plastid genes in their plastome, including *matK* and *rpoB* genes widely used as universal markers in various species. Extensive and in-depth studies with complete mitogenomes of diverse species in various fields will be possible through the pipeline.

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

PJ-0021

Research on Parallel Processing for NGS-Based Genotyping Pipelines for Distributed Processing in Response to Supercomputers

Kyu-Won Kim[1], Jin-Hyun Kim[2], Kwang Soo Kim[3*]

[1]Research Institute of Agriculture and Life Sciences, Seoul National University, 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Republic of Korea
[2]Genomics Division, National Institute of Agricultural Sciences, Jeonju 54874, Republic of Korea
[3]College of Agriculture and Life Sciences, Seoul National University, 1 Gwanak-ro, Gwanak-gu, Seoul 08826, Republic of Korea

Agricultural transitions into digital breeding and data-driven farming can be promoted using supercomputers, which allow to leverage bio big data such as genomics and transcriptomics in the fields of agriculture and biological engineering. Still, few tools for big data analysis such as fast NGS genotyping analysis pipelines have been optimized for supercomputers. In the present study, we have devised key elements needed for distributed processing in NGS genotyping pipelines for supercomputers. In particular, we analyzed and implemented the elements of parallelization for the widely recognized GATK genotyping pipeline under a supercomputing environment based on Linux shell. We found that multiple procedures of the GATK pipeline could induce the bottlenecks in execution time. Such procedures were modified to increase computing efficiency under parallel computing conditions. In addition, we implemented methods to predict and prevent the possibility of deadlocks arising from the distributed processes during parallel processing. Our results showed that a wide range of pipelines for bio big data can be improved to support distributed computing, which merits further development studies.

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***Corresponding Author:** Tel. 02-880-4556, E-mail: luxkwang@snu.ac.kr

PJ-0022

Albino phenotype caused by pseudogenization of the plastid *rpoB* gene in a commercial chimera cultivar ‘Melanie’ of *Cornus Kousa* in Cornaceae

HaYan Lee, Daewon Kang, Tae-Jin Yang*

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

Chimeric plants are utilized for ornamental purposes due to significant ornamental and economic values. Chimeric phenomena can arise from several origins: genetic mutations in nuclear or plastid genomes and transposable genetic elements. Recently, mutations in the plastid genome have emerged as a potential factor of chimeric phenomena. However, a plastid gene responsible for inducing the chimeric phenomenon in the *Cornus kousa* has not been reported yet. In this study, the plastid genomes and 45S nuclear ribosomal DNA (nrDNA) sequences from *C. kousa* cv. Melanie was newly assembled from both Green Leaf Tissue (GLT) and Albino Leaf Tissue (ALT) using the de novo assembly of Low Coverage Whole-genome sequencing (dnaLCW) method. Sequence comparisons between GLT and ALT were conducted using the newly assembled sequences. One Insertion/Deletion (InDel) was found in the plastid genome sequences, while no Single Nucleotide Polymorphism (SNP) or InDel was found in the 45S nrDNA sequences. The InDel was located within the *rpoB* gene and generated an internal stop codon, resulting in early termination of the gene. The *rpoB* gene is a plastid-encoded RNA polymerase (PEP) involved in the expression of photosynthesis-related genes. Using the single InDel found in the *rpoB* gene, we developed a High-Resolution Melting (HRM) marker to distinguish between GLT and ALT. In future study, we will apply the developed marker to additional *C. kousa* cultivars. We believe that our study is noteworthy for understanding the chimeric plants and the developed marker will be useful for the identification of the mutation causing the albino phenotypes.

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

PJ-0023

Discovering genomic loci associated with seed coat pigmentation in soybean using GWAS analysis

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

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

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

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

PJ-0024

SoyPedi: A phenotype search interface integrated with soybean pedigree for user-friendly access

Min-Gyun Jeong[1], Chaeyoung Lee[2,3], Jin Hyun Kim[2,4], Yoram Choi[1], Hye Jeong Kim[5], Young-Soo Chung[5], Hong Kyu Choi[5*]

[1]Department of Applied Bioscience, Dong-A University, Busan, Republic of Korea
[2]Department of Medical Bioscience, Dong-A University, Busan, Republic of Korea
[3]Dongnam Institute of Radiological & Medical Sciences, Busan, Republic of Korea
[4]Genomics Division, Department of Agriculture Biotechnology, National Institute of Agriculture Sciences, Rural Development Administration, Jeonju, Republic of Korea
[5]Department of Molecular Genetics, Dong-A University, Busan, Republic of Korea

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.

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

PJ-0025

Digital Breeding Information Digitalizing and Visualization Technology for Digital Breeding Transformation

Do-sin Lee, Kwang-hyun Cho, Jae-eun Oh, Ji-eun Kim, Hye-ri Jeong, Jeong-hee Lee*, Sung-Hwan Jo*

SEEDERS Inc., Daejeon, 34912, Republic of Korea

Digital breeding is an artificial intelligence and big data-based breeding technology that digitizes all genetic resource information to develop composite trait varieties that meet the needs of farmers and consumers. Here we present a web-based digital breeding platform connected with big data for the transition to digital breeding. Currently, it consists of whole genome sequencing (WGS) of more than 33 accessions of Capsicum annuum, including chili peppers and bell peppers. SNP analysis was performed in 33 C. annuum, and these accessions were aligned to the Capsicum annuum L. genome (v1.6). A total of 61,845,045 SNPs were identified from the obtained reads. Among the SNPs identified in genic regions, 14,773 haplotypes from genes have been confirmed across the C. annuum genome, which consists of 35,884 genes. WGS data from more than 111 accessions have been completed sequencing and are currently in the variant calling phase with the reference genome. These data will be added to the database by the end of 2023. The web-based digital breeding platform connected with big data introduces the following three functionalities. Through integration with the established database, users can conveniently access 1) lineage-specific Marker-Assisted Backcrossing (MABC) results, 2) GWAS marker information based on threshold variations, and 3) gene-specific haplotype information. Chromosome position information for MABC marker selection can be quickly grasped at a glance, and improved representation methods enable intuitive examination of specific traits through marker comparisons. The availability of GWAS results for different traits and the provision of results in various formats have increased data utilization. For interfamilly breeding combination design and marker reduction strategies for backcrossing selection, gene-based haplotypes provide fundamental information about LD blocks, including position, gene length, and frequency of haplotype. By developing and providing a web-based digital breeding platform linked to databases and analysis tools, we anticipate contributing to the practical implementation of molecular breeding and the transition to digital breeding as a user-friendly platform based on genomic information.

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

PJ-0026

OsSKS (*SKU5 Similar*) is required for pollen germination and male fertility in rice

Sang Dae Yun[1], Myung-Hee Kim[1,2], Eun Young Kim[1], Sung-Aeong Oh[1], Yu-Jin Kim[3], Ki-Hong Jung[4], Soon Ki Park[1*]

[1]School of Applied Biosciences, Kyungpook National University, Daegu 41566, Republic of Korea
[2]Genomics Division, Department of Agricultural Bio-Resources, National Institute of Agricultural Sciences, Rural Development Administration, Wansan-gu, Jeonju 54874, Republic of Korea
[3]Department of Life Science and Environmental Biochemistry, Pusan National University, Miryang 50463, Republic of Korea
[4]Graduate School of Biotechnology and Crop Biotech Institute, Kyung Hee University, Yongin 17104, Republic of Korea

In crop plants, pollen tube growth is crucial for the delivery of sperm cells to the ovule and affects grain yield. However, the molecular mechanisms underlying pollen germination and tube elongation remains unclear. Here, based on microarray data analyzed for developing anthers and pollen grains, *OsSKS* (SKU5 Similar family) gene showed late pollen-specific expression in anatomical expression analysis. In order to identify the functional role of *OsSKS*, we examined the segregation ratio in progeny for the T-DNA insertional mutants and the result demonstrated a distorted segregation ratio of 1:0.9:0.1 (wild-type:heterozygote:homozygote) which was frequently observed in gametophytic mutants. To determine whether the mutation caused a defect in male or female gamete transfer, we conducted reciprocal crosses. Notably, the experiments showed a significant reduction in transmission of the *ossks* gamete through the male lineage. Furthermore, both T-DNA insertional mutants and CRISPR/Cas9 knockout mutants of *OsSKS* displayed substantially low seed-setting rates. In comparison with wild-type pollen tubes, those of the *ossks* mutants ruptured more frequently when grown *in vitro.* Additionally, the growth of the *ossks* pollen tubes was failed to reach the embryo sac, thereby resulting in decreased male fertility. Next, our results demonstrate that OsSKS interacts with Mks1, cytME2, and ALDH2b confirmed by yeast two-hybrid assay and Co-IP assay. Transcriptome analysis revealed that 255 pollen-preferential genes were downregulated in *ossks-2* compared with the WT, and these genes are associated with cell wall modification. Thus, we propose that *OsSKS* plays a key role in pollen germination and tube elongation in rice.

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

PJ-0027

Genome-level and gene-level analysis of four rice isolines to identify the expression regulation-related elements of abiotic stress resistance traits

Ji Hun Hwang[1], Na-Hyun Shin[2], Jae-Hyuk Han[2], Joong Hyoun Chin[2], Kyung Do Kim[1*]

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

[2]Department of Integrative Biological Sciences and Industry, Sejong University, Seoul 05006, Republic of Korea

Climate change occurs flooding and drought that make reduce crop productivity, which causes global food crisis. To overcome the food crisis, the new isoline which has genes or QTLs (Quantitative Trait Locus) related to abiotic stress was bred by modern breeding. For example, Sub1 (Submergence1) and Pup1 (Phosphorus uptake1) isoline of IR64 (*Oryza sativa* subsp. Indica cv IR64) have abiotic stress resistance traits like submergence situations and phosphorus deficiency of soil. In recent research, the IPS (IR64-Pup1+Sub1), which pyramided Pup1 and Sub1's QTL was newly developed. IPS rice shows Sub1's submergence tolerance trait. However, IPS doesn't express Pup1's phosphorus uptake trait in phosphorus deficiency soil. To know the reason why Pup1's trait wasn't expressed, we performed genome-level and gene-level analyses. First, we perform genome assembly to identify the structural variation among four isolines for genome-level analysis. Each assembly of isolines shows about 98% completeness from the BUSCO (Benchmarking Universal Single-Copy Orthologs) assessment. We found that there is a common structural variation pattern except for the major QTL region between isolines by using global alignment. Additionally, we perform genome annotation to know the genome structure of each isoline. About 42,000 genes were annotated in each isoline and each annotation showed about 94% completeness from the BUSCO assessment. Among about 42,000 annotated genes, 34,742 genes from three isolines except IPS had orthologous with IPS and we checked 24,875 genes co-expressed from all isolines. Our genome-level and gene-level research results will be integrated for further analysis to identify the expression regulation-related elements.

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

PJ-0028

Determination and Accumulation of Gene Expression Data between Sorghum Genetic Resources by HPC

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

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

Plant genetic resources play a vital role in both in basic research as well as agricultural development such as digital breeding. Thus, many nations have dedicated substantial efforts to gather and to keep diverse genetic resources. In Korea, the National Agrobiodiversity Center (NAC) has undertaken significant measures to secure many resources including over 3,300 sorghum genetic resources. To ensure their effective utilization in agricultural research and development, it is crucial to estimate the differences of gene express between resources as well as between tissues in a resource. Considering this, we have developed an efficient pipeline using RSEM and edgeR. The pipeline has demonstrated exceptional efficiency and speed in estimating different expression level, analyzing 96 test samples from 8 representative genetic resources selected based on genotype data on RDA High-Performance Computing (HPC) system. Beside the transcriptome data, our team is committed to effort, aiming to determine genetic variants in over a thousand sorghum samples. Subsequently, the data will be publicly released through the National Agricultural Biotechnology Information Center (NABIC), contributing to broader agricultural knowledge and advancements.

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

PJ-0029

Deciphering *Saltol* QTL Functionality in Salinity Stress Tolerance: Comparative Transcriptome Analysis in MS11 and Backcrossed Inbred Lines

Jae-Hyuk Han[1,2], Na-Hyun Shin[1,3], Ian P. Navea[1,3], Il-Ryong Choi[2], Joong Hyoun Chin[1,3*]

[1]Department of Integrative Biological Sciences and Industry, Sejong University, 209 Neungdong-ro, Gwangjin-gu, Seoul 05006, Republic of Korea
[2]The International Rice Research Institute Korea Office, National Institute of Crop Science, Rural Development Administration, Iseo-myeon, Wanju-gun 55365, Republic of Korea
[3]Convergence Research Center for Natural Products, Sejong University, Republic of Korea

Salinity in soil affects almost all aspects of plant development. *Saltol*, located in chromosome 1, is a well-known QTL for salinity tolerance, which has been used to develop highly tolerant rice varieties in Southeast Asia, South Asia, and Africa. However, its functions remain unclear, and the molecular markers linked to *Saltol* have not always been effective in rice breeding programs. Two backcrossed inbred lines (BILs) harboring *Saltol* QTL were developed using marker-assisted backcrossing to improve salinity stress tolerance into MS11, a temperate *japonica* that can grow in tropical regions. Interestingly, despite both BILs containing *Saltol* QTL, they show very different phenotypes under salinity stress conditions. To account for the phenotypic differences of BILs under salinity conditions, RNA-seq analysis has been conducted with MS11 and two BILs. Shoot and Root tissues were collected at seedling stage, 1h after the salt treatment. By comparing the transcriptome profiles of MS11 and two BILs, A total of 2729 DEGs (1415 MS11, 993 MS11-SaltolA, and 1909 MS11-SaltolB) were identified in whole rice plant. Among these DEGs, GO enrichment analysis was performed only for genes common to MS11 and MS11-SaltolA and expressed differently only in MS11-SaltolA. GO enrichment analysis showed that genes encoding metabolic pathways and biosynthesis of secondary metabolites, including Organic acid, Small molecule, Carboxylic acid, and Oxoacid metabolic process. Through this study, we will contribute to the rice breeding of salinity-tolerant variety by identifying related candidate genes fully functional in *Saltol* QTL.

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

PJ-0030

Comparative Analysis of the Chloroplast Coding Sequence in the Malvaceae Family

Soon-Ho Kwon, Kyeong-Seong Cheon, Do-Yeon Kim, Young-Im Choi, Hanna Shin*

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

The Malvaceae family encompasses a wide range of species, from herbaceous to woody plants and is utilized for ornamental, medicinal, and industrial purposes. After completing chloroplast genome sequence of *Hibiscus syriacus*, our research explored the divergence process of the Malvaceae family through chloroplast coding sequences of 17 species from four genera: *Hibiscus*, *Abelmoschus*, *Gossypium*, and *Tilia amurensis.* The number of coding regions was 129 for *T. amurensis*, 133 for *Abelmoschus*, and 130 for the remaining two genera. In *T. amurensis*, the start codon of *infA* remained as an ambiguous pseudogene. Additionally, in the *Abelmoschus* genus, *rpl19*, *rpl22*, and *rpl16* were duplicated and included in the IR regions from the LSC region. The phylogenetic analysis indicated a clear divergence among genera. After the differentiation of the *T. amurensis*, *Gossypium* species, *Hibiscus* tree species, shrubs and herbaceous species of *Hibiscus*, and *Abelmoschus* were diverged in succession. *H. cannabinus* had the most SNP (806 bp) and InDel regions (71), while *H. syriacus* had the fewest (10 bp SNP and two InDel regions). *H. rosa-sinensis* exhibited the highest number of species-specific SNPs, representing 51.2% of the total SNPs. In contrast, the species with the fewest unique markers were *H. syriacus*, *H. mutabilis*, and *H. taiwanensis.* We found that coding region-based classification could be as effective as full-genome methods, with species divergence leading to an increase in gene count. Future research should further explore the functions of chloroplast genes to enhance our understanding of species divergence and chloroplast performance within species.

***Corresponding Author:** Tel. 031-290-1165, E-mail: hanna193@korea.kr

PJ-0031

A Pan-Genomic Approach to Discern Early and Late Flowering Mechanisms in 11 Rice Accessions

Yejin Lee[1,2], Dong U Woo[1,2], Yang Jae Kang[1,2*]

[1]Division of Bio & Medical Bigdata Department (BK4 Program), Gyeongsang National University, Jinju 52828, Republic of Korea

[2]Division of Life Science Department at Gyeongsang National University, Jinju, Republic of Korea

Background: Rice represents one of the pivotal staple food crops globally, with its flowering time playing a significant role in overall yield and productivity. Early and late flowering timeframes in rice are dictated by intricate genetic networks, the understanding of which is integral for the cultivation of novel rice varieties with enhanced yield and adaptability. However, the sheer size and diversity of the rice genome pose challenges to efficient sequencing and assembly.

Methods: In our study, we employed a pan-genomic strategy using nanopore technology, along with independent de novo assembly techniques, to sequence and assemble the genomes of 11 distinct rice accessions demonstrating varied flowering times. Following this, comparative genomics and transcriptomics were employed to pinpoint genetic variations and gene expression profiles associated with early and late flowering.

Results: We have conducted sequencing on 11 accessions and their corresponding tissue transcriptomes, including leaf, root, and flower, utilizing Nanopore and MGI sequencing technologies. The 11 accessions have undergone de novo assembly, and the gene contents have been prepared alongside the transcriptome data. Currently, we are in the process of constructing web services for the assemblies and gene catalogs.

Conclusion: This study accentuates the potential of a pan-genomic approach combined with nanopore technology and independent de novo assembly techniques in unraveling complex traits in large and diverse crop genomes. The results furnish novel insights into the genetic mechanisms underlying flowering time in rice, providing promising targets for crop improvement and contributing to potential reductions in carbon usage in rice cultivation.

***Corresponding Author:** Tel. 055-772-1352, Fax. 055-7721349, E-mail: kangyangjae@gnu.ac.kr

PJ-0032

Comparative analysis of transcriptome between omega-3 enhanced transgenic soybean and non-transgenic soybean

Sang-Gu Lee*, Seon-Woo Oh, Eun-Ha Kim, Hyoun-Min Park

Biosafety Division, National Institute of Agriculture Science. Rural Development Administration, Jeonju 54874, Republic of Korea

Soybean is major food crop for human globally, and it is used as a source of plant oil. Especially, α-linolenic acid, an omega-3 fatty acid is taken as health supplement. To develop transgenic soybean with high omega-3 fatty acid content, the *PfFAD3-1* gene, which is derived from *Physaria fendleri* called Lesquerella plant, strongly produces omega-3 fatty acid, was used to construct vector with seed-specific promoter. To identify gene expressions in metabolic engineering of fatty acid biosynthetic pathways, we compared between GM soybeans and Non-GM soybean using transcriptome analysis. We first identified gene expression pattern in leaves and analysis of seed is ongoing. The comparative analysis was carried out using three transgenic soybean lines with a copy of T-DNA and non-transgenic counterpart two Kwangan variety. Threre are 6,737 different expression genes (DEGs) in the comparative analysis between each sample. DEGs varied by comparison combination, especially between controls. Biological function analysis based on DEGs was performed between GM soybeans and Non-GM soybean. In result many DEGs are identified in order metabolic pathways and biosynthesis of secondary metabolites. In particular, we found that triacylglycoerol lipase SDP1 gene in DEGs related to lipid metabolism was up-regulated in all three transgenic soybeans line than the control. The result of these transcriptome analyses may identified unintentional gene expression between GM and Non-GM, but there are DEGs also in the control groups. Given this, the transcriptome analysis need to be utilized as safety assessment tech along with various method such as genomics and metabolomics.

***Corresponding Author:** Tel. 063-238-4720, Email: sangulee@korea.kr

PJ-0033

Highly Accurate Genome Assembly of *Geumgang1* with Various Assembly Strategies using Long-read HiFi sequencing

Muhyun Kim[1], Minyoung Song[1], Dohye Kweon[1], Yumi Ko[1], Sihyun Park[1], Ill-Min Jung[1], Jung-Hyun Gong[2], Backki Kim[2], Soon-Wook Kwon[2,3], Joohyun Lee[1*]

[1]Department of Crop Science, Konkuk University, Seoul 05029, Korea
[2]Department of Plant Bioscience, College of Natural Resources and Life Science, Pusan National University, Miryang 50463, South Korea
[3]Life and Industry Convergence Research Institute, Pusan National University, Miryang 50463, South Korea

For most crops, Yield is the upmost valuable factor in crop industry. *Geumgang1(Milyang307) rice* is super-high yield rice developed by Rural Development Administration, National Institute of Crop Science, Republic of Korea. *Geumgang1* is sorted by *Tongil* Variety known as high yield rice variety crossing of *Oryza Sativa subsp. Japonica* and *Indica* variety. To make a good use of molecular breeding to finding secrets of super-high yield of *Geumgang1*, WGS(Whole Genome Sequencing) of *Geumgang1* is needed to be done precisely. So, We generated sequence read data of *Geumgang1* by PacBio®HiFi sequencing and performed assembly. Genome assembly is performed two ways, one is reference-based assembly and the other one is *de novo* assembly. In Reference-based assembly, Due to *Tongil* variety's crossing, 3 different varieties of *Oryza Sativa L.* (*Oryza Sativa subsp. Japonica cv. nipponbare, Oryza Sativa subsp. Indica cv. IR64, Oryza Sativa subsp. Indica cv. R498*) are used. To assess assembly quality, Benchmarking Universal Single-Copy Orthologs (BUSCO) has been used, no differences between reference-based and *de novo* assembly. Moreover, Contig and scaffold N50 of all reference-based assembly shows approximately 30 - 32Mbp. However, N50 of *De-novo* assembly shows very short length. Several gaps are found in three reference-based alignment and those gaps are not able to fill with presented HiFi reads. Gap filling steps are carried out by filling gaps with query sequence which is reference genome or aligned *De novo* assembly that has no gaps within. Genome synteny analysis was performed through *Geumgang1* and three reference genomes to find large structural variants. Further, Gene annotation analysis, including synteny analysis, is performed for structural and functional annotation of *Geumgang1* genome.

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

PJ-0034

Transcriptomic comparison between purple-pigmented and normal leaves of soybean

Hee Jin You, Yeong-ho Kim, Seo Yoon Yang, Sungwoo Lee*

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

Purple-discoloration of the uppermost leaves has been observed on soybean accession 'PI 96983' in the later growth stages in recent years. Leaves on the uppermost(UP), middle(MD), and lower(LW) positions showed purple-pigmented, partially purple-pigmented, and green phenotypes, respectively. Potential molecular mechanisms of the symptom largely remain unknown. We performed RNA sequencing to compare transcriptomic changes between different colored leaves within the individual plants. The leaf samples at post R5 stage were collected at three positions of RILs with three biological replications. Differentially expressed genes (DEGs) of 2,971, 212, and 760 were respectively identified in the three comparisons; UP vs. LW, UP vs. MD, and MD vs. LW. Flavonoid 3 ' hydroxylase(*F3'H*) and dihydroflavonol 4-reductase(*DFR*) genes were significantly upregulated by up to 4-fold in UP leaves, 2-fold in MD leaves compared to LW, which was important for regulating flavonoid biosynthesis, which might be related to purple-discoloration. Gene Ontology(GO) and Kyoto Encyclopedia of Genes and Genomes(KEGG) enrichment analyses on the UP vs. LW comparison was performed. One of the significantly enriched GO terms in UP's up-regulated DEGs was GO:0004601(peroxidase activity), which was associated with physiological responses of plants to stress. Furthermore, in KEGG Orthology (KO) analysis, K00660(chalcone synthase) was highly enriched in the UP samples. Taken together, UP leaves were confronted with stress conditions and respond to stress through a series of external and internal changes, which was considered for the regulated leaf discoloration. In future work, we will focus on the mechanism by which candidate genes participate in purple-discoloration in PI 96983.

***Corresponding Author:** Tel. 042-821-5727, E-mail: sungwoolee@cnu.ac.kr

PJ-0035

The complete chloroplast genome and comparative analysis of four *Thypa* genus plants used as herbal medicines

Woojong Jang, Wook Jin Kim, Sumin Noh, Sungyu Yang, Goya Choi, Kyeonghee Kim, Byeong Cheol Moon*

Herbal Medicine Resources Research Center, Korea Institute of Oriental Medicine, 111 Geonjae-ro, Naju-si, Jeollanam-do 58245, Republic of Korea

Typha genus, including about 30 species of monocotyledonous flowering plants, is largely distributed around world, where it is found in a variety of wetland habitats. The dried pollen of some species in this genus is used as herbal medicine named ‘Puhuang’ in Korea and China. In this study, four representative plants of *Typha* genus distributed in Korea were collected to complete the chloroplast genome sequences. *Typha orientalis*, *T. angustifolia*, *T. laxmanni*, and *T. latifolia* were sequenced using Illumina Miseq platform, and each circular chloroplast genome was assembled by GetOrganelle software. Chloroplast genomes of the *Typha* species showed typical quadripartite structure divided by two copies of inverted repeats. The total length of newly assembled genome sequences ranges from 160,873 to 161,526 bp, and they identically encoded 114 unique genes including 80 protein-coding genes, 30 tRNA genes, and 4 rRNA genes. Average GC contents were estimated as 36.60%, 36.64%, 36.60%, and 36.69%, respectively, which exhibited well-conserved genomic structure and gene order within *Typha* species. Comparative analyses revealed higher similarity in the inverted repeat regions than in the single-copy regions. An average of 621 SNPs and 156.7 InDels were identified between each chloroplast genome, of which noticeable several InDels provided potential molecular markers for the specific *Typha* species identification. This study will provide essential information for understanding genomic characteristics of *Typha* species and for monitoring exemplary distribution of herbal medicines.

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***Corresponding Author:** Tel. 061-338-7145, E-mail: wjjang@kiom.re.kr

PJ-0036

Genetic studies of essential inorganic components to develop high-quality rice varieties

Sang-Beom Lee[1*], Sang-Won Park[2], Yong-Jin Park[3], Eok-Keun Ahn[1], Ung-Jo Hyun[1], Yoon-Seung Lee[1], Jeom-Ho Lee[1], Jong-Cheol Ko[1]

[1]National Institute of Crop Science, RDA, Suwon 16429, Republic of Korea
[2]Reserch Policy Bureau, Rural Development Administration, RDA, Wanju 55365, Republic of Korea
[3]Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 32439, Korea

Inorganic components in rice refer to the mineral elements that are essential for the growth and development of the rice plant. These elements play an important role in various physiological processes and are essential for human nutrition. The purpose of the study was to develop high-quality rice varieties that are well-adapted to the central and northern regions of Korea by searching for genetic markers associated with inorganic components. Thus, we conducted genome studies on 163 rice accessions, focusing on the contents of certain inorganic components: calcium (Ca), magnesium (Mg), copper (Cu), manganese (Mn), and zinc (Zn). The inorganic component contents in brown rice were analyzed using ICP-MS (Inductive Coupled Plasma Mass Spectrometry). To ensure the accuracy of their measurements, the recovery rates were verified for each component using a certified reference material (CRM). The content of these inorganic components showed significant positive correlations with each other at the $p<0.01$ level, and we detected 933,474 and 189,030 SNPs associated with inorganic components in the resequenced whole genome and 580K Axiom® SNP array, respectively. We confirmed significant markers ($-\log10(p) > 5$) among these SNPs. The study suggests that these significant markers can be utilized as important genetic data for future breeding programs aimed at developing high-quality rice varieties. Additionally, this study used resequenced whole genomes and high-density SNP arrays to improve the accuracy and predictability of trait-related markers in rice genome studies. This approach could contribute to more accurate and efficient breeding efforts in the future.

***Corresponding Author:** Tel. 031-695-4027, E-mail: cldst81@korea.kr

PJ-0037

Integrated omics studies to enhance pre-harvest sprouting resistance in rice (*Oryza sativa* L.)

Sang-Beom Lee[1*], Ung-Jo Hyun[1], Yong-Jin Park[2], Shingu Kang[1], Eok-Keun Ahn[1], Yoon-Seung Lee[1], Jeom-Ho Lee[1], Jong-Cheol Ko[1]

[1]National Institute of Crop Science, RDA, Suwon 16429, Republic of Korea
[2]Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 32439, Korea

Pre-harvest sprouting (PHS) in rice often leads to decreased grain quality and yield losses, particularly in regions with high humidity and rainfall before harvest. Therefore, it is crucial to gain a comprehensive understanding of the underlying mechanisms using integrated omics information to enhance PHS resistance in rice. It is known that the VP1 gene activates the expression of the PHS resistance gene Sdr4 through the ABA signaling pathway. In this study, we conducted functional haplotype analyses of the genomic sequences of the VP1 and Sdr4 genes using the resequenced whole genome of the Korea rice core collection, consisting of 417 accessions. The analyses revealed significant genetic variations in the promoter, intron, and exon regions of both the VP1 and Sdr4 genes. The genetic variations could potentially affect the expression and function of these genes, thus influencing PHS resistance in rice. To further investigate the association between genetic variations and gene expression, we performed Transcriptome Wide Association Studies (TWAS). The results identified a large number of SNPs associated with the expression of the VP1 (668,063 SNPs) and Sdr4 (720,156 SNPs) genes. Notably, we detected significant SNPs associated with VP1 expression on chromosomes 1, 2, 3, 5, and 11. Similarly, SNPs highly associated with Sdr4 expression were found on chromosomes 1, 10, and 11.

These identified SNPs can provide valuable insights into the specific genomic regions and potential candidate genes involved in PHS regulation, thereby advancing our understanding of this complex traits. In addition, they can facilitate the establishment of targeted strategies for breeding PHS-resistant rice cultivars.

***Corresponding Author:** Tel. 031-695-4027, E-mail: cldst81@korea.kr

PJ-0038

Functional and genetic characterization of *WOX3* genes in the trichome formation in tomato

Ji In Jang, Soon Ju Park*

Division of Applied Life Science, and Plant Molecular Biology and Biotechnology Research Center (PMBBRC), Gyeongsang National University, Jinju 52828, Republic of Korea

In plants, trichomes protect the plant body from pests and act as a safeguard against environmental stress. The molecular mechanism controlling trichome differentiation and formation has rarely been researched in tomatoes. Tomato trichomes have evolved into various types. Here, we characterized that three *SlWOX3* genes that are involved in the formation of types I, VI, VII trichome, as well as cell division of trichome cells. *SlWOX3* genes are specifically expressed in the types I, VI, VII trichome cells on the stem and leaflets. Overexpression of *SlWOX3* led to the overproduction of trichomes Type I, VI, and VII trichomes, while CR-*slwox3* alleles reduced trichome production in the epidermal cells of hypocotyls, stems, leaves, and flower buds. Since Woolly is the key gene in determining trichome cell fate, CR-*wo* resulted in a significant reduction of trichomes in aerial tissues. Genetic study revealed that CR-*slwox3s* CR-*wo* mutants exhibited significant reduction of all trichomes like CR-*wo* single mutant, indicating that *SlWOX3s* and *WO* have overlapping functions in trichome development. Taken together, Our results suggest that *SlWOX3s* are a set of downstream gene of *WO*, and plays a crucial role in trichome cell division for trichome formation.

***Corresponding Author:** Tel. 055-772-1356, E-mail: sjpark75@gnu.ac.kr

PJ-0039

Identification of QTLs Governing (-)-Epicatechin and Procyanidin B2 Contents in Soybean Seeds

Jae Ah Choi[1], Hakyung Kwon[1], Hyun-Ju Jang[2], Moon Young Kim[2], Suk-Ha Lee[1,2*]

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

(-)-Epicatechin (EC) and procyanidin B2 (PB2) are forms of flavanols predominantly found in plants responsible for pigmentation in seeds, which exhibit numerous health benefits. In soybeans, EC and PB2 are known to be rich only in black or brown seed. The genetic control of EC and PB2, end products of flavonoid biosynthesis pathway remains mostly veiled in soybeans. This study was performed to identify quantitative trait loci (QTLs) governing soybean EC and PB2 contents in seeds using a high-resolution single nucleotide polymorphism-based linkage map of a recombinant inbred line population of IT109098 (greenish brown seed) and K7-113 (black seed) via genotyping-by-sequencing. Both mapping parents showed high EC and PB2 and the progeny had normal distribution. The value of color components, L*, a* and b* in seed exhibited bimodal distribution in the progeny.

We identified 2 QTLs conferring seed flavanols contents on chromosomes 02 and 10, continuously identified for the three years 2020-2022. As a major QTL, *qECPBB10* on Chr10 explained 23.5-44.4% of phenotypic variation, showing high LOD scores of 15.4-44.3. Among 35 genes in *qECPBB10*, *Glyma.10G209800* and *Glyma.10G210000*, encoding phenylalanine ammonia-lyase 2 and calcium-dependent lipid-binding family protein, respectively, are likely to be candidate genes based on sequence variations and seed-specific expression.

Remarkably, QTLs for the flavanols contents were separately located on QTLs for L*, a* and b* values, indicating the major QTL, *qECPBB10* regulates flavanols in soybean seeds independently of seed color. This study will provide insights to improve our understanding of flavanol biosynthesis in soybean and breeding high-flavanols cultivars.

***Corresponding Author:** Tel. 02-880-4545, E-mail: sukhalee@snu.ac.kr

Special A.
Digital Breeding Based on Supercomputing (슈퍼컴퓨터 기반 디지털 육종)

SA-0001

Analysis of digital breeding big-data based on supercomputing

Donghwan Shim*

Department of Biological Sciences, Chungnam National University, 34134, Daejeon, Republic of Korea

We introduce a research methodology for analyzing digital breeding big data based on supercomputing. Digital breeding is an innovative method to develop species with improved traits by combining genomic analysis and phenotyping technology in the breeding process. In this study, we present a method to process and analyze large amounts of breeding data by utilizing supercomputing technology. By utilizing genomic information and phenotypic data collected from various breeding data sources, we can develop efficient machine learning and deep learning algorithms. By doing so, we can identify correlations between genomic information and breeding traits and explore superior genes. In addition, we aim to develop a platform that utilizes supercomputing clusters to process and analyze large-scale breeding big data at high speed. By leveraging parallel computing and distributed processing technologies, we can greatly reduce the complexity of digital breeding research, which enables us to obtain breeding results quickly. Our research results will demonstrate the effectiveness of supercomputing-based digital breeding big data analysis, and show its applicability to the breeding industry. By doing so, we hope to present a new breeding approach that can contribute to improving agricultural productivity and food security.

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***Corresponding Author:** Tel. 042-821-6279, E-mail: dshim104@cnu.ac.kr

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SA-0002

Establishment and support of a supercomputing infrastructure for digital breeding era

Tae-Ho Lee*

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

The advancement of technology has revolutionized breeding techniques, progressing from traditional methods to molecular breeding, and now to genomic breeding. Moreover, the rise of artificial intelligence (AI) technology is paving the way for a new era called digital breeding, which is a cutting-edge approach that integrates multi-omics big data, including genomics, metabolomics, and phenomics, with deep learning technology. By harnessing AI models trained on extensive datasets, digital breeding tackles challenges such as complex quantitative traits, multi-trait characteristics, and consideration of environmental factor that were previously difficult to address using human expertise or earlier AI methods. To successfully embrace the digital breeding era, three crucial components must be prepared: deep learning technology, comprehensive multi-omics data for agricultural resources, and high-performance computing (HPC) infrastructure. Among them, the establishment of a robust HPC infrastructure to accommodate the exponential growth of agricultural omics data is important. One of the optimal choices for such infrastructure is a supercomputer. Recognizing this need, the Rural Development Administration is presently constructing a supercomputing infrastructure and service environment. This initiative will serve as a fundamental cornerstone for the development and utilization of digital breeding technology. With the upcoming full operation of the supercomputer next year, digital breeding is poised to experience accelerated progress.

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

Special B.
Monitoring Strategy of GM Variety
(GM 품종의 관리방안)

SB-0001

Safty Management Measures for Non-approved LMO Seed for Seeds

Dongsun Kim*

Korea Seed & Variety Service, Gimcheon 39660, Republic of Korea

After the distribution of two varieties of LMO zucchini seeds that were not approved in Korea was confirmed in March 2023, it was found that unapproved LMO seeds that became breeding materials for the seeds were brought in and distributed in Korea.

As a cause, there was a quarantine procedure under the Plant Quarantine Act at the import stage, but it was not confirmed, and it was estimated that domestic distribution was possible because LMO was not checked at the time of the new plant variety application in 2015.

In order to prevent similar cases, we intend to prepare and promote the following improvement measures by reviewing the problems of the current system and implementation process.

First, as a measure to improve the import stage, importers are required to submit plant quarantine certificates for all seeds and the level of sanctions for violations of reporting obligations by importing seeds by post is strengthened as a penalty.

Second, as a measure to improve the domestic production and distribution stage, the LMO inspection target will be expanded from the current 8 to 37 crops by 2028, and legal grounds will be provided to attach LMO inspection results only for 37 crops until 2028.

In particular, five crops(tomato, papaya, bell pepper, paprika, melon) are subject to the expansion of LMO inspection at production and distribution stage this year.

***Corresponding Author:** Tel. 054-912-0231, E-mail: coinoia@korea.kr

SB-0002

Trends in commercialization of GM crops and the current status of practical application of herbicide-resistant GM zoysiagrass

Hyo-Yeon Lee[1,2*]

[1]Subtropical Horticulture Research Institute, Jeju National University, Jeju 63243, Republic of Korea
[2]Faculty of Biotechnology, Jeju National University, Jeju 63243, Republic of Korea

Genetically modified (GM) crops have shown a continuous increase in cultivation area since their first commercialization in 1994, reaching 190.4 million hectares in 2019. As of 2019, a total of 32 crops and 425 events have been approved globally, but there has not been a single approved event among the GM crops developed in Korea. In Korea, research on the commercialization of genetically modified (GM) crops has been conducted through the BioGreen21 program. However, as of 2023, the only GM crop event for which an unregulated petition for commercialization has been submitted is GM zoysiagrass developed by Jeju National University.

Jeju National University has developed a GM zoysiagrass (JG21) with herbicide tolerance for effective control of various weeds invading turfgrass areas. Additionally, a non-flowering GM zoysiagrass line (JG21-MS1) resistant to herbicides was developed to prevent gene flow through pollen dispersion. The developed GM zoysiagrass events exhibit resistance to the non-selective herbicide, basta, and have maintained stable expression of the target traits for over 15 years in confined field trials. Since these herbicide-resistant zoysiagrass events are genetically modified organisms, various environmental safety assessments need to be conducted prior to practical cultivation.

Over the past 20 years, our research team has conducted extensive studies on the human and environmental safety of herbicide-resistant zoysiagrass events. These safety assessments include molecular characterization, agronomic traits, gene flow, weediness potential, impacts on the surrounding ecosystem, and effects on human health. Based on the results of various safety assessments, there were no statistically significant differences observed between the herbicide-resistant or non-flowering herbicide-resistant zoysiagrass events and their conventional counterparts in terms of non-target traits. Furthermore, no adverse effects on the environment or human health were detected. Combining these research findings, we submitted a petition for a determination of nonragulated status of the non-flowering herbicide-resistant zoysiagrass event (JG21-MS1) in December 2014, which is currently under review by four institutions. Throughout the approximately 8-year review period, we have submitted a total of 23 sets of supplementary data requested by the four institutions. If the herbicide-resistant zoysiagrass events developed through this research are approved for cultivation, it is expected to contribute to cost reduction in turfgrass management, which represents the largest portion of weed control expenses, and increase income for turfgrass cultivation farmers.

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

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The Korean Society of Breeding Science's Award

2023년 한국육종학회 학회상 시상
The Korean Society of Breeding Science's Award

○ 시상일 : 2023년 6월 29일(목) 09:00~10:30

○ 장 소 : 라마다프라자 제주호텔 라마다볼룸 홀

○ 시상내용

1\. 한국육종학회상 품종상 (33호)

수상자	김성업(농촌진흥청 국립식량과학원)
품종명	건백(참깨), 품종등록번호 제5720호
수상내용	역병, 흰가루병 복합 저항성 참깨 품종 “건백”을 개발하여 농가 소득향상과 우량품종 보급에 기여함
포상내용	상장 및 부상 200만원 (한국육종학회)

2\. 한국육종학회 우수논문상

\- 한국육종학회지 -

수상자	박수형(농촌진흥청 국립원예특작과학원)
논문제목	- Korean J. Breed. Sci. 2020;52(1):41-52 - 저온에서도 결구가 잘 형성되는 배가 반수체 배추 ‘원교20051호’ 개발
포상내용	상장 및 부상 50만원 (한국육종학회)

\- Plant Breeding & Biotechnology -

수상자	조준현(농촌진흥청 국립식량과학원)
논문제목	- Plant Breed. Biotech. 2021;9:199-212 - Screening and Breeding for Biofortification of Rice with Protein and High Lysine Contents
포상내용	상장 및 부상 50만원 (한국육종학회)

3\. 농우육종학회상 (13호)

수상자	손범영(농촌진흥청 국립식량과학원)
수상내용	우리나라 사료용 옥수수 육종분야 및 종자 산업화에 기여함
포상내용	상장 및 부상 500만원 (농우바이오)

4\. 코레곤품종상 (8호)

수상자	이석하, 이영호, CJ제일제당(주)
품종명	콩/씨제이행복한1호, 출원 2014-306호
수상내용	콩나물 콩 “씨제이행복한1호”를 개발하여 대학, 기업, 농민 간 상생모델을 구축하여 종자산업과 식품산업 발전에 기여함
포상내용	상장 및 부상 200만원 (코레곤)

5. 월드그린시드피아 육종상 (4호)

수상자	강시용(국립공주대학교)
수상내용	국제원자력기구(IAEA)와 지구 식량문제 해결을 위한 국제협력 연구 및 방사선을 이용한 벼, 케나프 등 다양한 작물의 품종개발을 통해 방사선 육종 분야의 연구 기반 구축과 농산업 발전에 크게 공헌함
포상내용	상장 및 부상 1,500만원 (월드그린, 시드피아)

6. 월드그린시드피아 젊은육종가상 (7호)

수상자	서정현(농촌진흥청 국립식량과학원)
수상내용	우리나라 주요 식량작물인 콩에 대하여 내재해성, 다수성, 고기능성 유색콩 품종개발 및 우수한 연구성과를 이루었으며 미래 한국육종 발전을 견인할 젊은 과학자로 인정함
포상내용	상장 및 부상 500만원 (월드그린, 시드피아)

7. 한국육종학회 공로상

이주경(강원대학교), 35대 사단법인 한국육종학회장

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한국육종학회

Korean Society of Breeding Science

인 쇄 2023년 6월 28일
발 행 2023년 6월 28일
발행자 **사단법인 한국육종학회**
경기도 수원시 권선구 수인로 126 국립식량과학원 중부작물부 내
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세계와 경쟁할 수 있는 유전자원 발굴과 품종육성

국민 건강과 다양한 먹거리 채소 품종 개발을 위해 한국농수산대학을 거치면서 지금까지 40년간 종간 교배를 통한 신기능채소 연구에 매진해온 이관호 박사와 손잡고 세계종묘가 새롭게 도전을 시작합니다.

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피피에스

우리 **피피에스**는 지난 30년간 종자업을
통해 쌓은 노하우에 새로운 연구역량을 더해
한국종자산업의 대표주자로 우뚝 서고자 합니다.

⋮

- 1995년 피피에스 법인 설립
- 2018년 기흥 신사옥 준공
- 2020년 매출 100억 초과 달성
- 2020년 6월 기업부설연구소 설립
- 2022년 신규 육종연구소 이천에 개소