2020 KSBS International Conference on

Plant Digital Breeding

18nd(Tues) - 21th(Fri) August, 2020 / HOTEL ICC Daejeon, Republic of Korea

- **Host Organizer**
  The Korean Society of Breeding Science
  The Agricultural Genome Center, Agricultural Biotechnology Research Center
  Plant Molecular Breeding Center, Systems & Synthetic Agrobiotech Center
  New Breeding Technology Center, National Agricultural Genome Program
  National Agency for Crop Seed Improvement
- **Sponsors by**
  The Korean Association of Societies for Agriculture, Food, and Life Sciences
  The Korean Federation of Science and Technology Societies

The Korean Society of Breeding Science

사단법인 한국육종학회 The Korean Society of Breeding Science

2020년 한국육종학회 조직위원회

위 원 장	총괄	양태진(서울대학교)
	공동	문중경(국립농업과학원), 박순기(경북대학교), 고희종(서울대학교), 이상열(경상대학교), 정진철(국립식량과학원), 정영희(전남대학교), 안병옥(국립농업과학원 농업생명자원부), 강시용(한국원자력연구원)
총괄총무위원		이정동(경북대학교)
기획분과	위원장	이주경(강원대학교)
	위원	이점호(국립식량과학원), 강권규(한경대학교), 이긍주(충남대학교), 임기병(경북대학교), 박범석(홍익바이오), 손성한(국립농업과학원), 김기택(농업기술실용화재단), 박영훈(부산대학교)
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	위원	김완규(우리종묘), 박응준(국립산림과학원), 정종욱(충북대학교), 박희영(신젠타코리아), 정운화(코레곤), 최순호((주)농우바이오)
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	위원	정용석(제주대학교), 임진희(세종대학교), 김율호(국립식량과학원), 박성한(바이엘코리아), 강현중(국립농업과학원), 박교선(국립원예특작과학원), 최홍규(동아대학교)
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	위원	안경구(농업기술실용화재단), 이상직((주)농우바이오 생명공학연구소), 정영민(농업기술실용화재단), 최규환(그린국제특허법률사무소), 박한용(세종대학교), 서상기(홍익바이오), 조윤섭(전남농업기술원 원예연구소)
홍보분과	위원장	이병무(동국대학교)
	위원	이석우(국립산림과학원), 이승인(국립종자원), 심성철(세종대학교), 서학수(서울대학교), 서효원(농촌진흥청), 조영찬(국립식량과학원), 김행훈(순천대학교), 김진백(한국원자력연구원)
편집분과	위원장	권순욱(부산대학교)
	위원	이주현(건국대학교), 박철수(전북대학교), 김창수(충남대학교)
자문위원		오대근(한국농수산대학), 김홍식(충북대학교), 김용권(신경대학), 서용원(고려대학교), 조용구(충북대학교), 정영수(동아대학교), 안상낙(충남대학교), 박순기(경북대학교), 박수철(서울대학교)

2020년 한국육종학회 임원

회장	강시용(한국원자력연구원)
차기회장	양태진(서울대학교)
부회장	강권규(한경대학교), 강병철(서울대학교), 강성택(단국대학교), 김지강(국립원예특작과학원), 안경구(농업기술실용화재단, 종자산업진흥센터), 윤재복(주)고추와 육종), 이강섭(국립농업과학원), 이병무(동국대학교), 이석우(국립산림과학원), 이점호(국립식량과학원), 이주경(강원대학교), 이효연(제주대학교)
편집위원장	박순기(경북대학교), 양태진(서울대학교)
편집이사	박철수(전북대학교), 권순욱(부산대학교), 이정동(경북대학교), 이주현(건국대학교)
감 사	노재환(국립식량과학원 바이오에너지작물연구소), 최홍규(동아대학교)
사무총장	이정동(경북대학교)

2020년 한국육종학회지 사무국

경기도 수원시 권선구 수인로 126 국립식량과학원 중부작물부 내 (16429)
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- 1969년 창간된 한국육종학회는 연 4회(3월 1일, 6월 1일, 9월 1일, 12월 1일) 출판됩니다.
- 한국육종학회지 홈페이지 www.koreabreedjournal.org에서 논문검색 및 파일다운로드를 할 수 있습니다.

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This work was supported by the Korean Federation of Science and Technology Societies(KOFST) grant funded by the Korean government.

2020 KSBS International Conference on Plant Digital Breeding

유전체기반 디지털육종의 연구와 실용화전략

일시: 2020년 8월 18일(화)~8월 21일(금) / 장소: 대전ICC, www.breeding.or.kr

- 주관
  사단법인 한국육종학회
- 공동주관
  농생물게놈활용연구사업단, 농업생명공학연구단, 식물분자육종사업단,
  시스템합성농생명공학사업단, 신육종기술실용화사업단,
  국립농업과학원 포스트게놈다부처유전체사업단, GSP사업단 식량종자사업단
- 후원
  한국농식품생명과학협회, 한국과학기술단체총연합회
  ㈜농우바이오, ㈜코레곤, ㈜시드피아, ㈜월드그린

The Korean Society of Breeding Science

2020 KSBS International Conference on Plant Digital Breeding

Conference Information

○ Tile Digital Breeding Based on Genomics

○ Date 18nd(Tues) - 21th(Fri) August, 2020

○ Venue - August 18: HOTEL ICC Daejeon, Republic of Korea

- August 18~21: www.breeding.or.kr

○ Participating countries Korea, Canada, China, Germany, India, Phillipine, UK, USA

○ Important Date

- Abstract submission & Pre-Registration deadline: July May 31, 2020
- Opening of the conference: August 18, 2020 (HOTEL ICC, Daejeon)
- Closing of the conference: August 21, 2020 (Official Website)

○ Registration Fees

• Pre-Registration	100,000 KRW
• Onsite Registration	General Member 70,000 KRW
	Student Member 40,000 KRW
• Poster paper fee	20,000 KRW/1piece

○ Host Organizer

The Korean Society of Breeding Science

The Agricultural Genome Center, Agricultural Biotechnology Research Center

Plant Molecular Breeding Center, Systems & Synthetic Agrobiotech Center

New Breeding Technology Center, National Agricultural Genome Program

National Agency for Crop Seed Improvement

○ Sponsors by

The Korean Association of Societies for Agriculture, Food, and Life Sciences

The Korean Federation of Science and Technology Societies

2020 KSBS International Conference Program

Day 1 August 18, 2020		
10:00~11:00	Board & Organizing Committee	Convention Hall
11:00~12:00	KSBS's General Meeting & Award	
12:00~13:30	Lunch	
13:30~14:00	Opening Ceremony	
Plenary Session (1)		Convention Hall
14:00~14:40	5G Speed in Pepper Breeding Byoung-Cheorl Kang (Seoul National University, Korea)	
14:40~15:20	Deleterious mutations during domestication in the predominant selfing crop soybean Soon-Chun Jeong (Korea Research Institute of Bioscience & Biotechnology, Korea)	
Plenary Session (2)		www.breeding.or.kr
15:30~16:10	Evolution of homoeologous genes and domestication of horticultural traits in the Brassiceae vegetables Wang Xiaowu (Insitute of Vegetables and Flowers, CAAS, China)	
16:10~16:50	New cultivar and industry trend for Goji (Lycium species) in Genome era Ying Wang (Chinese Academy of Science, China)	
17:00~17:40	Moving Forward to a Digital Rice Genebank Kenneth McNally (International Rice Research Institute (IRRI), Phillipine)	
17:40~18:20	Genebank genomics bridges the gap between the conservation of crop diversity and plant breeding: a case study in barley Martin Mascher (Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) Gatersleben, Germany)	
18:20~19:00	Powerful, Scalable and Affordable genotyping solutions for Agrigenomics breeding applications from Thermo Fisher Scientific Kandalam, Arjun (Thermo Fisher Scientific, India)	

Day 2 August 19, 2020		
Concurrent Session		www.breeding.or.kr
09:00-12:00	CS-1 Genome Sequence & Genomics	CS-2 GWAS and Allele Mining
	CS-3 Highthroughput Genotyping & Phenotyping	CS-4 New Breeding Technology
13:30~17:00	CS-5 Breeding for Major Crops	CS-6 Breeding for Horticultural Crops
	CS-7 Genetic Resources & Special Crops	CS-8 Young Breeding Scientist

Day 3 August 20~21, 2020 (09:00~17:00)	
Oral Presentation & Poster Presentation	www.breeding.or.kr

Day 4 August 21, 2020 (11:00~12:00)	
Awards Ceremony and Closing Ceremony	www.breeding.or.kr

2020 KSBS International Conference 'Concurrent Session' Program

A. CS-01 Genome Sequence & Genomics		
No.	**Presentation Title**	**Speaker**
1	Application of best linear unbiased prediction (BLUP) on GWAS identifies candidate gene regulating branch development in soybean	Sangrea Shim (Seoul National University, Korea)
2	Epigenetic diversity in duplicated plant genomes	Kyung Do Kim (Myongji University, Korea)
3	Harnessing Retrotransposons for Crop Improvement	Jungnam Cho (CAS-JIC Centre of Excellence for Plant and Microbial Science, China)
4	Rice arbuscular mycorrhizal symbiosis requires the removal of the suppressor SMAX1	Jeongmin Choi (Department of Plant Sciences, University of Cambridge, UK)
5	Interactive analysis platform for data management, GWAS and marker development	Yei Soo Yu (DNACARE Co. Ltd., Korea)

B. CS-02 GWAS and Allele Mining		
No.	**Presentation Title**	**Speaker**
1	Combining GWAS and CRISPR-Cas9 for rapid identification of resistance genes to rice blast	Guo-Liang Wang (Ohio State University, USA)
2	Selection and use of rice bacterial blight resistant alleles based on both resistant gene structures and genome-wide data analysis	Kyu-won Kim (Kongju University, Korea)
3	Genetic diversity and genome-wide association study in a core collection of peanut germplasms using a high-density SNPs array	Tae-Hwan Jun (Pusan National University, Korea)
4	Uncovering candidate genes controlling major fruit-related traits in pepper via genotype-by-sequencing-based QTL mapping and genome-wide association study	Jin-Kyung Kwon (Seoul National University, Korea)
5	Genome-wide association study of eight fruit traits in cultivated tomato (*Solanum lycopersicum* L.)	Minkyung Kim (Sejong University, Korea)

C. CS-03 Highthroughput Genotyping & Phenotyping		
No.	**Presentation Title**	**Speaker**
1	Current status of high-throughput genotyping system for molecular breeding : practical considerations	Young-Min Jeong (Foundation of Agri. Tech. Commercialization & Transfer, Korea)
2	Multiplex Detection of Crop Genetic Mutations Based on Encoded Hydrogel Microparticles	Ki Wan Bong (Korea University, Korea)
3	High throughput phenotyping in cost-effective manners	Yong Suk Chung (Jeju National University, Korea)
4	Image-based Machine Learning Characterizes Root Nodule in Soybean Exposed to Silicon	Yoonha Kim (Kyungpook National University, Korea)
5	영상 및 분광정보를 활용한 우수 형질 비파괴 선발 방법	Byoung-Kwan Cho (Chungnam National University, Korea)
6	Establishment of high-throughput genotyping systems for *Panax ginseng*	Woojong Jang (Seoul National University, Korea)

D. CS-04 New Breeding Technology		
No.	**Presentation Title**	**Speaker**
1	RNA Guided Endonucleases based crop genome editing	Hyeran Kim (Kangwon National University, Korea)
2	Efficient and heritable gene edition using CRISPR/cas9system in tomato	Soon Ju Park (Wonkwang University, Korea)
3	Chloroplast-targeted transgene delivery and transient expression across varied plant systems using single-walled carbon nanotubes	Seonyeong Kwak (Seoul National University, Korea)
4	CRISPR/Cas9-mediated genome editing of Ehd1, a major inducer of flowering in rice, increases vegetative growth and grain yield potential	Lae-Hyeon Cho (Pusan National University, Korea)
5	Maintenance of net photosynthesis at the grain-filling stage increases crop productivity of indica rice	Dongjin Shin (National Institute of Crop Science, RDA, Korea)

E. CS-05 Breeding for Major Crops		
No.	**Presentation Title**	**Speaker**
1	Multiple abiotic stress tolerance improvement by the pyramiding QTLs in rice	Joong Hyoun Chin (Sejong University, Korea)
2	Genome sequence of Physic Nut (*Jatropha curcas* L.) provides insights into evolution of Euphorbiaceae family	Jungmin Ha (Gangneung-Wonju National University, Korea)
3	The barley pan-genome reveals the hidden legacy of mutation breeding	Murukarthick Jayakodi (Leibniz Institute of Plant Genetics and Crop Plant Research, Germany)
4	Development and utilization plans for high value colored wheat	Kyeong-Hoon Kim (National Institute of Crop Science, RDA, Korea)
5	Current Status and Prospect of Maize Quality Breeding	Jung-Tae Kim (National Institute of Crop Science, RDA, Korea)

F. CS-06 Breeding for Horticultural Crops		
No.	**Presentation Title**	**Speaker**
1	QTL mapping of bacterial wilt resistance in pepper (*Capsicum annuum* L.) using genotyping-by-sequencing analysis and two different isolates of *Ralstonia solanacearum*	Jundae Lee (Jeonbuk National University, Korea)
2	A high-contiguity Nanopore assembly of Brassica *nigra* genome allows localization of active centromeres and defines the ancestral Brassica genome	Sampath Perumal (Agriculture and Agri-Food Canada, Canada)
3	The Use of Genomic Information in Pome Fruit Breeding	Daeil Kim (Chungbuk National University, Korea)
4	Specific trait-targeted mutagenesis in radiation breeding	Sang Hoon Kim (Korea Atomic Energy Research Institute, Korea)
5	Whole-genome, transcriptome, and methylome analyses provide insights into the evolution of platycoside biosynthesis in balloon flower, a medicinal plant	Chang-Kug Kim (National Institute of Agricultural Sciences, RDA, Korea)

G. CS-07 Genetic Resources & Special Crops		
No.	**Presentation Title**	**Speaker**
1	A combinational approach of biparental QTL mapping and GWAS identifies candidate genes for phytophthora blight resistance in Sesame	Sung-Up Kim (National Institute of Crop Science, RDA, Korea)
2	Multi-Seeded(MSD1) regulates pedicellate spikelet fertility in sorghum through jasmonic acid pathway	Young Koung Lee (National Fusion Research Institute, Korea)
3	Population Analysis of *Angelica gigas Using* Chloroplast Based Markers for Molecular Breeding	Yi Lee (Chungbuk National University, Korea)
4	Perspectives and Actions in Breeding of Special-Purpose Trees	Jeong-Ho Song (National Institute of Forest Science, Korea)
5	Marker assisted selection (MAS) for breeding high oleic peanut (*Arachis hypogaea* L.) cultivars	Dr. Jalina (International Crop Research Institute of Semi Arid Tropics, India)
6	Influence of genome diversity on breeding and DNA barcoding of wildcrafted species.	Hyun-Seung Park (Seoul National University, Korea)

H. CS-08 Young Breeding Scientist		
No.	**Presentation Title**	**Speaker**
1	Customizing Solanaceae fruit crops for vertical farming by genome editing	Choon-Tak Kwon (Cold Spring Harbor, USA)
2	Characterization of the Common Japonica-Originated Genomic Regions in the High-Yielding Varieties Developed from Inter-Subspecific Crosses in Rice (*Oryza sativa* L.)	Jeonghwan Seo (Seoul National University, Korea)
3	An effective approach to accelerate rice pollen genetics utilizing omics data and genome editing technology	Woo-Jong Hong (Kyung Hee University, Korea)
4	Engineering Crassulacean Acid Metabolism (CAM) into C3 Plants to Improve Biomass and Water-Use Efficiency	Sung Don Lim (Kangwon National University, Korea)
5	Identification of *qLTG3-1* allele for low-temperature germinability in rice from the *Oryza rufipogon*	Kyu-Chan Shim (Chungnam National University, Korea)

2020 한국육종학회 국제공동학술발표회

국제공동학술발표회 개요

○ 행사명 2020년 한국육종학회 국제공동학술발표회

○ 일 시 2020년 8월 18일(화)~8월 21일(금)

○ 장 소 대전ICC, www.breeding.or.kr

○ 주 제 유전체기반 디지털육종의 연구와 실용화전략
(Digital Breeding Based on Genomics)

○ 참가국가 대한민국, 캐나다, 중국, 독일, 인도, 필리핀, 영국, 미국

○ 공동주관 식물분자육종사업단, 농생물게놈활용연구사업단, 농업생명공학연구단,
시스템합성농생명공학사업단, 신육종기술실용화사업단,
국립농업과학원 포스트게놈다부처유전체사업단, GSP사업단 식량종자사업단

○ 후 원 한국농식품생명과학협회, 한국과학기술단체총연합회

○ **일정 및 접수 방법 : 한국육종학회 홈페이지 www.breeding.or.kr**

○ 초록&등록비 마감일: 7월 1일(수)~31일(금)

구두 발표자료 마감일: 8월 10일, 포스터 발표자료 마감일: 8월 21일까지

○ 참가비 안내:
- 대면참가비 100,000원
- 비대면 참가비 일반회원 70,000원, 학생회원 40,000원
- 포스터 게재비 20,000 원 / 1편

○ 2020년 한국육종학회 국제공동학술발표회 일정

• 8월 18일(화)			* 진행방식
	10:00~13:00	정기총회, 학회상 시상	대면 (대전ICC)
	13:30~14:00	개회식	
	14:00~14:40	1부 기조발표 (1)	대면 & 비대면 (www.breeding.or.kr)
	15:30~16:10	1부 기조발표 (2)	비대면
• 8월 19일(수)시		2부 분과발표	비대면
• 8월 20(목)~21일(금)		3부 구두&포스터발표	비대면
• 8월 21일(금) 12시		학회 종료, 총회 영상 업로드 및 발표상 선정 발표	비대면

2020년 한국육종학회 국제공동학술발표회 일정

행사 진행방식에 따라 일정이 변경될 수 있습니다.

1. 2020년 8월 18일, 대전ICC		* 진행방식: 대면
10:00~11:00	이사회&조직위원회	2층 컨벤션홀C,D
11:00~12:00	정기총회 및 학회상 시상, 동오 농업과학기술인상, 시드피아, 월드그린 MOU 체결식	
12:00~13:30	중식	2층 컨벤션홀A
13:30~14:00	**개회식**	2층 컨벤션홀C,D
	사회 : 이정동 (사무총장, 경북대학교)	
	개회사 - 양태진 (조직위원장, 서울대학교)	
	환영사 - 강시용 (학회장, 한국원자력연구소)	
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		*** 진행방식: 대면/비대면**
14:00~14:40	5G Speed in Pepper Breeding: Time Matters	
	강병철 교수 (서울대학교)	
14:40~15:20	Deleterious mutations during domestication in the predominant selfing crop soybean	
	정순천 박사 (한국생명공학연구원)	
Plenary Session (2)		www.breeding.or.kr
		*** 진행방식: 비대면**
15:30~16:10	Evolution of homoeologous genes and domestication of horticultural traits in the Brassiceae vegetables	
	Wang Xiaowu (Institute of Vegetable and Flowers, CAAS, China)	
16:10~16:50	New cultivar and industry trend for Goji (Lycium species) in Genome era	
	Ying Wang (Chinese Academy of Science, China)	
17:00~17:40	Moving Forward to a Digital Rice Genebank	
	Kenneth McNally (International Rice Research Institute (IRRI), Phillipine)	
17:40~18:20	Genebank genomics bridges the gap between the conservation of crop diversity and plant breeding: a case study in barley	
	Martin Mascher (Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) Gatersleben, Germany)	
18:20~19:00	Powerful, Scalable and Affordable genotyping solutions for Agrigenomics breeding applications from Thermo Fisher Scientific	
	Kandalam, Arjun (Thermo Fisher Scientific, India)	

2. 2020년 8월 18~21일, www.breeding.or.kr		* 진행방식: 비대면
8월 18일(화)	**1부 Plenary Session**	

8월 19일(수)	**2부 한국육종학회 분과발표**	
시간	발표제목	좌장
09:00-12:00	CS-1 Genome Sequence & Genomics	강양제(경상대학교), 이태호(국립농업과학원)
	CS-2 GWAS and Allele Mining	김성길(전남대학교), 이주석(한국생명공학연구원)
	CS-3 Highthroughput Genotyping & Phenotyping	강성택(국립농업과학원), 김경환(국립농업과학원)
	CS-4 New Breeding Technology	정기홍(경희대학교), 김혜란(강원대학교)
13:30~17:00	CS-5 Breeding for Major Crops	하보근(전남대학교), 김재윤 (공주대학교)
	CS-6 Breeding for Horticultural Crops	이준대(전북대학교), 김도선(국립원예특작과학원)
	CS-7 Genetic Resources & Special Crops	조광수(국립식량과학원), 심동환(산림과학원)
	CS-8 Young Breeding Scientist	유수철 (한경대학교), 장철성 (강원대학교)

8월 20-21일	**3부 한국육종학회 구두&포스터발표 (발표시간 09:30-17:00)**

8월 21일(금)	**학회 종료, 총회 영상 업로드 및 발표상 선정 발표 (11:00~12:00)**

2020년 한국육종학회 공동심포지엄 분과발표 (Concurrent Session)

A. CS-01 Genome Sequence & Genomics

좌장: 강양제(경상대학교), 이태호(국립농업과학원)

순번	발표제목	발표자(소속)
1	Application of best linear unbiased prediction (BLUP) on GWAS identifies candidate gene regulating branch development in soybean	심상래(서울대학교)
2	Epigenetic diversity in duplicated plant genomes	김경도(명지대학교)
3	Harnessing Retrotransposons for Crop Improvement	조정남 (CAS-JIC Centre of Excellence for Plant and Microbial Science, China)
4	Rice arbuscular mycorrhizal symbiosis requires the removal of the suppressor SMAX1	최정민 (University of Cambridge, UK)
5	Interactive analysis platform for data management, GWAS and marker development	유의수(DNACARE Co. Ltd.)

B. CS-02 GWAS and Allele Mining

좌장: 김성길(전남대학교), 이주석(한국생명공학연구원)

순번	발표제목	발표자(소속)
1	Combining GWAS and CRISPR-Cas9 for rapid identification of resistance genes to rice blast	Guo-Liang Wang (Ohio State University, USA)
2	Selection and use of rice bacterial blight resistant alleles based on both resistant gene structures and genome-wide data analysis	김규원(공주대학교)
3	Genetic diversity and genome-wide association study in a core collection of peanut germplasms using a high-density SNPs array	전태환(부산대학교)
4	Uncovering candidate genes controlling major fruit-related traits in pepper via genotype-by-sequencing-based QTL mapping and genome-wide association study	권진경(서울대학교)
5	Genome-wide association study of eight fruit traits in cultivated tomato (*Solanum lycopersicum* L.)	김민경(세종대학교)

C. CS-03 Highthroughput Genotyping & Phenotyping

좌장: 강성택(국립농업과학원), 김경환(국립농업과학원)

순번	발표제목	발표자(소속)
1	Current status of high-throughput genotyping system for molecular breeding : practical considerations	정영민(농업기술실용화재단)
2	Multiplex Detection of Crop Genetic Mutations Based on Encoded Hydrogel Microparticles	봉기완(고려대학교)
3	High throughput phenotyping in cost-effective manners	정용석(제주대학교)
4	Image-based Machine Learning Characterizes Root Nodule in Soybean Exposed to Silicon	김윤하(경북대학교)
5	영상 및 분광정보를 활용한 우수 형질 비파괴 선발 방법	조병관(충남대학교)
6	Establishment of high-throughput genotyping systems for *Panax ginseng*	장우종(서울대학교)

D. CS-04 New Breeding Technology

좌장: 정기홍(경희대학교), 김혜란(강원대학교)

순번	발표제목	발표자(소속)
1	RNA Guided Endonucleases based crop genome editing	김혜란(강원대학교)
2	Efficient and heritable gene edition using CRISPR/cas9system in tomato	박순주(원광대학교)
3	Chloroplast-targeted transgene delivery and transient expression across varied plant systems using single-walled carbon nanotubes	곽선영(서울대학교)
4	CRISPR/Cas9-mediated genome editing of *Ehd1*, a major inducer of flowering in rice, increases vegetative growth and grain yield potential	조래현(부산대학교)
5	Maintenance of net photosynthesis at the grain-filling stage increases crop productivity of indica rice	신동진(국립식량과학원)

E. CS-05 Breeding for Major Crops

좌장: 하보근(전남대학교), 김재윤 (공주대학교)

순번	발표제목	발표자(소속)
1	QTL pyramiding을 이용한 다중재해저항성 벼 개발	진중현(세종대학교)
2	야트로파 유전체 염기분석을 통한 대극과 진화분석	하정민(강릉원주대학교)
3	범유전체학을 이용한 보리 돌연변이 육종	Murukarthick Jayakodi (Leibniz Institute of Plant Genetics and Crop Plant Research, Germany)
4	기능성 유색밀이 개발과 그 활용방안	김경훈(국립식량과학원)
5	옥수수 품질육종 현황 및 전망	김정태(국립식량과학원)

F. CS-06 Breeding for Horticultural Crops

좌장: 이준대(전북대학교), 김도선(국립원예특작과학원)

순번	발표제목	발표자(소속)
1	QTL mapping of bacterial wilt resistance in pepper (*Capsicum annuum* L.) using genotyping-by-sequencing analysis and two different isolates of *Ralstonia solanacearum*	이준대(전북대학교)
2	A high-contiguity Nanopore assembly of Brassica *nigra* genome allows localization of active centromeres and defines the ancestral Brassica genome	Sampath Perumal (Agriculture and Agri-Food Canada, Canada)
3	The Use of Genomic Information in Pome Fruit Breeding	김대일(충북대학교)
4	Specific trait-targeted mutagenesis in radiation breeding	김상훈(한국원자력연구원)
5	Whole-genome, transcriptome, and methylome analyses provide insights into the evolution of platycoside biosynthesis in balloon flower, a medicinal plant	김창국(국립농업과학원)

G. CS-07 Genetic Resources & Special Crops

좌장: 조광수(국립식량과학원), 심동환(국립산림과학원)

순번	발표제목	발표자(소속)
1	A combinational approach of biparental QTL mapping and GWAS identifies candidate genes for phytophthora blight resistance in Sesame (참깨 역병 저항성 연관 마커 개발)	김성업(국립식량과학원)
2	Multi-Seeded(MSD1) regulates pedicellate spikelet fertility in sorghum through jasmonic acid pathway (수수 유전체 육종 연구 현황)	이영경(국가핵융합연구소)
3	Population Analysis of *Angelica gigas Using* Chloroplast Based Markers for Molecular Breeding	이이(충북대학교)
4	Perspectives and Actions in Breeding of Special-Purpose Trees	송정호(국립산림과학원)
5	Marker assisted selection (MAS) for breeding high oleic peanut (*Arachis hypogaea* L.) cultivars	Janila Pasupuleti(ICRISAT)
6	Influence of genome diversity on breeding and DNA barcoding of wildcrafted species.	박현승(서울대학교)

H. CS-08 Young Breeding Scientist

좌장: 유수철 (한경대학교), 장철성 (강원대학교)

순번	발표제목	발표자(소속)
1	Customizing Solanaceae fruit crops for vertical farming by genome editing	권춘탁 (Cold Spring Harbor Lab., USA)
2	Characterization of the Common Japonica-Originated Genomic Regions in the High-Yielding Varieties Developed from Inter-Subspecific Crosses in Rice (*Oryza sativa* L.)	서정환(서울대학교)
3	An effective approach to accelerate rice pollen genetics utilizing omics data and genome editing technology	홍우종(경희대학교)
4	Engineering Crassulacean Acid Metabolism (CAM) into C3 Plants to Improve Biomass and Water-Use Efficiency	임성돈(강원대학교)
5	Identification of *qLTG3-1* allele for low-temperature germinability in rice from the *Oryza rufipogon*	심규찬(충남대학교)

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Plenary Session

Plenary Session

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<Research Interests>

1. QTL mapping and GWAS for major traits in pepper
2. Identification and characterization of genes controlling disease resistance in pepper
3. Identification and characterization genes controlling of capsaicinoid and carotenoid biosynthesis in pepper

<Education>

1. Seoul National University, Korea (1994 - 1999) Ph.D. in Plant Molecular Genetics
2. Seoul National University, Korea (1990 - 1992) M.S. in Plant Molecular Genetics
3. Seoul National University, Korea (1986 - 1990) B.S. in Horticulture

<Professional Experience>

1. Associate Dean of Research Affairs (2019. 8. - Present)
2. Director, Vegetable Breeding Research Center (SNU) (2010 - Present)
3. Director, Plant Genomics and Breeding Institute (SNU) (2014 - 2016)
4. Adjunct senior researcher, National Agricultural Products Quality Management Service (2009 - 2014)
5. Technical Advisory Board, Ministry for Food, Agriculture, Forestry and Fisheries, Republic of Korea (2012 - 2013)
6. Adjunct senior researcher, Rural Development Administration (2008 -2012)
7. Professor, Seoul National University, Seoul, Korea (2010 - Present)
8. Assistant Professor, Seoul National University, Seoul, Korea (2006. 3. - 2010. 3.)
9. Research Associate, Cornell University, Ithaca, NY (2002 - 2006)
10. Postdoctoral Associate, Cornell University, Ithaca, NY (1999 - 2002)
11. Researcher, Turfgrass and Environmental Research Institute, Samsung Everland Co., Anyang, Korea (1998 - 1999)

<Selected Publications>

1. Lee HY, Ro NY, Patil A, Lee JH, Kwon JK, **Kang BC**. 2020. Uncovering candidate genes controlling major fruit-related traits in pepper via genotype-by-sequencing based QTL mapping and genome wide association study. **Front Plant Sci**. 11: 1100
2. Yoon YJ, Venkatesh J, Kim J, Lee HE, Kim DS, **Kang BC**. 2020. Genome Editing of eIF4E1 in Tomato Confers Resistance to Pepper Mottle Virus. **Front Plant Sci** 11: 1098
3. Jang SJ, Jeong HB, Kim SA, Ha SH, Kwon JK, **Kang BC**. 2020. *Phytoene Synthase 2 can com*pensate for the absence of *Psy1* in pepper fruit (*Capsicum annuum*). **J Exp Bot**. 71:3417-3427
4. Jeong HB, Kang MY, Jung A, Han K, Lee JH, Jo J, Lee HY, An JW, Kim S, **Kang BC**. 2019. Single molecule real time sequencing reveals diverse allelic variations in carotenoid biosynthetic genes in pepper (*Capsicum* spp.). ***Plant Biotechnol J***. 17:1081-1093
5. Jelli V, **Kang BC**. 2019. Plant-pathogen interactions under changing temperatures: molecular and genetic perspectives. ***Curr Opin in Plant Biology***. 50:9-17
6. Park MJ, Lee J-H, Kan K, Jang S, Han J, Lim JH, Jung JW, **Kang BC**. 2019. A major QTL and candidate genes for capsaicinoid biosynthesis in the pericarp of *Capsicum chinense* revealed using QTL-seq and RNA-seq. ***Theor Appl Genet***. 132:515-529
7. Han KE, Jang S, Lee JH, Lee DG, Kwon JK, **Kang BC**. 2019. A MYB transcription factor is a candidate to control pungency in *Capsicum annuum*. ***Theor Appl Genet.*** 132:1235-1246.
8. Siddique MI, Lee HY, Ro NY, Han KE, Jelli V, Abate S, Patil A, Changkwian A, Kwon JK, **Kang BC**. 2019. Identifying candidate genes for *Phytophthora capsici* resistance in pepper (*Capsicum annuum*) via genotyping-by-sequencing-based QTL mapping and genome-wide association study. ***Sci Rep*** 9:9962
9. Han KE, Lee HY, Ro NY, Hur OS, Lee JH, Kwon JK, **Kang BC**. QTL mapping and GWAS reveal candidate genes controlling capsaicinoid content in *Capsicum*. ***Plant Biotech J***. 16: 1546-1558.
10. Kim SB. Kang -H, Hoang NH, Yeom -I, An JT, Kim S, Kang MY, Kim HJ, Jo YD, Ha Y, Choi D, **Kang BC**. 2016. Divergent evolution of multiple virus-resistance genes from a progenitor in *Capsicum* spp. ***New Phytol***. 213: 886-899.

PS-0001

5G Speed in Pepper Breeding

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The last decade has witnessed tremendous progress in genome sequencing and explosion of genome sequence information. This remarkable advancement in genomics provides unprecedented opportunities for crop improvement. Pepper (*Capsicum* spp.) is an important vegetable crop worldwide. Molecular markers for major traits are an essential tool to expedite development of new varieties in pepper. Our group has developed molecular markers linked to major genes including disease resistance using various genomics tools. Some of the genes have cloned (or are being) by the genomics-assisted method. For QTL mapping of quantitatively inherited traits, RILs and CC were developed and genotyped by the genotype-by-sequencing methods. Another approach, genome-wide association study (GWAS) has also applied for identifying genes associated to quantitative traits. Molecular breeding assisted by genomics tools enabled efficient selection of target traits and reduced costs of cultivar development. However, the very long generation time of pepper imposes another barrier in pepper breeding. Recently introduced “Speed Breeding”, which can shorten generation time of crop plants can accelerate pepper improvement by reducing the long generation time. To evaluate the speed breeding method in pepper, two *Capsicum* species with different flowering time were grown in controlled chambers with extended photoperiod (22 hours light/ 2 hours dark) and high temperature conditions. Both species showed remarkably reduced flowering time under the extended photoperiod condition, demonstrating that the speed breeding method can be applied in pepper breeding. We expect that combining genomic tools and speed breeding will enable 5G speed in pepper breeding.

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<Research Interests>

1. I have studied soybean genomics and genetics with a particular interest in the domestication process.
2. The soybean genomics studies sometimes lead to identification and genetic characterization of important genes. Currently, my gene-level studies focus on those genes that regulate dormancy, shattering, vine, waterlogging, etc.
3. I also conduct molecular characterization of genetically-modified organisms for their commercialization.

<Education>

1. BS, MS, Seoul Nation University, 1989, 1991
2. Ph.D. Oregon State University, 1997

<Professional Experience>

1. Research Associate, Virginia Tech, 1997-2001
2. Senior Researcher, Principal Researcher, Korea Research Institute of Bioscience and Biotechnology, 2002-present

<Selected Publications>

1. S.C. Jeong, J.K. Moon, S.K. Park, M.S. Kim, K. Lee, S.R. Lee1, N. Jeong, M.S. Choi, N. Kim, S.T. Kang, E. Park (2019) Genetic diversity patterns and domestication origin of soybean. Theoretical and Applied Genetics 132(4):1179-1193.
2. J.H. Kim, D.N. Bae, S.K. Park, N. Jeong, K. Lee, H. Kang, S.T. Kang, J.K. Moon, E. Park, and S.C. Jeong (2017) Molecular genetic analysis of a novel recessive white flower gene in wild soybean. Crop Science 57: 3027-3034
3. S.C. Jeong, J.H. Kim, D.N. Bae (2017) Genetic analysis of the *Lf1* gene that controls leaflet number in soybean. Theoretical and Applied Genetics 130:1685-1692.
4. N.R. Redekar, E.M. Clevinger, M.A. Laskar, R.M. Biyashev, R.V. Jensen, S.C. Jeong, S.A. Tolin, M.A. Saghai Maroof (2016) Candidate gene sequence analyses towards identifying *Rsv*3-type resistance to Soybean mosaic virus. The Plant Genome Vol. 9 No. 2. DOI: 10.3835/plantgenome2015.09.0088.
5. D.C. Ilut, A.E. Lipka, N. Jeong, D.N. Bae, D.H. Kim, J.H. Kim, N. Redekar, K. Yang, W. Park, S.T. Kang, N. Kim, J.K. Moon, M.A. Saghai Maroof, M.A. Gore, S.C. Jeong (2016) Identification of haplotypes at the Rsv4 genomic region in soybean associated with durable resistance to soybean mosaic virus. Theoretical and Applied Genetics 129: 453-468.
6. Y.G. Lee, N. Jeong, J.H. Kim, K. Lee, K.H. Kim, A. Pirani, B.K. Ha, S.T. Kang, B.S. Park, J.K. Moon, N. Kim and S.C. Jeong (2015) Development, validation, and genetic analysis of a large soybean SNP genotyping array. The Plant Journal 81, 625-636.
7. W.H. Chung, N. Jeong, J. Kim, W.K. Lee, Y.G. Lee, S.H. Lee, W. Yoon, J.H. Kim, I.Y. Choi, H.K. Choi, J.K. Moon, N. Kim, and S.C. Jeong (2014) Population structure and domestication revealed by high-depth resequencing of Korean cultivated and wild soybean genomes. DNA Research 2014; 21: 153-167.
8. W.K. Lee, N. Kim, J. Kim, J.K. Moon, N. Jeong, I.Y. Choi, .S.C. Kim, W.H. Chung, H.S. Kim, S.H. Lee, S.C. Jeong (2013) Dynamic genetic features of chromosomes revealed by comparison of soybean genetic and sequence-based physical maps. Theoretical and Applied Genetics 126:1103-1119.
9. D. Shim, S. Kim, Y.I. Choi, W.Y. Song, J. Park, E.S. Youk, S.C. Jeong, E. Martinoia, E.W. Noh, Y. Lee (2013) Transgenic poplar trees expressing yeast cadmium factor 1 exhibit the characteristics necessary for the phytoremediation of mine tailing soil. Chemosphere 90:1478-1486.
10. N. Jeong, S.J. Suh, M.H. Kim, S. Lee, J.K. Moon, H.S. Kim, and S.C. Jeong (2012) *Ln* is a key regulator of leaflet shape and number of seeds per pod in soybean. The Plant Cell 24: 4807-4818.

PS-0002

Deleterious mutations during domestication in the predominant selfing crop soybean

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As a predominant plant protein and oil source for both food and feed, soybean has a mating system that both domesticated and wild types are predominantly selfing. Here a genome-wide variation map of 781 soybean accessions that include 418 domesticated (*Glycine max*) and 345 wild (*Glycine soja*) accessions and 18 of their natural hybrids is generated. This map contains 10.6 million single nucleotide polymorphisms and 1.4 million indels that contribute to within- and between-population variations. Improved detection of domestication-selective sweeps enables to find drastic reduction of overall deleterious alleles in domesticated soybean relative to wild soybean during the domestication process. This resource enables the marker density of existing data sets to be increased to improve the resolution of association studies.

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<Research Interests>

1. Brassica Genomics
2. Molecular Genetics
3. Marker Assisted Breeding

<Education>

1. Jul. 2005 - Jul. 2008, PhD on Genetics and Breeding, Graduate School, CAAS.
2. Sep. 1989 - Jul. 1992, MsC on Plant breeding and genetics, Graduate School, CAAS.

<Professional Experience>

1. Jun. 2001 - Aug. 2002, PostDoc Position, The University of Warwick, School of Life Sciences, Coventry, United Kingdom
2. Jul. 1992 - present, Professor, Institute of Vegetables and Flowers, CAAS, Beijing, China

<Selected Publications>

1. Kun Lu, Lijuan Wei, Xiaolong Li, Yuntong Wang, Jian Wu, et al, Xiaowu Wang, Andrew H. Paterson & Jiana Li: Whole-genome resequencing reveals Brassica napus origin and genetic loci involved in its improvement. Nature Communications 03/2019; doi.org/10.1038/s41467-019-09134-9
2. Feng Cheng, Jian Wu, Xu Cai, Jianli Liang, Michael Freeling & Xiaowu Wang: Gene retention, fractionation and subgenome differences in polyploid plants, Nature Plants 04/2018; (4):258-268
3. Feng Cheng, Rifei Sun, et al., Guusje Bonnema, Jian Wu, Xiaowu Wang: Subgenome parallel selection is associated with morphotype diversification and convergent crop domestication in Brassica rapa and Brassica oleracea. Nature Genetics 08/2016; 48(10)., DOI:10.1038/ng.3634
4. Jinghua Yang, Dongyuan Liu, Xiaowu Wang, Changmian Ji, Feng Cheng, et al., Mingfang Zhang: The genome sequence of allopolyploid Brassica juncea and analysis of differential homoeolog gene expression influencing selection; Nature Genetics 09/2016; 48(10):1225-1232
5. Xiaowu Wang, Hanzhong Wang, Jun Wang, Rifei Sun, Jian Wu, Shengyi Liu, et al: The genome of the mesopolyploid crop species Brassica rapa. Nature Genetics 08/2011; 43(10):1035-9., DOI:10.1038/ng.919
6. Feng Cheng, Terezie Mandáková, Jian Wu, Qi Xie, Martin A Lysak, Xiaowu Wang: Deciphering the Diploid Ancestral Genome of the Mesohexaploid Brassica rapa. The Plant Cell 05/2013; 25(5)., DOI:10.1105/tpc.113.110486
7. Feng Cheng, Jianli Liang, Chengcheng Cai, Xu Cai, Jian Wu, Xiaowu Wang: Genome sequencing supports a multi-vertex model for Brassiceae species. Current opinion in plant biology 04/2017; 36:79-87., DOI:10.1016/j.pbi.2017.01.006
8. Feng Cheng, Chao Sun, Jian Wu, James Schnable, Margaret R Woodhouse, Jianli Liang, Chengcheng Cai, Michael Freeling, Xiaowu Wang: Epigenetic regulation of subgenome dominance following whole genome triplication in Brassica rapa. New Phytologist 02/2016; 211(1)., DOI:10.1111/nph.13884

PS-0003

Evolution of homoeologous genes and domestication of horticultural traits in the Brassiceae vegetables

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Polyploidy is an important genetic mechanism involved in plant evolution. Polyploidization produces a large number of multi-copy homoeologous genes. The processes by which these homoeologous genes are lost or retained to form new traits are key issues in plant evolution and domestication. Vegetables in the Brassiceae evolved from an ancient whole genome triplication (WGT) event. They developed special plant organs such as tuberous roots, swollen stems, leafy heads, and enlarged inflorescences. These make Brassiceae crop species ideal models for investigate the roles of gene lost and retention in both evolution and domestication. After analyzing several sequenced genomes Brassica species, we proposed "two-step" hypothesis to illustrate the evolution of WGT in Brassiceae species. In the first step, MF1 and MF2 merge and then undergo the first round of gene loss and chromosome rearrangement. In the second step, the evolved MF1-MF2 further merges with LF and undergoes the second round of gene loss and chromosome rearrangement. Finally, the gene density of LF is higher than that of MF1 and MF2. We found that “combined selection ofhomoeologous genes” underlies the domestication of complex horticultural traits, such as leafy heads in both Chinese cabbage and cabbage, tuberous root in turnip, and swollen stem in kohlrabi. Based on these findings, we proposed a molecular design strategy on "combined selection of homoeologous genes” for the genetic improvement of complex traits.

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<Research Interests>

1. Secondary metabolism of medicinal plants
2. Genetics and breeding of medicinal plants

<Education>

1. 1997/08 - 2002/05, Ph.D. Clemson University, Clemson, SC, US, Advisor: Profs. Greg Reighard and Albert Abbott, Major: Plant Genetics
2. 1994/08 - 1997/07, M.S. China Agricultural University, Beijing, China, Advisor：Zhenhai HAN, Major: Horticulture

<Professional Experience>

1. 2015/09 - now, Professor of Medicinal Plant Genetics and Genomics, South China Botanical Garden, Chinese Academy of Sciences
2. 2005/03 - 2015/08, Professor of Plant Genetics and Genomics, Wuhan Botanical Garden, Chinese Academy of Sciences

<Selected Publications>

1. Yang X, Lin S, Jia Y, Rehman F, Zeng S#, Wang Y#. (2020). Anthocyanin and spermidine derivative hexoses coordinately increase in the ripening fruit of *Lycium ruthenicum*. Food Chemistry, 311:125874
2. Wang X, Zhang J, He S, Gao Y, Ma X, Gao Y, Zhang G, Kui L, Wang W, Wang Y*, Yang S*, Dong Y* HMOD: an omics database for herbal medicine plants. Molecular Plant, 2018, 11:757-759.
3. Gong H*, Rehman F*, Yang T, Li Z, Zeng S, Pan L, Li Y, Wang Y# (2019) Construction of the first high-density genetic map and QTL mapping for photosynthetic traits in *Lycium barbarum* L. Molecular Breeding, 39(7):106
4. Huang WJ, Zeng SH, Xiao G, ,Liao S, Chen J, Sun W, Lv H, Wang Y*: Elucidating the biosynthetic and regulatory mechanisms of flavonoid-derived bioactive components in *Epimedium sagittatum*. Frontiers in Plant Science. 2015, 6:689.
5. Liu YL, Zeng SH, Sun W, Wu M, Hu WM, Shen XF, Wang Y*: Comparative analysis of carotenoid accumulation in two Goji (*Lycium barbarum* L. and *L. ruthenicum* Murr.) BMC Plant Biology. 2014, 14:269.
6. The Tomato Genome Consortium (Sato, S, … Wang Y (Principal Investigator)[14]… G Gianese): The tomato genome sequence provides insights into fleshy fruit evolution. Nature. 2012, 485(7400):635-641.

PS-0004

New cultivar and industry trend for Goji (Lycium species) in Genome era

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Lycium L. is a genus of Solanaceae containing about 80 species distributed in the temperate and subtropical zones. *Lycium* species are mostly found in dry, semi-saline environments. Chinese Pharmacopoeia recorded Lycii Fructus (*Gouqizi*, dry red fruit [RF] of *L. barbarum*), and Lycii Cortex (*Digupi*, dry root bark of *L. chinense* and *L. barbarum*). Black fruits (BF) of *L. ruthenicum* have been used as folk medicine, especially in Tibetan and Mongolian medicine. Therefore, Goji (or wolfberry, Gouqi) nowadays in China refers to the products prepared from *L. chinense*, *L. barbarum*, and *L. ruthenicum*, which is one of the most famous anti-aging herbs. Goji fruits have various phytochemical compounds, such as polysaccharides, polyphenols 23 , and carotenoids, dicaffeoylspermidine derivatives. Goji fruits have been used as both herbal medicine and functional fruits in China. *L. barbarum*, and *L. ruthenicum* whole genome sequencing projects have been carried out in order to facilitate the molecular breeding and secondary metabolism in Goji. With the development of economics and shortage of labor, mechanical harvest and fresh fruit consumption will be the future trend for Goji industry. New cultivars with terminated shoot growth and synchronized fruit ripening will be discussed.

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<Research Interests>

1. Genomics
2. Bioinformatics
3. Genetic Resources

<Education>

1. Ph.D. in Biochemistry, 1990, Oklahoma State University.
2. B.S. in Biology and Mathematics, 1982, Northwestern Oklahoma State University

<Professional Experience>

1. Mar 2019 - current. Head of Bioinformatics Cluster, IRRI
2. Feb 2018 - current. International Rice Informatics Consortium (IRIC) Coordinator
3. Jul 2010 - current. Senior Scientist II - Rice Genomics, IRRI
4. Jan 2004 - Jun 2010. Senior Scientist - Molecular Genetics, IRRI
5. Jul 2001 - Dec 2004. Scientist - Molecular Genetics, IRRI
6. Jul 1998 - Jun 2001. Affiliate Scientist - Molecular Biology, IRRI
7. Oct 1996 - Jun 1998. Project Scientist, IRRI
8. Sept 1994 - Aug 1996. Post-doctoral fellow, Plant Breeding, Cornell University
9. Aug 1990 - May 1993. Post-doctoral fellow, Biological and Marine Sciences, University of California at Santa Barbara
10. Nov 1988 - Nov 1989. Post-doctoral fellow, Microbiology and Immunology, University of Colorado Health Sciences Center

<Selected Publications>

1. Zhou Y, Chebotarov D, Kudrna D, Llaca V, Lee SH, Rajasekar S, Mohammed N, Al-Bader N, Sobel-Sorenson C, Parakkal P, Arbelaez LJ, Franco N, Alexandrov N, Hamilton NRS, Leung H, Mauleon R, Lorieux M, Zuccolo A, **McNally K**, Zhang JW, & Wing RA (2020) A platinum standard resource that represents the population structure of Asian rice. *Scientific Data* **7**:113. doi:10.1038/s41597-020-0438-2
2. Wang C, Yu H, Huang J, Wang WS, Faruquee M, Zhang F, Zhao X, Fu B, Chen K, Zhang H, Tai SS, Wei CC, Li J, **McNally K**, Alexandrov N, Gao X, Li Z, Xu J & Zheng TQ (2020) Towards a deeper haplotype mining of complex traits in rice with RFGB v2.0. *Plant Biotech J* **18**:14-16. doi:10.1111/pbi.13215.
3. Santos JD, Chebotarov D, **McNally KL**, Bartholomé J, Droc G, Billot C, Glaszmann JC (2019) Fine scale genomic signals of admixture and alien introgression among Asian rice landraces. *Genome Biol Evol* **11**:1358-1373. doi:10.1093/gbe/evz084.
4. Fuentes RR, Chebotarov D, Duitama J, Smith S, De la Hoz JF, Mohiyuddin M, Wing RA, **McNally KL**, Tatarinova T, Grigoriev A, Mauleon R, Alexandrov N (2019) Structural variants in 3,000 rice genomes. *Genome Res* **29**:870-880. doi:10.1101/gr.241240.118.
5. Wang D, Agosto-Perez F, Chebotarov D, Shi Y, Marchini J, Fitzgerald M, **McNally K**L, Alexandrov A & McCouch SR (2018) An imputation platform to enhance integration of rice genetic resources. *Nature Comm*, **9**:3519. doi:10.1038/s41467-018-05538-1.
6. Wang WS, Mauleon R, Hu ZQ, Chebotarov D, Tai SS, Wu ZC, Li M, Zheng TQ, Fuentes RR, Zhang F, Mansueto L, Copetti D, Sanciangco M, Palis KC, Xu JL, Chen S, Fu BY, Zhang HL, Gao YM, Zhao XQ, Shen F, Cui X, Yu H, Li ZC, Chen ML, Detras J, Zhou YL, Zhang XY, Zhao Y, Kudrna D, Wang CC, Li R, Jia B, Lu JY, He XC, Dong ZT, Xu JB, Li YH, Wang M, Shi JX, Li J, Zhang DB, Lee SH, Hu WS, Poliakov A, Dubchak I, Ulat VJ, Borja FN, Mendoza JR, Ali J, Li J, Gao Q, Niu YC, Yue Z, Naredo MEB, Talag J, Wang XQ, Li JJ, Fang XD, Yin Y, Glaszmann JC, Zhang JW, Li JY, Hamilton RS, Wing RA, Ruan J, Zhang GY, Wei CC, Alexandrov N, **McNally KL***, Li ZK & Leung H (2018) Genomic variation in 3,010 diverse accessions of Asian cultivated rice. *Nature* **557**:43-49. doi:10.1038/s41586-018-0063-9.
7. Stein JC, Yu YS, Copetti D, Zwick DJ, Zhang L, Zhang CG, Chougule K, Gao DY, Iwata A, Goicoechea JL, Wei S, Wang J, Liao Y, Wang MH, Jacquemin J, Becker C, Kudrna D, Zhang JW, Londono CEM, Song X, Lee SH, Sanchez P, Zuccolo A, Ammiraju JSS, Talag J, Danowitz A, Rivera LF, Gschwend AR, Noutsos C, Wu CC, Kao SM, Zeng JW, Wei FJ, Zhao Q, Feng Q, El Baidouri M, Carpentier MC, Lasserre E, Cooke R, da Rosa Farias D, da Maia LC, dos Santos RS, Nyberg KG, **McNally KL**, Mauleon R, Alexandrov N, Schmutz J, Flowers D, Fan CZ, Weigel D, Jena KK, Wicker T, Chen MS, Han B, Henry R, Hsing YIC, Kurata N, Costa de Oliveira A, Panaud O, Jackson SA, Machado CA, Sanderson MJ, Long MY, Ware D & Wing RA (2018) Genomes of 13 domesticated and wild rice relatives unveil genetic conservation, turnover and innovation across the genus Oryza. *Nature Genet* **50**:285-296. doi:10.1038/s41588-018-0040-0.
8. Mansueto L, Fuentes RR, Borja FN, Detras J, Abriol-Santos JM, Chebotarov D, Sanciangco M, Palis K, Copetti D, Poliakov A, Dubchak I, Solovyev V, Wing RA, Sackville Hamilton R, Mauleon R, **McNally K**L, Alexandrov N (2017) Rice SNP-seek database update: new SNPs, indels, and queries. *Nucl Acids Res* **45**:D1075-D1081. doi:10.1093/nar/gkw1135.
9. McCouch SR, Wright MH, Tung CW, Maron LG, **McNally KL**, Fitzgerald M, Singh N, DeClerck G, Perez FA, Korniliev P, Greenberg A, Naredo MEB, Mercado SMQ, Harrington SE, Shi Y, Branchini DA, Kuser-Falcao PR, Leung H, Ebana K, Yano M, Eizenga G, McClung A, Mezey J (2016) Open Access Resources for Genome Wide Association Studies (GWAS) in rice (Oryza sativa) illustrate the power of population-specific mapping. *Nature Comm* **7**:10532. doi:10.1038/ncomms10532.
10. 3K RGP (2014) The 3,000 rice genomes project. *GigaScience* **3**:7. doi:10.1186/2047-217X-3-7.

PS-0005

Moving Forward to a Digital Rice Genebank

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The 3000 rice genomes (3K RG) project provides a foundation to more deeply explore the genomic diversity within *Oryza sativa*. Within the 3K RGP dataset, we identified SNPs and structural variants (SVs) relative to the reference genome Nipponbare. Yet, having a single reference genome for analysis meant that variants in regions unique to one type or another could not be identified. Initial analysis of the 3K RG indicated nine subpopulations associated with geographic origin; further exploration allowed six additional subpopulations to be discerned. We now have constructed 15 long-read platinum standard reference sequences (PSRefSeqs) for each of these subpopulations. These reference genomes are being used to analyze the 3K RG and other resequencing data so that a more that a more thorough understanding of genomic variation is in hand. They will also facilitate building a pan genome for *O. sativa* with harmonized annotation and integrated variants. Additionally, we have begun the process to sequence 10K additional rice genomes across the range of diversity at >20X depth, the second step toward building a digital rice genebank. This new resource will significantly extend understanding of variation in rice relative to all subpopulations. Subsequently, we aim to sequence the remaining 100K accessions in the International Rice Germplasm Collection at lower coverage to complete the digital rice genebank. Ultimately, these resources will serve to identify variation for a range of traits including adaptation to stress resulting from climate change that can then be introduced into breeding programs.

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Dr. Martin Mascher

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Martin Mascher is head of the research group "Domestication Genomics" at IPK Gatersleben. A mathematician by training, his research focusses on topics in plant bioinformatics and computational genetics. He has developed algorithms and pipelines for assembling genome sequences and analysing resequencing data of crop diversity panels. Recently, his group has analysed sequence data from plant genetic resources, crop wild relatives and archaeological samples to understand domestication and crop evolution in cereals.

Since 2015	Independent group leader at IPK Gatersleben and member of the German Centre for Integrative Biodiversity Research Halle-Leipzig-Jena (iDiv)
2011-2014	Ph.D. in Bioinformatics, Bielefeld University
2011-2014	Research assistant, IPK Gatersleben
2006-2011	Diploma, Mathematics, Magdeburg University

PS-0006

Genebank genomics bridges the gap between the conservation of crop diversity and plant breeding: a case study in barley

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Genebanks hold comprehensive collections of cultivars, landraces and crop wild relatives of all major food crops, but their detailed characterization has so far been limited to sparse core sets. The analysis of genome-wide genotyping-by-sequencing data for almost all barley accessions of the German *ex situ* genebank provides insights into the global population structure of domesticated barley and points out redundancies and coverage gaps in one of the world's major genebanks. Our large sample size and dense marker data afford great power for genome-wide association scans. We detect known and novel loci underlying morphological traits differentiating barley genepools, find evidence for convergent selection for barbless awns in barley and rice and show that a major-effect resistance locus conferring resistance to bymovirus infection has been favored by traditional farmers. This study outlines future directions for the selection of useful genetic variation and its use in breeding programs, thus providing easier access to past crop diversity.

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<Research Interests>

1. Application of genotyping techniques in Agrigenomics research
2. Molecular profiling of solid tumors using advanced molecular techniques such as Proteomics and Transcriptomics

<Education>

Ph.D in Cancer Biology: Birla Institute of Technology and Science, Pilani, 2010
Thesis: Molecular Mechanisms involved in Intra-Ocular Tumor Progression.

M.Sc. Medical Laboratory Technology, Birla Institute of Technology and Science, Pilani, 2004. Project Thesis title: Role of P53 family proteins and Drug resistance proteins in Ocular tumors
Overall CGPA: 8.25/10.0

<Professional Experience>

2019 - Till date **Business Development Manager - Asia Pacific Japan at Thermo Fisher Scientific**
Developing a strong opportunities pipeline across APJ region, working closely with local commercial team to drive sales funnel and channel managers to manage distributors in the region. Identify new market avenues in Agrigenomics to achieve and exceed numbers every year. Work with Marketing Managers to participate in key events like conferences and conduct seminars to create product awareness and generate business opportunities. Collaborate internally with leadership Managers to manage and solve key issues in the business development.

2016 - 2019 **Genomics Product Specialist - Asia Pacific region at Thermo Fisher Scientific.**
Thermo Fisher Scientific Acquired Affymetrix and my role continued as Product Specialist for promoting all Affymetrix (Microarray) and Thermo Fisher Scientific products (NGS) products in Asia pacific region across 11 countries. Job profile is to involve in providing technical inputs to the application specialists, marketing team and sales team on Agrigenomics applications (Microarray and AgriSeq). Additionally, I am dealing with Clinical Diagnostic portfolio, Precision Medicine array products, next generation sequencing panels such as cancer panels, genetic disorders panel and genotyping product portfolio.

2014 - 2016 **Genomics Product Specialist - Asia Pacific Region (Affymetrix)**
Affymetrix - Specialist for Genotyping, AgBio and Clinical Diagnostics and Gene expression market for Asia Pacific Region. Worked in 11 countries for promoting Affymetrix products in the whole Asia Pacific region.

2013 - 2014 **Manager - Application Support** at Premas Biotech (Premas Life Sciences), India for Illumina NGS and Microarray platforms and consumables. (HiSeq, HiScanSQ, IScan and HiScan)

2011 - 2013 **Application support Specialist** at Spinco Biotech Pvt Ltd, India for Illumina NGS and Microarray platforms and consumables. (HiSeq, HiScanSQ, IScan and HiScan)
Pre and Post Sales of Illumina's real time PCR instruments.

Training in Singapore: Trained in Singapore on Application Support (Illumina, Biopolis, Singapore) for providing application technical support to customers on next generation sequencing technology.

<Selected Publications>

1. Ramaswamy Manimekalai , Gayathri Suresh, Hemaprabha Govinda Kurup , Selvi Athiappan, **Mallikarjuna Kandalam**. Role of NGS and SNP genotyping methods in sugarcane improvement programs. Crit Rev Biotechnol. 2020 Sep;40(6):865-880.
2. **Mallikarjuna K**, Sundaram CS, Sharma Y, Deepa PR, Vikas K, Tarun S, Lingam G, Biswas J, Krishnakumar S. Comparative proteomics analysis of differentially expressed proteins in primary retinoblastoma tumors. *Proteomics Clin. Appl* 2010:4 (4); 449 - 463. (Impact factor: 1.5) (citations 3)
3. **Mallikarjuna K**, Moutushy M, Biswas J, Krishnakumar S. Molecular Pathology of Retinoblastoma. *Middle East Afr J Ophthalmol. 2010*; 17:217-23. Review.
4. **Mallikarjuna K**, Pushparaj V, Biswas J, Krishnakumar S. Expression of epidermal growth factor receptor, ezrin, hepatocyte growth factor, and c-Met in uveal melanoma: an immunohistochemical study. *Curr Eye Res*. 2007 Mar;32(3):281-90. (Impact factor: 1.5) (citations 7)
5. **Mallikarjuna K**, Vaijayanthi P, Krishnakumar S. Cripto-1 expression in uveal melanoma: an immunohistochemical study. *Exp Eye Res*. 2007 Jun;84(6):1060-6. Epub 2007 Feb 7. (Impact factor: 2.6) (citations: 3)
6. **Mallikarjuna K**, Pushparaj V, Biswas J, Krishnakumar S. Expression of insulin-like growth factor receptor (IGF-1R), c-Fos, and c-Jun in uveal melanoma: an immunohistochemical study. *Curr Eye Res*. 2006 Oct;31(10):875-83. (Impact factor: 1.5) (citations 7).
7. Mitra M, **Mallikarjuna K**, Sundaram CS, Verma RS, Maheswari UK, Swaminathan S, Krishnakumar S. Reversal of stathmin-mediated microtubule destabilization sensitizes retinoblastoma cells to a low dose of antimicrotubule agents: a novel synergistic therapeutic intervention. *Invest Ophthalmol Vis Sci.* 2011;52:5441-8. (Impact factor - 3.8)
8. Moutushy M, **Mallikarjuna K**, Verma RS, Uma M, Krishnakumar S. Genome-wide changes accompanying the knock-down of EpCAM in retinoblastoma. *Mol Vis*. 2010:16:828-42 (Impact factor: 2.5).
9. Mohan A, **Mallikarjuna K**, Venkatesan N, Abhyankar D, Parikh PM, Krishnakumar S. The study of c-Src kinase and pStat3 protein expression in retinoblastoma. *Exp Eye Res*. 2006 Oct;83(4):736-40. Epub 2006 May 22. (Impact factor: 2.6)
10. Mohan A, **Mallikarjuna K**, Ramkumar HL, Gopal L, Krishnakumar S. Stem cell markers: ABCG2 and MCM2 expression in retinoblastoma. *Br J Ophthalmol.* 2006 Jul;90(7):889-93. (Impact factor: 2.9) (citations: 28)

PS-0007

Powerful, Scalable and Affordable genotyping solutions for Agrigenomics breeding applications from Thermo Fisher Scientific

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Molecular markers are now key components of crop improvement programs, and are applied to identify cultivars, analyze genetic diversity, construct linkage maps and identify quantitative trait loci (QTL). Molecular breeding can significantly reduce the cost and time required to deliver improved plant and animal species for agricultural use. Advancements in genomic technologies are accelerating these breeding programs by enabling higher-throughput genotyping across large populations than ever before. Applied Biosystems Axiom microarray and AgriSeq targeted genotyping by sequencing (GBS) solutions are our innovations that helps our customers economically deliver high-throughput plant and animal genotypes. Axiom Microarray with several advantages like custom design capabilities with fastest turn-around time, zero SNP dropouts and highly automated genotyping analysis are key to successfully implement Agrigenomics projects. The AgriSeq targeted GBS solution utilizes a highly efficient multiplexed PCR chemistry where hundreds to thousands of markers can be targeted and uniformly amplified in a single reaction. One of the powers of this technology is its capability to support multiple types of markers including single nucleotide polymorphisms (SNPs), multiple nucleotide polymorphisms (MNPs), insertions and deletions (InDels), and other structural variants (e.g. inversions, duplications). My talk would cover the overview of the Axiom and AgriSeq technologies and their applications in the Agrigenomics field.

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Concurrent Session

CA-0001

Application of best linear unbiased prediction (BLUP) on GWAS identifies candidate gene regulating branch development in soybean

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The number of branches is one of the important factors affecting the yield of soybean (*Glycine max* (L.)). Here, we conducted a genome-wide association analysis to identify candidate gene determining soybean branching based on the application of best linear unbiased prediction (BLUP). Five quantitative trait nucleotides (QTNs) were tightly associated with number of branches in a soybean core collection. Among these, a linkage disequilibrium (LD) block carrying *qtnBR6-1* was found to found to overlap a previously identified major quantitative trait locus *qBR6-1*. Using a set of near-isogenic lines (NILs) harboring high-branching (HB) and low-branching (LB) alleles of *qBR6-1* with 99.96% isogenicity and different branch numbers, we validated and narrowed down *qtnBR6-1*. A cluster of single nucleotide polymorphisms (SNPs) segregating into NIL-HB and NIL-LB was harbored in the LD block carrying *qtnBR6-1*. Among the five genes showing differential expression between NIL-HB and NIL-LB, transcriptional activity of *BRANCHED1* (*BRC1*; Glyma.06G210600) was significantly down-regulated in the shoot apex of NIL-HB. In addition, one missense mutation and two SNPs harbored in promoter region of *BRC1* were tightly associated with branch numbers in 59 additional soybean accessions. *BRC1* encodes TEOSINTE-BRANCHED1/CYCLOIDEA/PROLIFERATING CELL FACTORS 1 and 2 transcription factor and functions as a negative regulator of branching. Based on these results, we propose *BRC1* as a candidate gene regulating branching in soybean.

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CA-0002

Epigenetic diversity in duplicated plant genomes

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Plants have duplicated genes mostly due to whole-genome duplications (WGD) events that occurred in the ancestor species. Although a majority of duplicated genes are lost through non-functionalization or pseudogenization, many have been retained through balancing gene dosage/or functional divergence. DNA methylation can contribute to the regulation of gene expression in plants, yet little has been investigated to the role of DNA methylation in the functional divergence of paralogous genes. Using high-resolution methylation maps of accessions of domesticated and wild soybean, we show that in soybean, a recent paleopolyploid with many paralogs, DNA methylation likely contributed to the elimination of genetic redundancy of polyploidy-derived gene paralogs. Transcriptionally silenced paralogs exhibit particular genomic features as they are often associated with proximal transposable elements (TEs) and are preferentially located in pericentromeres, likely due to gene movement during evolution. In addition to DNA methylation, divergent distributions of small RNA abundance in soybean, which have not yet been seen in any plant species, will be presented.

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CA-0003

Harnessing Retrotransposons for Crop Improvement

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Transposable elements (TEs) are mobile DNAs that jump around the genomes. Their mobile nature has contributed vastly to the genetic variability of many crops, which serve as important breeding resources. With the aim of harnessing TEs for creating new genetic variations and ultimately crop improvement, we have been striving to develop methods to identify active TEs and detect their mobilization in real time. In this talk, I will discuss our novel sequencing method ALE-seq (***A***mplification of ***L***TR of ***e***clDNAs followed by sequencing) that identifies active retrotransposons in complex crop genomes. ALE-seq detects the extrachromosomal linear DNA (eclDNA), the final intermediate of retrotransposition, by specifically sequencing the 5' long terminal repeat (LTR). Using ALE-seq in rice and tomato, we detected eclDNAs for novel LTR retrotransposons, *Go-on* and *FIRE*, which are activated in the heat-stressed rice and tomato pericarps, respectively. Besides, we recently established a fluorescence-based retrotransposition reporter system RUM (***R***eal-time j***UM***ping of retroelements) that allows us to detect TE mobilization in real time and at single-cell resolution. RUM adopts truncated fluorescence gene engineered in the LTR region of a retroelement, which can be reconstituted to an intact and functional fluorescence gene during the retrotransposition life cycle. Overall, the novel methods to study retrotransposon behavior unveil the hidden natural driver for genomic variability which will help accelerate crop breeding process.

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CA-0004

Rice arbuscular mycorrhizal symbiosis requires the removal of the suppressor SMAX1

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Under limited nutrient conditions, more than 80% terrestrial plants are engaged with the symbiotic fungi, arbuscular mycorrhizae (AM), to obtain minerals such as phosphate. AM symbiosis initiates with a bidirectional biochemical dialogue where both symbiotic partners send and receive diffusible signals to recognize each other. The receptor complex, alpha/beta-fold hydrolase, Dwarf14-like (D14L), and the F-box gene, Dwarf3 (D3), are vital for sensing AM fungi in rice. The same receptor complex recognizes the smoke derived-compound karrikin, triggering seed germination and seedling growth post-wildfire in Arabidopsis. In this study, we investigated a downstream component of *D14L/D3* receptor complex during AM symbiosis and identified *Suppressor of MAX2 -1 (SMAX1)* as a critical component. Loss of function *smax1* mutation led to an elevated level of colonization than wild-type, suggesting SMAX1 functions as a suppressor of AM symbiosis. Furthermore, genetics study placed *SMAX1* epistatically downstream of the receptor complex, *D14L/D3*. Consistently, SMAX1 protein was accumulated in both *d14* and *d3* receptor mutant, indicating that the receptor complex is involved in the degradation of the suppressor. Based on the nuclear localization of SMAX1, we tested whether SMAX1 suppresses transcription of AM symbiosis genes. RNAseq analysis of uninoculated *smax1* mutant indeed revealed the activation of a set of genes that are known to be regulated by AM symbiosis, including ones that that are involved in the bidirectional chemical dialogue. In summary, we discovered that the removal of the SMAX1 suppressor is required for the successful establishment of AM symbiosis by transcriptional reprogramming the rice for the endosymbiosis.

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CA-0005

Interactive analysis platform for data management, GWAS and marker development

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

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CB-0001

Combining GWAS and CRISPR-Cas9 for rapid identification of resistance genes to rice blast

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Rice blast, caused the fungal pathogen *Magnaporthe oryzae*, is one of the most serious diseases of rice and affects global food security. Use of resistance genes is the most effective approach to control the disease. To identify new resistance genes to *M. oryzae*, we used genome-wide association study (GWAS) and the Rice Diversity Panel 1 and 2 (RDP-1 and 2) to map and clone major and QTL genes against the *M. oryzae* populations in Asia and Africa. The RPD-1 population contains about 350 rice accessions and genotyped with about 700K SNPs and the RPD-2 population contains 584 rice accessions and are genotyped with 700K SNPs. The rice cultivars were either inoculated with single blast isolates in growth chambers or grown in the blast nurseries for natural infection. Association mapping was conducted using the disease resistance phenotypic data and the SNP genotype data. We mapped over 100 QTLs that are effective to different *M. oryzae* isolates. In addition, we identified QTLs that are associated with field resistance in the blast nurseries. Using the SNP markers tightly linked to two candidate genes, RNAi and CRISPR-Cas9 gene editing technologies, we cloned one major and one QTL resistance gene. Finally, over 100 rice cultivars that confer broad-spectrum resistance to *M. oryzae* have been found and provided to rice breeders for rice blast resistance improvement. These results demonstrate that combining GWAS and CRISPR-Cas9 is a powerful approach to rapid identification of new major and minor resistance genes to rice blast.

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CB-0002

Diversity of alleles related to major agronomic traits in rice

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We had previously identified the genomic diversity of Korean rice core set using next generation sequencing (NGS). Now we examined the diversity of alleles related to major agronomic traits of the extended Korean rice core set. We performed genome-wide resequencing, chip genotyping, and RNA-Seq on the rice population. We identified genome-wide SNPs from all the rice sets and identified alleles for all known genes in the rice. We compared the distribution of alleles related to major agronomic traits, such as starch synthesis and bacterial leaf blight resistance, and the distribution of alleles among ordinary genes.

Keyword: allele, core set, diversity, genome, rice, SNP

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CB-0003

Genetic diversity and genome-wide association study in a core collection of peanut germplasms using a high-density SNPs array

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Due to the recent domestication of peanuts derived from a single polyploidization event, the genetic diversity of cultivated peanuts was extremely low. In order to expand the genetic variation in breeding programs, the use of core collections has many benefits and it will be a good starting material for association analysis. High-density SNP arrays have been widely used in many applications that require a large number of markers such as GWAS and genome selection. In the study, the population structure and genetic diversity of 384 peanut germplasms including a total of 284 peanut core collections were evaluated using a high-density 58 K SNPs, and a GWAS was performed using compressed mixed linear model in GAPIT package of R software for seed shape trait. A total of 6,144 filtered SNPs and seed aspect ratio data were analyzed for GWAS. A total of 4 candidate SNPs showing significant association with seed aspect ratio were identified on chromosome Aradu.A09, Araip.B08 and Araip.B09 with significant *P*-value < 0.0001. The distribution of observed -log10(p) for each SNP was compared with the expected distribution in a QQ plot, representing that the population structure and kinship relationship were well controlled in the GWAS for the trait. Our study showed the possibility of GWAS analysis using a core collection and a high density SNPs array in peanut, and we also identified significant markers associated with seed aspect ratio. It is expected that various other agronomic traits of peanut can be analyzed using the same way in the future.

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CB-0004

Uncovering candidate genes controlling major fruit-related traits in pepper via genotype-by-sequencing-based QTL mapping and genome-wide association study

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All modern pepper accessions are products of the domestication of wild *Capsicum* species. However, due to the limited availability of genome-wide association study (GWAS) data and selection signatures for various traits, domestication-related genes have not been identified in pepper. Here, to address this problem, we obtained data for major fruit-related domestication traits (fruit length, width, weight, pericarp thickness, and fruit position) using a highly diverse panel of 351 pepper accessions representing the worldwide *Capsicum* germplasm. Using a genotype-by-sequencing (GBS) method, we developed 187,966 genome-wide high-quality SNP markers across 230 *C. annuum* accessions. Linkage disequilibrium (LD) analysis revealed that the average length of the LD blocks was 149 kb. Using GWAS, we identified 111 genes that were linked to 64 significant LD blocks. We cross-validated the GWAS results using 17 fruit-related QTLs and identified 16 causal genes thought to be associated with fruit morphology-related domestication traits, with molecular functions such as cell division and expansion. The significant LD blocks and candidate genes identified in this study provide unique molecular footprints for deciphering the domestication history of *Capsicum*. Further functional validation of these candidate genes should accelerate the cloning of genes for major fruit-related traits in pepper.

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CB-0005

Genome-wide association study of eight fruit traits in cultivated tomato (*Solanum lycopersicum* L.)

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Genome-wide association study (GWAS) is an effective approach to identify favorable alleles with high mapping resolution. Advances on high-throughput genotyping technologies facilitate GWAS in crop species. We conducted GWAS to investigate quantitative trait loci (QTL) for eight fruit traits in a collection of 162 cultivated tomato accessions. The traits used in this study included fruit height, fruit width, fruit shape index, fruit weight, Brix, locule number, pericarp thickness and fruit firmness. Phenotypic variations of these traits in the tomato accessions were evaluated with three replicates in field trials over two years. For genotyping, the 51K Axiom® tomato array was used, and 34,550 confident SNPs were selected for further analysis. STRUCTURE analysis revealed seven sub-populations in the tomato collection and the resulting membership coefficients were used to account for population structure along with a kinship matrix. GWAS detected a total of 81 SNP loci which were significantly associated with the eight fruit traits at $P < 0.01$, explaining 4.30% to 21.09% of total phenotypic variations. Of these, 35 SNP loci were detected over two years and the other 46 SNP loci were year-specific. In addition, eight SNP loci showed significant associations with multiple traits, suggesting pleiotropic effects of the QTL. Interestingly, we found 46 loci associated with novel QTL and 27 candidate genes in the vicinity of these loci based on *in silico* analysis. These results will accelerate development of molecular tools for improving fruit traits via marker-assisted selection and genomic selection in breeding programs.

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CC-0001

Current status of high-throughput genotyping system for molecular breeding : practical considerations

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For efficient molecular breeding, high-throughput genotyping (HTG) system is essential. There are two main components for HTG: DNA extraction and genotyping. In high-throughput DNA extraction, the most critical factor is the extraction cost per sample. Automated systems usually use magnet bead-based method, which provides good DNA quality but with a high cost. In contrast, sample preparation methods for direct-PCR are cost-efficient. In the case of genotyping, HTG platforms can be categorized by the genotype numbers per sample. Next-generation sequencing-based methods are generally suitable for analyzing very large number of genotype analysis in a small number of samples. On the other hand, HTG systems such as Array Tape-based equipment is suitable for analyzing a small number of target genes in plenty of samples. Instruments such as microarray and Fluidigm have a fixed genotype/sample ratio but it can be cost-efficient. Since the efficiency of HTG is greatly affected by DNA extraction and genotyping methods, appropriate combinations can be utilized according to the diverse procedures of molecular breeding.

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CC-0002

Multiplex Detection of Crop Genetic Mutations Based on Encoded Hydrogel Microparticles

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Genetic mutations in crops are closely related to the target traits and they play an important role as key markers for crop breeding. Current techniques to detect these genetic mutations are generally based on microwell array which uses microliter reaction system and 2D chip which uses 2D surface reaction system. However, they contain some limitations such as low sensitivity, lack of multiplex capacity, requirement of target amplification process, and high detection cost. Herein, we present a highly sensitive multiplex detection of crop genetic mutations based on encoded hydrogel microparticles. Hydrogel microparticles can provide high probe activity in a water-like environment and high target sensitivity in a picoliter-scale three-dimensional reaction system. Furthermore, high multiplex capacity can be obtained since each particle can be loaded with a probe and a graphical code to identify the probe. Utilizing the encoded hydrogel particle technology, we succeeded in detecting multiple origin-related genetic mutations in genomic DNA of ginseng and classifying the origin of ginseng. We also show a colorimetric labelling method that enables the field detection of genetic mutations. Finally, we demonstrate a high-throughput automated analyzer that could allow for rapid analysis of hydrogel microparticles.

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CC-0003

High throughput phenotyping in cost-effective manners

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Advent of high throughput phenotyping in recent years excited breeders by showing the possibility to solve the bottleneck, “phenotyping enough number of breeding population”. However, breeders has been soon doomed by the complexity of the cutting edge technologies from multi-crossed research areas and the costs of equipment and facilities presented by phenomics-specialized companies strengthened their disappointment turning hope to break bottleneck into illusion. Thus, I am very delighted to share the methods for high throughput phenotyping in cost-effective manners. In this presentation, I would present simple-but-solid methods for various target traits so that breeders and researchers so that they could apply those to their own purposes under their own circumstances. I hope they could develop even better methods out of this presentation.

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CC-0004

Image-based Machine Learning Characterizes Root Nodule in Soybean Exposed to Silicon

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Silicon promotes nodule formation in legume roots which is crucial for nitrogen fixation. However, it is very time-consuming and laborious to count the number of nodules and to measure nodule size manually, which led nodule characterization not to be study as much as other agronomical characters. Thus, the current study incorporated various techniques including machine learning to determine the number and size of root nodules and identify various root phenotypes from root images that may be associated with nodule formation with and without silicon treatment. Among those techniques, the machine learning for characterizing nodule is the first attempt, which enabled us to find high correlations among root phenotypes including root length, number of forks, and average link angles, and nodule characters such as number of nodules and nodule size with silicon treatments. The methods here could greatly accelerate further investigation such as delineating the optimal concentration of silicon for nodule formation.

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CC-0005

영상 및 분광정보를 활용한 우수 형질 비파괴 선발 방법

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작물의 생산량과 품질은 재배 환경의 상태와 조건에 큰 영향을 받는다. 다양한 환경에서 작물의 생육이 잘 이루어지기 위해서는 abiotic/biotic 스트레스 등에 민감하지 않은 우수한 형질의 작물을 선발하는 것이 중요하다. 작물 선발은 작물 자체나 최종 산물인 종자의 표현형을 통해 이루어질 수 있다. 스트레스에 대한 작물의 반응, 특정 유용 성분이 많은 식량 종자 등을 선발하기 위해서는 형질이 다음 세대로 전달될 수 있는 비파괴적인 선발이 필요하며 객관성이 낮은 육안 관찰보다 영상 및 분광측정 장치 등을 활용한 객관적이며 정량적인 표현형 검정이 필요하다. 본 연구에서는 인삼 및 콩의 표현형 비파괴적 정량 분석을 위해 초분광 영상 장치와 분광기를 활용하였다. 초분광 영상을 이용하여 인삼의 고온스트레스(abiotic)와 뿌리썩음병(biotic) 스트레스를 지상부의 인삼 잎사귀로 진단하고, 콩의 유용성분 비파괴 분석을 위해 분광분석 기술을 활용하였다. 본 연구를 통하여 분광 및 영상기술이 스트레스 내성 품종 선발 및 특정 성분 함량이 높은 종자의 비파괴 신속 선발에 활용될 수 있음을 확인할 수 있었다.

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CC-0006

Establishment of high-throughput genotyping systems for *Panax ginseng*

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Panax ginseng which has various pharmacological efficacy is one of the most valuable medicinal herb in Korea. Many eloquent studies have been carried out for this crop, but the fields of efficient breeding are still poor. In order to develop useful molecular markers for ginseng, it is necessary to understand its complex genome structure. Genotyping-by-sequencing method using various ginseng genetic resources was applied to reduce the complexity and to discover high-throughput SNP information. Informative SNPs were selected based on strict parameters from regions where flanking sequences exist in a single copy within the genome. These SNPs were converted into kompetitive allele specific PCR (KASP) markers and Fluidigm SNP chips suitable for high-throughput genotyping systems. As a results, 36 KASP markers and 3 set of SNP chip (48x48) including 131 SNPs evenly distributed in the genome were successfully developed. These genetic tools accurately and quickly confirmed the genotypes of various ginseng genetic sources. Most of the accessions were distinguished from each other and grouped according to the useful genotype information. Based on the KASP markers and SNP chip sets developed in this study, high-throughput genotyping systems for *P.ginseng* was successfully established. The presence of these genetic tools will provide useful information on efficient management of germplasms currently being managed and will be used for practical ginseng breeding applied to various genetic resources.

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CD-0001

RNA Guided Endonucleases based crop genome editing

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RNA-guided programmable nuclease (RGEN), such as a CRISPR/Cas9 or a CRISPR/Cpf1, is the representative molecular scissor for precision genome editing. RGENs were rapidly implemented for targeted mutagenesis in living cells and precision molecular breeding in various organisms. Previously, we had reported DNA-free genome editing tools for precision crop editing with both CRISPR-Cas9 RNP and CRISPR-Cpf1 RNP. To successfully editing in a target gene, it is essential to apply specifically designed and validated CRISPR tools in a target genome. Here, I will describe RGENs-mediated genome editing in both Korean soybean cultivars and whole-genome sequenced peppers and share about established guide-RNA screening tools for soybean and pepper.

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CD-0002

Efficient and heritable gene edition using CRISPR/cas9system in tomato

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CRISPR/cas9 technology provides precise sequence editing in the targets of single or multi-genes in research and crop improvement. In this study, we examined the methods for inducing mutations in multi-genes using multi-target CRISPR/cas9 system and the isolation of single gene mutation using backcrossing of the mutations. Four sgRNAs efficiently edited two loci with double targets on each locus but were less effective to four loci with single target in each locus. This methods back-crossed multi-loci mutant with wild type, which resulted in easily isolating single-loci mutants as T-DNA free generation. In addition, we also set up homology-directed repair (HDR) system mediated by CRISPR/cas9-geminiviral replicon to gain a function in tomato. DNA double strand break (DSB) and donors copied by geminiviral replicon effectively complemented determinate growth tomato into indeterminate tomato. Thus, our methods provide the efficient processes of genome editing for genetic researches and tomato breeding.

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CD-0003

Chloroplast-targeted transgene delivery and transient expression across varied plant systems using single-walled carbon nanotubes

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Plant genetic engineering is essential for crop improvement, pharmaceutical biosynthesis, sustainable agriculture, and fundamental plant biology. Chloroplast genetic engineering provides a level of containment that rarely leads to the outcrossing of transgenes since the plastid genome is maternally inherited in most higher plants, motivating the development of plant organelle-specific nanocarriers. We design chitosan-complexed single-walled carbon nanotubes, utilizing the lipid exchange envelope penetration (LEEP) mechanism to maximize the trafficking efficiency of the plasmid DNA-SWNT complexes into the chloroplasts without any external biolistic or chemical aid.

We achieved chloroplast-targeted transgene delivery by visualization of transient expression of a marker gene, yellow fluorescent protein, in mature *Eruca sativa*, *Nasturtium officinale*, *Nicotiana tabacum*, and *Spinacia oleracea* plants and isolated *Arabidopsis thaliana* mesophyll protoplasts. Our approach is simple, easy to carry out, cost-effective, and does not require specialized equipment. This chloroplast-selective transgene delivery nanocarrier offers practical advantages over current gene delivery techniques for mature non-model plants to benefit plant bioengineering.

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CD-0004

CRISPR/Cas9-mediated genome editing of *Ehd1*, a major inducer of flowering in rice, increases vegetative growth and grain yield potential

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Flowering time is elaborately controlled by various environment factors, but is ultimately induced by florigens such as FT or FT-like molecules. Increasing vegetative growth period could promote biomass and grain yield. In rice, *Early heading date 1* (*Ehd1*) is a major inducer of florigen gene expression. However, the molecular mechanism by which this protein regulates downstream genes is poorly understood. For studying its molecular function, *Ehd1* knockout mutants were generated by the CRIPSR/Cas9 method. In the T1 generation, *ehd1* KO plants showed delayed flowering under short- or long-day conditions when compared with the WT. The KO plants also exhibited increased panicle number and grain yield per plant, and plant height. Ehd1 is highly homologous to the type-B response regulator (RR) family in the cytokinin signaling pathway. To elucidate whether exogenous cytokinin influences the length of vegetative phase, we applied 6-benzylaminopurine to plants at various developmental stages. This treatment delayed flowering time by 8 to 9 d when compared with mock-treated plants, but only at the stage when the flowering signals were produced. Transcript levels of florigen genes, *Heading date 3a* (*Hd3a*) and *Rice Flowering locus T1* (*RFT1*), were significantly reduced by the treatment, but expression of *Ehd1* was not altered. Cytokinin treatment induced expression of two type-A response regulators, OsRR1 and OsRR2, that physically interacted with Ehd1, a type-B response regulator. These observations suggest that cytokinin maintain the vegetative phase by increasing the levels of OsRR1 and OsRR2, which inhibit the transition to reproductive phase by interfering Ehd1 activity.

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CD-0005

Maintenance of net photosynthesis at the grain-filling stage increases crop productivity of indica rice

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Increasing grain productivity is critical agronomic agenda to meet the food demand for the growing population in the World. Diverse strategies including trait improvement have been tried to increase the crop yield. Chlorophyll degradation during leaf senescence has important functions translocating nutrients from leaves to storage organs. The functional stay-green with slow leaf yellowing and photosynthesis activity maintenance at senescence stage has been considered one of strategy for increasing crop productivity. Leaf senescence and grain filling rate of *indica* rice varieties are normally faster and lower than those of *japonica* rice varieties on rice cultivation environment in Korea. We hypothesized that maintenance of net photosynthesis during senescence maybe increase grain filling rate and crop yield of *indica* rice varieties. Here, we have identified the *Stay-Green* (*OsSGR*) gene on chromosome 9 controlling the leaf senescence time with chlorophyll content by map-based cloning. Promoter variations in the *OsSGR* gene encoding the chlorophyll-degrading Mg^{++}-dechelatase were found to trigger higher and earlier induction of *OsSGR* in *indica*, which accelerated senescence of *indica* rice cultivars. *Japonica OsSGR* alleles introgressed into *indica*-type cultivars in Korean rice fields lead to delayed senescence, with increased grain yield and enhanced photosynthetic competence. Taken together, these data establish that naturally occurring *OsSGR* promoter and related lifespan variations can be exploited in breeding programs to augment rice yield.

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CE-0001

Multiple abiotic stress tolerance improvement by the pyramiding QTLs in rice

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Climate change in rice production will be significant in Korea as well as in other countries. Facing the possible adverse effects caused by unpredictable weather conditions, several breeding strategies have been applied to rice. Out of them, highly valuable traits were found from the landraces and wild relatives of rice through remote crossing programs. We have applied major QTLs for highly efficient phosphorus uptake, and also for drought resistant, salinity resistance, etc. Some of the successful near isogenic lines containing QTLs showed some beneficial effects, not only for the original target stress tolerances, but also for salinity and high temperature stress. The selected sister lines containing the QTLs showed very different phenotypes under the stresses, thus, the differential genomic constitutions of the lines are being studied. By pyramiding multiple biotic and abiotic QTLs in the novel japonica and indica varieties, some high-quality and stress tolerant varieties were developed. The more total effective temperature increase in the cropping duration in Korea might be helpful for growing indica rice. On the other hand, the immigration or the advent of new pathogens or insect biotypes will affect rice production in the future. Consistent support on breeding multiple stress resistances is critical in achieving climate change resilience in food security with rice.

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CE-0002

Genome sequence of Physic Nut (*Jatropha curcas* L.) provides insights into evolution of Euphorbiaceae family

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Jatropha curcas (physic nut), a non-edible oilseed crop, represents one of the most promising alternative energy sources due to its high seed oil content, rapid growth and adaptability to various environments. We report ~339 Mbp draft whole genome sequence of J. curcas var. Chai Nat using both the PacBio and Illumina sequencing platforms. We identified and categorized differentially expressed genes related to biosynthesis of lipid and toxic compound among four stages of seed development. Triacylglycerol (TAG), the major component of seed storage oil, is mainly synthesized by phospholipid:diacylglycerol acyltransferase in Jatropha, and continuous high expression of homologs of oleosin over seed development contributes to accumulation of high level of oil in kernels by preventing the breakdown of TAG . A physical cluster of genes for diterpenoid biosynthetic enzymes, including casbene synthases highly responsible for a toxic compound, phorbol ester, in seed cake, was syntenically highly conserved between Jatropha and castor bean. Transcriptomic analysis of female and male flowers revealed the up-regulation of a dozen family of TF s in female flower. Additionally, we constructed a robust species tree enabling estimation of divergence times among nine Jatropha species and five commercial crops in Malpighiales order. Our results will help researchers and breeders increase energy efficiency of this important oil seed crop by improving yield and oil content, and eliminating toxic compound in seed cake for animal feed.

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CE-0003

The barley pan-genome reveals the hidden legacy of mutation breeding

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Genetic diversity is key to crop improvements under threats of climate change and population growth. Due to the prevalence of genomic structural variation (SV), a single reference genome is inadequate to capture the full landscape of diversity within a crop species. Multiple high-quality sequence assemblies are an indispensable component of a pan-genome infrastructure. Barley (*Hordeum vulgare* L.) is an important cereal crop with a long history of cultivation and adapted to a wide range of agro-climatic conditions. Here, we report the construction of chromosome-scale sequence assemblies for 20 barley genotypes, comprising landraces, cultivars and one wild barley selected as representatives of global barley diversity. We catalogued genomic presence/absence variants and explored the use of structural variants for quantitative genetic analysis with whole-genome shotgun sequence of 300 genebank accessions. We discovered abundant large inversion polymorphisms and analysed in detail two inversions frequent in current elite barley germplasm; one likely the product of mutation breeding and the other tightly linked to a locus involved in geographic range expansion. This first-generation barley pan-genome makes previously hidden genetic variation accessible to genetic studies and breeding.

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CE-0004

Development and utilization plans for high value colored wheat

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In general, seed coat (wheat bran) contains a large amount of functional ingredients, and is known to be particularly rich in dietary fiber. Colored wheat is known as a wheat that has a pigment by coloring the seed coat with purple or black.

According to HPLC for the contents of the anthocyanin pigment series, a colored wheat, Ariheuk, contained 1.53㎍/g of C3G(cyanidin-3-O-glucoside), 0.38㎍/g of Pn3G(peonidin-3-O-glucoside), but normal Korean wheat such as Keumkang did not be detected. Ariheuk was also determined higher functional ingredients including tannins, total phenolic compounds and antioxidant capacity using an alkali hydrolysis method than Keumkang. In particular, anthocyanin content from Ariheuk revealed 10 times higher than that of conventional Korean wheat. The content of polyphenols and flavonoids was detected the highest value at 33 days after fertilization (DAF), and then decreased. In addition, the extracts from seed coat using 70% ethanol for 12 hours was shown the highest value of antioxidant capability. These extracts help to survive the cell by suppressing apoptosis of the cells in the high-fat induced hepatocytes, and also can help maintain liver health by inhibiting lipid accumulation in the liver cells.

Therefore, it is thought that Ariheuk can be used for the production of functional foods using the seed coat of colored wheat, and it is expected to be used as a potential food material that can simultaneously increase the functional and sensory elements for various processed foods.

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CE-0005

Current Status and Prospect of Maize Quality Breeding

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In Korea, the systematic start of maize breeding began in the 1960s. From 1960s to 1980s, the method of maize breeding was developed into synthetic and single cross varieties, and then the goal of maize breeding was stability high yielding. Since the 1990s, most of the maize varieties in Korea have been developed into a single-cross, and the breeding target has also been converted to high quality. Beginning in the 1990s, edible maize breeding centered on waxy maize was initially focused on maize starch research. The study of waxy maize was mainly carried out on improving palatability such as glutinous improvement and pericarp thickness. Silage maize was conducted on the study of the stay-green character and high yield for the development of whole crop maize varieties. Since the 2000s the consumers demand has diversified in maize quality. In edible maize, it is required to develop a variety with added functional ingredients such as antioxidant and anti-cancer as well as good taste. In recent years, demand for sweet maize and super sweet maize has been increasing due to changes in the population structure and consumer needs. There is also a growing new and variable demand for the development of maize varieties for feed crop. The new quality characteristics of feed maize is required by improvement of digestion rate, early maturing and late planting adaptability, suitable for the cropping system. Research on raising lysine content which is an insufficient essential amino acid in maize is also needed for study of grain maize.

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CF-0001

QTL mapping of bacterial wilt resistance in pepper (*Capsicum annuum* L.) using genotyping-by-sequencing analysis and two different isolates of *Ralstonia solanacearum*

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Bacterial wilt caused by *Ralstonia solanacearum* became one of the most devastating diseases in chili pepper (*Capsicum annuum* L.) production due to the rising temperatures in Korea. The most efficient solution is to develop the resistant pepper varieties to bacterial wilt. Therefore, in this study, we aimed to identify QTLs resistant to bacterial wilt in the F_2 population obtained from a self-pollinated strong resistant pepper cultivar 'Konesian hot' using genotyping-by-sequencing (GBS) analysis and two different isolates of *R. solanacearum* including HS with moderate pathogenicity and HWA with strong pathogenicity. Two sets of 96 F_2 individuals were evaluated for the resistance with disease index scores 0 (resistant) to 3 (susceptible) at every seventh day after inoculation for six weeks. A total of 12,227 and 19,044 SNPs were obtained through GBS analysis in two populations following the inoculation with HS and HWA isolates, respectively. Two pepper genetic linkage maps consisting of 1,168 and 1,267 SNP markers were constructed. The maps contained 12 linkage groups with a total linkage distance of 2,320.2 and 2,311.3 cM. QTL analysis using a composite interval mapping (CIM) method revealed four QTLs (*Bwr6w-7.1*, *Bwr6w-9.1*, *Bwr6w-9.2*, and *Bwr6w-10.1*) conferring resistance to HS isolate and two QTLs (*Bwr6w-5.1* and *Bsw6w-9.1*) resistant to HWA isolate. In addition, six high-resolution melting (HRM) markers were developed, which were closely linked to each QTL. These QTL information and HRM markers will accelerate the development of pepper varieties with strong resistance to bacterial wilt.

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CF-0002

A high-contiguity Nanopore assembly of *Brassica nigra* genome allows localization of active centromeres and defines the ancestral Brassica genome

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High-quality nanopore genome assemblies were generated for two *Brassica nigra* genotypes (Ni100 and CN115125); a member of the agronomically important *Brassica* species. The N50 contig length for the two assemblies were 17.1 Mb (12 contigs), one of the best among 324 sequenced plant genomes, and 0.29 Mb (424 contigs), respectively, reflecting recent improvements in the technology. Comparison with a *de novo* short-read assembly for Ni100 corroborated genome integrity and quantified sequence related error rates (0.2%). The contiguity and coverage allowed unprecedented access to low complexity regions of the genome. Pericentromeric regions and coincidence of hypo-methylation enabled localization of active centromeres and identified a novel centromere-associated ALE class I element which appears to have proliferated through relatively recent nested transposition events (<1 million years ago). Genomic distances calculated based on synteny relationships were used to define a post-triplication *Brassica* specific ancestral genome and to calculate the extensive rearrangements that define the evolutionary distance separating *B. nigra* from its diploid relatives.

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CF-0003

The Use of Genomic Information in Pome Fruit Breeding

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Apple and pear are most representative pome fruits and are included in Pomoideae, Rosaceae. The pome fruit trees have 17 basic chromosomes and their genomic information can be shared with other Rosaceae, including peach, cherry, and strawberry. The high heterozygosity by SI and long juvenile phase until flowering have limited genetic analysis deriving the precise breeding programs in pome fruits. Depending on the development of genome analysis, investigating genetic characteristics has become possible in fruit trees. In pome fruits, genetic analysis has been conducted using reference genome data to apply genetic information in whole breeding process. The NGS generated data were analyzed using a customized bioinformatics pipeline suitable for heterozygous genome at the beginning of genetic analysis in pome fruits. This analysis allowed in exploring informative SNPs for pome fruits. Genome structure based core collections and high density genetic linkage maps were constructed using genomic information. Pseudo-chromosome based linkage maps were used to identify loci associated with target traits. Candidate genes controlling traits were investigated through RNA-sequencing. The GWAS was also performed in pome fruits that is difficult in segregation based genetic analysis. Genetic information produced by genome analysis in pome fruits could be applied extensively in Rosaceae family. Precise phenotyping of target traits is required priorly to increase accuracy and application of achievements from genetic analysis in fruit tree breeding and cultivation. Moreover, efficient analytical populations and analysis systems of genetic and genomic studies are necessary for to improvement of fruit tree breeding.

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CF-0004

Specific trait-targeted mutagenesis in radiation breeding

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Radiation such as γ-rays and X-rays is generally known to induce mutations randomly in the plant genome. Thus, it is difficult to predict the pattern of mutations induced by radiation. This study focuses on developing a method to reduce the randomness of mutation. It is based on the hypothesis that specific genes could be relatively more affected by radiation when they are highly expressed. We selected flower-color and leaf-color as target traits for this purpose in chrysanthemum and oriental *Cymbidium*, respectively. To up-regulate genes encoding proteins in anthocyanin and chlorophyll pathways, we used sucrose and plant hormones, and dark/light treatment, respectively. γ-ray was irradiated when those genes were highly expressed. The high expression of genes in the anthocyanin pathway was observed with 50 mM sucrose treatment for 18 h. Sucrose with methyl jasmonate (MeJA) treatment was optimal to up-regulate genes in the anthocyanin pathway. To up-regulate genes in the chlorophyll pathway, dark treatment for 60-75 days, followed by light treatment for 10 days appeared to be optimal. Sucrose with MeJA pre-treatment followed by γ-irradiation resulted in a 1.5-fold increase in the frequency of flower-color mutants compared with γ-irradiation alone in chrysanthemum. Dark/light pre-treatment followed by γ-irradiation resulted in a 1.4 to 2.0-fold increase in the frequency of leaf-color mutants compared with γ-irradiation alone in oriental *Cymbidium*. These results suggest that random mutation by radiation could be reduced to some extent by controlling the expression of genes related to specific traits.

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CF-0005

Whole-genome, transcriptome, and methylome analyses provide insights into the evolution of platycoside biosynthesis in balloon flower, a medicinal plant

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A balloon flower (*Platycodon grandiflorus*) has been traditionally used to treat bronchitis and asthma in East Asia. Triterpenoid saponins (TSs) are common plant defense phytochemicals with potential pharmaceutical properties. The oleanane-type TSs, platycosides, are a major component of the *P. grandiflorus* root extract. Recent studies show that platycosides exhibit anti-inflammatory, anti-obesity, anti-cancer, anti-viral and anti-allergy properties. However, the evolutionary history of platycoside biosynthesis genes remains unknown. In this study, we sequenced the genome of *P. grandiflorus* and investigated the genes involved in platycoside biosynthesis. The draft genome of *P. grandiflorus* is 680.1 Mb long and contains 40,017 protein-coding genes. Genomic analysis revealed that the *CYP716* family genes play a major role in platycoside oxidation. The *CYP716* gene family of *P. grandiflorus* was much larger than that of other Asterid species. Orthologous gene annotation also revealed the expansion of *β-amyrin synthases* (*bASs*) in *P. grandiflorus*, which was confirmed by tissue-specific gene expression. In these expanded gene families, we identified key genes showing preferential expression in roots and association with platycoside biosynthesis. Additionally, whole-genome bisulfite sequencing showed that *CYP716* and *bAS* genes are hypomethylated in *P. grandiflorus*, suggesting that epigenetic modification of these two gene families affects platycoside biosynthesis. Thus, whole-genome, transcriptome, and methylome data of *P. grandiflorus* provide novel insights into the regulation of platycoside biosynthesis by *CYP716* and *bAS* gene families.

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CG-0001

A Combinatorial Approach of Biparental QTL Mapping and Genome-Wide Association Analysis Identifies Candidate Genes for Phytophthora Blight Resistance in Sesame

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Phytophthora blight, caused by pathogen *Phytophthora nicotianae,* is responsible for a huge reduction in sesame (*Sesamum indicum* L.) crop yields. In this study, we utilized a combinatorial approach involving biparental QTL mapping and genome-wide association (GWAS) analysis to identify genes associated with Phytophthora blight resistance in sesame. Evaluation of resistant of the parental varieties (Goenbaek, Osan and Milsung) and the RILs of both the populations in greenhouse conditions suggested the qualitative nature of the trait.. The genetic map comprised thirteen LGs covering a total map length of 887.49 cM with an average inter-marker distance of 4.69 cM. Significant QTLs explaining phenotypic variation in the range of 2.25% to 69.24% were identified on chromosomes 10 and 13 (Chr10 and Chr13). A resistance locus detected on Chr10 was found to be highly significant. The association of this locus to PBR was also identified through BSA and single marker analysis in Goenbaek x Milsung cross and through genome-wide association mapping of 87 sesame accessions. The GWAS analysis identified 44 SNP loci significantly associated with Phytophthora disease-resistant traits on Chr10. Further, the haplotype block analysis conducted in order to find whether the SNPs associated with resistance in this study showed that the SNPs are in high LD with the resistance QTL. We obtained a total of 68 candidate genes, which included a number of defense-related *R* genes. One of the genes, *SIN_1019016* (*At1g58390)* showed high expression in the resistant parent. The results from this study would be highly useful in identifying genetic and molecular factors associated with Phytophthora blight resistance in sesame.

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CG-0002

MULTISEEDEDs regulates pedicellate spikelet fertility in sorghum through the jasmonic acid regulatory module

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Inflorescence architecture mainly contributes to grain number per panicle (GNP) and is a major determinant of grain yield in cereals. Sorghum [*Sorghum bicolor* (L.) Moench] inflorescence is basically composed of one fertile sessile spikelet (SS) and two infertile pedicellate spikelets (PS). To identify regulatory factors involved in the inflorescence architecture, we screened an EMS mutagenesis population from the pedigreed sorghum mutant library. We found inflorescent architecture mutants, named as *multiseeded* mutants (*msd1,2,3,4*) with gained fertile ability in PS. A detailed dissection of developmental stages of wild type and *msd1,2,3* and *4* described that the PS in wild type do not have floral organs, including ovary, stigma, filament and anther, while the *msd* mutants generate intact floral organ in the sessile spikelet. We found *MULTISEEDED1* (*MSD1*) encoded a TCP (Teosinte branched/Cycloidea/PCF) transcription factor, and lipoxygenase (LOX) domain-containing gene, *MULTISEEDED2* (*MSD2*) encoded lipoxygenase (LOX) domain-containing protein which plays a role in the jasmonic acid (JA) biosynthetic pathway. *MSD4* encoded an alcohol dehydrogenase, which plays a role in late step of the jasmonic acid (JA) biosynthetic pathway. Young *msd1* panicles have 50% less JA than wild-type (WT) panicles, and application of exogenous JA can rescue the *msd1* and *msd2* phenotype. Recent results reveal a new mechanism for increasing GNP, with the potential to boost grain yield, and provide insight into association of JA pathway with sorghum panicle development and spikelet fertility. In addition, these finding will elucidate the molecular and regulatory network of spikelet development via JA regulations.

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CG-0003

Population Analysis of *Angelica gigas* Using Chloroplast Based Markers for Molecular Breeding

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Angelica species is a representative medicinal plant that has been used in medicinal methods, especially in traditional Asian herbal medicine. In this study, chloroplast insertion or deletion (cpInDel) markers were developed from chloroplast sequences of *Angelica gigas* Nakai to provide insight into intraspecific and interspecific genetic diversity in *Angelica* species. We found insertion or deletion regions from the comparative analyses of five *A. gigas* chloroplast genome sequences and successfully designed 25 primer sets. Finally, 24 cpInDel markers were developed by polymorphism testing using *A. gigas* accessions. These markers were applied to 88 *A. gigas* accessions for intraspecific comparison. The average polymorphism information content (PIC) value was 0.20 and the average number of genotypes (NG) was 2.33. The interspecific comparison using 13 *Angelica* species (115 accessions) showed a PIC value of 0.40 and the average NG and the average availability were 4.63 and 0.99, respectively. The newly developed 24 cpInDel markers would be useful tools for the exploration of the variation present in *A. gigas* and could be used in phylogenetic classification and genotypic grouping for *A. gigas* breeding and genetic relationship studies of *Angelica* species.

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CG-0004

Perspectives and Actions in Breeding of Special-Purpose Trees

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It is known that 4,221 native plants are distributed in Korea. Exploring indigenous plant resources suitable for domestic climate and developing new varieties are seriously important in responding to market-opening pressure such as Free Trade Agreement (FTA) and establishing plant sovereignty. Most of all, it could contribute to creating new income to farmers by providing new high-value-added cultivars of native species. Changes in lifestyle and enhancement of living standard brought about social concerns for healthy life and credible food. To keep up with the trend, various new cultivars of special-purpose trees are developing in Division of Special forest Products, National Institute of Forest Science. The aim of breeding of special-purpose trees is also changing from quantitative breeding for high-yield in the past to qualitative breeding for high-functionality and high-value-added forest products. So far, 28 cultivars were developed in seven species, for example, *Kalopanax septemlobus* (Thunb.) Koidz., *Rubus coreanus* Miq., *Actinidia arguta* (Siebold & Zucc.) Planch., and so on. These cultivars are characterized in use of Korean native species, high productivity, high functionality, early harvest or ease of cultivation. Currently, along with breeding of new cultivars, establishment of standard cultivation guideline for various species is also carried out to improve the stability of cultivation against extreme weather conditions and strengthen consumption competitiveness through the certification of Good Agricultural Product (GAP). Various efforts to supply excellent new cultivars and cultivation methods to farmers and achieve stable income frame in mountain villages is conducted by Division of Special forest Products, National Institute of Forest Science.

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CG-0005

Marker assisted selection (MAS) for breeding high oleic peanut (*Arachis hypogaea* L.) cultivars

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High oleic peanut/groundnut cultivars are preferred by food industry for extended shelf-life benefits, and have consumer health benefits. Marker Assisted Selection (MAS) approach was used for early generation selection using SNP genotyping for FAD mutant alleles conferring high oleic trait, and two major QTLs governing resistance to rust and late leaf spot. FAD2B mutant allele was selected using SNP markers, while FAD2A mutant allele was selected using Near Infrared Reflectance Spectroscopy (NIRS). Kompetitive allele-specific PCR (KASP) based High-Throughput Genotyping Platform (HTGP) was used for SNP genotyping, for which leaf discs were sent to service provider. More recently, single seed chip based SNP genotyping was standardized resulting in enhanced operational efficiency. First high oleic peanut varieties were identified for commercialization in India during 2019; Girnar 4 (ICGV 15083) and Girnar 5 (ICGV 15090) have oleic acid content of 80+2%, and recorded superior pod yield and agronomic performance than the national checks in the national testing conducted under All India Coordinated Research Project on groundnut (AICRP-G). The high oleic cultivars wer Kompetitive allele-specific PCR (KASP)e commercialized in 8 years as against 12-15 years required in general from crossing to commercialization. The fast-track development was possible through use of low-cost controlled conditions for reducing generation interval and early generation multi-location testing. The 'high oleic' peanut lines in Spanish and Virginia Bunch types suitable for cultivation in Asia and Africa under rainfed conditions are bred at ICRISAT and over 100 lines were shared by ICRISAT to its collaborators in nine countries including Australia.

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CG-0006

Influence of genome diversity on breeding and DNA barcoding of wildcrafted species

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Genome diversity is one of the key factors for contemporary breeding. However, most of the herbal plants are still wildcrafted or cultivated with undomesticated collections and natural diversity of them is often not taken seriously. Misunderstanding of genome diversity as well as genetic characteristics often cause misapplication of DNA marker and rather intensify the confusion in species identification. In this study, we compared the organelle genomes of 81 seed plants, plastid and mitochondria, and revealed that the mitochondrial genomes contained plastid originated sequences, called MTPT. Moreover, when organelle genomes of *Cynanchum wilfordii and C. auriculatum* were sequenced as a case study, the similarity of MTPTs between species was closer than that of plastid genome and their sequences were highly different to current plastid sequences. Considering the insertion time of MTPT and the divergence time of species, the MTPTs had been transferred at their common ancestor and maintained in conserved form due to the slow mutation rate of mitochondrial genome. Co-amplification of these sequences can cause misapplication of DNA barcoding for species authentication. Additionally, four plastid genomes of *C. wilfordii* was characterized and their intraspecific diversity can also lead to misidentification of wildcrafted target species with other relative species.

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CH-0001

Customizing Solanaceae fruit crops for vertical farming by genome editing

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A modern revolution in agriculture is emerging that allows cultivation in urban environments to provide local low input food production. However, space restrictions and the need for rapid crop cycling have limited vertical farms to lettuce and related 'leafy green' vegetables. Fruit crops are highly desired, but developing new varieties whose architectures and productivities are optimized for these specific growth parameters is challenging. From the identification of a regulator of tomato stem length, we devised a trait-stacking strategy that combines mutations causing rapid flowering, precocious growth termination, and condensed shoots. Application of our strategy using CRISPR-Cas9 genome editing restructured vine-like growth of tomato plants into a compact, early yielding plants suitable for urban agriculture. We confirmed yields were maintained by field-based productivity trials, and demonstrated cultivation in indoor farming systems. Targeting the same stem length regulator alone in the Solanaceae berry plant groundcherry also provided rapid customization. Our approaches can expand the repertoire of crops for vertical farming.

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CH-0002

Common *Japonica* Type Genomic Regions Present in the High-Yielding Varieties Derived from *Indica-Japonica* Crosses in Rice (*Oryza sativa* L.)

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The inter-subspecific crossing between *indica* and *japonica* subspecies in rice have been utilized to improve the yield potential of rice. As the result of these efforts, high-yielding varieties (HYVs) have been developed in different East Asian countries, including Korea, Japan, and China. In Korea, HYVs developed in this manner has been called 'Tongil-type'. In this study, a comparative study of the genomic regions in the eight HYVs was conducted with those of the four non-HYVs. The Next-Generation Sequencing (NGS) mapping on the Nipponbare reference genome identified a total of 14 common genomic regions of *japonica*-originated alleles. Interestingly, the HYVs shared *japonica*-originated genomic regions on nine chromosomes, although they were developed through different breeding programs. A panel of 94 varieties was classified into four varietal groups with 38 single nucleotide polymorphism (SNP) markers from 38 genes residing in the *japonica*-originated genomic regions and 16 additional trait-specific SNPs. As expected, the *japonica*-originated genomic regions were only present in the *japonica* (JAP) and HYV groups, except for Chr4-1 and Chr4-2. The *Wx* gene, located within Chr6-1, was present in the HYV and JAP variety groups, while the yield-related genes were conserved as *indica* alleles in HYVs. Conventional rice breeding program for HYV development utilizing *indica* parents in East Asia has maintained some *japonica*-originated regions, which have contributed to quality acceptability without trade-off of yielding mostly inherited from *indica* parents. The *japonica*-originated genomic regions and alleles shared by HYVs can be employed in molecular breeding programs to further develop the HYVs in temperate rice.

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CH-0003

An effective approach to accelerate rice pollen genetics utilizing omics data and genome editing technology

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Successful sperm delivery is a factor that affects crop yield. However, the study of this mechanism in rice is poorly understood due to absence of homozygous mutants for gamete transfer defect genes and also due to functional redundancy originated from genome duplication events. To overcome these limitations and facilitate pollen genetics research in rice, we have constructed and perform a research strategy utilizing omics data and genome editing technology. Here, as an early process, we present an intuitive tool for the investigation of CRISPR target genes according to their functional redundancy in rice (CAFRI-Rice; cafri-rice.khu.ac.kr). This tool can generate a phylogenetic heatmap that can be used for estimation of the functional redundancy of the queried rice gene, based on 2,617 phylogenetic trees and eight tissue RNA-sequencing data sets. Among 55,801 MSU7 annotated rice genes, 33,483 genes were sorted into 2,617 Pfam families, and about 24,980 genes were tested for functional redundancy using a phylogenetic heatmap approach. As a result, it can predict that 7,075 genes would have functional redundancy according to the threshold value validated by an analysis of 111 known genes functionally characterized using knockout mutants and 5,170 duplicated genes. Lastly, we showed the usefulness of the CAFRI-Rice-based approach by overcoming the functional redundancy between two root-preferred genes via loss-of-function analyses as well as confirming the functional dominancy of three genes through a literature search. We hope that CAFRI-Rice-based target selection will accelerate functional genomic studies not only in rice but also be expanded to other plant species.

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CH-0004

Engineering Crassulacean Acid Metabolism (CAM) into C_3 Plants to Improve Biomass and Water-Use Efficiency

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Crassulacean acid metabolism (CAM) is a specialized photosynthetic mode to increase a water-use efficiency (WUE) that exploits a temporal CO_2 pump with nocturnal CO_2 uptake and concentration to reduce photorespiration to improve the adaptability of plants to hotter and drier climates. CAM species, with their inverted stomatal behavior, display water demands that are typically 4- to 7-fold less than of comparable C_4 and C_3 photosynthesis species, respectively. Thus, introducing the CAM pathway into C_3 photosynthesis plants (CAM Biodesign) is expected to confer enhanced photosynthetic performance and WUE. Functional analysis of the genes encoding C_4 enzymes in common ice plant including *Mc*β*CA2*, *McPPCK1*, *McPPC1*, *McNAD(P)-MDHs*, *McNAD(P)-MEs*, *McPPDK*, and McPPDK-RP of both the carboxylation and decarboxylation modules and cognate circadian clock-controlled promoters were installed to reconstitute the appropriate temporal expression of the CAM pathway in the C_3 model *Arabidopsis*. Furthermore, developing an effective multi-gene assembly tool for the large number of C_4 enzyme gene cassettes is necessary to ensure proper expression of each CAM gene cassette in the target species. Current steps achieved to date for CAM Biodesign will be summarized including subcellular localization and phenotypic analysis of individual ice plant C_4 enzyme genes, circadian clock-controlled promoter mining, vector set construction for multi-gene circuit assembly, and the phenotypic effects of engineering a four-gene carboxylation module, three-gene decarboxylation module, and seven-gene synCAM in *Arabidopsis*.

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CH-0005

Identification of *qLTG3-1* allele for low-temperature germinability in rice from the *Oryza rufipogon*

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Low-temperature germinability (LTG) is a desired trait for direct-seeding cultivation in rice. In our previous study, two QTLs, *qLTG1* and *qLTG3*, were identified using the population derived from a cross of Hwaseong and *O. rufipogon* (IRGC 105491). In this study, we characterized and analyzed the interaction between the two QTLs, by developing an F_2 population derived from a cross between near-isogenic line TR20 which harbors *qLTG1* and *qLTG3* of *O. rufipogon* alleles and Hwaseong. The F_2 plants with both *qLTG1* and *qLTG3* alleles from *O. rufipogon* showed higher LTG scores than the plants with only *qLTG1* or *qLTG3*. No significant interaction between the *qLTG1* and *qLTG3* was observed. Based on its location, *qLTG3* appears to be allelic with *qLTG3-1*, a major QTL known to control LTG. In the exon region, three sequence variations which lead amino acid changes were detected between Hwaseong and *O. rufipogon*. Among these variations, a non-synonymous substitution at the 62nd amino acid site, had not previously been reported. To know the cause of the LTG variations between parents, we genotyped three sequence variations of *qLTG3-1* in 98 Asian cultivated rice accessions. The 98 accessions were classified into 5 haplotypes, based on three variations and a 71-bp deletion. Mean low-temperature germination rates were compared, and haplotype 5 (*O. rufipogon*-type) showed a significantly higher germination rate than haplotype 2 (Nipponbare or Hwaseong- type), and haplotype 3 (Italica Livorno-type). The *O. rufipogon qLTG3-1* allele will be utilized for the improvement of LTG in rice breeding program.

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Poster Session

PA-0001

Characterization of complete chloroplast genome of *Sinomenium acutum* (Menispermaceae)

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We generated the complete chloroplast genome sequence of *Sinomenium acutum*, a species of the Menispermaceae family, and characterized from the *de novo* assembly of Illumina HiSeq paired-end sequencing data. The total length of the chloroplast genome of *S. acutum* was 162,787 bp with a large single-copy (LSC) region of 91,430 bp, a small single-copy (SSC) region of 21,245 bp, and a pair of identical inverted repeat regions (IRs) of 25,056 bp. The total of 131 genes were annotated in the chloroplast genome of *Sinomenium acutum*, including 85 protein-coding genes, 38 transfer RNA (tRNA) genes, and 8 ribosomal RNA (rRNA) genes. The phylogenetic analysis of *S. acutum* with 11 related species revealed the closest taxonomical relationship with *Menispermum dauricum* in the *Menispermaceae* family.

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PA-0002

Synthetic promoter technology for Improving Drought Tolerance

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Drought is one of the most costly natural disasters affecting crop productivity. Developing drought-tolerant crops is a major challenge in modern agriculture. Modern agriculture faces new challenges due to climate changes brought about by global warming and drought conditions in many arid and semi-arid regions of the world. Therefore, we set the goal of the study to establish the feasibility of using synthetic promoter for the production of drought-tolerant agricultural, horticultural, and forestry crops. In order to achieve the goal, we used bioinformatics and an integrated molecular biology approach. Previously we created 4 synthetics (stress-inducible) promoters that can drive strong expression of target genes in a drought-specific manner. In this study, we generated and characterized transgenic plants that express drought tolerance genes driven by the selected synthetic promoters. The outcome of this project will lead to a biotechnological means for protecting crop yield under drought stress.

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PA-0003

Molecular Cytogenetic Analyses on *Sisymbrium irio* using Repetitive DNA Sequences

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Sisymbrium irio has not gained enough fame compared to its close relatives. Nevertheless, the species is still known to possess traits making it on the list of economically important plants. There has not been much genome information generated from it. Thus, molecular cytogenetic analyses have been carried out using genomic DNA, Cot DNA, and known repetitive sequences to evaluate the chromosomal distribution of repetitive elements and to determined chromosome structure similarities and differences from its closely related species. Fluorescence in situ Hybridization (FISH) and Genomic in situ Hybridization (GISH) techniques were implemented as important tools for directly detecting chromosome targets. The probes were either labeled with digoxigenin 11-dUTP and biotin 16-dUTP. Ribosomal RNA loci were constituted of 4 terminal signals of 18S rDNA juxtaposed to 4 signals of 5S rDNA. Arabidopsis-type subtelomere repeats have been detected in all of the chromosomes. Interestingly, gDNA probe and Cot DNAs have hybridized on all of the pericentromere and rDNA regions suggesting that majority of its repetitive elements are concentrated in the centromere regions. These data are essential to give an insight of its genomic organization and could potentially become a benchmark for future genome assembly.

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PA-0004

Differences in DNA methylation contribute to synchronous pod maturity in mungbean (*Vigna radiata* L.)

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Cytosine methylation in genomic DNA affects gene expression, potentially causing phenotypic variation. Mungbean, an agronomically and nutritionally important legume species, is characterized by nonsynchronous pod maturity, resulting in multiple harvest which costs extra time and labor. To elucidate the epigenetic influences on synchronous pod maturity (SPM) in mungbean, we determined the genome-wide DNA methylation profiles of eight mungbean recombinant inbred lines (RILs) and their parental genotypes, and compared DNA methylation profiles between high SPM and low SPM RILs, thus revealing differentially methylated regions (DMRs). A total of 3, 18, and 28 pure DMRs, defined as regions showing no significant correlation between nucleotide sequence variation and methylation level, were identified in CpG, CHG, and CHH contexts, respectively. These DMRs were proximal to 20 genes. Among the 544 single nucleotide polymorphisms identified near the 20 genes, only one caused critical change in gene expression by early termination. Analysis of these genome-wide DNA methylation profiles suggests that epigenetic changes can influence the expression of proximal genes, regardless of nucleotide sequence variation, and that SPM is mediated through gibberellin-mediated hormone signaling pathways. These results provide insights into how epialleles contribute to phenotypic variation and improve SPM in mungbean cultivars.

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PA-0005

Gene expression analysis for drought stress during vegetative and reproductive stage using RNA-seq in maize

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Maize are often subjected to periods of drought stress during their life cycle. The objective of this study was attempted to determine stage-specific genes at vegetative and reproductive stage of maize under drought stress by using network-based transcriptome analysis. The 144 RNA-seq data of B73 at seedling and development stage were obtained from NCBI database. The raw data were filtered for quality control of the reads with the FASTQC tool, and the filtered reads were pre-proceed using the BBDUK tool. The sequencing reads were aligned to the reference genome by STAR tool. The data were analyzed using the HTSeq software based on the read count data that were obtained from expression profiling. Differential expression analysis was performed using the DESeq2 R package. We conducted a systemic study by using the weighted gene correlation network analysis (WGCNA) method to identify modules related to drought stress. Significantly, 38 modules were detected based on the RNA-seq data. Among them, 6 modules (darkgrey, lightpink4, novajowhite2, red, salmon, and salmon4) related to the feature of drought stress. Interestingly, network feature analysis confirmed that the red modules demonstrated a remarkably correlation with drought stress at seedling stage. This module was related to signaling pathway, apoptosis, cell wall degradation, and cellulose synthesis. Eleven genes (GRMZM2G150893, GRMZM2G134947, GRMZM2G173128, GRMZM2G127490, GRMZM2G002128, GRMZM2G171818, GRMZM2G325907, GRMZM2G000818, GRMZM2G003406, GRMZM2G017268, and GRMZM2G353076) in red module were related to peroxidase, BHLH transcription factor, MYB transcription factor, and zinc finger protein.

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PA-0006

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

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Biological and cellular processes in plants are regulated by many mechanisms, such as controlled gene expression, protein synthesis, protein modification, protein degradation, and interactions among molecules. E3 ubiquitin ligases are a central modifier of plant signaling pathways that act through targeting proteins to the degradation pathway. U-box E3 ligases play crucial roles in regulating plant development, reproduction, cellular protein degradation and responses to biotic and abiotic stresses. However, comprehensive analysis of the U-box gene family in wheat (*Triticum aestivum* L.) has not been analyzed yet. We identified a total of 265 U-box genes in wheat genome and these genes were further divided into various subgroups based on specific domains. Gene ontology, KEGG, and KOG analysis of U-box genes were investigated. Transcriptome analysis revealed differential expression patterns of U-box genes which were specifically expressed in various developmental stages and tissues, and abiotic stress condition. The genome-wide analysis of U-box genes provides new opportunities for characterization of candidate U-box genes and elucidation of biological roles in wheat development and stress responses.

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PA-0007

Comprehensive RNA-seq resource for abiotic responses in *Capsicum annuum L.*

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Hot pepper (*Capsicum annuum L.*) is one of the most consumed vegetable crops in the world and useful to human as it has many nutritional and medicinal values. Like other crops, peppers are threatened by diverse environmental conditions due to different pathogens and abiotic stresses. High-quality reference genomes with massive datasets of transcriptomes from various conditions can provide clues to preferred agronomic traits for breeding. However, few global gene expression profiling datasets have been published to examine the environmental stress-resistant mechanisms in peppers. In this study, we performed RNA sequencing (RNA-seq) analysis of pepper treated with heat, cold, salinity, and osmotic stress at six different time points. A total of 78 RNA samples, containing three biological replicates per time point for each of the abiotic stresses and a mock control, were tested by RT-PCR for the expression of abiotic stress-specific marker genes, and libraries were constructed. Analyses of the transcriptome data in this study will provide useful information for basic studies of various stimuli to facilitate the development of stress-resistant pepper cultivars.

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PA-0008

Overexpression of *BrTSR53* Gene Improves drought Tolerance in Rice seeding stage

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Drought is a major environmental stress affecting crop yield adversely in the world. Recent climate change increases drought stress with severity in crop field. Thus, improving crop performance under drought conditions is an important goal to support world food requirements in agricultural industry. To cope with drought stress, plants need molecular mechanisms that coordinate expression of genes to protect them from water deficient conditions and increase the chance of survival in arid regions. Transcripton factor, *BrTSR53* gene is a putative stress-related gene isolated from *Brassica rapa*. We generated *BrTSR53*-overexpression transgenic rice plants using Agrobacterium-mediated transformation method. To investigate regulation of *BrTSR53* expression in rice, quantitative real-time PCR was performed using RNAs from tissues and western blot analysis. To further understand the role of *BrTSR53* in stress tolerance, we studied responses of *BrTSR53*-overexpression rice plants to salt stress conditions.

To investigate the function of *BrTSR53* in reponse to drought stress, we generated *BrTSR53*-overexpression transgenic rice plants and wild-type plants and dehydration test were performed. Two types rice plants grown on soils for 4 weeks. These four-week-old transgenic line and wild-type plant were exposed to water-deficient conditions for two to four days and then were rehydrated. After re-watering, The transgenic lines showed better recovery from water deficient condition and higher survival rates improved compared to wild-type plants. These results suggest that the transcription factor *BrTSR53* gene played an important role in the tolerance of rice to water deficient conditions.

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PA-0009

LegCompara: A genome data-linked bioinformatic platform for legume comparative analysis

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Comparative genome analysis is a powerful approach to look into the genomic organizations among different, but evolutionary related, species, to predict function of certain genes of interest and to interpret evolutionary relationships between compared species. For such reasons, development of efficient and automated bioinformatic visualization tool is essential in this research field. To achieve this goal, we intended to construct an interactive and flexible bioinformatic interface for the comparative analysis focused on legume genomes, named 'LegCompara'. This platform consists mainly of two parts: a web-based user interface and corresponding relational databases. The database harbors a diverse array of genomic information (e.g., functional annotation, ortholog groups) for seven legumes (M. truncatula, G. max P. vulgaris, C. cajan, V. radiata, C. arietinum) and two model plants (A. thaliana, O. sativa). This genome browser, unlike other traditional genome browsers, was designed for researchers to dynamically interact with user interface, so it can navigate multiple chromosomes of different or same species simultaneously, resulting in genome-wide and/or regional comparisons by depicting corresponding syntenies with either blocks or lines between orthologous regions or genes. It is expected that LegCompara may provide researchers and breeders with useful resources for more efficient and user-friendly comparative genome analysis.

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PA-0010

LegExpress: a bioinformatic platform for translational transcriptome analysis for legumes

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

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PA-0011

Chromosome-level genome assembly through Hi-C scaffolding and gap-filling: Case of the Korean sesame variety Goenbaek

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The construction of a high-quality genome assembly is a key point to address important biological questions related to plant growth, resistance mechanism against biotic and abiotic stresses, and genomics-assisted plant breeding. As part of our sesame genome project, we previously generated an initial genome assembly of the Korean sesame variety Goenbaek, using Falcon-Unzip algorithm with Pac-Bio long-reads. In order to reach a chromosome-level genome assembly, the proximity ligation technology of Dovetail Genomics® was employed. As a result, a set of 13 pseudomolecules and unanchored contigs were constructed spanning 281,760,649 bp. The contiguity was drastically improved from N50 = 2,554,306 bp (L50 = 30) to N50 = 19,200,389 bp (L50 = 7). The number of pseudomolecules is identical to the Chinese reference genome, suggesting the high accuracy of the scaffolder algorithm. However, a total of 195 gaps in the whole scaffolds and 183 gaps in the 13 pseudomolecules were identified. To distinguish if those gaps are from the primary assembly artifacts or real gaps, we mapped sequences of 183 gaps to three different assemblies: contigs from Illumina short-reads of Goenbaek using Soapdenovo v. 2.0, contigs from PacBio long-reads of Goenbaek using CANU v. 1.8, and scaffolds from Illumina short-reads of Chinese cultivar Zhongzhi 13. The sequence comparisons showed the presence of 35 pseudo gaps. The PCR amplifications on regions including the gaps followed by Sanger sequencing showed that 33 gaps could be filled. The combination of various assemblies from short reads and long reads followed by PCR allows the identification and filling of gaps derived from the incompleteness of genome assemblers.

Keywords: sesame, genome, Hi-C scaffolding, gap filling

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PA-0012

Comparative genomics in *Sesamum* L. genus revealed genome expansion/contraction and potential tetra-ploidy pattern of putative *Sesamum schinzianum*

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Sesamum L. genus is composed of about 20 accepted species including 19 wild relatives. Previous cytogenetic studies suggested three main sets of chromosome number including 2n = 26, 2n = 32, and 2n = 64. However, due to the lack of genomic data, the mystery about the genome organization relationship between sesame species remains unexplored. Therefore, we designed this study in order to investigate the differences and similarities between three sesame species *viz Sesamum indicum* cv Goenbaek, *Sesamum alatum*, and a putative *Sesamum schinzianum*. Taking advantage of the long reads sequencing technologies, we performed the primary assemblies of the three species using both Falcon-Unzip and Canu assemblers. The primary assembly sizes from the string graph based-assembler Falcon were 282 Mb, 504 Mb, and 692 Mb for *S. indicum cv* Goenbaek, *S. alatum*, and *S. schinzianum* respectively. The Bogart-based CANU assembler generated longer assemblies with 298 Mb and 536 Mb for *S. indicum* cv Goenbaek and *S. alatum* respectively; while relatively shorter 684 Mb for *S. schinzianum*. However, the most contiguous assemblies were noted for all Canu assemblies with N50 values of 4.4 Mb, 6.6 Mb and 6.3 Mb for *S. indicum* cv Goenbaek, *S. alatum* and *S. schinzianum* respectively. Using Artemis v 18.0.0, macrosynthenies investigation between the three species revealed re-arrangement patterns as well as expansion/contraction events. Surprisingly, *S. schinzianum* known in the literature as octoploid showed a tetraploidy pattern based on the nucmer alignment. These preliminary results suggested a requalification of the ploidy number for *S. schinzianum*.

Keywords: sesame, genome, comparative genomics, ploidy

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PA-0013

Evolutionary analysis of *Perilla citriodora* genome

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Perilla is an annual short-day plant that belongs to the family Lamiaceae which is widely cultivated not only as an oilseed but also as a vegetable in East Asia. Polyploidy, or whole-genome duplication (WGD), has been recognized as a major evolutionary force in plants. However, *Perilla citriodora* (diploid) which have been known to contribute the formation of *frutescens. var. acuta* (tertaploid) remains poorly understood in evolutionary mechanisms on genomic levels. In the present study, to investigate an evolutional relationship of *Perilla citriodora* with 12 species of Lamiaceae we tried to identify clusters of orthologous genes using OrthoFinder (version 2.3.1). Whole-genome duplication (WGD) and species divergence time were estimated by finding orthologs and paralogs within and between species and plotting their Ks (synonymous substitutions per site) distribution, respectively. OrthoFinder results from 6 species exhibited that 9,664 groups had at least one protein sequence and 35 (243 genes) clusters were unique to *Perilla citriodora*. 11 species also showed that 17,607 groups and 7,268 groups had at least one protein sequence, respectively. Phylogenetic analysis indicates that the divergence of diploid *Perilla citriodora* was estimated as 30 MYA (million years ago). Genome diversity information of *Perilla citriodora* provides insights for the evolutionary clues in Lamiaceae.

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PA-0014

Complete chloroplast genome sequence of *Solanum demissum* and development of *S. demissum* specific markers for the discrimination from other Solanum relatives

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The hexaploid *Solanum demissum*, a wild tuber-bearing species from Mexico is one of the oldest wild species in the history of modern potato breeding and has been widely used in breeding for late blight caused by *Phytophthora infestans* in potatoes. In this study, we obtained the chloroplast genome sequence of *S. demissum* by next-generation sequencing technology and compared it with those of other *Solanum* species to develop specific markers for *S. demissum*. The chloroplast genome has a total sequence length of 155,558 bp. Its size, gene content, order and orientation are similar to those of the other *Solanum* species. Phylogenic analysis with eleven other Solanaceae species revealed that *S. demissum* is most closely located to *S. hougasii* and *S. stoloniferum*. After detailed comparisons of the chloroplast genome sequences of the seven *Solanum* species, we identified two InDels and 12 SNPs specific to *S. demissum*. Based on these InDels and SNPs, we developed two allele-specific PCR markers for discriminating *S. demissum* from other *Solanum* species. The results obtained in this study will aid in exploring the evolutionary aspects of *Solanum* species and accelerating breeding using *S. demissum*.

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PA-0015

A GBS-based linkage map for anchoring scaffold sequence in tetraploid *P. frutescens*

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De novo genome assembly of the tetraploid *P. frutescens* is in progress. To make pseudomolecule of *P. frutescens* genome, we constructed the high-density linkage map using GBS from two mapping population. One group is the 192 RILs obtained by crossing Daesildeulkkae and Ipdeulkkae-1ho, and the other group is the 96 F2 lines obtained by crossing Pureunchajogi and Namcheon. Among 622,815 polymorphic SNP between the parental lines of RIL, we picked out 9,276 SNP in *Ape*KI for GBS library and made each SNP genotyping matrix. Among 3,659,790 polymorphic SNP between the Pureunchajogi and Namcheon, we picked out 5,462 SNP in *Pst*I-*Msp*I for GBS library and made each SNP genotyping matrix. The high-resolution genetic map was created with 2,418 and 3,147 SNP markers in RILs and in F2 mapping population, respectively. These maps comprised 2,278 and 2,454 SNP markers and spanned total genetic distance of 1713.365 cM across the 24 linkage groups and 2169.316 cM across the 21 linkage groups. It anchored a total of 20 assembled scaffolds that covered about 1122.716 Mb (97.38%) of the 1152 Mb assembled genome and 81.36% of the 1379 Mb predicted genome size. The GBS approach presented here provides a powerful method of developing high-density linkage map in species without a completed genome while providing valuable tools for anchoring and ordering physical maps.

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PA-0016

Evaluating the dynamic plastome evolution of early vascular plants: *Selaginella*

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The *Selaginella* genus belongs to the Selaginellaceae family consisting of around 750 species inhabiting various environments around the world. As a sole genus, *Selaginella* is located in an important position in evolutionary history which makes it a valuable resource for studying plant evolution. *Selaginella* species have unique features which differentiate them from other higher land plants. In this study, we sequenced and assembled plastid genome sequences of three *Selaginella* species, *S. tamariscina*, *S. stauntoniana*, and *S. involvens* using Illumina and Oxford Nanopore sequencing platforms. The complete plastomes of the three *Selaginella* species along with 13 other *Selaginella* species and 3 non-*Selaginella* species registered in NCBI were utilized in a comparative analysis to understand phylogenetic relationships and other unique features that this genus displays. As a result, most species within the *Selaginella* species had atypical plastid genome structures containing a long single copy (LSC), short single copy (SSC), and two direct repeat (DR) blocks instead of inverted repeats (IR) commonly found in higher land plants. Major block inversions containing one repeat region caused dynamic structural rearrangements between IR and DR structures within the genus. We also present other uncommon characteristics such as small plastid genome sizes, gene losses as well as intron losses, abundant RNA editing, high GC contents, and intraspecies diversity within *S. tamariscina* individuals.

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PA-0017

Genome assembly of soft-shelled adlay (*Coix lacryma-jobi* variety *ma-yuen*), a cereal and medicinal crop in the Poaceae family

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Coix lacryma-jobi, called adlay or Yulmu, is an annual herbal plant belonging to the Poaceae family and has been cultivated as cereal and medicinal crop in Asia. We generated a draft genome of the *C. lacryma-jobi* variety *ma-yuen* (soft-shelled adlay) Korean cultivar, Johyun, by *de novo* assembly using PacBio and Illumina sequencing data. A total of 3,362 scaffold sequences, 1.28 Gb in length, were assembled, representing 82.1% of the estimated genome size (1.56 Gb). We found that approximately 77.0% of the genome is occupied by repeat sequences, most of which are *Gypsy* and *Copia*-type retrotransposons, and evidence-based genome annotation predicts 39,574 protein-coding genes. We further predict that soft-shelled adlay diverged from a common ancestor with sorghum 9.0-11.2 MYA. Transcriptome profiling revealed that 1,470 genes were strongly up-regulated in seeds and the most enriched Gene Ontology terms were assigned to carbohydrate and protein metabolism. In addition, we identified 76 storage protein genes and 13 candidate genes involved in biosynthesis of benzoxazinoids (BXs) including coixol, a unique BX compound found in *C. lacryma-jobi* species. Our genome sequence data will provide a valuable resource for molecular breeding and pharmacological study of this plant species. The genome assembly and annotation information are available in NCBI (Bioproject accession PRJNA573577, https://www.ncbi.nlm.nih.gov/bioproject/PRJNA573577) and *Coix lacryma-jobi* Genome DB (http://phyzen.iptime.org/adlay/index.php).

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PA-0018

Natural occurrence of antibiotic resistant and attenuated isolates of *Burkholderia glumae*

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Burkholderia glumae is the causal agent of bacterial panicle blight, which produces phytotoxin, toxoflavin, and oxalate in a quorum sensing (QS)-dependent manner. To determine whether the genome diversity of *B. glumae* isolates originated from different ecological niches has pathological implications, we performed Pacbio sequencing of 58 isolates of *B. glumae* acquired from diseased rice panicles, broken seeds, and wilted solanaceous crops. Genomic organizations of isolates from solanaceous crops were very similar to those of the reference BGR1 strain, which indicated that *B. glumae* might be cross infect rice in the paddy field and other solanaceous crops. However, we found inversion, rearrangement, and mergence of chromosomes in the genome of the different isolates. There was an insertion of the DNA fragment carrying antibiotic-resistant genes in the upstream region of the toxofalvin biosynthetic gene cluster in isolates from broken seeds, which caused the reduction of toxoflavin biosynthesis and virulence and conferred resistance to kanamycin and spectinomycin. Most isolates acquired from broken seeds produced fewer amounts of QS signals and oxalate compared to those produced by BGR1. Less production of oxalate by the isolates from broken seeds caused the lethal environmental alkalization when they were grown in Luria-Bertani (LB) medium. Pathogenomic analysis of *B. glumae* isolates from diverse ecological niches indicated how variations of *B. glumae* genome affect genotypes, virulence, and survival. It would be interesting to find what kinds of selection pressure are involved in the genome evolution of *B. glumae*, especially when it interacts with different host plants.

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PA-0019

Whole Genome Sequence and Genetic Diversity of Basmati Rice

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Basmati is considered as a unique varietal group of rice due to their aroma and superior grain quality characteristics. Despite various efforts, defining Basmati genomic variation and its origin is unclear. In the present study, the genomes of three traditional Basmati varieties were resequenced and mapped to Nipponbare, Kasalath, and Zhenshan 97 reference genomes. By comparing the sequences, we detected common SNPs in the genic regions of three Basmati varieties, revealing that Basmati had less SNP variations with *aus* group compared to *japonica* and *indica* groups. Analysis of gene ontology (GO) associations indicated that SNPs present in the genes encoding various biological, molecular and cellular functions. Additionally, the metabolic process involved in cellular aromatic compound was found to be associated with common mutated gene cluster, which supported that aroma is an important specific genome feature in Basmati varieties. Further, total of 30 traditional Basmati varieties were classified into 22 *aromatic*, four *aus* and four *indica* groups based on genome-wide SNP markers. All 22 *aromatic* group Basmati varieties possessed flavoring *Badh2* allele. Additionally, some of agronomic and grain quality traits of Basmati rice were also comparatively evaluated, length width ratio of grain (LRG), panicle length (PL) and amylose content (AC) showed significant difference between aromatic and *indica*/*aus* groups. Comparative analysis of genome structure based on genome variation and GO analysis, inferred that Basmati genome derived mostly from *aus* and *japonica* groups. In addition, the whole genome sequence data and genetic diversity information from this study will serve as an important resource for molecular breeding and genetic study using Basmati varieties.

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PA-0020

Characterization of major flowering time genes via vernalization response in Carrot (*Daucus carota* L. *ssp. sativus*)

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The Carrot (*Daucus carota* L. *ssp. sativus*) is an important root vegetable crop in the world with having various root colors. Although carrot is categorized as a green plant vernalization type (A low temperature treatment for a long period; about 2-3 months), little is known about the flowering time genes. Here, we ascertained the key flowering genes of carrot (FLOWEING LOCUS T (FT), SUPPRESSOR OF OVEREXPRESSION OF CONSTANS 1 (SOC1), CONSTANCE (CO), GIGANTIA (GI), LATE ELONGATED HYPOCOTYL (LHY), FLOWERING LOCUS C (FLC), FRIGIDA (FRI), VERNALIZATION 1 (VRN1), GA REQUIRING 1 (GA1) and GIBBERELLIN INSENSITIVE (GAI)) according to the genome information. As a result, 4 *DcFTs*, 6 *DcSOC1s*, 3 *DcFLCs*, 3 *DcCOLs*, 2 *DcVRN1s*, 2 *DcGAIs*, 1 *DcGI*, 1 *DcLHY*, 1 *DcFRI*, and 1 *DcGA1* were identified in four flowering pathways. We constructed phylogenetic trees and the chromosomal location of the flowering genes. Furthermore, we performed RT-qPCR analysis to investigate vernalization response of the key flowering genes in two early bolting carrot inbred lines under a long period of plant adapt vernalization (80 days). The result of RT-qPCR indicated that flowering activators including integrator genes were significantly increased to the vernalization (*DcFTs*, *DcSOC1s*, *DcCOLs*, *DcGI* and *DcVRN1*), whereas a strong repressor *DcFLCs* were remarkably decreased in both lines. However, *DcLHY*, *DcFRI*, *DcGAI* and *DcGA1s* showed modest response to the vernalization in the lines. Our analysis has provided useful information for long-term plant vernalization and valuable sequence resource of major flowering genes in Carrot.

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PA-0021

A low-pungency S3212 genotype of *Capsicum frutescens* caused by a mutation in the *putative aminotransferase* (*p-AMT*) gene

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The purpose of this study was to identify the genetic mechanism underlying capsinoid biosynthesis in S3212, a low-pungency genotype of *Capsicum frutescens*. Screening of *C. frutescens* accessions for capsaicinoid and capsiate contents by high-performance liquid chromatog- raphy revealed that low-pungency S3212 contained high levels of capsiate but no capsaicin. Comparison of DNA coding sequences of pungent (T1 and Bird Eye) and low-pungency (S3212) genotypes uncovered a significant 12-bp deletion mutation in exon 7 of the *p-AMT* gene of S3212. In addition, *p-AMT* gene transcript levels in placental tissue were positively correlated with the degree of pungency. S3212, the low-pungency genotype, exhibited no significant *p-AMT* transcript levels, whereas T1, one of the pun- gent genotypes, displayed high transcript levels of this gene. We therefore conclude that the deletion mutation in the *p-AMT* gene is related to the loss of pungency in placental tissue and has given rise to the low-pungency S3212 *C. frutescens* genotype.

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PA-0022

Rapid identification of the cultivated species by sequencing and PCR-RFLP analysis of two starch synthase genes

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The objective of this study was to develop a PCR-RFLP method to identity the cultivated species of grain amaranth based on variations in the sequences of their starch synthase genes. We sequenced the *SSSI* and *GBSSI* loci in 126 accessions of cultivated grain amaranth collected from diverse locations around the world. We aligned the gene sequences and searched for restriction enzyme cleavage sites specific to each species for use in the PCR-RFLP analysis. Our analyses indicated that EcoRI would recognize the sequence 5′-GAATT/C-3′ in the *SSSI* gene from *Amaranthus caudatus* L., and *TaqI* would recognize the sequence 5′-T/CGA-3′ in the *GBSSI* gene from *Amaranthus hypochondriacus* L. The PCR products obtained using gene-specific primers were 423 bp (*SSSI*) and 627 or 635 bp (*GBSSI*) in length. These products were cut with different restriction enzymes resulting in species-specific RFLP patterns that could be used to distinguish among the cultivated grain amaranths. The results clearly showed that *A. caudatus* and *A. hypochondriacus* were easily differentiated at the species level using this method. Therefore, the PCR-RFLP method targeting amaranth starch synthase genes is simple and rapid, and it will be a useful tool for the identification of cultivated species of grain amaranth.

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PA-0023

밀 종실 크기 관련 대립유전자 조합에 따른 종실 특성

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국내 밀 품종 41개의 종실 크기 관련 대립유전자 중 표현형에서 유의적인 차이를 나타낸 4개의 유전자좌(*TaCWI-4A, TaCWI-5D, TaGW2-6A, TaSus2-2b*)의 대립유전자 조합에 따른 종실 특성을 분석하였다. 기존에 천립중의 무게를 올린다고 보고된 대립유전자는 각각 *Hap-4A-T*, *Hap-5D-C*, *A*, *H*이며, 이 조합을 가지고 있는 품종의 종실 특성은 천립중, 리터중, 종자 길이, 종자 폭, 종자 두께 각각 39.2g, 826g, 6.36mm, 3.29mm, 2.78mm로 나타났다. 10개의 대립유전자 조합 중 천립중의 무게 순으로 정리하였을 때 8번째로 무거운 조합으로 기존에 알려진 결과와는 상반되는 결과를 나타냈다. 이러한 결과는 국내 밀 품종에서 *TaCWI-4A*유전자좌의 대립형질 *Hap-4A-T*와 *Hap-4A-C* 간에 천립중의 차이가 유의하지 않았고, *TaGW2-6A*유전자좌의 대립형질 *A*와 *G*, *TaSus2-2b* 유전자좌의 대립형질 *H*와*L*에서 천립중의 무게를 올린다고 보고된 대립형질 *A*와 *H* 보다 오히려 *G*와 *L*의 형질을 가지고 있는 품종이 천립중, 종자 길이, 종자 폭, 종자 두께가 유의적으로 높게 나타났기 때문이다. 대립유전자와 표현형의 불일치는 다양한 유전자 배경의 차이로 발생 한다고 생각되며, 추후 종자 무게 및 크기에 관련된 유전자형이 다른 유전자좌에 의해 종실 크기의 특성 변이가 발생하는지 탐색하는 연구가 필요 할 것이다.

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PA-0024

장수형 밀 집단을 이용한 이삭길이 관련 QTL분석

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긴이삭을 가진 태중밀과 금강밀을 교배한 장수형 집단 94계통(F_{10} RILs) 을 2017년부터 3년간 이삭 길이 관련 형질을 조사하였다. 장수형 집단의 수장(spike length)과 이삭의 수밀도(compactness)는 짧은 수장과 낮은 수준의 수밀도에 치우친 분포를 나타내었으며, 수장은 경수와 수축 길이와는 부의 상관을 나타내었다. 1,761 SNP marker가 2787.07 cM에 분포하였으며, A게놈에 29.7%(523개), B 게놈에 38.9%(685개), D 게놈에 31.4% (553개)분포하였다. 본 연구에서는 이삭 길이 관련 4개의 QTL을 찾았는데, 수장 관련 2개의 QTL, *qSL*-1 과 *qSL*-2은 각각 5A와 6A 염색체에 위치하였으며, 장수형 집단의 이삭 길이를 각각 16.9%와 30.0% 설명이 가능하였고, 5B와 6A 염색체에 위치한 2개의 수축 길이 QTL, *qLCR*-1과 *qLCR*-1는 31.5%과 15.9%의 변이 설명이 가능하였다. *qSL*-2과 *qLCR*-2 의 위치는 동일한 것으로 나타났으며, 이들 QTL을 이용하여 이삭길이 관련 표현형 변이가 30%이상 설명이 가능하기 때문에 수장 증가를 통한 국산밀 수량 증대를 위해 밀 육종 프로그램에서의 활용을 검토할 필요가 있다.

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PA-0025

Analysis of Structure and Function Relationship of Soybean *FLOWERING LOCUS T* Homologs

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FT is the major floral activator in photoperiod-dependent flowering pathway. To understand the role of *FT* homologs in flowering time control of short-day (SD) plant soybean, we identified ten soybean *FT* homologs (*GmFTs*) and characterized the biological functions of these *GmFT* homologs in soybean flowering. Overexpression phenotypes in *Arabidopsis* and day length-dependent expression patterns of *GmFT* homologs suggest that a subset of these homologs, including *GmFT2a/2b*, *GmFT3a/3b*, and *GmFT5a/5b*, promote flowering in response to floral inductive SD conditions, while *GmFT1a/1b*, *GmFT4*, and *GmFT6* delay flowering in these conditions. To understand the molecular mechanisms of antagonistic functions of floral activator GmFT2a/GmFT5 and floral repressor GmFT4, we first conducted the homology modeling analysis. The homology modeling analysis using amino acids sequences of GmFT2a and GmFT4 and Hda3, a rice FT homolog, as a template suggested that these two soybean proteins share similar structural features. Moreover, we performed the yeast two-hybrid (Y2H) screening using GmFT5a and GmFT4 as a bait, to test whether these two antagonistic proteins share same binding partners or have their specific ones. From the Y2H screening, we isolated 144 and 38 binding proteins of GmFT5a and GmFT4, respectively. Further analysis of their binding suggested that GmFT5a and GmFT4 exhibit similar interaction properties to isolated proteins. Taken together, our results suggest that floral activator and repressor GmFT homologs play their opposite roles in modulation of soybean flowering not by regulating the different biological pathways, but by differentially regulating the same biological pathway with floral activator or repressor GmFT homolog-specific manner.

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PA-0026

Effects of High Ambient Temperature on Soybean Growth and Flowering

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Since the cultivation environment of crops is changing rapidly, such as drought, salinity, and high temperature caused by global warming, we investigated the effect of the high temperature on growth and flowering in soybean. Flowering time and growth characteristics were investigated in both 'Williams 82', early maturing cultivar, and 'IT153414', medium-maturing cultivar, grown at normal atmospheric temperature (normal field) and high temperature conditions (atmospheric temperature +3℃, Climatron). To investigate the effects of rising temperature on the expression of various flowering genes, we analyzed their mRNA levels in the leaves of soybean accessions tested. RT-PCR analysis revealed that soybean flowering genes exhibited different expression patterns in response to elevated temperature compared to normal growth temperature. We also analyzed the expression patterns of flowering genes in soybean plants grown at 20℃ and 30℃ conditions of growth chamber under short- and long-day conditions, respectively. Moreover, higher temperature also differentially affects growth, flowering time, and productivity of two soybean accessions tested. First of all, higher temperature accelerated flowering of both soybean accessions. In early flowering accession, Williams 82, the plant length was increased, but the yields composed by the number of pods and seeds tended to decrease. In medium flowering IT153414 accession, the numbers of pod were reduced, but the seed numbers were increased at higher temperature conditions. The results indicated that higher temperature had worse effect on the yields of early flowering accession than that of medium flowering accession. Our results provide valuable information for breeding soybean cultivars suitable for changing climate conditions.

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PA-0027

Comparison of *fatty acid biosynthesis 2* genes in diploid and tetraploid perilla

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

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PA-0028

Seqping analysis for *Perilla citriodora*

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Perilla is one genus in the mint family, Lamiaceae, and has long been used as oil crop and a medicinal herb in East Asia. For the annotation analysis of *Perilla citriodora*, the raw data of the sequenced perilla 12 transcripts samples were preprocessed for high accurate assembly and the pair read by reading correction after quality trimming was used for analysis. For protein-coding gene prediction analysis, Seqping was used by using major transcript sequence as the input file, perilla de novo repeat sequence generated by repeatModeler, plant RefSeq protein sequence of NCBI, and Gypsy Database (GyDB). As a result, 43,175 genes, 43,664 transcripts, and 36,015 CDs were predicted. In addition, coding region was found using TransDecoder for Transcript base sequences obtained from TACO and Seqping, and BLAST and hmmsearch were performed using NCBI RefSeq plant protein and Pfam DB. The BLAST and HMMER were performed to calculate the statistical significance and to deduce the function by comparing with the gene database which was already known about the selected genes. As a result, 32,279 of the 32,447 hit proteins of perilla in NCBI RefSeq plant protein DB, and the function of 24,445 proteins were detected in Pfam. The BLAST2GO analysis showed the highest ratio in a cellular process, binding, and cell sections. Using the BUSCO and plant lineage dataset, 1,330 genes of the perilla pseudomolecule sequence and gene set were evaluated to be as high as 92.4%.

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PA-0029

품종판별을 위한 맥주보리 유전체 정보 생산과 InDel 마커 개발

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전라북도 완주군 이서면 혁신로 181 국립식량과학원

보리는 2배체로 5.1 Gb (haploid genome size)의 큰 genome size를 가지며 단순 반복서열이 80% 이상으로 시퀀스 분석, DNA 마커 개발 등에 어려움이 있다. 한편 2017년에 보리의 표준유전체('Morex')가 발표되어 genome 정보를 이용한 resequencing 등의 다양한 분석이 가능해졌다. 최근 DNA 수준에서 보리 품종간의 유연관계분석 및 품종 판별 그리고 이러한 DNA 마커를 이용한 분자육종의 요구가 증가하고 있다. 맥주보리를 이용한 고품질 맥아 생산을 위해서는 품종간 혼종을 방지하여 종자의 균일한 발아가 가장 중요하다.

본 연구에서는 호품을 포함한 6개 맥주보리 품종의 NGS 분석을 통해 품종간 DNA 상의 변이 (SNP, InDel)를 분석하였으며, 이를 이용하여 InDel 마커를 개발하고 품종판별에 이용하였다. 각 품종의 genomic DNA 추출은 Genomic DNA prep kit(Biofact, Korea)를 이용하였으며, DNA 농도는 Bioanalyzer(Agilent Technologies, USA)를 이용하여 분석하였다. 이후 paired end sequencing library를 제작하고 Illumina HiSeq X platform에서 염기서열 분석을 실시하였다. 생산된 염기서열정보로부터 low quality read를 Trimmomatic 프로그램(version 0.38)을 이용하여 제거하고, High-quality read는 Burrows-Wheeler Aligner (BWA) 프로그램(version 0.7)을 이용하여 BAM 형식으로 변환하였다. 이를 Genome Analysis Toolkit (GATK, version 3.5)의 HaplotypeCaller module를 이용하여 변이를 선발하고 VCF 파일을 작성하였다. 6개의 샘플에 대한 FastQC 결과 Q20(%)은 97%이었다. 표준유전체('Morex)에 Mapping 된 Read들은 87~89%, 평균 depth는 6~10X이었다. 6개 품종에 대한 SNP와 InDel 변이는 각각 615,878, 50,732개로 나타났다. 필터링을 통해 이 중에서 20bp 이상이면서 high-quality InDel 329개를 선발하고 17~25mer, GC content 50% 내외, Tm 50~60℃, PCR product 크기는 300~500bp인 프라이머를 제작하였다.

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PA-0030

Integrated transcriptomic and metabolomic analysis of four *Panax* species to identify genes involved in the ginsenoside biosynthesis

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The *Panax* genus belonging to the Araliaceae family has been used as a traditional medicinal plant, benefitting human health over the ages and producing various triterpene compounds such as ginsenosides. Characterization of multiple key pathways and enzymes involved in triterpenoid biosynthesis is an essential step for understanding genomic information of the biosynthesis mechanism. In this research, comparative transcriptome and metabolomic analysis was conducted to characterize the diversity of genes related to the triterpenoid biosynthesis pathway among the four *Panax* species (*Panax ginseng* [PG], *Panax quinquefolius* [PQ], *Panax notoginseng* [PN], *Panax vietnamensis* [PV]). Squalene epoxidase (SQE) and 2,3-oxidosqualene cyclases (OSCs) such as dammarenediol II synthase (DDS), beta-amyrin synthase (β-AS), lanosterol synthase (LSS), cycloartenol synthase (CAS) and lupeol synthase (LUS) are the important genetic factors for triterpenoid biosynthesis including plant sterol and ginsenosides. Through comparison of the expression from SQE to OSCs, it was found that the patterns changed in various ways for each species. Metabolite profiling revealed that multiple compounds were detected in adventitious roots from four species such as protopanaxadiol (PPD), protopanaxatriol (PPT), ocotillol (OT) and oleanane (OA) type. Most PPD type ginsenosides are abundant in PG and PN, while most PPT type ginsenosides are rich in PG and PQ. This study will provide the insight of dynamics of triterpenoid biosynthesis among *Panax* species.

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PA-0031

Designed GWAS and GEN databases to construct a multi-dimensional database system

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In order to efficiently utilize the exponentially growing various omics information in crop research and development, research on efficient management and utilization of raw data (primary information, first dimension) such as genomes and phenotypes as well as high-dimensional information such as SNP (2nd) and GWAS (3rd) is essential. To ensure that the multi-dimensional information can be effectively used for crop research, we are building databases to provide combined omics-information. As the first step, we designed databases for two 3rd dimensional information, GWAS(Genome-Wide Association Study) and GEN(Gene Expression Network). The GWAS and The GEN databases contain 7 and 14 tables, respectively. By a chromosome entity, the databases are connected not only to each other but also to other databases such as variant and gene expression DB. If the foundation for using multi-dimensional information is established with the databases, many agricultural research and development such as genome based breeding can be performed more efficiently.

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PA-0032

To study of genetic diversity base on complete chloroplast genome among *Panax* species in Vietnam

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Panax species (Araliaceae) are regarded as the king of herbal medicinal plants. However, their evolutionary, taxonomical relationship, and origin remain largely unresolved. In recently, we were successful in developing efficient 18 chloroplast gene-derived SNP markers to authenticate the 7 *Panax* species (*P quinquifolius* and *P. trifolius* from North America and five species, *P. ginseng*, *P. notoginseng*, *P. japonicus*, *P. vietnamensis*, and *P. stipuleanatus* from Asia). In Vietnam, *P. vietnamensis* is represented by three varieties: *P. vietnamensis* Ha et Grushv. var. *vietnamensis* (Ngoc Linh ginseng), *P. vietnamensis* var. *fuscidiscus* K. Komatsu, S.Zhu et S. Q. Cai (Lai Chau ginseng) and *P. vietnamensis* var. *langbianensis* (a new variety). It is difficult to distinguish these varieties due to the high similarity in flowers and fruits, and the wide variation in rhizomes, roots, and leaves. Furthermore, 18 SNP markers in the previous study are limited to discriminate on these varieties. Therefore, in an urgent work to investigate, preserve, and research these seriously endangered wild medicinal resources, high-resolution genetic markers must be developed to discriminate between these varieties. In this study, the complete chloroplast genomes of three *P. vietnamensis* var. *fuscidiscus* and two *P. vietnamensis* var. *langbianensis* were assembled and analyzed for the first time. Sixteen chloroplast gene-derived SNP markers were developed to distinguish the three varieties. The results of this study will be beneficial for taxonomic research, identification and conservation of Vietnam *Panax* wild resources in the future.

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PA-0033

팥 품종판별・다양성 분석과 유전체 육종을 위한 유전체정보 해석

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팥은 일년생 콩과작물로 동아시아에서 널리 재배하고 있으며 최근 평균수량은 173kg/10a으로 알려져있다. 팥 유전체연구는 2015년도 The Beijing University of Agriculture에서 De novo assembly를 수행하여 Vigan1.1로 명칭하는 유전체를 작성하였다. 그리고 한국에서는 경원 팥품종을 이용하여 De novo assembly를 수행하여 보고하였다. 위의 표준유전체(Vigan1.1, 약 538Mb)를 기반으로 팥의 유전체육종과 LD 분석, 품종판별을 위해 팥 유전체 정보를 해석하였다. 공시재료는 종자원에 등록된 14 품종 중 주요 7품종(충주, 아라리, 경원, 홍언, 서나, 홍진, 홍다)을 선택하였다. NGS Sequencing raw data에서 BWA-0.7.17-r1188을 이용하여 표준유전체(Vigan1.1)에 mapping을 하였다. 그 결과 생성된 BAM 파일은 GATK4.0.11.0를 이용하여 vcf 파일을 작성하였다. vcf 분석은 vcftools, bcftools를 이용하여 mapping quality, base quality, depth 등의 기준에 따라 filtering 수행하여 62,770개의 Single Nucleotide Polymorphisms(SNP; 58,356)&Insertion/ Deletion(Indel; 4414) 리스트를 확보하였다. Allele frequency에 따른 SNP&Indel 리스트를 분석한 결과 0.5에 해당하는 갯수는 21,570이며 이는 품종판별마커 제작에서 변이 다양성이 높은 마커를 선발하는 기준이 된다. 프라이머 4개를 이용하여 SNP 위치를 Direct sequencing 한 결과 해당 부분에 SNP가 존재하였고 Linkage Disequilibtium(LD) 현상이 나타나서 62,770의 다형성을 대상으로 LD 분석을 수행하였다. 그 결과 LD의 R-square값에 대한 데이터를 확보하였고 Block 수와 각 블락에 따른 linking된 SNP의 목록을 정리 중이다. 이후 품종판별마커를 제작할 때 LD Block 정보를 활용하여 마커를 선발하는 데 효율적으로 수행할 수 있을 것이라 기대한다. 그러므로 팥 7개 품종에 대한 다양성을 확인하고 품종 특이적 마커와 품종 판별을 위한 마커 조합을 도출할 예정이다.

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PA-0034

Reconstitution of cytokinin signaling pathway in rice protoplasts

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Cytokinin (CK) signaling pathway consists of three components; type B response regulator (RR), histidine phosphotransfer protein (HP) and histidine kinase (HK) which transmit signals through sequential phospho-relay reactions from a receptor (HK) to a transcription factor (type B RR). Each component has multiple genes and is able to make combinations of hundreds signaling pathways. Thus, we tried to characterize activities of genes and CK signaling pathway using luciferase assay system in rice protoplasts. Firstly we constructed TCSn:fLUC consisting of CK-response synthetic promoter and firefly luciferase. Then we monitored how signaling components take effects on TCSn:fLUC in rice protoplasts depending on 6BA. We performed luciferase assay using four genes in type B RRs, HPs and HKs respectively. All of type B RRs activated TCSn:fLUC strongly. Especially OsRR18 and OsRR19 showed hyper-sensitive activities to 6BA. The four HPs showed quite similar activities even though OsHP1 and OsHP2 represent higher sensitivity to 6BA than others. Unexpectedly over-expression of HKs showed low activities and less sensitive to 6BA compared to type B RR and HPs. Finally, we selected OsRR18, OsHP2 and OsHK3 which showed the highest sensitivity to 6BA. And then the three genes were co-transformed to reconstitute the CK signaling in rice protoplasts, it was confirmed that the OsHP2 increased trans-activity and sensitivity to 6BA of the OsRR18 and the OsHK3 increases the overall trans-activity regardless of 6BA. Taken together, protoplast-luciferase assay system based on the CK responsive reporter system facilitates high-throughput characterization of each gene function in CK signaling.

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PA-0035

Roles of F-box proteins containing LRR-repeat domain in wheat

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The F-box proteins have specific roles of the regulation of various development processes such as flowering, circadian rhythms, photomorphogenesis, seed development, leaf senescence, and hormone signaling by post-translational modification. F-box proteins contain recognizable substrate domain, such as Leu-rich repeats (LRRs), WD repeats, or kelch-repeats that are thought recognize specific proteins for degradation. We isolated three F-box genes from wheat developmental stages. The cDNA encoding *TaFBX1*, *TaFBX2*, and *TaFBX3* contained 495, 1215, and 1140bp open reading frames, respectively. All deduced TaFBXs contained an F-box domain (IPR001810) and a Leu-rich repeat domain (IPR032675). The expression pattern of *TaFBX*s was analyzed by qRT-PCR according to wheat development stages. The *TaFBX* genes were differentially expressed in wheat vegetative stages and grain developmental stages. TaFBXs green fluorescent protein signals were localized in the nucleus and plasma membrane. Using the yeast two-hybrid screen, we screened some proteins that interact with TaFBXs. And also, we performed yeast two-hybrid assay to investigate protein-protein interaction between TaFBXs and various wheat SKP-like proteins (TaSKP1 and TaSKP6). The Y2H interaction and BiFC assay revealed that TaFBX3 specially interacts with the GPI-AP. We confirmed that GPI-AP is targeted by TaFBX3 for degradation by the 26S proteasome using tobacco leaves treated with MG132, a proteasome inhibitor. These results indicate that TaFBX3 acts as a connector between GPI-AP and SCF complex.

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PA-0036

High-Density SNP Linkage Map Construction and QTL Analysis of Firmness in Octoploid Strawberry (Fragaria × ananassa)

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The allo-octoploid cultivated strawberry (*Fragaria x anananssa Duchesne*) has been produced around the world because of its pleasant flavor and health benefitting properties. Recently, with advances in sequencing and scaffolding technology, chromosome-scale octoploid genome information is now available. In addition, with the development of various molecular markers, it is possible to construct high-density linkage maps that can be useful for molecular breeding. In this study, we constructed a high-density bin map using IStraw90 Axiom® SNP array and genotyping-by-sequencing (GBS)-based markers, and an F2 populations derived from inbred lines. As a result, a high-density linkage bin map of 3,974.6 cM in length was constructed, consisting of 1,245 bins and 33 linkage groups, covering 87.7% of the total physical length of the octoploid genome. This high-density linkage map was used to improve the quality of the octoploid reference genome, 'Camarosa'. The chromosomes 1-2, 2-1, 6-2, and 6-4 of 'Camarosa', which has scaffolding errors in large scale, were reassembled based on the linkage map constructed in this study. Furthermore, this high-density linkage map was used to analyze QTL for firmness, one of the traits that is important for the quality of strawberry fruits. As a result of QTL analysis of two linkage bin maps, 'L80' and 'T137', major QTL was detected only in the 'L80' population. In summary, the high-density linkage maps, 'L80' constructed in this study will be a framework for molecular breeding of agriculturally important traits in strawberry.

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PA-0037

In silico Analysis for Selecting Restriction Enzyme Suitable for GBS Library Construction in Kiwifruit

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Kiwifruit (*Actinidia* spp.) is an autopolyploid species and heterozygosity increases with ploidy levels. *In silico* analysis is a prerequisite to select a suitable restriction enzyme in genotyping-by-sequencing (GBS) library preparation. Therefore, this study was performed *in silico* analysis to investigate suitable restriction enzymes for GBS library construction in kiwifruit. *In silico* analysis was performed using SimRAD packages v0.96 in R Studio v.4.0.0. 'Red5' (*A. chinensis*) PS1_1.69.0 was used as the reference genome. A total of 13 restriction enzymes, including methylation sensitive and insensitive enzymes, were selected for *in silico* analysis. The reference genome sequences were digested using restriction sites of those 13 restriction enzymes and the number of fragments ranged from 201 to 500 bp were investigated. Among those 13 restriction enzymes, *Mse*Ⅰ could produce the largest number of fragments, while *Avr*Ⅱ was expected the lowest fragment production. The number of fragments was high in the order of *Hin*fⅠ, *Tfi*Ⅰ, *Aci*Ⅰ, *Sau*96Ⅰ, *Hha*Ⅰ, *Ape*KⅠ, *Eco*RⅠ among methylation-sensitive enzymes, and *Mse*Ⅰ, *Mfe*Ⅰ, *Bsr*GⅠ, *Hin*dⅢ, *Sph*Ⅰ, *Avr*Ⅱ among the methylation-insensitive enzymes. Properties of each restriction enzyme will be considered for produce genome-wide SNPs as well as GBS library construction.

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PA-0038

Simultaneous accumulation of a broad range of flavonoids and changes in transcriptional profile in a chrysanthemum (*Chrysanthemum morifolium* Ramat.) mutant cultivar producing dark-purple petals

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'ARTI-Dark Chocolate' (AD) is a chrysanthemum cultivar with dark-purple rays that was developed through mutation breeding using gamma-rays. We performed HPLC-DAD-ESIMS using AD and its original cultivar 'Noble Wine' (NW) for metabolic characterization. A total of 26 phenolic compounds were detected, among which three anthocyanins and eight other flavonoids were identified specifically in AD. In all subgroups of flavonoids classified according to aglycone type (derivatives of apigenin, acacetin, luteolin, and diometin), the amounts were 8.0-10.3 times higher in AD. This indicated dramatic and simultaneous accumulation of flavonoids in AD. To elucidate the mechanism on flavonoids accumulation in AD, we performed transcriptome analysis. As the result, we found that most of unigenes in flavonoid biosynthetic pathway were not significantly up-regulated in AD. Instead, genes coding proteins involved in post-translational regulation were enriched in down-regulated genes. Especially, we found a DNA mutation on an F-box gene. This implies the suppression of post-translational regulation-related genes rather than that of transcriptional regulators of flavonoids biosynthetic genes might be a mechanism underlying high accumulation of flavonoids in AD.

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PA-0039

Coumestrol and phytohormonal cross-talk in soybean

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Soybean is a major crop in the world, that is consumed due to its nutritional value and protein contents. Coumestrol is one of the isoflavones, acting as phytoestrogen and is an important hormone in the animals also found in most of the leguminous plants. Reports suggested that coumestrol displays potent α-glucosidase inhibitory activity and can potentially be helpful in curing various diseases such as diabetes and menopause. It is also reported that coumestrol contents in plants may vary depending on the age of the plant with more coumestrol contents in the old plants. Therefore, it could also be involved in important physiological processes such as senescence. We, therefore, were interested to see the physiological changes due to coumestrol treatment to soybean leaves. Our results suggested that the coumestrol contents in the 126 days old leaves were the highest compared to the 98- and 35-days old leaves with different colors. Coumestrol treatment also induced adventitious roots initiation compared to control leaves. These results suggested a possible crosstalk between coumestrol and other phytohormones. Therefore, we were interested to see coumestrol contents after different phytohormone applications to the soybean leaves. Interestingly, the Ethephon which is a precursor to ethylene and MeJA combined with Ethephon showed more coumestrol contents suggesting a possible interaction between coumestrol and ethylene during the senescence process. We also studied the coumestrol biosynthetic pathway by studying the expression of key genes involved in the biosynthetic pathway. The results suggested that the two up-stream genes, *GmIFS1* and *GmIFS2* in the coumestrol biosynthetic pathway were highly up-regulated in Ethepon and Ethepon combined with MeJA treated plants at 3 days after treatment. At the same time, the S-nitrsothiol (SNO) contents were also increased. The presence of SNO can be deemed to the high accumulation of nitric oxide (NO) which in the recent past has become a tremendous signaling molecule. Therefore it is suggested that NO might regulate the coumestrol contents through the ethylene pathway in plants. However, further investigation is required to unravel the underlying mechanism that how NO, ethylene, and coumestrol interact to bring physiological changes in plants.

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PA-0040

Selective induction of recombinant protein expression in Arabidopsis protoplasts by using Gal4/UAS gene expression system and abiotic stress

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Constitutive high expression of recombinant proteins can inhibit the growth of transgenic plants and further reduce recombinant protein productivity itself. Selective induction of recombinant protein expression is one of the ways to solve problems of growth retardation of transgenic plants and degradation of expressed recombinant proteins during plant growth. However, high cost and low protein expression were disadvantages of selective induction method. Previously, we modified Gal4/UAS expression system to be suitable for high production of recombinant proteins in plant tissues. Here, we utilized ABA response element (ABRE) motif of ABI1 promoter to induce expression of Gal4-VP16 transcription factor by treatment of abiotic stresses (NaCl, drought etc.). Newly generated inducible promoter (6xABRE_A) was composed of 6 repeats of ABI1 ABRE motifs and 35S minimal promoter. We co-transformed *6xABRE_A/35-m::Gal4-VP16* and *6xAS/35-m::At1g53000-sGFP* into Arabidopsis protoplasts. By treatment of 1uM ABA, 6xABRE_A successfully induced expression of Gal4-VP16 and then At1g53000-sGFP was expressed by Gal4-VP16 transcription factors sequentially. The fusion vector (*6xABRE_A/35-m::Gal4-VP16 - 6xAS/35-m::At1g53000-sGFP*) combined with two inducible expression cassettes also induced the recombinant protein well by ABA treatment. Combination of selective induction of Gal4-VP16 and Gal4/UAS high expression system allows transgenic plants to grow normally and produce high amount of recombinant proteins simultaneously. It can be further developed as an effective strategy to increase recombinant protein productivity in transgenic plants.

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PA-0041

Comparative analysis of complete chloroplast genome sequences of three *Hibiscus syriacus* local varieties

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Hibiscus syriacus L. is distributed all over the world, and has an important meaning as a national flower in South Korea. However, since *H. syriacus* has not yet been identified as the origin, research and investigations have been conducted. Chloroplasts are well preserved in organism and have been used as a good material for identifying species differentiation, evolution and migration. There is only a small amount of genetic variation among species and even varieties. In this study, three different local varieties were selected to find a variation in chloroplasts and to make a basis for data to identify the origin. Total genomic DNA was produced raw data through illumina tru-seq flatform. After that, the circular chloroplast sequence was completed using NOVOplasty v4.1 program. And alignment analysis is carried out with clustal omega program. As a result, the complete genome was constructed with Jeju 2 (160,899 bp), Gyeongbuk 1 (161,022 bp), and Gyeonggi 3 (161,027 bp). Compared with the reference sequence, variants 0.22% (indel locus 50, substitution locus 27) in Jeju 2, 0.017% (indel locus 20, substation locus 2) in Gyeongbuk 1, and 0.013% (indel locus 19, substitution locus 1) in Gyeonggi 3 were confirmed. The results of this study will be used to identify the origin and species differentiation of *H. syriacus* and other relative species.

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PA-0042

Transcriptome analysis pipeline based on RNA-sequencing

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Next-generation sequencing (NGS) technologies have facilitated the identification of novel genetic markers and examination of genetic variation in plant genomes and transcriptomes. Currently there are many tools for transcriptome sequence assembly and analysis. We build the pipeline using proper tools to analyze transcriptome sequencing for plants based on RNA-sequencing (RNA-seq). The transcriptome analysis pipeline is three parts: transcriptome assembly, identification of differentially expressed genes (DEGs), and function annotation. Using this pipeline, patterns might contribute to understanding the genetic basis of heterosis. This pipeline would be useful in breeding program.

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PA-0043

Development of nuclear DNA markers based on short-read WGS data of *Cynanchum wilfordii*

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Cynanchum wilfordii is a domestic functional plant in Korea. The cultivation of *C. wilfordii* for commercial purposes has increased since it was proved to show medicinal effects such as alleviating menopausal symptoms and reducing cholesterol levels. Currently, cultivars or inbred lines of *C. wilfordii* do not exist because artificial pollination methods and molecular breeding systems have not been established for it. Considering buoyant demand for *C. wilfordii*, application of molecular breeding technologies is required. In this study, we developed nuclear DNA markers using short-read WGS data. First, four accessions of *C. wilfordii* were sequenced using Illumina MiSeq. One accession was selected and its sequencing data were assembled *de novo*. 834,864 variants were called by mapping the other three sequencing data to the previous *de novo* assembly result. The variants were filtered through 15 steps which required various conditions such as quality depth, allele frequency and proportion of variations. 340 SNPs were then selected as final candidates. Primers targeting 11 SNPs were designed and validated with HRM tests. Developed nuclear DNA markers will contribute to the breeding of *C. wilfordii* as an efficient tool for identification of accessions, investigation of zygosity and marker-assisted selection.

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PA-0044

Genetic diversity analysis of *Schisandra chinensis* using mitochondrial DNA markers

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Schisandra chinensis is a vine plant belonging to the Schisandraceae and is a deciduous broad-leaved vine plant of the genus *Schisandra*. Schisandraceae is native to Korea and includes S. *chinensis*, *Schisandra repanda*, and *Kadsura japonica*. Among them, *S. chinensis* is used for medicinal purposes in Korea. In this study, *S. chinensis* genetic resources were collected from 13 regions and Next Generation Sequencing analysis was performed using Illumina Hi-seq platform. Insertion or deletion (InDel) markers with more than 6 base pair (bp) difference and simple sequence repeat (SSR) markers with 3 to 6 bp motif were developed. A total of 19 markers were developed and applied to the collected genetic resources to characterize the markers using PowerMarker software. Eleven markers with 0.5 or higher Polymorphism Information Content (PIC) value were applied to the 13 resources collected in Korea for phylogenetic analysis. The molecular marker developed in this study could be used for genetic diversity analysis and molecular breeding of *S. chinensis*.

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PA-0045

Development of Molecular Markers for the Identification of *Panax ginseng* Genetic Resources

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Ginseng (*Panax ginseng* CA Meyer) is divided into cultivated ginseng and wild ginseng depending on the presence of cultivation by farmers. Wild-simulated ginseng refers to the ginseng cultivated in mountain areas without artificial facilities and pesticides. The place where wild-simulated ginseng is cultivated is a forest with cool, shaded mountains and under the trees older than 20 years. Ginseng varieties, wild ginseng, and wild-simulated ginseng genetic resources were collected and DNA was extracted using a DNA extract kit and CTAB method. Insertion or deletion (InDel) loci were identified through next generation sequencing analysis. Genotyping was performed using electrophoresis and fragment analysis. We developed one mitochondrial InDel and two chloroplast InDels and more than 20 nuclear InDels using the collected genetic resources. Our result would be a helpful tool for the selection of adequate variety of ginseng for the wild-simulated ginseng production.

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PA-0046

Chloroplast genome diversity and chromosome structures of two *Cynanchum* species

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Indigenous plants *Cynanchum wilfordii* (Cw) and *C. auricualtum* (Ca) have been used as medicinal plants for a long time in Korea and China, respectively, but research on the genome is insufficient. We collected various Cw germplasms from Korean local farms, and many different morphological traits have been found in the shape of their leaves and roots that led to the reflection of genetic diversity. We found five InDels and six SNPs within Cw chloroplast genomes through comparative analysis of five Cw and two Ca individual sequences, and 253 InDels and 973 SNPs were identified between two species. Four of five intra-species InDels originated from tandem repeats, and three were located in the genic region. One of the six intra-species SNPs was located in the genic region, and the rest in the inter and intra-genic regions. As a result of genotyping 165 Cw individuals using seven intra-species markers, 2 to 5 types were found in each allele. 26 chlorotypes classified into two major clades were identified. The estimated total genome size was 212~272 Mbp, and 11 chromosomes pairs with juxtaposed 5S and 45S nrDNA regions were observed. The tandemly located structures of 5S and 45S were assembled, and three intra-species and 16 inter-species variations were found in the 45S region. 15 inter-species variations were found in the 5S inter-genic spacer region, but the 5S sequence was conserved. Basic genome structure, diversity, and marker information in our study will provide basic data for breeding research of Cw.

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PA-0047

Differentiation of *Ziziphus jujuba* Varieties Using Nuclear Based InDel Markers

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Ziziphus jujuba is a tree of the Rhamnaceae family. It is mainly distributed in subtropical and tropical regions of Asia and America. *Z. jujuba* has undergone various modification over a long time due to natural evolution and artificial selection, and more than 800 varieties have been found. Its fruit is edible in the shape of an oval and contains hard seeds. It has potential nutritional benefits, including high nutritional value and antioxidant activity. To protect the genetic resources of jujube and increase its value as a crop, it is necessary to identify varieties of *Z. jujuba* that are cultivated and distributed. We developed insertion or deletion (InDel) markers based on nuclear DNA to differentiate varieties. InDel loci were identified through next generation sequencing analysis. Genotyping was performed using electrophoresis and fragment analysis. We successfully developed 26 InDel markers from the *Z. jujuba* nuclear DNA. Nuclear InDel markers varied in size from 6 to 50 base pairs. As a result of phylogenetic analysis by applying 8 nuclear InDel markers, 95 samples were divided into 35 groups. Our results would contribute significantly for the differentiation of *Z. jujuba* varieties.

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PA-0048

Differentiation of *Ziziphus jujuba* Varieties Using Mitochondria InDel Markers

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Ziziphus jujuba is an economically important species in Rhamnaceae. It is one of the oldest cultivated fruit trees in the world and has domesticated 7,000 years ago. The size of *Z. jujuba* is usually 2~3 cm and the weight is 10~13 g. *Z. jujuba* is an economically important crop, and the fruit is used for raw fruits, snacks, cooking as well as for medicine. To protect the genetic resources of jujube and increase its value as a crop, it is necessary to identify varieties of *Z. jujuba* that are cultivated and distributed. The organelle, the mitochondria, has independent DNA. We developed insertion or deletion (InDel) markers based on mitochondrial DNA to differentiate varieties. InDel loci were searched through next generation sequencing (NGS) analysis. Genotyping was performed using electrophoresis and fragment analysis. We successfully developed 21 InDel markers from the *Z. jujuba* mitochondrial DNA. Mitochondrial InDel markers varied in size from 2 to 200 base pair. As a result of phylogenetic analysis, 95 samples were successfully divided into 15 groups. Our results will contribute significantly for the differentiation of *Z. jujuba* varieties.

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PA-0049

Establish infrastructure for advancement of Agrobiological genome information

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Various and huge genome information is being produced by utilizing next-generation sequencing (NGS) technologies and is difficult to analyze with general computing tasks. The demand for bioinformatics research, which is used to develop genome-based molecular markers and superior traits, is rapidly increasing. Large-scale genome information of 17 items produced through the first stage of "Korea Post-Genome project" has been utilized. However, it is difficult to apply the current bioinformatics analysis pipeline for large and complex genome items, the amount of genome sequencing information of onion is hundreds of terabytes. The research on advancement of existing genomic information and quality improvement is required. We optimized and built the genome assembly pipelines. Finally, we will implement the user-friendly interface and this system is useful to researcher for studying genomics in breeding.

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PA-0050

Machine learning-based estimation of disease-related QTLs

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Model crops such as rice and soybean have been cumulated various QTLs for importance agricultural traits such as yield, biotic/abiotic resistances, and amount of beneficial compounds. Especially in the case of rice QTL finding efforts have accumulated ~ 35000 loci for highly detailed traits such as biochemical property, abiotic/biotic stress, anatomy, yield, vigor, sterility, quality and developments. With increasing number of newly sequenced orphan crops, it would be practically helpful for breeders if rice QTLs can be translated into newly sequenced genome. Comparative genomics revealed that the gene contents within certain genomic regions are highly conserved between species evidenced by collinearity of genes. It suggests that similar gene clusters may contribute similar function for phenotype. Based on this hypothesis, we tried to translate the QTL regions into newly sequenced genome using gene contents information in fixed length genomic regions. Here, we trained stress-related QTL prediction model using protein domain profiles of genomic regions of rice QTL information and tested in other monocot genomes. We found the model works with acceptable accuracy. We will further develop automated marker development pipeline based on the prediction. This approach will help marker development of newly sequenced crops for stress-resistance breeding.

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PB-0001

GWAS analysis of flowering time variation in cowpea

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Cowpea is an essential food for African countries or developing countries. For the genetic improvement of plants, flowering time is one of the major selection criteria. This study aims to investigate the flowering time-related genes using genome-wide association analysis (GWAS). A total of 384 cowpea germplasm were planted in the field of Chonnam National University and day to flowering time was evaluated in 2018 and 2019, respectively. The main genetic component of day to flowering time was identified by Genome Association and Prediction Integrated Tool (GAPIT) and Elastic-Net analysis. From the GAPIT, 22 SNPs were identified among five different chromosomes (chr.2, chr.3, chr.7, chr.9, and chr.11), and Elastic-Net analysis identified 15 SNPs across seven different chromosomes (chr.1, chr.2, chr.3, chr.4, chr.5, chr8, and chr.9). From both analyses, the major seven genes from Vigun01g084000, Vigun01g088200, Vigun01g227200, Vigun02g062600, Vigun03g291600, Vigun03g296800, and Vigun08g216600 were considered as candidate genes controlling flowering time in cowpea. These results confirmed that day to flowering time was strongly controlled by multiple genes affecting early flowering, delay flowering time, and repressing the transition to flowering, etc. This could help to better understand the genetic basis and explore the mechanism of flowering time in cowpea.

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PB-0002

GWAS analysis targeting on genes and genomic loci associated with seed pigmentation of soybean

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

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PB-0003

Homeodomain-like transcriptional regulator is a candidate gene elevating α-linolenic acid in an EMS-induced soybean, PE2166

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When soybean [*Glycine max* (L.) Merr.] is consumed directly as food, linoleic acid (LA, ω-6) and α-linolenic acid (ALA, ω-3) are essential fatty acids for human diet among fatty acid compositions. Intake of fatty acids with high ω-3 concentration or lower ω-6/ω-3 ratios is more desirable for human health. Through mutagenesis of Pungsannumul, PE2166 was identified to be contained ~14% ALA in our previous study. The objective of this present study was to unveil a novel candidate gene controlling the elevated ALA concentration in PE2166. Major QTLs, *qALA5_1* and *qALA5_2*, were detected on chromosome 5 through QTL mapping analyses of RILs population. With next generation sequencing (NGS) of parental lines and Pungsannamul, and analyses of recombination, a candidate gene controlling elevated ALA concentration was identified to be a major causal gene, *Glyma.05g221500* (*HOME*) which is homeodomatin-like transcriptional regulator. This causal gene as transcription factor may regulate in the expression level of microsomal ω-3 fatty acid desaturase (*FAD3*) genes which is responsible for conversion of LA into ALA in fatty acid biosynthetic pathway in soybean. Further research will be required to reveal the association of *HOME* and *FAD3* genes. In addition, we hypothesized that utilization of two genes including *HOME* gene from PE2166 and either of microsomal delta-12 fatty acid desaturase 2 (*FAD2*) genes can reduce seed ω-6/ω-3 ratio. With a population segregating *HOME*, *FAD2-1A* and *FAD2-1B* genes, combination of a mutant allele of *HOME* gene from PE2166 and either of *FAD2-1* genes can reduce the seed ω-6/ω-3 ratio.

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PB-0004

An integrated GWAS analysis pipeline construction using Multiple NGS data

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Analysis of next-generation sequencing (NGS) data, which are many produced for genome study, depend on correct calling of Single Nucleotide Polymorphisms (SNPs) and genotypes. Therefore, SNPs are an increasingly important tool for the study of Genome Wide Association Study (GWAS).

But, the existing method of the SNP and GWAS analysis pipeline has the inconvenience of inputting NGS data into the application of each step and executing the corresponding program to analyze the data obtained by the process. Therefore, to improve this inconvenience, a modified analysis pipeline was constructed, and a multi-genome data was input to extract the SNP at a time to develop a system capable of GWAS analysis.

It is a user-friendly, independent platform system for extracting integrated SNPs for multiple genomic data and then evaluating effective GWAS utilization for bias patterns observed in genomic data.

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PB-0005

Genome-wide association study to identify loci associated with agronomic traits in mungbean

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Dissecting the genetic basis of important agronomic traits will assist future breeding programs in mungbean, an important vegetable and protein source in Asia. We performed genome-wide association study in mungbean using 7551 SNP markers developed using genotyping by sequencing on 222 cultivated mungbean accessions from all over the world. The traits being evaluated were flowering time, maturity time, pod formation time, seed weight, number of seeds per pod, peak harvest, cumulative weekly harvest, final yield, and synchronicity. Using two different association methods, 77 and 79 markers were found to be significantly associated with some of the traits at p-value <0.0001 respectively. Some of the genes that intersect with significant markers share homology with soybean genes and QTL that could explain their role in trait formation, which makes them attractive candidates for follow up studies. The data can be used as a basis for mapping studies or parental selection in mungbean breeding programs.

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PB-0006

Genetic dissection of tiller number in rice by genome-wide association studies

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Tiller number is the key determinant of rice plant architecture and panicle number and consequently controls grain yield. Thus, it is necessary to optimize the tiller number to achieve the maximum yield in rice. However, comprehensive analyses of the genetic basis of tiller number, considering the development stage, tiller type, and related traits, are lacking. We sequenced 219 Korean rice accessions and constructed a high-quality single nucleotide polymorphism (SNP) dataset. The tiller number at different development stages and heading traits involved in phase transitions were evaluated. By a genome-wide association study (GWAS), we detected 20 significant association signals for all traits. Five signals were detected in genomic regions near known candidate genes. Most of the candidate genes were involved in the phase transition from vegetative to reproductive growth. In particular, HD1 was simultaneously associated with the productive tiller ratio and heading date, indicating that the photoperiodic heading gene directly controls the productive tiller ratio. Multiple linear regression models of lead SNPs showed coefficients of determination (R^2) of 0.49, 0.22, and 0.41 for the tiller number at the maximum tillering stage, productive tiller number, and productive tiller ratio, respectively. Furthermore, the model was validated using independent japonica rice collections, implying that the lead SNPs included in the linear regression model were generally applicable to tiller number prediction. We revealed the genetic basis of tiller number in rice plants during growth by a GWAS and formulated a prediction model by linear regression. Our results improve our understanding of tillering in rice plants and provide a basis for breeding high-yield rice varieties with the optimum tiller number.

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PB-0007

Estimation of regression equation for predicting tiller angle variation in rice

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Tiller angle is an important influencing factor in rice plant architecture that affects planting density and yield per unit area. Molecular tools to predict tiller angle contribute to breeding programs which aim optimizing rice plant architecture. In this study, several SNP markers related to tiller angle were developed and used with a model population to define a linear regression model for the prediction of tiller angle in rice. The resulting linear regression model, consisting of eight SNP markers as independent variables, was assessed using an independent test population. Overall, the regression model achieved an adjusted R2 of 0.51 and exhibited consistent predictive accuracy with an R2 of 0.61. Three of the eight independent variables, namely, PIN2-1, LIC1-1, and TAC1, contributed substantially to the linear regression model. These three major effect markers were also major determinants of tiller angle in the independent test population. Allelic combinations of the three major effect markers modulated tiller angle in the range of 5.6-19°. The DNA markers and linear regression model developed in this study will facilitate rice breeding programs for improving plant architecture.

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PB-0008

밀 고온내성 정도에 따른 ROS 소거 관련 유전자, *WHI1*의 차등 발현

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최근 기후변화에 따른 다양한 내재해성 밀 품종이 요구되며 유전체 데이터를 기반으로 하는 신육종기술이 각광받고 있다. 본 연구는 국내 밀 등숙기에 갑작스런 고온에 따른 밀 품질 저하를 예방하기 위하여 고온내성 품종 선발을 위한 유전체 정보를 수집하고자, 고온에 강한 품종과 약한 품종에서 고온처리 시 ROS를 소거해 주는 효소 관련 유전자의 발현을 분석하였다. 각 밀 품종의 고온처리 시 발현되는 대표적 ROS 소거 유전자를 전사수준에서 quantitative RT-PCR을 수행하여 유식물 및 출수기에 고온내성과 발현 양상이 일치하는 유전자인 *WHI1*(wheat heat induced gene 1)을 주목하였다. 고온에 강한 조품과 약한 올그루, 중간 특성을 보이는 금강으로부터 각각*WHI1* 의 cds 및 promoter를 클로닝하여 염기서열을 분석하였다. *WHI1*은 밀 6번 A, B, D 염색체에 각각 존재하며, 그들간 아미노산 서열 상동성이 95% 이상으로 거의 유사하였다. 50개 아미노산으로 구성된 D게놈의 *WHI1*은 국내품종에서는 아미노산 서열이 동일하였으며, A게놈 *WHI1*은 조품과 Chinese spring의 아미노산 서열은 동일한 반면, 금강과 올그루는 3개와 4개 아미노산에서 차이가 존재하였다. 아울러 *WHI1*-6A promoter 서열에서는 품종간 다양한 염기서열의 차이가 보였다. 품종간 *WHI1*의 cds 및 promoter 차이가 고온에 어떠한 기능적 영향을 미치는지 확인하고자 애기장대 등 모델식물에서 유전자 기능검정을 수행하고 있다. 추후 이 연구결과를 토대로 고온내성 밀 정밀육종에 이용할 선발 마커 개발에 도움이 되길 기대한다.

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PB-0009

QTL identification for arsenic in rice using genome-scale profiling, high-throughput analysis

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The ionomics is defined as the measurement of total inorganic components in organism. Recently, ionomics studies have been progressed to high-throughput element profiling to find genes involved in ions, its subjects have been expanded from rice and maize to human cells.

Arsenic (As) with toxicity as a non-essential element, had been widely used in pesticides, feed additives, *etc*. and it induces infertile ears of plants and threatens human health. Rice is known to approximately tenfold elevated in As exposure than other crops because it is ingested by more than 50% of the world population

This study conducted network analysis to investigate the interaction between As and functional mineral. Also, the genome-wide association study was performed to verify genetic variants associated with As under different environmental conditions. In addition, *Japonica* (Nipponbare) and *Indica* reference genome (MH63) were used for 273 rice varieties to minimize false positive, respectively.

As a result of network analysis between As and other inorganic components, their interaction was influenced by ecotype and environmental conditions. Besides, the As content of *Japonica* and *Indica* group under contaminated soil conditions showed high association ($-\log10(p) > 5$) with genetic variants than non-contaminated soil. This study presumes that the genetic variants associated with arsenic and the interaction on inorganic components may vary by environmental factors. Therefore, these results can be used as useful data to understand the relationship between As and other inorganic components and to investigate genetic factors on As in terms of food safety.

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PB-0010

The identification of QTL associated with arsenic and iron in rice (*Oryza sativa* L.)

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Arsenic (As) is a toxic inorganic element, it exists in the form of arsenite (As^{3+}) or arsenate (As^{5+}) according to the redox state and pH of soil.

As^{3+} is more toxic and soluble than As^{5+}, also it is well absorbed by rice in flooded condition. The As in soil not only causes physiological disorders of rice plant, but also it induces cancer and skin disease in human and animal. The rice absorbs various inorganic components such as Fe, Ca and Zn as well as As via roots. In particular, Fe combines with As in the form of ferrous hydroxide or ferric hydroxide, so that it cannot be absorbed into rice. OsNIP1 and OsIRT2 are currently known to be the major genes involved in As and Fe, respectively, but the genetic factors involved in these traits are not yet clear. In this study, genome-wide association study (GWAS) was performed to find common quantitative trait loci (QTL) related to As and Fe.

As a result of GWAS for rice core collection (284 varieties), 25 candidate genes commonly associated with As and Fe in *Indica* were identified. The functions of candidate genes were metal ion transporter activity, ethylene response factor, zinc/iron permease protein *etc*. In the future, these results are expected to be used as useful data for minimizing toxic minerals and maximizing functional minerals by identifying common QTLs associated with As and Fe. Therefore, the verification of candidate genes and the study of metabolites and mechanisms involved in minerals are required.

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PB-0011

Genome-Wide Association Analysis of the Content of Phenol Compounds in 137 Rice Germplasm

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Phenolic compounds are representative secondary metabolites and are known to relate with various physiological activities such as antioxidants and anti-cancer. In this study, Genome Wide Association Study(GWAS) were performed using 137 rice accessions, to find SNP markers were related catechin, hesperetin and the sum of targeted 54 phenolic compounds in rice.

Five SNP markers on chromosome 1 associated with content of catechin. We found 35 candidate genes which were located within ~50kbps on chromosome 1. To narrow the range, Haplotype analysis was conducted and detected 4 candidate genes. Also, in GWAS analysis of content of hesperetin, we discovered 5 SNP Markers on chromosome 3 and 32 candidate genes were found on chromosome 3. Two candidate genes were detected through haplotype analysis. Lastly, From the sum of targeted 54 phenolic compounds, we detected 5 SNP markers on chromosome 3 based on Manhattan plot and discovered 20 candidate genes. We also used haplotype analysis to narrow the range and 7 candidate genes were identified. Several candidate genes were detected from GWAS analysis related to phenolic compounds, but the candidate genes through GWAS is required to further research for discover genes which concerned with phenolic compounds in rice.

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PB-0012

SNP identification related to Grain Size using a Genome-Wide Association Study of Korea Rice landrace and KRice Core in Rice (*Oryza sativa* L.)

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Grain size is one of major components determining grain yield in rice. Identification of desirable allele related to grain size through GWAS would be effectively. In this study, the traits for Grain Length (GL) and Grain Width (GW) analyzed by conducting a Genome-Wide Association Study (GWAS) using 217 Korea Rice landrace accessions and 137 KRice Core accessions, respectively. In landrace, the average of GL was 5.01cm and the range of GL was 4.22cm to 6.21cm. The average of GW was 2.95cm and the range of GW was 2.38 to 3.46. In KRice core, the average of GL was 5.34cm and the range of GL was 4.50cm to 6.09cm. The average of GW was 2.52cm and the range was 1.62cm to 3.05cm. In GL, Landrace was more variable than KRice core, but in GW, KRice core skewed to narrow than Landrace. Genotyping of Landrace was done using 583K genotyping array and Genotype of KRice core was done using whole genome resequencing. Finally, 134K SNPs of Landrace and 3460K SNPs of KRice core were used for GWAS, respectively. In case of landrace, significant regions of GL were detected on chromosome 2, 6 and 8 and GW were found on chromosome 4, 9, 10 and 11. Otherwise, In KRice core, significant regions of GL were on chromosome 2, 3, 6 and 9 and GW were on chromosome 4, 6, 9 and 11.

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PB-0013

Identification of bakanae disease resistance resource from Korean Rice Landrace through genome wide association study

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The outbreak of rice bakanae disease causes the most important problems for rice producing countries and affects almost all known rice cultivars. To identify Bakanae disease resistance in Korean Rice Landrace with diverse genetic sources is important for efficient breeding. Genotyping was performed using KNU Axiom Oryza 580K Genotyping Array. The GAPIT package (Genome Association and Prediction Integrated Tool) was used to conduct association analysis for the bakanae resistant resources of 217 landrace accessions (Lipka et al. 2012). The mixed linear model (MLM) was performed, where a kinship (K) matrix as the variance-covariance matrix between the individuals was combined with population structure from PCA. Considering both -log(P) and -log(FDR adjusted P), a compromised threshold at -log(P) $\geq$ 2.7 was used to screening significant SNPs associate to bakanae resistant. The potential candidate genes were identified on chromosome 2,3 and 10 relating to the resistance of bakanae disease. Gene Ontology analysis of this genes is ranked in the top 5%: intracellular part(GO:0044424), intracellular organelle(GO:0043229), intracellular (GO:0005622), cell-part(GO:0044464), cell(GO:0005623), organelle(GO:0043226). Protein description analysis related to the disease showed that 7 genes on chromosome 2, 3 genes on chromosome 3 and 5 genes on chromosome 10 respectively.

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PB-0014

Genome Wide Association Analysis Related to Salt tolerance at the Seedling Stage in Rice

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Salinity is one of the major constraints in soil problems and is considered as a limitation to increase rice production for rice growing countries. Generally, rice is relatively tolerant to stress during germination, active tillering, and maturity but is particularly sensitive at the seedling stage and reproductive stage. This experiment was conducted a genome wide association study (GWAS) to understand the genetics basis of salt tolerance in rice at the seedling stage. The GAPIT package (Genome Association and Prediction Integrated Tool) was used to conduct association analysis for the salt tolerance of 217 Korea rice landrace accessions. Genotyping was done with 266,040 single nucleotide polymorphisms (SNPs) using KNU Axiom Oryza 580K Genotyping Array. After filtering the genotype with the minor allele frequency 0.03, 134620 SNPs were left to analyze.

We evaluated all cultivars on salt screening at normal condition and salt stress (14dS/m) condition in seedling stage. Based on salt stress score, 4 highly resistant cultivars, 23 resistant cultivars, and 29 moderately resistant cultivars were selected. Significant marker trait associations were determined based on a threshold of -lg(P) as ≥ 4.0. Adjacent significant SNP associated with the trait within a physical distance of 200 kb upstream and downstream were regarded as a candidate region. The significant regions related to salt stress score were found in chromosome 3 and 12.

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PB-0015

Genome-Wide Association Study of Cold Tolerance at Seedling Stage in Rice (*Oryza sativa* L.)

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Rice is a temperature-sensitive crop and yield is severely affected by low temperature. In particular, cold stress at seedling stage cause to delay heading stage. To understand the genetic basis of cold tolerance in rice, we evaluated the cold tolerance at the seedling stage of KRICE_CORE 137 rice cultivars. Two weeks after sowing, 137 cultivars were treated at 17±1℃ for 7 days under relatively humid of 70% at Chuncheon Substation, National Institute of Crop Science (NICS), Republic of Korea. For evaluation, the seedlings were scored 1 to 9. Average score of total 137 lines is 6.17. Among the tested cultivars, temperate japonica is the most cold-tolerance group and the most tolerance lines are Pyeongbuk and Gou 405. GWAS analysis is implemented with GAPIT. Selection of SNP refer to manhattan plot and threshold of -log(p) is 5. Lead SNPs are identified and then searched that located in various genes on chromosome 1,9 and 10. The candidate gene in ±200kb range of the selected SNP position. The result of Gene Ontology is identified that 42 of 141 candidate genes are related to Catalysis of a biochemical reaction at physiological temperatures. Meanwhile, a total of four genes containing SNP are expected to be one in chromosome 1, one in chromosome 9, and two in chromosome 10.

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PB-0016

Genome-wide association study of root system development at the seedling stage in rice

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For rice, root system plays a crucial role for growth process, understanding the mechanism of molecular genetics, screen the root-related merit germplasm, which showed essential for improving the root system development and future breeding.

In this study, whole panel contain 137 rice varieties were chosen from Korean rice core set (KRICE_CORE), 2 million high-quality SNPs as the genotype filtered from row data (6.5 milion SNP). Genome-wide association study (GWAS) was performed by measurement of maximum root length (MRL) and total root weight (TRW) during rice seedling stage. Analysis combined with Principal Components Analysis (PCA) and Kinship matrix, finally two quantitative trait loci (QTLs) were related to MRL and two QTLs were related to TRW were detected in chromosome (Chr) 3, 6 and 8, respectively. candidate region (230kb) as the candidate region for detection of candidate genes according to Linkage Disequilibrium (LD) decay analysis results. Five reported genes that related with root development were found, four unreported genes that as the candidate genes were filtered using RNA-seq data, gene annotations and quantitative real-time PCR (qRT-PCR). Among these, promoter analysis showed two genes contain SNPs that location at root-relate motif. Diverse haplotypes of these genes showed significant related with phenotype variation.

Based on these, two novel genes highly possible as functional gene associated with root development, and the significant haplotypes were beneficial for future breeding. This study supports a basic theory in molecular breeding and genetic for root system development at rice seedling stage.

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PB-0017

Genome-wide Association Study for Leaf Morphological Traits in Pear (*Pyrus* spp.)

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Leaf is the organ for performing photosynthesis and leaf shape affects plant growth. Therefore, searching for the gene(s) controlling leaf development is important to increase the photosynthetic efficiency of crops. Genome-wide association study (GWAS) is a method for detecting genes based on the association between genome-wide markers and phenotypes. This study was performed to detect locus related with morphological trait of pear leaf at the genome level. Seven leaf morphological traits (Leaf length (L), leaf width (D), L/D ratio, petiole length, apex, margin, and base) were investigated. At the 60 days after full bloom, 10 mature leaves in the middle of the shoot were collected per pear accession. Genotyping-by-sequencing (GBS) was performed using a total of 202 pear accessions. After GBS analysis, 46,961 GBS-SNPs were used for analysis. GWAS was performed through the Genomic Association and Prediction Integrated Tool (GAPIT) package version 3 with general linear model (GLM) in R. We detected candidate SNP related to L/D ratio in chromosome 9. S3_8191731, S6_423386, S9_20170900 and S14_17984819 SNPs located in the chromosomes 3, 6, 9, and 14, respectively were associated with the development of leaf margin. Those significant SNPs controlling leaf morphological traits could be used as foundation data for development of molecular markers.

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PB-0018

Two different genomic regions of the soybean cultivar Sochung2 respectively confer resistance to two different isolates of *Phytophthora sojae*

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Phtophthora sojae is a soilborne oomycete pathogen that causes severe damages to susceptible soybean plants and the management of this disease has been primarily relied on genetic resistance to *P. sojae* controlled by *Rps* (resistance *Phytophthora sojae*) genes. In the soybean breeding, identifying different *Rps* genes and introducing multiple resistance genes to cultivar is taken seriously for management disease in field environment. Such qualitative resistance is often race-specific and determined by interaction between resistance (*R*) and avirulence (*Avr*) proteins. Depending on this interaction, when there exist multiple resistance genes in a soybean variety, different *Rps* genes of the genotype may provide resistance to different races or isolates of *P. sojae*.

Sochung2 is a Korean soybean cultivar with black seed coat and presents resistance to two different *P. sojae* isolates 40412 and 2457. To identify genetic locations of genes for resistance, 103 recombinant inbred lines (RILs) developed by a cross of Daepung x Sochung2 were tested for their reactions to the two *P.sojae* isolates. Differential inheritance of resistance were observed in the RILs for the respective *P. sojae* isolates. Genetic mapping identified two different genetic regions of Sochung2 that respectively contribute resistance to each of isolate 40412 and 2457. This result suggests the possibility of discovering new resistance locus and it will be valuable resource for breeding soybean cultivars resistant to *P.sojae*.

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PB-0019

Combined genome-wide association analysis and linkage analysis identified resistance loci for *Phytophthora sojae* in soybean [*Glycine max* (L.) Merr.]

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Single dominant *Rps* (Resistance to *P. sojae*) genes can provide primary protection against infection of *P. sojae*. The objective of this study was to identify and verify resistance loci against *P. sojae* isolate 2457. Genome-wide association study (GWAS) and linkage analysis were performed using 180K SNP data and the disease phenotype. In GWAS, one and twenty SNPs were identified on chromosomes 3 (3,990,383 bp) and 8 (20,826,396 to 21,323,168 bp). The locus on chromosome 8 is a novel region first reported in the present study. No *Rps* allele has been reported near the region. The locus on chromosome 3 overlapped to the well-known *Rps* region identified by many previous studies, where several genes encoding nucleotide binding site-leucine-rich repeat (NBS-LRR) protein are annotated. A recombinant inbred line (RIL) population derived from a cross of Daepung x Daewon was used for validating the results from GWAS; Daewon is resistant, while Daepung susceptible to the isolate 2457. In single-marker analysis of variance (ANOVA), twelve SNP markers on chromosome 3 (4,200,520 to 4,752,915 bp) were identified significantly associated with resistance to *P. sojae*. Linkage analysis revealed that an interval (3,893,390 to 4,642,893 bp) on chromosome 3 was highly associated with the resistance, which overlapped to the genomic region identified by GWAS. More details will be discussed. This is the first report of existence of *Rps* gene in the Korean soybean variety. The findings of this study will be a meaningful framework for investigation of soybean-*P. sojae* interaction and the resistance germplasm will be a valuable source for breeding of the *P. sojae* resistance.

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PB-0020

A novel symptom of soybean: discoloration on upper leaves and a primary genetic analysis

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Climate change or severe weather phenomena often cause usual, un expected phenotypes in plants and these are new challenges in contemporary plant breeding and improvement. In recent years, discolored leaves were observed on upper leaves of soybean varieties; which looked like symptom of 'sunburn' or Cercospora leaf blight. In this study, two recombinant inbred line populations derived from a cross of Daepung x PI 96983 and Daepung x Wooram were used to score the symptom in the fields located in Cheonan, 2018 and in Daejeon, 2019. Upper leaves of PI 96983 and Wooram showed purple-discoloration in mid-to-end August, while those of Daepung did not. Levels of discoloration were segregated in the populations, and highly heritable. Two distinct locations of the chromosome 6 were detected in each population. The genomic regions accounted for ~60% of the phenotypic variance. To our best knowledge, such symptom is first report in this study. More details in sequence variation among major Korean soybean varieties and additional analytic efforts will be addressed.

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PB-0021

Genetic Analysis and Evolutionary Relationship of *ALK* (*Starch Synthase II-3*) Gene in 475 Rice Accessions

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Eating and Cooking Quality (ECQ) is essential in evaluating rice quality. One main parameter of ECQ, Gelatinization Temperature (GT), is controlled by the *ALK* gene, which encodes a putative soluble starch synthase called II-3 (*SSII-3*) in chromosome 6 of rice. Analyses on genetic diversity, as well as its evolutionary relationships and its carrying gene among the diverse groups of origin, are crucial. In this investigation, we used 475 different rice accessions belonging to different subgroups of origins and then performed bioinformatic analyses on their variations in resequencing, haplotyping and characterizing. The results indicated that there were, in total, 32 non-synonymous SNPs by five different exons of chromosome 6. There were, in total, 70 haplotypes, of which haplotypes 1, 7, 37 and 38 showed the highest accumulation of rice accessions, and then Hap-37 and Hap-38 were present only for cultivated rice accessions. As for *FST* values, *Temperate Japonica* thoroughly share their genetic characteristics with other subgroups, but *Indica* showed no more subdivisions for this gene (*ALK*) with its *Tropical Japonica* and *Admixture*.

Keywords: *ALK*, GT in starch biosynthesis, genetic relationship, cultivated rice

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PB-0022

Genetic Variations in Haplotype Analysis and Population Structure of *BE1* (*Starch Branching Enzyme 1*) Gene in 475 Rice Accessions

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The starch-branching enzymes (*BEs*) are a part of starch biosynthesis, playing an important role in determining the structural and physical properties of the starch granules, especially amylopectin. *BE* itself has two differently functioning isoforms (*BEI and BEIIa/b*) and they are based on their difference in the chain-length pattern by the degree of polymerization (DP) which mainly contributes to the amylopectin chain length distribution in starch biosynthesis. The gene expression of *BEI* is later in development than that of *BEII* and some cereals and its contribution to amylopectin synthesis is active only in intermediate amylopectin chains. The *BEI* gene divergence was also evolved prior to *BEII* in the monocots and dicots. For the development of genetic works, the diversity and related analyses for this *BEI* gene are crucial for its characterization among the diverse groups of origin. In this investigation, we used 475 rice accessions belonging to different subgroups of origins and then performed bioinformatic analyses on their variations in resequencing, haplotyping and characterizing. The results indicated that there were a total of 33 non-synonymous SNPs by 10 different exons of chromosome 6. There were 43 haplotypes of which many of *Temperate Japonica* rice belonged to the *Reference*-contained haplotype (OS06G0726400) and haplotype 3 (Hap_3) showing the accumulation of most *Indica* accessions.

Keywords: BE1, amylopectin chain length, haplotype analysis, cultivated rice

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PB-0023

Evolutionary Analysis of *Pullulanase* (*PUL*) Gene in 475 Rice Accessions

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Pullulanase (*PUL*) is a debranching enzyme which has seen wide utilization in terms of hydrolyzing the α-1,6 glucosidic linkages in starch, amylopectin, pullulan, as well as related oligosaccharides. This enables a complete and efficient conversion of the branched polysaccharides into small fermentable sugars during the saccharification process. It has also been indicated that PUL is a novel indicator of inherent RS (Resistant Starch) formation in rice. Through this analysis, we specifically studied trait-specific genetic works, genetic diversity, along with other related analyses of the *PUL* gene on 475 rice collected from different origins. Through the course of this investigation, we performed bioinformatic analyses on their variations via resequencing, haplotyping, and the construction of genetic relationships among the groups. The results indicated that there were a total of 33 non-synonymous SNPs by 14 different exons of chromosome 4. There were 63 haplotypes, of which the *Wild* group is obviously implicated in the functioning of their SNPs. A nucleotide diversity (π) and Tajima's D test for this gene exhibited a highter degree of SNPs for the *Wild* group compared to that of other tested groups.

Keywords: *Pullulanase*, resistant starch biosynthesis, genetic distribution, cultivated rice

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PB-0024

Resequencing of 475 Rice Accessions for Their Genetic Linkage and Population Structure of *Starch Synthase IIC* (*SSIIC*) Gene

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Starch synthase proteins in rice are categorized into five classes: *SS* (from *I* to *IV*) and *GBSS* (*I* and *II*). Under this scheme, *SSIIC* (also known as *SSII-1*), one isoform of *SSII* is steadily expressed in root, leaf, and endosperm during the grain filling stage. Like with other *SS* isoforms, *SSIIC* also contributes to amylopectin synthesis during starch biosynthesis. For purposes of familiarizing with genetic information regarding this gene, we investigated 475 rice accessions belonging to different subgroups of origins. We subsequently performed bioinformatic analyses on their variations in resequencing, haplotyping, and structuring based on different groups of the population. The results revealed that there were 53 non-synonymous sites on nine different exons of chromosome 4. Of which 53 haplotypes, many wild accessions are individually separated as their own haplotypes, presenting multiple SNPs. According to nucleotide diversity, the *Wild* group presented the highest values, with the lowest value observed in the *Admixture, and* no variation was observed in the *Aroma* group. It was also revealed that the *Temperate Japonica* group highly shared its genetic characteristics with other subgroups, mostly with *Indica, Tropical Japonica,* and *Aroma* groups.

Keywords: *SSIIC*, starch biosynthesis, genetic distribution, cultivated rice

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PB-0025

Genetic Diversity and Characterization of *SSIIIB* (*Starch Synthase IIIB*) Gene in 475 Rice Accessions

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Starch Synthase IIIB (*SSIIIB*) is the main component of *Starch Synthase* (*SS*) which plays an important role in amylopectin chain length elongation during starch biosynthesis. Despite its two different isoforms (*SSIII-B/A*, mostly used as *SSIII-1/-2*), *SSIIIB* was mainly expressed in the leaves. Its suppression in rice can reduce amylopectin synthesis and consequently contributed to an increase in amylose phenotype. For the development of trait-specific genetic works, genetic diversity and related analyses are crucial, together with its carrying gene characterization among the diverse groups of origin. In this investigation, we used 475 different rice accessions belonging to different subgroups of origins and then performed bioinformatic analyses on their variations in resequencing, haplotyping, and characterizing. The results indicated that there were 20 non-synonymous SNPs in total by 9 different exons of chromosome 4. There were 67 haplotypes, of which more than 58% of *Temperate Japonica* rice belonged to different haplotypes, and most of them (exactly 243 accessions) were in the same haplotype, indicating a statistically non-significant difference with its other subgroups.

Keywords: *SSIIIB*, amylopectin biosynthesis, haplotype network, cultivated rice

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PB-0026

Comprehensive Genome-Wide Association Studies for Lipophilic Phytonutrients in Rice

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We have performed comprehensive genome-wide association studies (GWASs) on lipophilic phytonutrients in rice. We sampled three independent fields of 296 Korean rice core sets. In total, 42 GWASs were performed, and, among the results, the inflation factors of 30 results were within the acceptable range and 3 were ideal. Significantly associated regions were found in four lipophilic phytonutrients. The fact that there are overlapping and nonoverlapping regions of significant candidate regions between lipophilic phytonutrients suggests that some parts of the variance of the content of lipophilic phytonutrients were caused by the same gene.

Keywords: GWAS, Korean rice core sets, lipophilic phytonutrients, rice

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PB-0027

Genetic diversity of *AGPS2* gene isoforms in rice

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ADP-glucose pyrophosphorylase small subunit 2 (*AGPS2*) is an enzyme involved in amylose synthesis during starch biosynthesis. *AGPS2* has 4 gene isoforms (*Os08t0345800-01, Os08t0345800-02, Os08t0345800-03, Os08t0345800-04*). It is important to be aware of gene isoform biogenesis for understanding gene function. To investigate the polymorphisms and genetic distribution of AGPS2, we implemented variant calling by employing a total of 475 resequencings including 54 wild and 421 cultivated rice strains. As a result, gene isoforms of *AGPS2* were confirmed to be a different haplotype. Particularly in *Os08t0345800-01* and *Os08t0345800-02*, non-synonymous SNPs altering amino acid coding were observed. In addition, the *AGPS2* of the gene network was linked via starch and sucrose metabolism. This study suggests that the distribution of gene isoforms of *AGPS2* in Korean rice is expected to be used as an important data point to develop new rice varieties.

Keywords: *AGPS2*, starch, gene network, gene isoform

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PB-0028

Genetic diversity and gene network of *AGPL4* in 475 accessions of rice genetic resources

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ADP-glucose pyrophosphorylase large subunit 4 (*AGPL4*) is an enzyme involved in starch synthesis during starch biosynthesis. We analyzed the genetic diversity of 475 Korean rice genetic resources, including 54 accessions of wild rice. As a result, *AGPL4* was located on chromosome 7, and a total of 38 mutations were confirmed in 16 exons. Particularly in exon 1, a 20 bp mutation was caused by a frameshift mutation. We observed 16 non-synonymous SNPs altering amino acid coding. In addition, the *AGPL4* of gene networks was linked to starch and sucrose metabolism.

Keywords: *AGPL4*, starch, gene network, non-synonymous

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PB-0029

Genetic diversity of *DPE1* in 475 accessions of rice genetic resources

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Disproportionating enzyme 1 (*DPE1*) is the functional gene in storage starch synthesis in rice (*Oryza sativa* L). We performed a mutational analysis of *DPE1* to provide important background data for improving starch quality based on genome information in rice breeding. To investigate the polymorphisms and genetic distribution of *DPE1*, we implemented variant calling using a total of 475 resequencing data including 54 wild rice and 421 cultivated rice. As a result, *DPE1* (*Os07g0627000*) was located on chromosome 7, and a total of 23 mutations were confirmed in 16 Exons. Particularly in exon 1, 6 non-synonymous SNPs altering amino acid coding were observed.

Keywords: *DPE1*, starch synthesis, genetic distribution, cultivated rice

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PB-0030

The genetic diversity and gene network related to starch biosynthesis gene using 475 accessions

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Isoamylase 1 (*ISA1*) is associated with starch synthesis. The mutation of *ISA1* leads to endosperm sugar accumulation. Using 475 accessions of genotype data, we analyzed the genetic diversity and gene network of *ISA1*. As a result, *ISA1* was located on chromosome 8, and a total of 27 mutations were confirmed in 18 exons. In addition, the *ISA1* gene network was linked to the biosynthesis of secondary metabolites. This allowed us to gather information on its genetic diversity, enabling more systematic identification of varieties associated with starch content.

Keywords: *ISA1*, starch synthesis, gene network, diversity

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PB-0031

Genetic diversity of the rice starch synthase gene *SSIIIa* in 475 accessions of rice genetic resources

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Soluble starch synthase *IIIa* (*SSIIIa*) is a key enzyme involved in amylose synthesis during starch biosynthesis. More particularly, *SSIIIa* is double repression of soluble starch synthase. We analyzed the diversity of 475 Korean rice genetic resources, including 54 accessions of wild rice. Our analysis of the *SSIIIa* mutation information found that a large number of mutations exist in *SSIIIa*. Specifically, a total of 104 mutations that alter amino acid coding were confirmed in exon 3. These results suggest that the *SSIIIa* gene could be potential candidate marker for rice functional research and breeding.

Keywords: *SSIIIa*, starch synthesis, amylose, diversity, haplotype

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PB-0032

Genetic diversity and eQTL of *GBSSII* gene in rice

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Granule-bound starch synthase II (*GBSSII*) is an enzyme involved in amylose synthesis during starch biosynthesis. We performed a mutational analysis of *GBSSII* to provide important background data for improving starch quality based on genome information in rice breeding. To investigate the polymorphisms and genetic distribution of the *GBSSII*, we implemented variant calling using a total of 475 resequencing data, including 54 wild rice and 421 cultivated rice. As a result, *GBSSII* was located on chromosome 7, and a total of 39 mutations were confirmed in 14 exons. In addition, the eQTL analysis of the *GBSS II* was conducted using a core group of 297 key clusters of KRICE CORE. Our analysis of the *GBSS II* mutation information found that a large number of SNP and indel mutations exist in the *GBSS II* of the domestic core resource. These findings of *GBSS II* will provide important information for the improvement of new varieties in the future.

Keywords: *GBSSII*, starch, amylose synthesis, eQTL

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PB-0033

Gene-to-metabolite study of *BADH2* with high-throughput analysis for precise fragrance control in rice

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Genomic analysis was performed using next generation sequencing (NGS). It encompassed whole genome resequencing, a total of 475 rice core sets with an average coverage of approximately 10X on the Illumina Hiseq 2000 and 2500 sequencing systems platform (Illumina Inc., USA), the 421 KRICE_CORE, and 54 wild rice. We also combined the KRICE_CORE with 3K RGP (rice genome project by CAAS, BGI and IRRI) of Asian cultivated rice for the haplotyping study. We conducted variant calling for a 475 rice core set, identification of the expression quantitative trait loci (eQTLs) for the *BADH2* gene using RNA-Seqs from 297 rice accessions, the protein levels on the 64 core set using LC-MS/MS the quantitative analysis of 2-acetyl-1-pyrroline (2-AP) contents for 60 rice accessions, and phynotyping for 426 rice accessions. The result exhibited that a total of 58 alleles in the coding region of *BADH2* were detected from the 475 core sets, and the 46 novel alleles among them. The newly identified alleles contained 14 non-synonymous SNPs and deletion leading to functional changes, manifesting in 111 rice accessions. The eQTLs of the Os08g0424500 represented a significant association with the *BADH2* gene, while the metabolites having a relative amount of 2-acetyl-1-pyrroline were consistent with the phenotype of 7 haplotypes in cultivated rice.

Keywords: Next generation sequencing (NGS), Fragrance rice, *BADH2* gene, 2-AP, pQTL, eQTL

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PB-0034

Genetic diversity of the rice fragrance gene (*BADH2*) in diverse wild rice base on DNA chip data

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The wild species of genus *Oryza* is regarded as a valuable resource for rice improvement because of its high genetic diversity. The rice fragrance given off by this species results from a loss in function of the betaine aldehyde dehydrogenase (*BADH2*) gene contained in chromosome 8. In this study, DNA chip data analysis was used to examine a total of 150 wild rice accessions. Single nucleotide polymorphism (SNP) variant sites of 150 wild rice accessions were performed using PowerCore software to discern the functional, novel alleles in BADH2 compared with the Nipponbare genome. A total of 39 haplotypes based on nucleotide polymorphism were detected within the coding sequence of the *BADH2* gene. We discovered 9 fragrance alleles leading to non-synonymous mutations in the coding region, which manifested in 30 wild rice accessions. This discovery of the novel functional *BADH2* alleles and haplotypes will be employed in a *BADH2* diversity study to improve the breeding of new varieties of fragrant rice.

Keywords: Wild rice, *BADH2* gene, haplotype analysis, DNA chip

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PB-0035

Discovery of the novel fragrance alleles and development of functional SNP markers for breeding of fragrant rice

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In the global market, fragrant rice which contributes to 15-18% of the world's massive rice trade has received special attention from rice breeders who take into consideration the fragrance of rice for the main purpose of propagating the commercial varieties of rice. A fragrant trait in rice is mainly controlled by the beta-aldehyde dehydrogenase gene 2 (*BADH2*) on chromosome 8. In this study, the whole-genome sequencing data of 475 rice germplasms reveal *BADH2* in 50 cultivated and 31 wild rice accession numbers. Twenty-six alleles were detected to be non-synonymous in the coding sequence of *BADH2* that presented 112 aromatic rice accessions. Ten of these were known alleles and the remaining sixteen were novel alleles. Furthermore, ten SNP functional markers out of twenty-six alleles were developed, and nine of them distinguished by a tetra primer amplification refractory mutation system-polymerase chain reaction (ARMS-PCR). One of them was discriminated through a Taman probe fluorescent assay in *badh2*-E2-476C>A using the CFX96 Real Time System (Bio Rad). Forty-six accessions were selected to verify the benefit of these markers. The ARMS-PCR technique is fast, low-cost, reliable, and uncomplicated for needy laboratories. However, the Real Time PCR method was also very fast and precise. We recommended it for examining a huge sample, the breeding population and high GC contents in the PCR product will be inexpensive. We expect that these *BADH2* genotyping markers for ARMS-PCR and Real Time PCR will be used for marker-assisted selection (MAS) and the development of hybrid fragrant rice and new fragrant rice varieties through breeding programs.

Keywords: Fragrant rice, *BADH2*, marker-assisted selection (MAS), SNP marker

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PB-0036

Haplotype analysis and genetic study of grain size, GS3 gene, for selection events in wild and cultivated Rice (*Oryza sativa L.*)

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Rice yield potential and quality are partially affected by grain size, weight and shape, which associates with a great number of genes and QTLs. The grain size and shape are significantly associated by excavating single nucleotide polymorphisms (SNPs). GS3 gene is a putative regulator that plays a role in grain size determination. Here, a total of 475 germplasms (54 wild types and 421 cultivated types) were collected from around the world, sequencing with high average coverage (~15.88X) and product ~3.42T raw data. To explore the evolution in rice genetics, artificial selection (π_w/π_c), F_{ST}, population structure, haplotype and phylogenetic analyses are combined in this analysis. We observed 10 haplotypes and H_1 showed that 316 accessions are the same sequence with a reference gene. H_10 was found 1 bp deletion at the position 20839640 and 20841433 in wild type. The changes SNPs (T/G and G/T) at the position, 20839323 and 20839383, in exon 1 were found in both cultivated and wild types. Temperate japonica types are clearly separated from other types in principal component analysis (PCA). In the haplotype network, wild types are clearly separated from other groups. Our finding plays a foundation for further functional validation and breeding utilization.

Keywords: Grain size, haplotype, population structure, rice

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PB-0037

Studies of rice heading date (Hd1) haplotypes reveal adaptation of flowering time in different ecotype groups

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Heading date directly determines planting districts and seasons, and thus plays an important role in the production and introduction of varieties. It is a crucial trait for rice expansion to high latitudes, determined by both genetic factors and environmental cues. Cultivars with an appropriate heading date will be conductive to high grain yield by fully utilizing the light and temperature resources in their growing regions. Here, a total of 475 rice accessions were collected from around the world, sequencing with high average coverage (~15.88X), product ~3.42T raw data and observed haplotype variation for Hd1 gene. We found 54 different haplotypes, including both SNPs and indels sites. Among the different haplotypes, the deletion sites were mostly found (pink color) as opposed to the insertion site (blue color), and the SNPs showed the yellow highlighted color in the haplotype table. Wild types were clearly separated from other differing ecotype groups in the principal component analysis. For the population structure analysis, temperate japonica types were clearly observed in K3, K4 and K7.

Keywords: Heading date, haplotype, Principal component analysis, rice

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PB-0038

Haplotype analysis and genetic study of semi-dwarf 1 gene, SD1, for selection events in different groups of rice (*Oryza sativa L.*)

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Semi dwarfing is one of the most important traits in cereal crops, including rice. The rice semi-dwarf 1 gene (SD1) is well-known as the "green revolution gene." This gene contributed to the significant increase in crop production in the 1960s and 1970s, especially in Asia. Conventional breeding procedures have introduced the SD1 gene. Still, this gene's importance makes the identification of SD1 highly desirable for the efficient production of high-yield crops via genetic engineering. A total of 475 rice accessions were collected from the world sequencing with high average coverage (~15.88X) and product ~3.42T raw data. To explore the evolution and improve rice genetics, artificial selection (π_w/π_c), F_{ST}, population structure, haplotype, and phylogenetic analyses are combined in the analyses. We observed 19 haplotypes, and H-11 and H-12 were found 7 bp insertion in exon 1 at the position, 38382415, in wild type. The changes SNP (A/G) at the position, 38385057, in exon 3 were found in both cultivated and wild types. Japonica types are clearly separated from other types in the principal component analysis (PCA). In the phylogenetic tree analysis, wild types are clearly separated from other groups.

Keywords: semi-dwraf 1, population structure, haplotype, rice

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PC-0001

Overexpression of *OsASR* enhances tolerance to environmental stress and improves productivity by modulating stomatal closure in transgenic rice plants

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Abscisic acid-, stress-, and ripening-induced (*ASR*) genes are involved in responding to abiotic stresses, but their precise roles in enhancing grain yield under stress conditions remain to be determined. We cloned a rice (*Oryza sativa*) *ASR* gene, *OsASR1*, and characterized its function in rice plants. *OsASR1* expression was induced by abscisic acid (ABA), salt, and drought treatments. Transgenic rice plants overexpressing *OsASR1* displayed improved water regulation under salt and drought stresses, which was associated with osmolyte accumulation, improved modulation of stomatal closure, and reduced transpiration rates. *OsASR1*-overexpressing plants were hypersensitive to exogenous ABA and accumulated higher endogenous ABA levels under salt and drought stresses, indicating that *OsASR1* is a positive regulator of the ABA signaling pathway. The growth of *OsASR1*-overexpressing plants was superior to that of wild-type (WT) plants under paddy field conditions when irrigation was withheld, likely due to improved modulation of stomatal closure via modified ABA signaling. The transgenic plants had higher grain yields than WT plants for four consecutive generations. We conclude that *OsASR1* has a crucial role in ABA-mediated regulation of stomatal closure to conserve water under salt- and drought-stress conditions, and *OsASR1* overexpression can enhance salinity and drought tolerance, resulting in improved crop yields.

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PC-0002

Expression analysis of genes associated with sucrose accumulation in mungbean (*Vigna radiata* (L.) Wilczek) leaves after depodding

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Mungbean (*Vigna radiata* [L.] Wilczek), an important source of carbohydrate and protein in Asia, is characterized by nonsynchronous pod maturity; consequently, harvesting is labor intensive. Because pod maturity is associated with synthesis and remobilization of sucrose, we examined changes in sucrose levels and transcriptome in leaf (source) tissues after pod (sink) removal using two genotypes, VC1973A and V2984; VC1973A had higher synchronicity in pod maturity than V2984. After pod removal, much higher number of pods were produced in V2984 than VC1973A. The sucrose content of leaf tissues significantly decreased in V2984 because it continued to utilize assimilates from leaves for producing new pods, but significantly increased in VC1973A because of the loss of sink. Transcriptome analysis revealed that the number of differentially expressed genes was approximately fourfold higher in VC1973A than in those of V2984 after pod removal. The expression of two paralogous genes (*Vradi01g05010* and *Vradi10g08240*), encoding beta-glucosidase enzymes, significantly decreased in VC1973A after pod removal and was significantly lower in depodded VC1973A than depodded V2984, indicating these two genes may participate in sucrose utilization for seed development by regulating the level of glucose. The results of this study will help elucidate the genetic basis of synchronous pod maturity in mungbean and facilitate the development of new cultivars with synchronous pod maturity.

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PC-0003

Screening of soybean genetic germplasm with high sucrose content using a simple enzyme method

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Sugar content in soybean [*Glycine max* (L) Merr.] seed is an important quality attribute for soyfood and soymilk. Rapid extraction and quantification of soluble sugars in soybean seeds are essential for large-scale breeding selections without an instrument such as HPLC. In this study, we used the enzyme method based on the enzymatic reactions of invertase and glucose oxidase (GOD). To extract soluble sugar, 150mg of grounded seeds were added to 1.5ml deionized (DI) water and the mixture was incubated at 50℃ for 15 min hours, respectively. Hydrolyzed glucose was reacted with glucose oxidase (GOD) reagent and absorbance was measured at 490nm wavelength using a spectrophotometer to estimate sucrose content. To verify the colorimetric method, sucrose content was measured with a HPLC-RI. Sucrose contents of 903 soybean accessions were measured by this colorimetric method, and 6 genotypes with more than 8% sucrose content were selected. This colorimetric method is a fast, simple, and inexpensive tool for the quantitative determination of sucrose in soybean.

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PC-0004

Determining factors of Anthocyanin Biosynthesis in Rice Pericarp

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Some rice pericarps exhibit black and brick red color due to the accumulation of anthocyanins and proanthocyanidins, respectively, while these flavonoid pigments are missing in most cultivated rice. Several studies reported that pigmented rice seeds have nutritionally good traits including the accumulation of various phytochemicals, such as phenolics, carotenoids and γ-oryzanols and beneficial effects on human health as antioxidants. Due to the health-promoting properties, enhancing anthocyanin in crops is interesting project for breeders and researchers. Anthocyanins biosynthesis is cooperatively regulated by a conserved MBW (MYB-bHLH-WDR) transcriptional factors (TF) complex. However, the molecular mechanism underlying specific organ pigmentation is not clear.

To investigate the anthocyanin biosynthesis mechanism, we isolated and characterized the MBW TFs. The expression pattern of MYB and bHLH TF except for WDR was correlated well with those of anthocyanin biosynthetic genes. Through the subcellular localization analysis, it confirmed that both of MYB and bHLH were exclusively localized in nucleus, but WDR was found both in nucleus and cytoplasm. Yeast two hybrid assay reveled that bHLH interacted with MYB and WDR. With the steroid receptor-based inducible activation system with rice protoplasts, it confirmed that simultaneous expression of MYB and bHLH TFs can activate the transcript level of anthocyanin biosynthetic genes. Based on the sequence variation in anthocyanin biosynthetic genes, we developed the marker for identifying the pericarp color before seed set. Taken together these results, it revealed that the MYB and bHLH TF identified in this study can control the anthocyanin accumulation in rice pericarp.

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PC-0005

A transcriptional network of anthocyanin biosynthesis in Radish taproot

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Radishes (*Raphanus sativus* L.), belonged to the brassicaceae, are economically important vegetable crops cultivated for producing seed oil and sprouts, as well as edible taproots. They showed the various colors in taproot including white, red, purple and green due to the presence or absence of anthocyanins and/or chlorophylls, respectively. To perform the quantitative real-time PCR with different colored taproots radishes, we confirmed the transcript levels of anthocyanin biosynthetic genes and regulatory genes in all the red radish cultivars. To investigate the anthocyanin biosynthetic mechanism, we analyzed the role of *RsMYB1*, a key regulator for anthocyanin biosynthesis in red radishes. It was confirmed that RsMYB1 ($RsMYB1^N$) derived from red radishes showed the difference at nucleotide sequences RsMYB1($RsMYB1^M$) derived from white radishes. Yeast two hybrid analysis revealed that $RsMYB1^N$ physically interacted with RsTT8, while $RsMYB1^M$ was unable to interact with RsTT8. Transient assay with radish cotyledons and tobacco leaves, respectively, was performed to investigate the anthocyanin biosynthetic mechanism on the roles $RsMYB1^N$ and $RsMYB1^M$. As expected, $RsMYB1^N$ actively induced the transcript level of anthocyanin biosynthetic genes resulting in anthocyanin accumulation, whereas $RsMYB1^M$ did not induce the anthocyanin biosynthetic genes expression and anthocyanin accumulation. Through the promoter activation assay, it confirmed that $RsMYB1^N$ has the function to activate the *RsCHS* and *RsDFR* promoter, but $RsMYB1^M$ did not. Based on the variation between $RsMYB1^N$ and $RsMYB1^M$, we developed the marker for discriminating the taproot color in radishes. Overall, it suggested that RsMYB1 is a key regulator on anthocyanin biosynthesis in radish taproots.

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PC-0006

Evaluate genetic homogeneity between seeds in a genetic resource by genotyping

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Many countries have been making various efforts to secure genetic resources, which are the key materials for agricultural research and development. NAC (National Agrobiodiversity Center) has secured more than 280,000 agricultural genetic resources in Korea. In the era of the genome, it is essential to obtain genotype information about genetic resources to utilize agricultural genetic resources efficiently. However, there is not yet a system for efficiently securing genotype data of the huge number of genetic resources. Therefore, we aim to construct a model system by using 3,300 sorghum genetic resources managed by NAC. As the first step, we evaluated the genetic homogeneity between seeds in a genetic resource by genotyping. 5 seeds for each resource were sown out of 45 sorghum resources determined by the Powercore. As a result, most resources show relatively high genetic homogeneity. For the next two years, we will evaluate over a thousand sorghum resources and the data would be helpful in breeding.

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PC-0007

A High-resolution Bin-map Facilitates QTL mapping of Lodging-related Traits using Milyang23/Gihobyeo Recombinant Inbred Lines (MGRILs)

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Rice (*Oryza sativa* L.) is one of the most important staple crops in the world, and its productivity has been dramatically increased after Green revolution. However, lodging has been a severe problem of reducing yield, grain quality and mechanical harvesting efficiency, and it becomes a major target in rice breeding. In this study, quantitative trait loci (QTL) mapping based on high-resolution map were performed with phenotypes of lodging-related traits, including culm length, panicle length, panicle number per plant, branch number per panicle, grain number per plant, 100-grain weight, stem internode length and diameters (1^{st}, 2^{nd}, 3^{rd}, 4^{th}). In genetic analysis, we resequenced the whole-genome of recombinant inbred lines derived from a cross between Milyang23 and Gihobyeo (MGRILs). To increase the efficiency of QTL mapping, we constructed high-resolution map using sliding window approach in which 3,563 bins were positioned as genetic markers. As a result, a total distance was 1,278.62 cM, and an average of marker density was 0.36 cM among rice chromosomes. A total of 65 QTLs were detected in lodging-related traits, and 22 of them were classified to major QTLs which explained by more than 10% of phenotypic effects. These results showed that the bin-based genetic map was a powerful method for a rapid QTL mapping with high-resolution, and will be helpful for fine-mapping and cloning of significant QTLs/genes.

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PC-0008

Prediction accuracy of genomic selection using core SNP sets for fruit traits in cultivated tomato (*Solanum lycopersicum* L.)

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Genomic selection (GS) is an efficient breeding strategy for genetically complex traits to increase genetic gain per breeding cycle. Advances in high-throughput genotyping technologies with genome-wide SNPs have facilitated GS in crop species. The present study was conducted to optimize GS for seven fruit traits including Brix, height, width, shape index, weight, locule number, and pericarp thickness in cultivated tomato. A collection of 162 breeding lines with diverse genetic backgrounds was used as a training population. We evaluated phenotypic variations of these traits in this population in field trials with three replicates over two years. For genotyping, the 51K Axiom^{TM} tomato array was used and a total of 49,960 SNPs were detected across 12 chromosomes. Of these, 34,550 SNPs were filtered based on the minor allele frequency and missing data rate for calculating genomic estimated breeding values (GEBVs) with the Ridge Regression model. The correlation coefficients between GEBVs and observed phenotypes ranged from 0.612 (Brix) to 0.872 (pericarp thickness) for the 34,550 SNP markers. A subset of 48 SNP markers associated with QTL for the fruit traits showed correlation coefficients of 0.601 (Brix) to 0.835 (pericarp thickness). Furthermore, similar levels of correlations (0.639 to 0.861) were found with another subset of 96 SNP markers including additional QTL with minor effects, suggesting that the use of QTL-associated markers is a cost-effective approach to increase prediction accuracy of GS. The results from this study can accelerate the development of a GS pipeline for improving fruit traits in tomato breeding programs.

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PC-0009

Development and Application of *Indica-Japonica* SNP marker sets using Fluidigm System in Rice

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Molecular markers are efficient and essential genotyping tools for molecular breeding and genetic analysis of rice. We developed two 96-plex *indica-japonica* single nucleotide polymorphism (SNP) genotyping sets for genetic analysis and molecular breeding in rice using the Fluidigm platform. Informative SNPs between *indica* and *japonica* were selected from SNP data of the Rice Diversity database, HapRice world SNP data of the Q-TARO database, and our 40 rice cultivar resequencing dataset. SNPs in set 1 were evenly distributed across all 12 rice chromosomes at a spacing of 4 - 5 Mb between adjacent SNPs. SNPs in set 2 mapped to the long genetic intervals in set 1 and included 14 functional or linked SNPs in genes previously cloned and associated with agronomic traits. Additionally, we used the SNP sets developed in this study to perform genetic diversity analysis of various cultivated and wild rice accessions, construction and validation of a subspecies diagnostic subset, linkage map construction and quantitative trait locus (QTL) analysis of *japonica* × *indica* F_2 population, and background profiling during marker-assisted backcrossing. Furthermore, we identified subspecies-specific SNPs and discuss their distribution and association with agronomic traits and subspecies differentiation. Our results indicate that these subspecies-specific SNPs were present in wild rice prior to domestication. This genotyping system will serve as an efficient and quick tool for genetic analysis and molecular breeding in rice.

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PC-0010

Identification of a locus conferring compound raceme inflorescence in mungbean (*Vigna radiata* (L.) R.Wilczek)

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A compound raceme inflorescence is common in leguminous species including mungbean (*Vigna radiata* [L.]). To improve yield-related traits in mungbean, understanding genetic basis of the compound raceme is necessary. Therefore, the present study was performed to identify a locus controlling the compound raceme in mungbean. We first identified a natural mutant IT208075 showing a simple raceme having no secondary inflorescence and branch and developed a recombinant inbred line (RIL) population of VC1973A (compound raceme) x IT208075 (simple raceme). An observed segregation ratio of compound and simple racemes fitted to a Mendelian 1:1 ratio in the population, indicating a single gene controlling the compound raceme, designated as *Comraceme*. Using a genotyping-by-sequencing-based genetic map, *Comraceme* was located at Chr4_26997427… Chr4_27545988 on chromosome 4, spanning 520 kb containing 55 genes with function annotations. Besides, ten RILs carrying heterozygous fragment around *Comraceme* showed the compound raceme, indicating that *Comraceme* is dominant. *Comraceme* also had syntenic relationships with soybean QTLs associated with inflorescence-related traits. Among several development-related genes with sequence variations between the mapping parents, *Vradi04g00002481* encoding an B3 DNA-binding domain transcription factor only had two insertions in the upstream region, specific to IT208075 and different from VC1973A and two other genotypes. From the shoot apical tissue, *Vradi04g00002481* was upregulated in VC1973A and IT208075 at the early and late vegetative stages, respectively. Based on these results, *Vradi04g00002481* is likely a candidate gene responsible for the compound raceme. Our findings provide valuable genetic resources to develop mungbean cultivars with desirable yield traits relevant with inflorescence architecture.

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PC-0011

A Mechanism to trigger the immune response in *Arabidopsis thaliana* against *Pseudomonas syringae* pv. *actinidiae* NZ V13 type III secreted effector HopF4b

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Plant recognizes the invasion of phytopathogenic microbes in both direct and indirect ways. Plant harbors disease resistance (*R*) genes, which play a key role to recognize the existence or activity of the effector protein injected from pathogen through type III secreted system (T3SS). The successful recognition of the effector by R protein results in an immune response, such as hypersensitive response (HR).

A type III effector HopF4b from *Pseudomonas syringae pv. actinidiae* NZ V13 triggered HR in *Arabidopsis* Ct-1, but not in Col-0. Likewise, the bacterial growth of *Pseudomonas syringae* pv. *tomato* DC3000 carrying HopF4b was restricted in Ct-1, but not in Col-0. This result indicates that Ct-1 can recognize HopF4b and trigger the immune response which lacks in Col-0.

To map the corresponding genetic locus, we will use the F2 population and the Recombinant Inbred Lines (RILs) between Ct-1 and Col-0. Once the HR-responsible locus becomes clear, NLR genes in this region will be tested as a primary candidate.

Finally, this study aims to elucidate the mechanism mediating HopF4b recognition in *Arabidopsis thaliana* Ct-1.

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PC-0012

Identification of transcription factors involved in triacylglycerol biosynthesis

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During the seed development, triacylglycerol (TAG) is accumulate in cotyledon. The TAG is used as an energy source for seedling development in germinated seeds. Complex network of transcription factors (TFs) regulate genes involved in TAG biosynthesis. LEAFY COTLYLEDON 2 (LEC2) is the master regulator in TAG biosynthesis. LEC2-downstream TF networks in the process of TAG synthesis has not been study well. In this study, we identified 25 seed-specific TFs that are upregulated by LEC2. To identify novel transcription factors that regulate TAG or fatty acid biosynthesis in LEC2 regulatory network, each of 25 seed-specific candidate TF has been transforming to overexpress in tobacco leaf using *Agrobacterium* infiltration. Qualitative and quantitative analysis of TAG and fatty acid in transformed leaf are underway by thin layer chromatography (TLC) and gas chromatography (GC) to see if each TF can induce TAG and fatty acid synthesis. The discovery of novel TFs that regulate the synthesis of TAG or fatty acid can be usefully used to enhance the oil content of plants.

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PC-0013

Genetic Diversity Analysis of Wild-simulated Ginseng using Simple Sequence Repeat and Insertion/Deletion Markers

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Panax ginseng C. A. Meyer is wild-simulated ginseng (WSG) in Korea which depends on an artificial forest growth method. WSG samples were collected from nine areas in Korea. After polymerase chain reaction (PCR) amplification using the primer pair labeled with fluorescence dye (FAM, NED, PET, or VIC), fragment analysis were performed. PCR products were separated by capillary electrophoresis with an ABI 3730 DNA analyzer. From the results, WSG cultivated in Korea showed very diverse genetic background. In this study, we tried to develop a method to discriminate between WSG using 8 simple sequence repeat (SSR) and 12 insertion/deletion (InDel) markers. Furthermore, we analyzed the genetic diversity of WSG collected from nine cultivation areas in Korea. These results could be used for further research on cultivar development by using molecular breeding techniques and for conservation of the genetic diversity of *P. ginseng*.

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PC-0014

Phyllotaxis derived phenotypic makers for high throughput phenotyping (HTP) data analysis

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High throughput phenotyping (HTP) data are generating enrich information of plant physical description at any given time point. However, many HTP studies were utilized single dimension data such as projected area (PA) from obtained plant images were to study traits of interests. There were abundant morphological variation in natural population and it cannot be explained with only PA. We collected and analyzed of wild *Lactuca* species known as "*Lactuca denticulata*" with next generation sequencing (NGS) to separate different population structures. Phyllotaxis describing arrangements among plant organs is a new concept among plant breeders. Previous studies in *Arabidopsis* discovered that phyllotaxis is associated with multiple genes Virus-infected *Arabidopsis* showed statistically different rosette shapes with HTP. Also, multiple genes control the leaf angles of crops. Hence, we applied phyllotaxis derived phenotypic markers to separated collections of wild *Lactuca* species. In result, each collection separated with phyllotaxis derived phenotypic markers. The result indicated that effectiveness phyllotaxis marker to study population in the post-genomics era.

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PC-0015

Transcriptome sequencing of onion(*Allium cepa* L.) to develop SNP marker set

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Onion (2n=2x=16) is an economically and nutritionally important vegetable crop worldwide and is widely cultivated. The molecular genetic information of onion is insufficient to develop effective markers for agronomic traits because of large genome size. Among other types of molecular markers, SNP (single nucleotide polymorphism) is mostly used in genetic diversity analysis due to its abundance and accuracy. To search a useful set of SNPs, we performed transcriptome sequencing using Illumina Nextseq500. In toal, 30 onion lines were constructed using lines developed in the National Institute of Horticulture and Herbal Science and breeding company. The average of short reads mapping rate was about 90.73%. We identified 1,515,410 SNPs by aligning contigs of 30 onion lines. Among the total SNPs, 68 SNPs were selected based on the stringent filtering parameters such as genotype and allele, segregation ratio (1:2:1), distinguishable species (1:1), single copy number, polymorphism information content (PIC~0.5) value, adjacent SNPs (60 bp). To validate the SNP markers, genotyping and phylogenetic analysis of 30 lines were performed. Thus the markers designed in the present study can be employed to identify onion germplasm resources and to accelerate onion molecular breeding.

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PC-0016

Gene expression analysis of sweetpotato putative genes in response to *Fusarium oxysporum*

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Fusarium wilt disease caused by the fungal pathogen *Fusarium oxysporum* f. sp. *Batatas*, is widespread in sweetpotato production areas in Korea. The symptoms on sweetpotato plants include wilting, leaf yellowing and browning of vascular tissues in the lower stems. Development of disease-resistant varieties is a crucial goal of sweetpotato breeding. However, studies on the identification of *F. oxysporum* resistance-related genes in sweet potatoes have been rarely conducted and the mechanism of disease resistance is not clear. This study was carried out to assay the disease severity index of fusarium wilt by rapid screening method via hydroponic system in sweetpotato. The disease severity index was varied according to cultivars. Three cultivars, 'Pungwonmi', Shingeonmi and Yeseumi, were resistant, while Annobeni were susceptible. To gain insight into the cause-and-effect on different furarium wilt symptom between sweetpotato cultivars, we compared the expression of genes (include *NAC*, *MYB*, resistance (*R*) genes, pathogenesis-related (*PR*) genes and genes involved in the salicylic acid (*SA*) and jasmonic acid (*JA*) signaling pathways) related in the disease response to fusarium wilt. Among them, *PR10*, *R-1* gene, *JA* and *SA* signaling gene were significantly up-regulated in the resistant cultivars 'Singeonmi' and 'Pungwonmi', respectively. These data can be used to understand the molecular mechanisms of disease resistance and will contribute to the development of sweetpotato with fusarium wilt resistance.

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PC-0017

Development of fluorescence-based SNP markers for identification of Korean wheat cultivars

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The hexaploid common wheat (*Triticum aestivum*), one of 3 worldwide staple food crops, has a large genome size of about 17 Gbp that makes genome identification difficult. Demand for domestic wheat cultivars is increasing, but cultivation cannot satisfy demand for wheat processing due to the admixture of cultivars. To increase the use of domestic cultivars and thus improve the domestic wheat industry, we developed a new cultivar identification system based on fluorescence signals to analyze multiple samples efficiently and reliably. We obtained complete chloroplast genome sequences of 7 major Korean wheat cultivars using NGS analysis. Based on comparative analysis with 14 wheat cultivars registered in NCBI, 4 SNPs were identified for the classification of 7 major cultivars. Additionally, we used the wheat genome SNP database (https://www.cerealsdb.uk.net/cerealgenomics/CerealsDB/) to select 902 SNPs among 93,363 SNPs by filtering out single-copy nuclear genome regions to avoid paralogous targets and tested 32 SNPs using Allele-specific-PCR (ASP) markers. As a result, we developed fluorescence-based qualitative markers (Taqman) from 5 nuclear- and 2 chloroplast-derived SNPs that show diversity among 7 major cultivars, applied them to 35 domestic cultivars using Real-Time PCR, and confirmed that 7 major cultivars clustered into 6 groups. By developing additional SNP-based markers, we will establish a high-throughput identification system of Korean wheat cultivars.

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PC-0018

Design and characterization of 50K SNP chip array for Genomic Selection of Korean Red Pine (*Pinus densiflora*) Trees

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Pinus densiflora (Korean red pine) is a species of evergreen conifer that is distributed in Korea, Japan, and China, and of economic, scientific, and ecological importance. The National Institute of Forest Science has made great efforts in Korean red pine breeding for the past 60 years. Nevertheless, we still have a lot of challenges to solve the limitation of tree breeding which takes a lot of time and labor. In order to overcome of these limitations, we are attempting a new paradigm tree breeding method by integrating NGS big data and ICT. Genomic Selection (GS) is one of the accelerating breeding methods. With the advent of high throughput molecular technology, numerous molecular markers distributed throughout the whole genome can be developed to characterize many genetic entries involving new perspectives in methodology of selection. In tree breeding the GS could significantly reduce the cost of genetic improvement schemes by limiting the size and number of field experiments. In this study, we used 5,228 trees of 46 half-sib F1 families from 6 environments in Korea and we got 97,647 SNPs via GBS (Genotyping by Sequencing). And then, we designed the high-resolution DNA chip (200K chip) to validate whole SNPs. Finally, we selected and produced the 50K SNPs chip for genotyping of Korean red pine trees. Now, we are preparing to analyze 4,412 trees which are confirmed the pedigree. We expect that the red pine SNP chip will make a great contribution to shortening the tree breeding period. In addition, it may be useful for early selection and development of disease-resistant bio-markers.

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PC-0019

RNA-seq analysis of poplar (*Populus alba* × *P. glandulosa* and *Populus euramericana*) in response to elevated CO_2 concentration

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The present research was conducted to investigate the transcriptome change of *P. alba* × *P. glandulosa* hybrid poplar clone (Clivus) and *Populus euramericana* clone I-476 in response to elevated CO2 concentration. The impact of CO2 concentration on poplar is not clearly understood because of the experimental difficulties in accomplishment of long-term CO2 treatment. To study the effect of elevated levels of ambient CO_2 on poplar, three open-top chambers (OTCs) were utilized. We analyzed the differences in the transcriptomes of *P. alba* × *P. glandulosa* hybrid poplar clone (Clivus) and *Populus euramericana* clone I-476 using high-throughput RNA sequencing techniques and elucidated the functions of the differentially expressed genes. Plants were grown at ambient (400 ppm) and elevated CO_2 concentrations (1.4 × ambient CO_2, 560 ppm and 1.8 × ambient CO_2, 680 ppm) during 16 weeks in OTCs. We obtained 272,355 contigs and identified 207,063 unigenes by Trinity transcriptome assembly. Differential expression analysis identified 2,477 induced and 1,285 repressed genes in the leaves by elevated CO_2. Elevated CO_2 decreased the expression of genes related to Golgi membrane, zinc ion binding and lipid localization, but enhanced the expression of heat shock protein, oxidative stress related genes and starch synthase. We also identified 49,467 and 41,826 potential specific simple sequence repeats (SSRs) from the transcriptome of Clivus and I-476, respectively. These results give valuable information for tree improvement program under climate change.

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PC-0020

콩나물 대량검정을 위한 20립 종자 콩나물 재배 및 특성 평가방법

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경상남도 밀양시 점필재로20 국립식량과학원 남부작물부 밭작물개발과

콩나물용 콩 품종개발 시 콩나물 특성을 평가하는 것은 중요한 선발 지표가 된다. 그 이유는 유전형에 따라 발아특성과 콩나물 생육 특성이 다르기 때문이다. 하지만 일반적으로 콩나물 재배특성을 평가하기 위해서는 다량의 종자가 소요되어 평가 규모가 제한적이고 종자 생산량이 확보되기 전인 저세대 및 다량의 유전분석 집단 등 대량검정에는 어려움이 있다. 본 실험은 최소량의 종자로 콩나물 재배특성을 평가하기 위한 방법을 개발하기 위해 수행되었다. 선행연구에서 10립, 20립 30립 재배 및 300g으로 재배한 경우를 비교하였을때 20립 평가 시 300g 재배와 차이가 가장 적은 것으로 분석되었다. 2년간(2019년~2020년) 22종의 소립 나물용 품종을 시험재료로, 20립 및 300립, 각 3반복으로 콩나물을 재배하여 전장, 배축장, 근장, 배축굵기, 부패립, 경실립, 미발아립, 수율을 조사하고 상관관계를 분석하였다. 20립 재배는 50ml 팔콘튜브를 사용하였으며 300립 재배는 플라스틱 박스를 사용하였다. 콩나물 재배는 4시간 침종 후 암실에서 수온 및 기온 20±1℃에서 매 4시간마다 관수하여 5일간 재배하였다. 분석 결과 20립 재배 및 300립 재배간 상관계수가 전장 0.91***, 배축장 0.91***, 근장 0.86***, 배축굵기 0.01ns, 부패율 0.68***, 경실율 0.35ns, 미발아율 0.06ns, 콩나물 수율 0.85***로 분석되었다. 종자 립수를 파악하는 경실립, 미발아립은 시료 채취에 따라 그 변이가 편중될 수 있어 상관관계가 낮은것으로 생각되었으나, 콩나물의 외관 특성과 무게를 나타내는 수율은 그 상관계수가 높아 콩나물 재배특성 평가에 20립 방법을 활용할 수 있을 것으로 생각된다.

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PC-0021

국내 육성 벼 300품종의 호남지역 도열병 저항성 연차 간 변이 분석

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전라북도 완주군 이서면 혁신로 181 국립식량과학원

본 연구는 1982년부터 2017년까지 국내에서 육성된 벼 300품종의 도열병 저항성을 2018, 2019년 전주, 남원에서 측정한 후, 연차 및 지역별 균주 변이에 따른 저항성 반응의 차이를 연구하기 위하여 수행하였다. 잎도열병 유묘검정은 농촌진흥청 표준분석기준법에 의거하여 강(1~3), 중(4~6), 약(7~9)으로 실시하였다.

2018년에는 국립식량과학원 본원(완주) 및 운봉시험지(남원)에서 각 7월 6일, 6월 26일 파종하였고, 8월 7일에 검정하였다. 파종 후 검정일까지 누적평균기온은 각 1,015.7℃, 1,173.8℃, 누적합계일조시간은 320.4, 322.9시간이었다. 2018년도 도열병 저항성 검정결과는 다음과 같다. 300개 품종 중 완주에서는 31%(92개), 남원에서 48%(145개)가 도열병에 강한 저항성을 보였다. 자포니카 품종의 잎도열병 저항성 평균은 완주, 남원지역별로 5.36, 4.08이었고, 통일형 품종은 각 1.76, 1.95로써 도열병 저항성이 유의하게 약하였다($p<.001$, Tukey). 특히, 통일형 품종은 지역 관계없이 안정적으로 도열병 저항성에 강하였다.

통일형 품종들은 안정적인 잎도열병 저항성을 보였다 완주조생종이 중생종, 중만생보다 도열병 저항성에 강한 경향을 보였다.

2019년에는 완주, 남원에서 각 7월 1일, 6월 24일 파종하였고, 8월 7일, 8월 9일에 검정하였다. 파종 후 검정일까지 누적평균기온은 1,051.7℃, 1128.4℃ 누적합계일조시간은 218.6, 240.0시간이었다. 2019년도 도열병 저항성 검정결과는 다음과 같다. 300개 품종 중 완주에서는 64%(192개), 남원에서는 76%(230개)가 도열병에 강한 저항성을 보였다. 완주에서는 조생종이(도열병 저항성 평균 : 2.6) 중생종(4.0), 중만생종(4.5)보다 도열병 저항성에 강한 경향을 보였으나($p<.001$, Tukey), 중생종과 중만생종의 도열병 저항성은 유의한 차이를 보이지 않았다. 남원에서는 조생종(2.0)이 중생종(3.6)에 비해 유의하게 도열병 저항성이 강하였으나, 중만생종(3.1)과 큰 차이를 보이지 않았다.

2018년과 2019년 국내 육성 300품종의 도열병 저항성은 연차 간으로 유의한 차이가 있었다($p<.001$). 조생종은 중생종, 중만생종에 비해 연차・지역에 비교적 안정적으로 도열병 저항성에 강한 것으로 나타났고, 2018년도에는 중생종이 중만생종보다 도열병 저항성에 강한 경향을 보였으나 2019년도에는 큰 차이를 보이지 않았다. 호남지역에서 뿐만이나라, 중부, 영남지역에서의 도열병 저항성 평가결과를 종합적으로 분석하여 지역 및 연차 간 도열병 균주의 변이를 모니터링하고, 이를 도열병 저항성 품종 육종에 기여할 것으로 기대한다.

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PC-0022

Expression of Curculin, a New Type of Alternative Sweetener in Transgenic Rice

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Sweet tasting and taste modifying proteins are the natural alternative to flavor enhancers and artificial sweeteners. Curculin is a unique protein, which has both sweet tasting and taste modifying properties. In this study, pinII Ti plasmid vector was constructed with curculin gene, where the gene encoding curculin protein was placed under the control of the duel cauliflower mosaic virus 35S (2× CaMV 35S) promoter into rice (*Oryza sativa* L. var. Japonica cv. Dongjinbyeo) by *Agrobacterium*-mediated transformation to generate transgenic plants. Here, twenty-six plant lines were regenerated and the transgenic rice plant lines were confirmed by different molecular analysis. The genomic PCR result revealed that all of the plant lines were transgenic. The single copied and intergenic plant lines were selected by Taqman PCR analysis and FST analysis, respectively. Expression of curculin gene in transgenic rice resulted in the accumulation of curculin protein in the leave. The transgenic lines obtained in next generation, where curculin protein was also accumulated in the plant leave. Sensory analysis result suggested that the curculin protein expressing transgenic lines exerted both sweet and taste modifying activities. These results demonstrated that curculin was expressed in transgenic rice plants.

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PC-0023

QTL analysis for Cold induced Yellowing Tolerant at seedling stage using 93-11/ Milyang352 doubled haploid(DH) lines in rice

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Seedling of rice is easily damaged to low temperature and results in yellowing, growth retardation, reduced tiller, which can cause severe yield losses. Especially rice, *Indica* varieties, is a highly sensitive to low temperature below 15-20℃ because of originating from tropical or subtropical climates. So, this study was the rice doubled haploid(DH) lines derived from cross of *indica* cultivar 93-11 and *japonica* line Milyang352 were used in genetic mapping and QTL analysis studies of cold induced Yellowing Tolerant (CYT). We used 234 polymorphic SNP markers in the whole genome region including 100 KASP markers and 134 Fluidigm markers to build genetic map. We observed cold phenotype of 128 DH population in cold screening test facility at Chuncheon Branch. And then, chlorophyll content of this population was measured from these rice seedlings. For observation of cold tolerant phenotype of DH population in cold screening test facility, we treated cold stress by 13℃ water for 10 days when seedling stage of 3 leaf base. QTL analysis was performed with QTL IciMapping program. We named QTLs as and Cold induced Yellowing Tolerant (CYT) in cold screening test facility. Two major QTLs for CYT was detected on chromosome 2 and 10. Among these QTLs, *qCYT10* on chromosome 10 showed 29.3 LOD score with 59.1% of phenotypic variation. *qCYT10* on chromosome 10 was identified in the facility experiment on both 2018 and 2019. These results may provide useful information for a marker-assisted breeding program to improve cold tolerance in rice.

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PC-0024

Identification of new mutant alleles of *AUGMIN* subunits broadens a spectrum of AUGMIN function during sexual reproduction in Arabidopsis.

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In flowering plants, production of functional gametophytes is prerequisite for double fertilization that leads to successful proliferation. Pollen grains as male gametophytes in *Arabidopsis thaliana* are uniquely patterned with two sperm cells inside a vegetative cell. To better understand genetic regulation underlying the pollen development, we morphologically screened the DAPI-stained mature pollen in a mutant population generated in this study. As a result, we identified two independent lines, *AL318* and *AL434,* exhibiting similar mutant phenotypes regarding nucleus number and pollen pattern. Genetic analysis showed that the two mutants are maintained in heterozygotes but not in homozygotes due to highly reduced genetic transmissions from both sexes. Developmental analysis revealed that mutant microspores at polarized stage either completely fail to enter pollen mitosis I or abnormally divide with altered division asymmetry, resulting in mature pollen without the male germline. We found that the defects arise from genetic lesions in *AUG2* and *AUG4* genes, members of AUGMIN complex that mediates microtubule (MT)-dependent MT nucleation in broad species. Collectively, our study provides genetic evidence that AUGMIN complex plays critical roles not only in correct execution but also in mitotic entry for pollen mitosis I, broadening a spectrum of AUGMIN function during sexual reproduction in Arabidopsis.

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PC-0025

STICKY GERM CELL suppresses callose deposition in newly forming germ cell to ensure the germ cell internalization and differentiation during pollen development in Arabidopsis

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Double fertilization in flowering plants that occurs between male and female gametophytes located in distance is facilitated by a unique pattern of the male gametophyte (pollen) - two sessile gametes (sperm cells) within a vegetative cell producing a pollen tube. In a morphological screen to elucidate genetic control governing this strategic patterning of the pollen, we isolated a heterozygous *sticky germ cell* (*sgc*) mutant that dehisces abnormal pollens with the germ cell immobilized at the pollen wall. Detailed analyses revealed that the *sgc* allele is specifically detrimental to pollen development causing ectopic callose deposition that impedes separation and differentiation of the germ cell. We identified the *SGC* gene to encode a highly conserved domain of unknown function 707 gene that is broadly expressed but germline-specific during pollen development. In addition, transgenic plants co-expressing fluorescently fused SGC and known organelle markers showed that SGC is detected in the endoplasmic reticulum, Golgi apparatus and vacuole. Interestingly, a yeast-two-hybrid screen with a SGC bait identified a thaumatin-like protein gene we termed GCTLP1 of which some homologues are reported to bind and/or digest β -1,3-glucan, a main constituent of callose. Moreover, GCTLP1 is expressed in a germline-specific manner and co-localized with SGC during pollen development, further supporting the GCTLP1 as a putative SGC interactor. Collectively, we report that SGC suppresses callose deposition in newly forming germ cell, thereby ensuring the germ cell to be internalized into the vegetative cell and correctly differentiated probably in conjunction with the GCTLP1 function during pollen development in Arabidopsis.

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PC-0026

Development of SNP chips for efficient breeding in *Panax ginseng*

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Ginseng (*Panax ginseng*) has been used as a representative medicinal herb in Korea. However, due to the long cultivation period up to harvesting and slow growth rate, developing useful genetic tools for efficient ginseng breeding is desperately needed. Ginseng has undergone whole genome duplication events which leads to its allotetraploid nature. Therefore, molecular markers need to be developed by exploring single copy regions to avoid misinterpretations caused by paralogous sequences. Genotyping-by-sequencing method was used to reduce genome complexity and to analyze various genetic resources. Multiple SNPs were discovered and high-quality SNPs that existed in single copy regions within the genome were selected. After filtering processes, 144 informative SNPs were filtered out and 3 SNP chips were designed. They were applied to 92 ginseng breeding accessions for final verification and selection of 131 SNPs that were separated into three sets of 48 x 48 Fluidigm SNP chip based on genome-wide distribution of SNPs. In conclusion, this is the first case of SNP chip development in ginseng and can be used in various fields such as cultivar breeding, seed purity testing, and classification of domestic ginseng resources.

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PC-0027

Genome-wide analysis of late pollen-preferentially expressed genes and identification of segregation distortion lines in rice

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Understanding the pollen development in cereal crops is a major key component for maintaining and increasing crop production and responding to climate change. We identified 627 late pollen-preferentially expressed genes using the public transcriptomes database (http://www.ncbi.nlm.nih.gov/geo/). To identify the functions of these genes, we performed genotyping analysis and evaluated the functions using the 200 T-DNA insertion mutant lines in rice. We obtained 17 segregation distortion lines including 1:1:0 segregation (wild type: heterozygote: homozygote) and less homozygote lines. We selected five segregation distortion lines for further study. In addition, we also utilized the CRISPR/Cas9 system and generated primary 20 transgenic plants per line to confirm the phenotype of five segregation distortion lines. We will perform sequence analysis of transgenic lines to identify the homozygous plants and evaluae the gene functions.

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PD-0002

Bulk segregant analysis (BSA) for leaf and seed related traits in *Perilla frutescens* using SSR markers

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In this study, bulk segregant analysis (BSA) was performed to detect simple sequence repeat (SSR) markers associated with leaf- and seed-related traits in *Perilla frutescens*. We detected 18 SMTAs involving 12 SSR markers associated with the six phenotypic traits. The four SSR markers (KNUPF15, 21, 29, 60) were associated with leaf surface color (LC), and four SSR markers (KNUPF11, 15, 21, 60) were associated with reverse side leaf color (RLC). Moreover, the five SSR markers were associated with seed related traits. KNUPF11 and 29 were associated with seed coat color (SCC), while KNU29 was associated with seed size (SS). KNUPF12, 16, 42 markers were associated with seed hardness. Among these significant markers, KNUPF11 and 29 were co-segregated between RLC/SCC and LC/SCC, respectively. To validate significant markers for leaf color and seed related traits, dendrogram of 11 F_3 population, which two bulk groups consist of 6 green/green and 5 purple/purple, was constructed using six SSR markers related LC and RLC traits, and were well clustered into two groups according to their LC and RLC. We also constructed dendrogram using five significant markers associated with seed related traits. 16 F_3 population were relatively clear divided into three groups, and group I and III were only BLS (brown-large-soft) type. Moreover, a total of F_3 population were clearly grouped based on SCC using five significant SSR markers associated with seed related traits. In conclusion, these results may support opportunities to improve crop quality by MAS.

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PD-0003

Genetic variation and association mapping in *Perilla* accessions using seed characteristics and SSR markers

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A total of 38 accessions of cultivated var. *frutescens* and related weedy types were selected for association analysis according to their seed characteristics. Correlation analysis showed that the seed germination rate (SGR) and seed size (SS) combination had high positive correlation coefficients. Genetic diversity analysis was performed on 38 *Perilla* accessions using 29 SSR primers. The average genetic diversity (GD) and polymorphic information content (PIC) value were 0.597 and 0.550, respectively. Moreover, the 38 *Perilla* accessions were divided into two groups in population structure analysis. Association analysis was performed with 29 SSR markers and three seed characteristics in the 38 *Perilla* accessions. This study was detected 6 SSR markers associated with the SGR trait, 8 SSR markers associated with the seed hardness (SH) trait, and 7 SSR markers associated with the SS trait. Among these significant markers, three SSR markers (KNUPF3, 25, 60) were simultaneously associated with the SGR, SH and SS traits. The phylogenetic tree was revealed that accessions of cultivated var. *frutescens* could be clearly distinguished from weedy type accessions of var. *frutescens* and var. *crispa* by using 29 SSR markers. In addition, the selected SSR markers related to the three seed characteristics clearly distinguished accessions of cultivated var. *frutescens* and related weedy types. Therefore, these results are very important for understanding the seed characteristics of cultivated and weedy types of *Perilla* crop, for effectively selecting and utilizing existing germplasm accessions, and for improving the crop seed quality of *Perilla* varieties in breeding programs.

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PD-0004

Increased production of α-linolenic acid and yield in FAD3-1 transgenic soybean seeds

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Soybeans are generally cultivated as economical and nutritious crops in many regions of the world. In addition, Soybean is the main crop used as a source of vegetable oil for human use. Omega 3, an essential fatty acid, is mainly consumed through health supplement and fish. To produce competitive crops, a transgenic soybean with high a-linolenic acid content was developed using the *PfFAD3-1* gene isolated from Resquerella. *PfFAD3-1* gene was introduced into soybean by *Agrobacterium*-mediated transformation method. *PfFAD3-1* gene and T-DNA insertion were identified by using PCR, qRT-PCR and Southern blot analysis. Moreover, the expression of the transgene was confirmed by RT-PCR. The content of α-linolenic acid in the transformed seeds (T_2) was confirmed by gas-chromatography analysis, and it was measured 4-times higher than wild type soybean seeds.

Agronomic characters of 6 transgenic lines (T_2) with high α-linolenic acid content were investigated in the GMO field. As a result, the yield was improved in harvested T_3 seeds with increased size. Flanking sequence analysis is also in progress by selecting 6 lines with superior phenotype and α-linolenic acid content among T_3 generations.

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PD-0005

식감을 저해하는 고구마 섬유질 표준 분석법 확립을 위한 조건 탐색 및 국내 주요 품종의 섬유질 특성 평가

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고구마는 환경적응성이 뛰어나 다양한 지역에서 재배가 가능하며 단위면적당 생산량이 높아 주요 식량자원으로 이용되고 있다. 국내에서 고구마는 주로 식용으로 이용되기 때문에 식감과 당도가 주요한 품종 선발 지표가 되고 있다. 고구마 품종의 주요 문제점 중 하나는 괴근에 발생하는 섬유질이며 조리 시 육질의 식감을 저해한다. 또한 괴근에 발생한 섬유질은 식감 뿐 아니라 가공 품질을 저해하기 때문에 고구마 판매에 부정적인 영향을 미치고 있다. 이러한 고구마 섬유질 발생을 줄이기 위해서는 섬유질 발생원인 구명과저감기술 개발이 필요하다. 본 실험에서는 먼저 고구마 섬유질을 분리할 수 있는 표준 분석 방법을 확립한 뒤, 주요 품종별로 특성 평가를 진행하였다. 고구마 섬유질의 분석 조건으로 마쇄 시간, 효소 처리 유무, 세척 횟수 등을 확인하였다. 결과적으로 막자사발을 이용하여 2분간 마쇄하고 2L씩 3회 세척한 뒤 amylase 처리를 통한 섬유질 분리방법이 적절하다고 판단되었다. 또한 섬유질 간이 분석을 위해 생고구마를 수직으로 절단한 후 Phloroglucinol-HCl을 처리하여 염색된 부분의 면적을 촬영하고 분석하였다. 수동측정(manual)과 프로그램(‘Image J’)을 이용한 염색부위 면적 계산 시 측정값의 차이 오차범위 5% 이내로 적어 Phloroglucinol-HCl처리와 ‘Image J’ 프로그램을 활용한 섬유질 측정방법이 신뢰성 높은 간이 분석법임을 확인 할 수 있었다.

본 실험결과는 고구마 섬유질 분석 체계 확립에 필요한 기초자료로 사용될 것이다. 또한 품종 및 재배환경에 따른 고구마 섬유질 특성 파악에 활용될 수 있을 것이다. 향후 고구마 섬유질 발생양상 구명하고 이를 통해 섬유질 저감 기술이 개발된다면 고품질 고구마 생산에 기여할 수 있을 것이다.

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PD-0006

Sterilization and pre-inoculation of soil provide a prerequisite for consistent screening of *Fusarium* wilt disease resistance

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A soil-borne fungus *Fusarium oxysporum f. sp. sesami* (*Fos*) is one of major pathogens that hamper sesame cultivation in Korea. The screening of plant materials is a prerequisite for discovering resistant genotypes, disease resistant genes or molecular markers. Although various screening methods for *Fusarium oxysporum* species have been suggested, the soil treatment as well as the inoculation timing effects on the disease proliferation speed is not well characterized. Therefore, this study is designed to assess the variability of the wilt disease incidence following the soil preparation type and the inoculation timing. The experiment was set with 4 soil preparations, *viz.* sterilized and pre-inoculated soil (7 days before transplantation), sterilized and transplantation-day-inoculated soil, non-sterilized and pre-inoculated soil, non-sterilized and transplantation-day-inoculated soil. The seeds of the sesame cultivar Goenbaek were germinated in petri dishes. Young plants showing same growth rate at 4 leaves stage were selected and transplanted in pots containing inoculated soil (1.0×10^7 conidia/ml). Disease incidence including wilting, growth retardation and death were observed in the growth chamber (25℃ and 12/12 hours (day/night)) for 14 days. We observed the highest disease incidence (100%) under sterilized and pre-inoculated soil condition followed by sterilized and transplantation-day-inoculated soil (80%) and non-sterilized and pre-inoculated soil (33.3%). The lowest incidence (0%) was observed under non-sterilized and transplantation-day-inoculated soil. This result shows that the soil sterilization and pre-inoculation provide essential soil condition for *Fusarium* wilt disease incidence.

Keywords: Sesame, Fusarium wilt disease, Disease resistance screening

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PD-0007

The Correlation between Legal Definitions of GMO and Policy Decisions on the Regulation of Genome Edited Crops- Global Trends

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As an emerging technology, genome-editing has a huge potential in knowledge-based crop breeding. Many challenges including increased global food and feed demand, technologies for sustainable agricultural practice and climate changes have been forcing us to seek various solutions. Genome editing is definitely one example of technological solutions of which we can take advantages. However, the uncertainty in the area of regulation may act as a biggest threat to the further development and utilization of the technology. Especially, whether genome edited crop would be regulated as genetically modified ones is the key issue in the controversy. Since regulatory oversight is a legal action, legislative provision makes the basis of the regulatory system. Each and every legislation contains provisions of 'definition' and 'scope'. In this poster presentation, we compare such provisions and regulatory decision of each government and jurisdiction in order to have an insight regarding current and future movement related to policy decision regarding the regulation of genome edited crops in Korea.

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PD-0008

Application of double-stranded RNAs in *Arabidopsis thaliana*

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RNA interference (RNAi) is an RNA-dependent gene silencing process regulated by interaction of RNA-induced silencing complex (RISC) and double-stranded RNA (dsRNA). Exogenous dsRNA is imported directly into the cytoplasm and cleaved to short dsRNA fragments of 20-25 base pairs called small interfering RNAs (siRNAs) by Dicer. Guide strand of which siRNAs incorporated in RISC interacts with target mRNA sequence, induces the cleavage and thus degrades target mRNAs by ribonucleases in cells. Recent studies show that dsRNA treatment on plants can induce RNAi. However, the application methods and delivery system of dsRNA are poorly explored. In this study, dsRNA is applied in *Arabidopsis thaliana* by two kinds of methods, dipping and spray. We synthesized diverse dsRNAs which designed to target fluorescent gene A and chloroplast development-related gene B in *Arabidopsis thaliana* genome. After application of dsRNA that targets gene A, we found the reduction of fluorescent expression through fluorescence microscope and mRNA expression level using qRT-PCR in gene A overexpressing transgenic *Arabidopsis thaliana*. In addition, after dsRNA application that targets gene B, we observed growth repression of wild type *Arabidopsis thaliana*. The data revealed that application of target gene specific exogenous dsRNA with dipping and spray methods can induce suppression of target genes of interest. This study might provide a foundation of understanding the processes of dsRNA application and delivery system in plants that can be contributed to RNAi-based technology.

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PD-0009

Molecular marker for selecting Gray leaf spot resistant or susceptible tomato

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토마토 점무늬병(Gray Leaf Spot, GLS)은 *Stemphylium lycopersici*에 의해 발생하는 곰팡이 병의 하나이며, 일반적으로 고온, 다습한 환경의 시설재배 포장에서 많이 발생한다. 병원균이 감염된 후 5일 이내에 병 증상이 나타나게 되며, 회갈색 내지 암갈색의 작은 부정형 반점을 형성하게 되고 심하게 감염될 경우 잎이 황색으로 변하며 마르고 떨어지게 된다. 점무늬병에 감염된 식물체의 경우 전염의 위험성으로 인하여 폐기하여야 하므로 전체 생산량에 심각한 문제를 일으키게 된다. 점무늬병 저항성 유전자인 Sm은 야생종인 *Solanum pimpinellifolium* 계통으로부터 유래되었으며, 다양한 육종라인에 사용되고 있다. 그러나, 이를 판별하기 위한 분자마커 개발은 아직 미비한 상황이다. 본 연구팀은 점무늬병 저항성 및 이병성 계통의 염기서열 분석을 통해 두 계통 간의 다형성을 확인하였으며, 이를 바탕으로 Hybridization probe melting(HybProbe) 기법을 이용하여 저항성 유무 판별 마커를 개발하였다. 또한, 개발된 분자마커의 유효성을 확인하기 위해 실제 포장에 존재하는 *Stemphylium lycopersici*를 수집, 배양하였으며 병리검정을 통해 저항성 판별 마커의 유효성을 확인하였다. 마지막으로 저항성 및 이병성 계통의 F2 분리집단을 대상으로 분자마커를 이용해 토마토 점무늬병 저항성 유무를 판별하고 병리검정을 통해 이를 검증하였다. 본 연구는 토마토 점무늬병 저항성 및 이병성 계통의 유전체 염기서열 내 다형성을 분석하고, HybProbe 기법을 이용하여 저항성 유무 판별 마커를 개발하였으며, 병리검정을 통해 이를 검증하였다. 이러한 연구는 앞으로 토마토 점무늬병에 저항성을 나타내는 토마토 품종을 효율적으로 판별 및 육성할 수 있어 육종에 소요되는 시간, 비용 및 노력을 절감하는데 매우 유용할 것으로 기대된다.

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PD-0010

농업생명공학에 대한 효율적 온라인 정보제공

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본 연구는 농업생명공학기술에 대해 소비자들이 원하는 정보의 요구 및 정보제공 방식을 파악하는 한편, 현재 제공되고 있는 농업생명공학에 대한 온라인 정보제공의 문제점 및 개선을 통하여 효율적인 농업생명공학 정보제공 방안을 도출하고자 수행되었다. 이를 위해 2020년 3월부터 4월까지 제주도를 제외한 전국 성인 남녀 1,869건을 대상으로 웹조사를 수행하였다. 적절한 농업생명공학에 대한 온라인 정보이용 인식조사를 위해 농업생명공학 인지 무경험자와 정보 수집 경험이 없는 대항을 제외하여 1,046명의 유효표본을 대상으로 설문 분석을 수행하였다. 조사내용은 농업생명공학 관련 인지 및 지식 문항, 농업생명공학에 대한 의견, 태도 관련 질문, 농업생명공학에 대한 정보수집 관련 문항, 농업생명공학 온라인 정보 제공 방식에 관련 문항, 응답자 조사 사항의 항목으로 구성되었다. 농업생명공학에 대한 온라인 정보탐색 여부는 경험이 있는 경우가 32.2%로 조사되었으며, 만족도는 매우 만족 1.2%, 만족 26.9%, 보통 62.3%, 불만족 9.7%로 나타났다. 농업생명공학의 유익성 정보는 식량 및 농가 소득 증대가 가장 높았으며, 유해성 정보로는 자연환경 파괴와 식품 위해성이 가장 높았다. 농업생명공학 정보의 영향을 조사한 결과 유해성 정보(81.1%)가 유익성 정보(73.6%)에 비해 인식에 큰 영향을 준 것으로 파악되었다. 생명공학에 대한 온라인 정보수집 사이트의 중요도 조사 결과 '검증된 자료 및 출처 제시'와 '객관적 내용 제공'이 가장 높게 나타났다. 콘텐츠 유형별 선호도 및 선호 요인을 조사한 결과 사진, 표와 그래프, 동영상 등 시각적 콘텐츠에 수요가 높았으며 콘텐츠 유형별 선호요인에서 유의미한 차이가 나타나는 것으로 조사되었다. 본 연구결과는 생명공학 정보제공 사이트에서 사용자들의 배경 및 특성에 맞는 콘텐츠 유형을 맞춤형으로 제공하는 기초자료로 활용될 수 있을 것으로 판단된다.

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PD-0011

Fact-checking of Anti-GMO Arguments Appeared in Pros & Cons Contentions

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Genetically modified organism, GMO is a highly contentious topic especially in the area of agriculture. For more than 25 years, crop breeding via plant biotechnology has been drastically expanded not only in terms of global area of GM crop adoption but also of number of traits and crop species amenable to be developed. However, anti-GMO activists continue to claim that GM technology is risky so that agricultural products using the technology should be banned until its safety is surely proved. However, evidences and references they provide are usually ones misunderstood as well as misrepresented. In this presentation, facts appeared to support anti-GMO arguments are critically reviewed.

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PD-0012

Metabolic response of poplar (*Populus alba* × *P. glandulosa* and *Populus euramericana*) in elevated CO_2 concentration

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Poplar is an important model species for understanding abiotic stress response in trees. This study was conducted to investigate the level of metabolites in *Populus alba* × *P.glandulosa* (Clivus) and *P.euramericana* (I-476) in response to elevated CO_2 concentration for selecting tree species adaptive to climate change. The trees were grown in open-top-chambers (OTCs) with elevated CO_2 concentration: (i) CO_2 400 μmol mol^{-1} (control, ambient), (ii) CO_2 560 μmol mol^{-1} (1.4 × ambient CO_2) and (iii) CO_2 680 μmol mol^{-1} (1.8 × ambient CO_2) for 16 weeks in OTCs. The growth phenotype, photosynthetic pigment levels, soluble sugar, proline, H_2O_2, and malondialdehyde (MDA) were measured to evaluate the effects of elevated CO_2 on plant growth and physiology. The growth phenotype was measured at 16 weeks after growth in OTCs. There were no significant differences among treatments in levels of chlorophyll b, proline, and total soluble sugar. I-476 had lower level of chlorophyll a, total chlorophyll, carotenoid, and MDA in the OTCs with elevated CO_2 than in the controls, respectively. However, the elevated CO_2 treated I-476 showed higher H_2O_2, and starch levels than the controls, respectively. In addition, the elevated CO_2 treated Clivus had higher carotenoids and MDA levels than the controls. These findings may give a better understanding of metabolic and physiological responses of poplar to elevated CO_2.

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PD-0013

CRISPR-Cas9-mediated gene editing to produce *bar*-knockout rice lines

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The clustered regularly interspaced palindromic repeats (CRISPR)/CRISPR associated 9 (Cas9) system generates site-specific double strand breaks (DSBs) at user-defined genomic sequences, which has been applied in diverse plant species for targeted mutagenesis. In this study, we edited a herbicide-resistant *bar* gene in a Bt-resistant transgenic rice BT-T07 by using CRISPR/Cas9 system to achieve disruption of PAT protein expression. Three single guide RNAs (sgRNA) at 108-130bp, 269-291bp and 394-415bp from transcription initiation site of *bar* gene respectively were selected and confirmed successful sgRNA cleavage efficiencies in vitro assay. For each target region, a total of 172, 614 and 864 of rice regenerants were generated respectively. Sequence deletion or single nucleotide polymorphism (SNP) were detected on the *bar* gene from 3, 20 and 2 regenerant T_0 plantlets, showing 1.7%, 3.3% and 0.2% of mutation rates for each target site respectively. T_1 seeds were harvested from T_0 plants and immuno script assays indicated a T_1 population targeted on 108-130bp region of *bar* gene showed significant segregations on PAT protein expressions, but slight differences on PAT expression of other T_1 populations. Mutation types and transformation cassette were analyzed for T_1 plants, aimed to find out *bar* knockout progeny homologous lines without cas9 cassette. These knockout lines would benefit to development of biosafety assessment on transgenic plants derived from gene editing technology.

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PD-0014

Development of Global Biotechnology Information Sharing System

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This research is being carried out with the aim of strengthening domestic research competitiveness and supporting the establishment of an efficient safety management system through the establishment of a real-time information sharing system related to global agricultural biotechnology technology and utilization. To that end, the Korea Biotechnology Information Center (KBIC), a global network of ISAA (International Service for Acquiring Agri Biotech Applications), has been set up to collect and provide global biotechnology research information. The collected information is classified and translated by issue and provided through KBIC's website (http://isaaa-korea.or.kr), and KBIC newsletter is emailed to more than 1,000 subscribers every quarter, providing convenience for scientists to use easily. We are also operating on-line communication programs for the people's right to know through KBIC's website and SNS communication. On the other hand, public discussions for the general public are held regularly to resolve the public's curiosity, and various opinions are collected through them. Through these efforts, we are striving to support the vitalization of agricultural biotechnology research by securing competitiveness in the agricultural biotechnology field and establishing scientific and objective information sharing and proper utilization ways. This work was supported by a grant from the Next-Generation Bio-Green 21 Program (No. PJ01367503), Rural Development Administration, Republic of Korea.

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PD-0015

유전자교정 육종 소재 개발을 위한 옥수수 형질전환 파이프라인 구축

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옥수수는 식용, 사료, 에너지, 산업소재, 제약 원료 등 여러 분야에 광범위하게 사용되는 세계 3대 작물 중의 하나로 생명공학 소재 개발이 가장 활발하게 진행된 작물이다. 신육종 기술의 하나로 등장한 유전자 교정 기술로 형질이 개선된 옥수수 개발이 전 세계적으로 수행되고 있다. 본 연구는 유전자 교정을 통한 신품종 개발의 기반 강화를 위해서 농과원에서 확립된 형질전환 기술을 소개하고자 한다. 또한 이를 활용하여 국내외 옥수수 계통들의 형질전환 여부 및 효율성을 조사하고자 하였다. 이를 위하여 국내 옥수수 7계통 (HW3, KS140, KS141, KS197, KS202, 강다옥, 다청옥)과 국외 2계통 (B73, B104)을 포장재배 하여 미성숙 배를 분리하여 사용하였다. 선발마커로 제초제 저항성 유전자 *bar*를 4x CaMV35S 프로모터에 융합하여 제작된 벡터를 *Agrobacterium*균주 AGL1과 EHA101에 도입 한 후 분리된 미성숙배에 *Agrobacterium*공동배양법을 이용하여 형질전환을 진행하였다. 형질전환 기술이 확립된 옥수수 HiⅡA 미성숙 배에 유전자 교정 여부 및 효율을 검정하고자 유전자 교정을 확인 할 수 있는 마커 유전자로 알비노 유도 유전자 교정 벡터를 *Agrobacterium*균주 EHA101에 도입하여 형질전환 하였다. 현재 아그로박테리움으로 감염된 미성숙배로부터 bialaphos가 포함된 선발 배지에서 캘러스 형성을 유도하는 과정 중에 있다. 금후 계획으로 국내 옥수수 품종 및 계통 형질전환 효율 및 유전자 교정 효율을 검정할 예정이다.

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PD-0016

튀김부피향상을 위한 국내육성 팝콘옥수수 적정 수확시기

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국내 극장 및 놀이공원 등에서 소비되는 팝콘용 옥수수의 원료는 수입에 의존하고 있다. 옥수수연구소에서는 수입산 팝콘원료를 대체하기 위하여 1997년부터 튀김옥수수 연구를 시작하여 현재 오륜팝콘, 지팝콘, 오륜2호, 기찬팝콘을 개발하여 국내 재배농가에 보급하고 있다. 국내 유통되는 수입산의 가격은 1,600원/kg에 수입되고 있는 반면 국내 생산 원료곡은 5,000원/kg에 유통되고 있어 가격차이가 3~4배정도 유지되고 있어 유통이 활발하게 이루지고 있지는 않다. 하지만 최근 국내산을 찾는 수요가 확대되면서 소비가 공급을 따라가지 못하고 있다. 전국적으로 재배면적은 2017년도에 11ha 정도 재배되었으나, 2020년에는 68ha가 재배되고 있다. 유통업체에서 수입산을 찾는 가장 큰 이유는 원료곡의 균일성과 가격경쟁력 때문이다. 기존에 국내산 원료곡은 품질기준이 마련되어 있지 않아서 알곡의 균일성이 떨어지고, 튀김부피에 영향을 주는 알곡의 수분이 일정하지 않아 가공되었을 때 튀겨지지 않는 알곡의 비율이 높아 유통업체로부터 외면을 받아왔다. 낮은 원료가격과 품질의 우수성이 수입산을 이용할 수 밖에 없는 구조를 만들었다. 옥수수연구소에서는 국내산 품종의 품질을 높이기 위해 2017년부터 지역특화과제로 수확 후 관리 기술개발을 위해 저장온도 및 저장방법 등 표준화 기술을 개발하여 국내산 팝콘품질을 수입산과 대등하게 높여 나가고 있다. 국산 품종의 소비를 높이기 위해서는 생산비를 낮추고 수량이 높은 품종을 개발하고, 재배가 쉬운 품종을 개발하다면 팝콘원료의 수입을 대체할 수 있을 것이다. 따라서 본 연구는 국내산 원료곡의 품질을 향상시키기 위해 국내육성품종의 적정수확시기별 튀김부피를 조사하여 수확기를 설정하고자 수행하였다. 옥수수 수염이 출현하는 출사기를 기준으로 40, 50, 60, 70에 각각 수확하여 품종별 일반성분 및 튀김부피 등 품질을 조사하였다. 국내육성 품종의 적정 수확시기는 출사 후 60~70일 정도가 튀김부피을 높이는 수확시기로 나타났다. “지팝콘”과 “기찬팝콘”은 60일, “오륜팝콘”과 “오륜2호”는 70일에서 튀김부피가 높아졌다. 일반성분 분석에서는 “오륜팝콘”의 경우 수확 시 알곡수분 함량은 40일 31.37%에서 70일 수확에서는 17.26%로 낮아졌다. 대신 단백질 함량은 40일 7.53%에서 70일 10.46%로 높아져 수분이 줄어드는 대신 단백질 등 일반성의 함량은 높아졌다. 튀김부피는 40일 수확 시 29.8㎤/g, 50일 32.8㎤/g, 60일33.4㎤/g, 70일 34.8㎤/g으로 수확기가 늦을수록 튀김부피가 늘어나는 경향을 보였다. 따라서 품종별 적정 수확시기를 설정하고 이에 맞게 수확을 한다면 국내산 원료곡의 알곡 품질도 향상될 것으로 기대한다.

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PD-0017

Measurement of genetic diversity and relationship in gamma-ray irradiated soybean mutants using transposon-based marker system

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Transposable elements (TEs) or transposon have major impact on genome evolution and contribute considerably to size, structure and plasticity of genomes. PONG and MITE are two of the major class II DNA transposon in the soybean genome. In this study, we developed a marker system based on targeted region amplification polymorphism with TIRs of transposon (TE-TRAP) that use consensus of TIRs sequence information of the PONG, MITE-stowaway (M-s) and MITE-tourist (M-t). In order to define the applicability of TE-TRAP, we used 210 soybean MDP that had been selected through M_{12} generation to investigate genetic diversity and inter-relationship in mutant population. In total, 12 TE-TRAP primer combinations produced 407 amplicons in the mutant lines. Among the different TE-TRAP primer combinations, polymorphism level and polymorphism information content (PIC) value obtained average 57.98% and 0.14, respectively. Dendogram and principal component analyses revealed that in cluster analysis, only clustering pattern of PONG did permit clear distinction and divided the MDP into 3 major groups. According to an analysis of molecular variance, AMOVA of M-t, M-s and Pong showed 2,209 (20%), 2,776 (18%) and 3.151 (29%) variation in inter mutant population, respectively; whereas the variation of intra mutant population of M-t, M-s and PONG was 8.957 (80%), 12,385 (82%) and 7.646 (71%), respectively. These results indicated that M-s and M-t had higher aspect of mobilization than that of PONG in gamma-ray irradiated soybean mutants. The TE-TRAP marker system reveals a high level of genetic diversity, which provides a useful marker resource for mutation breeding research.

Keywords: Soybean; Transposable element; mutation breeding; gamma ray, TE-TRAP

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PD-0018

CRISPR/Cas9-Mediated Gene Editing of the *OsESP4-1* Gene to Enhance the Tolerance to Phosphate Deficiency in Rice

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Phosphorus is one of the macronutrients essential for plant growth and development, as well as crop productivity. Many soils around the world are deficient in phosphate (Pi) that plants can utilize. Previously, we identified novel knock-out mutant (*hypersensitive to phosphate deficiency*, *hpd*) involved in phosphate (Pi) starvation signaling in *Arabidopsis*. The *hpd* mutant exhibits enhanced Pi uptake and *PSI* gene expression and altered root architectural under Pi starvation compared to wild-type. The *hpd* mutant phenotype is caused by the lack of *ENHANCED SILENCING PHENOTYPE4* (*ESP4*) gene whose function is proposed in mRNA processing. The results indicated that loss of *ESP4* function can induce tolerance to Pi deficiency in plants. We intend to develop transgenic rice tolerant to Pi starvation stress through the CRISPR/Cas9-mediated gene editing targeting *OsESP4* gene. In rice genome, there are two *ESP4* homologs, *OsESP4-1* and *OsESP4-2*, and their transcripts were induced by starvation of both Pi and K nutrients. We generated transgenic rice plants expressing sgRNAs targeting *OsESP4-1* and confirmed several types of deletion mutations in *OsESP4-1* gene by targeted deep sequencing. Transgenic rice with loss of function of *OsESP4-1* gene exhibit higher Pi content than wild-type and altered root development phenotypes under Pi starvation conditions. These results indicate that the conservation of *ESP4* function between dicot and monocot plants. We will select homozygote mutant rice plant (T2) without T-DNA insertion and investigate the tolerance of *OsESP4* gene editing plants to Pi starvation.

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PD-0019

CRISPR/Cas9-mediated Editing of *P34* Gene to Yield Low Allergenic Soybean

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Soybean is a major source of edible oil and protein for human and animal nutrients. However, allergenic proteins that cause allergies to sensitive individuals limit its extensive use in the food industry. Many soybean allergenic proteins have been identified and studied. These soybean allergens fall into five groups: the seed storage proteins Gly m 6 (glycinin G1, G2, G3, G4, and G5), Gly m 5 (β-conglycinin), Gly m TI (Kunitz trypsin inhibitor), Gly m Bd 30K (P34), and Gly m Bd 28K. P34 is a papain superfamily cysteine proteinase type of enzyme occupying <1% of the total seed proteins and regarded as a major soybean allergen to which more than 65% of soy-sensitive patients react. To develop P34-null low allergenic soybean, we generated CRISPR/Cas9 constructs expressing sgRNAs targeting single *P34* gene (Glyma08g116300) in pMDC123 vector and both *P34* and its homolog (Glyma08g116400, 88.6% similarity) simultaneously in pECO210 multiplex vector (donated from Prof. Sang-Gyu Kim, KAIST). These two constructs were transformed into 'Williams 82' soybean cultivar using *Agrobacterium*-mediated transformation method. Moreover, to verify the most efficient Cas9 proteins in soybean, we generated gene editing vectors expressing sgRNAs targeting *P34* gene and various types of SpCas9 proteins, including plant codon-optimized Cas9, Arabidopsis codon-optimized Cas9, human codon-optimized Cas9, and plant codon-optimized Cas9 with high GC contents, respectively. This approach would provide valuable information to develop the efficient gene editing system in soybean.

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PD-0020

Development of Low Phytate and Early Maturity Soybean by CRISPR/Cas9-mediated Gene Editing

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Phytic acid (InsP6) is the major storage form of phosphorus (P) in crops accounting for about 75% of total P in mature seeds. Soybean contains phytate contents between 1.0 and 4.6%. Humans and nonruminant animals cannot digest phytate because they lack sufficient phytase in their digestive system. The undigested phytate is excreted in animal waste leading to phosphorus pollution and eutrophication of waterways. Furthermore, phytate can chelate cationic metal micronutrients such as iron and zinc, and may interact with proteins making them nutritionally unavailable. Thus, phytate is the one of the antinutritional factors that could be eliminated from soybean seeds to broaden soybean usage. To develop low phytate soybean, we generated CRISPR/Cas9 constructs expressing sgRNAs targeting single *GmIPK1* gene (Glyma14g072200), which catalyze the final step in phytate biosynthesis, and multiplex vector expressing sgRNAs targeting both *GmMIPS1* gene (Glyma08g116300), which is the first and rate limiting gene in phytate biosynthesis, and its close homolog (Glyma18g018600, 99.4% similarity) simultaneously in pECO210 multiplex vector (donated from Prof. Sang-Gyu Kim, KAIST). Moreover, to develop early flowering and maturity soybean, we generated multiplex CRISPR/Cas9 constructs expressing sgRNAs targeting both *GmE2* gene (Glyma10g221500), which function as a repressor of flowering and maturity in soybean, and its close homolog (Glyma20g170000, 97.4% similarity) simultaneously in pECO210 vector. These three constructs were transformed into 'Williams 82' soybean cultivar, respectively, using *Agrobacterium*-mediated transformation method and now, we are regenerating transgenic soybean plants.

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PD-0021

Genomic Selection of Fruit-Related Traits in Pepper (*Capsicum spp.*)

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In Korea, pepper (*Capsicum.*spp) is an important crop for spices as well as fresh fruit. Among the various traits, fruit related traits are critical determinants of marketable quality in pepper. Fruit traits are controlled by a number of genes. To develop an effective breeding method on these traits, we examined the potential of genomic selection in pepper. We used the two populations, pepper core collection and PD RILs, and generated SNPs by genotyping by sequencing (GBS) and whole genome re-sequencing. After filtering and imputation, a total of 18,663 SNP markers common in both populations were selected. As target traits, fruit length and fruit weight data were used. To select the most effective genomic selection model, we conducted 10 fold cross-validation using our core collection data for training. Based on the training results, we selected three models, 'gblupRR', 'RKHS', 'Random Forest' and tested prediction models. Using the selected models, SNP markers were subjected to estimation of breeding values in the testing population (PD RILs). Then, model performances were evaluated by comparing correlations between predicted values and observed phenotype values of PD RILs. For fruit weight, 'RKHS' showed the highest accuracy with an average value of 0.558. For fruit length, 'RKHS' and 'gblupRR' showed the same accuracy with an average value of 0.290. In general, differences of linkage disequilibrium pattern and genetic diversity between training and test population could lead the lower prediction accuracy in testing populations. In our case, even though parental lines were included in the training population, the prediction accuracy was lower than expected in the testing population.

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PD-0022

유전자가위 기술을 이용한 고부가가치 당근 개발

박다솜, 정선금, 김미진, 정민, 양희범, 류영우, 김윤성*

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당근 (*Daucus carota*)은 세계적으로 재배되며 베타카로틴과 안토시아닌 같은 건강에 유익한 물질을 함유한 주요 웰빙 채소 중 하나이다. 국내에서도 다수 재배되고 있으나 고품질 고가 당근 교배종 시장은 해외 종자기업들이 선도하고 있다. 오랫동안 사용 되어온 관행육종 또는 분리육종 은 개발 기간이 길고 많은 비용이 들어가는 단점과 함께 고품질의 해외 품종을 넘는 품종개발이 어려운 실정이다. 따라서 고품질 품종 육성을 위해 첨단생명공학 기술을 이용한 신규 유전자원 개발이 필요한 상황이다.

본 연구는 CRISPR/Cas9을 활용하여 당근의 색소 합성유전자, 개화유전자, 병저항성 관련 유전자를 교정함으로서 기존 형질을 유지하면서 고부가가치 형질을 획득하는 기술을 개발하고자 진행하였다. 먼저 보유한 엘리트 당근 계통을 이용하여 embryogenic callus를 확보하였다. 또한 주요형질을 도입하기 위해 관련 타겟 유전자를 선정하여 각 유전자를 타겟하는 sgRNA를 제작하였으며, 제작된 sgRNA 시퀀스를 선발 계통에서 확인하였다. 현재는 embryogenic callus에서 분리한 원형질체에 PEG 방법을 이용하여 sgRNA/Cas9 complex를 주입하여 교정체 생산을 위한 배양을 수행 중에 있다.

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PD-0023

Increase of oleic acid by application of base editing in Arabidopsis *FAD2* gene

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The demand of vegetable oils is steadily increasing worldwide. Vegetable oils are used mainly for diet and cooking. It is desirable to reduce the unsaturation of fatty acid in order to increase the storage stability against the rancidity of vegetable oil and to reduce the trans-fat generated during cooking. Fatty acid desaturase 2 (FAD2) is the first enzyme to synthesize polyunsaturated fatty acid. Mutation of *FAD2* prevents the conversion of monounsaturated fatty acid, oleic acid, to polyunsaturated fatty acid, linoleic acid, to enhance the production of oleic acid. Recently, base editor, which can change only one base pair without forming a double strand break (DSB), has been developed and it has become possible to use this technology to modify activity of certain gene. However, it has never been applied to research on changing in plant lipid metabolism. In this study, the base pair in the window of guide RNA (gRNA) of targeted FAD2 gene was successfully substituted by the cytosine base editor. A total of four missense mutations were observed. Except for one (A295V) mutation, three are new mutation. The oleic acid content was highly increased according to amino acid residue in missense sequences. The one of mutation line, CBE321 line (A295V, T296M), increased up to 62% in T4 seeds. In addition, the oleic acid in T4 plant leaf was increased up to 40%. Based on these results, cytosine base editing in FAD2 suggests new biotechnology method in lipid metabolic engineering.

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PD-0024

Development of rice mutant pool and GE crops using genome editing of upstream open reading frames (uORF) for an alternative to GM crops

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As the global population continues to expand, crop productivity will demand to be increased by 70% until 2050. The genetically modified (GM) crops have been developed for high crop productivity. However, there were many restrictions for the successful commercialization of GM Crops. Therefore, alternative strategies have been attempted to develop biotech crops, such as gene-editing (GE) crops. The CRISPR/Cas9 technology is useful for gene-editing to generate targeted mutants and has played an essential role in the global gene-editing market. Recently, the USDA approved the commercialization of modified white button mushrooms that resisted browning using CRISPR-Cas9. Although the CRISPR-Cas9 system has been widely used and studied for genome editing, so far, its usage is limited to target gene knockout. We focus on overexpression of the target gene by mutating upstream open reading frames (uORFs), controlling the translation of downstream ORF, by the CRISPR-Cas9 system for an alternative to GM crops. To identify the target of endogenous uORF for genome editing in rice, we attempt to analyze the uORF sequence on genes isolated in our lab for stress tolerance and high yield GM crops. We have found 20 uORFs and are currently analyzing the function of uORFs in rice protoplasts by the Dual-luciferase system. The identified uORF will continue editing by the CRISPR-Cas9 system for target gene overexpressing rice. This study would indicate that editing uORFs in rice provides an efficient method for alternatives to GM crops and a new approach in genome editing technology.

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PD-0025

Development of Drought Tolerant Crops using noncoding RNAs

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Abiotic stresses are major constraints of agricultural productivity. Drought, the most serious stress, and its negative impacts are likely to increase worldwide. Recent studies have shown that abiotic stresses induce aberrant expression of many noncoding RNAs, including miRNAs, thus suggesting that miRNAs may be promising targets for genetically improved crop tolerance to abiotic stresses. In general, abiotic stress induces miRNAs to downregulate their target mRNAs, and their downregulation leads to accumulation and activation of positive regulators. This implies that miRNAs do not control directly plant growth and development but control indirectly plant development by mediating a miRNA-target gene network. Therefore, it is evident that endogenous miRNAs have been shown to work as developmental switches and to regulate drought-responsive genes under drought stress. Previously, we identified the rice noncoding RNAs (66 miRNAs and 98 lncRNAs), whose expressions were highly regulated by drought conditions, and whose transcript levels were negatively correlated with the putative target genes. For a further investigation of the biological functions of each miRNA, we generated 12 miRNA overexpressing and knockout lines using constitutive GOS2 promoter and CRISPR/Cas9, respectively. During cultivation, we found several phenotypes in the overexpression lines, including premature leaf senescence, increased number of tillers and grain yield along with the drought tolerance phenotype. The use of miRNA-overexpressing and knockouts and their targets will be a promising technique for determining the native functions of individual miRNAs in response to drought stresses. The identification of the specific positions of miRNAs underlying their regulatory networks represents a convincing research area to pursue in the future.

Keywords: Noncoding RNA, Drought tolerance, Grain yield, Target gene, CRISPR/Cas9

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PD-0026

국내 주요 밀 품종의 미숙배 채취 시기별 조직배양 효율 분석

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전라북도 완주군 이서면 혁신로 181 국립식량과학원

밀은 국내 제2의 주곡작물로써 국내 환경 및 용도별 맞춤 품종 육성을 목표로 다양한 국산밀 품종 개발을 하고 있다. 최근 소비자 요구가 다양해지고 있으며, 아울러 기후변화에 따른 다양한 내재해성 밀 품종이 요구되어짐에 따라 데이터를 기반으로 하는 신육종기술이 각광받고 있다. 이 시대적 흐름에 발맞추고자 디지털 기반 정밀육종에 필수적 단계인 유전자편집 기술을 구축하기 위하여 국내 대표 밀 품종을 파종 시기를 달리하여 미숙배 채취 시기별 조직배양 효율을 분석하였다. 4종의 밀 품종 (금강, 백강, 조품, 아리흑)을 기내에서 발아시킨 후 냉장실에서 춘화처리한 후 비닐하우스에서 2월에서 3월까지 2개월간 포트에 파종하여 개화시기를 달리하였다. 미숙배 채취는 각 식물체의 이삭별 개화 후 2주에 채취하여 조직배양에 이용하였으며, 캘러스 형성율과 재분화율을 조사하였다. 캘러스 형성율은 품종과 시기에 관계없이 대부분 발생하였으며, 재분화 효율은 백강이 가장 우수하였고, 금강이 그 뒤를 이었다. 개화 시기는 3월 초에 파종하여 5월초에 개화하여 얻은 미숙배에서 가장 질 좋은 캘러스와 재분화율을 보였다. 본 연구결과를 토대로 국산밀의 효율적인 유전자교정 시스템 구축을 기대한다.

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PD-0027

Measurement of callus induction efficiency using immature embryo in the heading date control system by Speed Breeding condition in Wheat (*Triticum aestivum*) cultivar 'Bobwhite'

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The tissue culture using immature embryo in wheat is one of the useful materials to increase transformation efficiency. However, tissue culture using an immature embryo is very labor-intensive and time-restrictive method, as sampling must only be done at the optimized time after flowering. In this experiment, 'Speed Breeding' was used as a breeding method that reduces the heading date by extended photoperiod. The growth controled room was constructed by adjusting the photoperiod (22-hour light/2-hour dark) using LED light at 22℃. The wheat variety 'Bobwhite' were vernalized at 4℃ and planted in pots to investigate the heading date. The average heading date was 42 days after sowing. The 11th day after the flowering, 20 immature embryos of 1 mm to 1.5 mm of diameter were placed onto the callus induction medium. After incubation of 2 weeks, sub-cultures were performed on callus induction medium for same cultivation condition. Four weeks after callus induction, the calli were transfer to regeneration medium for shoot induction. All induced calli and regenerated plants in each stage were measured efficiency of tissue culture. As a results, there was no difference in tissue culture efficiency using immature embryos collected under 'Speed Breeding' condition. This study can be useful information in the development of the wheat transformation system.

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PD-0028

Recurrent parent genome recovery analysis based on KASP marker for marker-assisted backcross breeding (MABC) in rice

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Brown rice (Oryza sativa) is rich in nutrients such as protein, fat, dietary fiber and vitamins. The consumption of brown rice is increasing annually in Korea. The eating quality and yield potential are the main goals of rice breeding programs. Marker-assisted backcrossing(MABC) is useful for selecting an offspring with a highly recovered genetic background of a recurrent parent at early generation. The objective of this study is to investigate physico-chemical, textural properties related to eating quality of brown rice derived from 'Seolgaeng' and to identify candidate genes related to aleurone layer synthesis and starch synthesis. The recurrent parent, Samgwang, was backcrossed with BC1F1 plants as a pollen parent and analyzed a recurrent parent genome(RPG) recovery with 96 Kompetitive allele-specific PCR(KASP) markers. SNP mapping was performed by trimming paired-end read sequences of Samgwang, Seolgang, and Ilpum. As a result, mutation sites were identified, and a total of 211 genes were extracted from this site which 200 genes were in protein-coding region. A total of 72 genes were identified with SNPs between Samgwang and Seolgang. Marker effectiveness analysis between Samgwang and Seolgang was performed using 779 KASP markers, and finally 96 KASP markers were selected. These markers were presented in all twelve chromosomes. The background analysis revealed that the extent of recurrent parent genome recovery ranged from 50% to 90 % in BC1F1 generations.

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PD-0029

Identification of stress tolerances through CRISPR/Cas9-targeted knockout of *PUB* genes in rice

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Genome modification technologies have been successfully applied to improve various crop traits. Among them, CRISPR/Cas9 system is now conveniently available as a precise and efficient genome engineering tool. Targeted mutagenesis using CRISPR/Cas9 system is especially useful for gene functional analysis and plant breeding. In this study, we applied the CRISPR/Cas9 system to modify U-box genes to generate stress tolerance lines in rice. Binary vectors harboring expression cassettes of Cas9 nuclease, single guide RNA (sgRNA) targeting the U-box type E3 ubiquitin ligase (PUB) and bar as a selection marker gene were constructed and used for production of transgenic rice plants via Agrobacterium-mediated transformation. Targeted mutations were analyzed in bar-resistant shoots by sequencing of the PCR products of the edited PUB genes using NGS analysis. The gene edited plants containing DNA mutations such as nucleotide substitutions, insertions and deletions of the target site, which varied depending on the different edited lines. We are investigating biotic and abiotic stress tolerance in the edited lines. And this presentation will be discussing relationship between types of mutations and stress tolerances in the gene edited lines in rice.

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PD-0030

Highly efficient protoplast isolation with *Agaricus bisporus* for genome-editing

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Agaricus bisporus is one of the widely consumed mushrooms in the world because of good taste and flavor. The production of A. bisporus has increased in China, the United States, Poland and the Netherlands. In Korea, *A. bisporus* has been one of the most popular edible mushrooms and the total Korean production of *A. bisporus* was 11,348 MT (71 billion won) in 2018. Many protoplast are needed as a material for high efficient genome-editing of *A. bisporus.* This study was carried out to select cell wall degrading enzymes for maximizing protoplast yield. The protoplasts were released from young mycelia cultured on DT-80 medium for 3~4 days using commercial cell wall degrading enzymes after 15 days culturing. The highest yield of protoplasts was obtained from the homogenized mycelia treated with the enzyme combination of Lysing Enzymes from Trichoderma harzianum, cellulase and yatalase.

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PD-0031

Optimization of Ca^{2+}-alginate based regeneration methods in *Arabidopsis thaliana* protoplasts

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Protoplast has been regards of as an ideal material for studies of totipotency. To date, it has been used as the best material for transformation and transfection of macromolecules. An aspect for improved plant production, this goal required efficient protoplast-based regeneration methods. In the case of the most popular CRISPR technology today, genome editing has been successfully applied to isolated protoplasts from various plant species, but only a few plant species have reported success in plantlet formation from protoplasts undergoing genome editing. In cases of *Arabidopsis thaliana* Col-0, one of the major model species, few studies in biotechnological studies with protoplast-based regeneration have been reported. This is probably because required efficiency for each technology has been unsatisfied. To resolve this problem. This research checked protoplast regeneration efficiency between ecotypes. The optimal mediums required each steps of regeneration technique were found. Also, the best conditions and material for root induction were selected. This method can advance two months to acquire regenerated plant. Based on improved protoplast-based regeneration methods, this protocol is more user-friendly, requires shorter times and provides opportunity for various research than previous studies.

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PD-0032

Overexpression of OsPYL/RCAR7, an ABA receptor, improves drought tolerance without defects in growth of rice

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

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PD-0033

Identification of a synthetic partial ABA agonist, S7, improves drought tolerance

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The stress hormone abscisic acid (ABA) helps plants to survive under abiotic stresses; however, its use as an agrochemical is limited by its chemical instability and expense. Here, we isolated chemicals able to induce ABA signalling responses in rice (*Oryza sativa*) protoplasts system. This system consists of an ABA-hypersensitive synthetic promoter containing ABRE and DRE motifs driving a luciferase reporter gene. After efficiently transfecting rice protoplasts with this construct, we screened chemicals library with a similar molecular weight and chemical structure to ABA and identified one chemical, S7, that induced ABA signalling by mediating interactions between the group I and II OsPYL receptors and certain OsPP2CAs in a yeast two-hybrid assay. In an in vitro pulldown assay, S7 was found to mediate a weak interaction between OsPYL5/8 and various OsPP2Cs. S7 treatments did not affect seedling growth or seed germination, but could reduce water loss. Rice seedlings treated with S7 exhibited transcriptome profiles that partially overlapped those treated with ABA. Taken together, we concluded that S7 is a new partial ABA agonist, which has potential use in future dissections of ABA signalling and as an agrochemical.

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PD-0034

Transcriptomic and physiological analysis of null lines generated by knockout of *OsCAO1* using CRISPR/Cas9 system in rice

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Rice chlorophyllide a oxygenase (*OsCAO1*), identified as the chlorophyll b synthesis under light condition, plays a critical role in regulating rice plant photosynthesis. In this study, the development of edited lines with pale green leaves by knockout of *OsCAO1* gene known as a chlorophyll synthesis process is reported. Eighty-one genetic edited lines out of 181 T_0 plants were generated through CRISPR/Cas9 system. The edited lines have short narrow flag leaves and pale green leaves compared with wild type 'Dongjin' plants (WT). Additionally, edited lines have lower chlorophyll b and carotenoid contents both at seedling and mature stages. A transcriptome analysis identified 580 up-regulated and 206 downregulated genes in the edited lines. The differentially expressed genes (DEGs) involved in chlorophyll biosynthesis, magnesium-chelatase subunit (CHLH), and glutamate-1-semialdehyde2, 1-aminomutase (GSA) metabolism decreased significantly. Meanwhile, the gel consistency (GC) levels of rice grains, chalkiness ratios and chalkiness degrees (CD) decreased in the edited lines. Thus, knockout of *OsCAO1* influenced growth period, leaf development and grain quality characters of rice. Overall, the result suggests that *OsCAO1* also plays important roles in chlorophyll degradation and ROS scavenging to regulate both natural and induced rice senescence.

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PD-0035

Image analysis of micro-tome growth for TYLCV sap inoculation screening

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Tomato yellow curl virus(TYLCV) is one of major disease in green house tomato cultivation. usually PCR test has been used TYLCV tomato infection test. But PCR test is not efficient infection test for massive tomatoes. Normally growth pattern of virus infected plant is different from healthy plant. Image analysis is simply possible to observing plant growth differences. In this study, we try setting sap inoculation condition and screening TYLCV infected tomato using image analysis. For setting condition for TYLCV sap inoculation, we tested variable material, different optical density(OD) level and sap inoculation tools. Then we analyzed image of healthy and TYLCV infected micro-tome for growth differences. In this study, result shows different by material, OD level, sap inoculation tools test. In follow study, we try to identifying TYLCV resistance genes and TYLCV resistance cultivar using image analysis.

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PD-0036

세라믹큐브 및 HRM을 통한 토마토 유전자교정체 초기세대의 신속한 검정법 확립

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유전자교정식물체의 초기세대(T0, T1)검정 방식은 연구자마다 다양하나, 보편적으로 유전자교정식물체의 gDNA를 추출하여 PCR를 통해 운반체DNA를 확인하고 유전자서열분석을 통해 편집부위의 편집여부를 확인하는 과정을 거친 후 세대진전 라인을 선발한다. 이와 같은 기존의 검정법은 본 연구의 검정법과 비교했을 때, 비용 및 시간, 노동력이 많이 소요된다는 단점이 있다. 따라서 본 연구에서는 토마토를 대상으로 유전자가위기술(CRISPR/Cas9)을 이용하여 얻어진 유전자교정 T0과 T1 식물체의 운반체DNA 여부를 세라믹큐브를 통해 direct PCR 검정하는 조건을 확립하였다. 또한 교정부위의 교정여부를 확인하는 방법도 세라믹큐브를 통한 HRM검정법을 확립하여 분석한 결과 기존 gDNA기반 검정 결과와 동일한 결과를 얻었다. HRM 분석을 통한 유전자교정여부에 대한 검증은 NGS장비를 통한 InDel분석을 통해 확인하였다. 이렇듯 세라믹큐브 및 HRM을 통한 초기 유전자교정체에 대한 검정법 확립을 통해 비용 및 시간, 노동력을 절약하여 빠르게 검정할 수 있다. 이후 선발된 유전자교정식물체는 전장유전체서열 분석을 통해 운반체DNA 여부, on-, off-target에 대한 검증 및 확인을 진행하여 최종적으로 유전자교정식물체를 확보할 예정이다.

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PD-0037

Production of male-sterile tomatoes using genome editing techniques

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The demand for tomatoes is increasing every year worldwide, an economic problem arises in that the cost of seed production of tomato hybrids (F1) through artificial mating with superior varieties is higher than the selling cost. This problem can be solved using the tomato male-sterility system for the production of F1 seeds is not necessary. In this study produces genetically engineered tomatoes with male-sterility using genetic scissors technology (CRISPR/Cas9). We selected 10 candidate genes related to tomato surgical development, produced 5 vectors for this gene, and transformed them into M82, a tomato for processing. Through the genome sequence analysis of the produced transformants (T0), it was confirmed whether to edit the gene and the male sterility characteristics of T1 generation and T0 plant were analyzed. Currently, M82 has 26 lines acquired from T0 generation and 14 lines from T1 generation. Based on DNA vector, editing information, and separation ratio results, two lines of T1 generation and one line of T2 generation were selected, and all 159 seeds were sown. We obtained 55 individuals from which DNA vector was removed and confirmed whether they were edited by performing HRM analysis of the obtained individuals. Of these, 29 lines selected individuals confirmed the gene-editing through InDel analysis. Finally, a stable heterozygous edited crop from which the CRISPR / Cas9- vector was removed was obtained.

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PD-0038

Generation and Transcriptome Profiling of slr1-d7 and slr1-d8 Mutant Lines with New Semi-dominant Dwarf Allele of *SLR1* using CRISPR/Cas9 System in Rice

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The rice *SLR1* gene encodes the DELLA protein, and a loss-of-function mutation is dwarfed by inhibiting plant growth. We generate *slr1-d* mutants with a semi-dominant dwarf phenotype to target mutations to the DELLA/TVHYNP domain using CRISPR/Cas9 genome editing in rice. Sixteen genetic edited lines out of 31 transgenic plants were generated. Deep sequencing results showed that the mutants had six different mutation types at the target site of TVHYNP domain of *SLR1* gene. The homo-edited plants selected individuals without DNA (T-DNA) transcribed by segregation in the T_1 generation. The slr1-d7 and slr1-d8 plants caused a GA-insensitive dwarf phenotype with shrunken leaves and shortened internodes. A genome-wide gene expression analysis by RNA-seq indicated that the expression levels of two GA-related genes, $GA_{20}OX_2$ (Gibberellin oxidase) and GA_3OX_2, were increased in the edited mutant plants suggesting that $GA_{20}OX_2$ acts as a convert of GA_{12} signalling. These mutant plants are required by altering GA responses, at least partially by a defect in the phytohormone signaling system process and prevented cell elongation. The new mutants, namely slr1-d7, slr1-d8 lines are valuable semi-dominant dwarf alleles with potential application value for molecule breeding using CRISPR/Cas9 system in rice.

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PD-0039

Knockout of *MS10*^{35} gene (Solyc02g079810) encoding a bHLH transcription factor using CRISPR/Cas9 system, confers male sterility phenotype in tomato

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The utilization of male sterility into hybrid seed production reduces its cost and ensures high purity of tomato varieties because it produces no pollen and has exserted stigmas. Here, we report the generation of edited lines with male sterility phenotype by knockout of *MS10*^{35} gene (Solyc02g079810) encoding a bHLH transcription factor that regulates both meiosis and cell death of the tapetum during microsporogenesis in tomato. Twenty-eight genetic edited lines out of 60 transgenic plants were selected. Of these, 11 different mutation types at the target site of Solyc02g079810 were selected by deep sequencing analysis. These mutations were confirmed to be transmitted to the next generations. The null lines without the transferred DNA (T-DNA) was obtained by segregation in the T_1 and T_2 generation. In addition, we showed that the cr-ms10-1-3 mutant line exhibited dysfunctional meiosis and an abnormal tapetum during flower development, resulting in no pollen production. RT-PCR analysis showed that most of the genes associated with pollen and tapetum development in tomato had lower expression in the cr-ms10-1-3 mutant line compared to WT. We demonstrate that directed gene modification of the Solyc02g079810 gene via CRISPR/Cas9-mediated genome editing results in male sterility in tomato plants. Our results suggest an alternative approach to generating male sterility in crops.

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PD-0040

Agrobacterium-mediated transformation of tomato cultivar microtome using genome edition of *Pelo1* gene

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Tomato cultivar microtome is easy to transform using *Agrobacterium*. Genome editing based on CRISPR technology, *Agrobacterium*-mediated stable expression and virus mediated transient expression of CRISPR/Cas9 system are evolving in the genomies assisted breeding of horticultural crops. To develop varieties of virus-resistant tomato using gene editing to guide RNA of *Pelo1* gene which is a well known viral-resistant gene. The seeds were germinated on an MS medium, and grown for 7 days in an invitro environment. Then, the cotyldons and hypocotlys were cut into 7-8mm segments for *Agrobacterium*-mediated transformation and inoculated on shoot induction (SI) medium. After 3-4 weeks, the occurrence a callus induction was observed and transferred to the shoot elongation (SE) medium. To confirm the existence of *Pelo1* gene, genomic DNA was isolated from leaves of non-transgenic and transgenic (T_0 plant) and confirmed using PCR. The results of the current study can be extended for the development a potential CRISPR/Cas9 system in horticultural crops to develop new varieties using genome editing techniques.

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PD-0041

DNA-Free Genome Editing of *Petunia x hybrida* Protoplasts Using CRISPR-Cas9 Ribonucleoprotein Complexes

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CRISPR/CAS9 system has emerged as an alternative tool for targeted genome modification in many horticulture crops. Petunia (*Petunia x hybrida*) belonging to *Solanaceae* family, an important ornamental and a model plant for comparative research. In this study we investigated the functional role of a flavonoid biosynthetic pathway gene called *F3H* (*flavanone 3-hydroxylase*) through site-directed mutagenesis using the direct delivery of purified Cas9 protein and single guide RNA (sgRNA) into Petunia (*cv*. 'midnight') protoplast cells. Using transient introduction of RNPs complex with sgRNAs targeting *F3Ha* and *F3Hb* regions, InDel mutations at the target loci were analyzed by targeted deep sequencing. This resulted in mutation frequencies ranged from 9.99-26.27 % as evidenced by Indel detection by amplicon analysis through Cas-Analyser. Seven mutant lines that contain mutations in either *F3HA* or *F3HB* gene with wild-type flower color of purple violet (RHS 93A) and one complete mutant line having mutations in both *F3H* genes with modified flower color of pale purplish pink (RHS 69D) accounted for 11.94 % of the total regenerated 67 T0 plants. In summary, we demonstrated the suitability of DNA-free genome editing of ornamental plants for the first time, which will pave the way for regeneration of precisely mutated crops without the use of transgenesis.

Keywords: CRISPR/Cas system; *flavanone 3-hydroxylase*; Petunia; Protoplast; Ribonucleoproteins; Site-directed mutagenesis

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PD-0042

Resistance Gene Analysis for Biotic Stresses in Indica Rice Breeding Lines Using Gene-Specific DNA Markers

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Rice varieties with multiple resistance to biotic stresses are stabilizing to rice production in diverse environment. This has to necessarily overcome new emerging pathogens and pests and possible adverse effects from climate change. Host-plant resistance is the most desirable and economic strategy for the control or management of rice blast and bacterial blight diseases and BPH. The present study was carried out to detect positive alleles to resistance genes for blast, and bacterial blight and brown planthopper in indica breeding lines using candidate gene-specific DNA markers. In 9 R-genes analysis for blast resistance, Pib and Pik-m alleles are harbored 67 (90.5%) and 71 (96%) in 77 indica breeding lines, respectively. The alleles for Pia, Pita (Pita-2), Pi5, Pi40 (Piz-t) and Pik-h (Pi54) are contained to 15, 37, 11, 11, and 5 lines, respectively. In 7 R-gene analysis for bacterial blight, four R genes of Xa1, Xa3, Xa4, and Xa21 were detected to positive alleles in 22, 8, 64, and 10, respectively in 77 breeding lines. Two R-genes, xa5 and Xa7 were detected to positive alleles in IR79643-39-2-2-3 and Basmati370, respectively, however, those genes were not detected to any lines developed from the crosses of these parents. A recessive gene xa13 was not detected to all parents and breeding lines analyzed in this study. In 11 R-gene analysis for brown planthopper, nine R genes of Bph1, bph2, Bph3, Bph6, Bph14, Bph18, Bph21, Bph26, and Bph32 were detected to positive alleles in 23, 31, 22, 29, 9, 12, 25, 12, and 36, respectively in 77 breeding lines. All putative candidate alleles from analyzing gene-specific DNA markers could not express to resistance, but these alleles would be showing more stable field resistance than those of non-alleles. These results would be analyzed to relationship with phenotyping results, and used to indica rice breeding program.

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PD-0043

Functionality evaluation and metabolite profiling of diverse *Peucedanum japonicum* collections towards breeding of elite cultivars

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Peucedanum japonicum (PJ) is perennial plant belonging to the Apiaceae family, and has been used as a traditional medicine for a long times in Korea, Japan and China. Researches on the chemical compounds and functionality of PJ have been conducted in various ways. In this study, intra-species diversity of the secondary metabolites was analyzed using LC-MS chromatogram and anti-inflammation in LPS-induced RAW 264.7, DPPH radical scavenging activity, Ultraviolet B (UVB) protection effect in HaCaT keratinocytes were evaluated against 10 PJ species with morphologically diverse characteristics. UPLC-UV-QTof MS analysis was conducted to the leaf (PJL) and root extract (PJR). Each chromatogram peak was identified and unique components for leaf and root were found, such as caffeoylquinic acid for leaf and peujaponiside for root. PJL and PJR both showed reduced NO production within individual and organ dependent difference and regulated gene expression on inflammatory response. DPPH radical scavenging activity showed different antioxidant efficacy between organ. PJL has high effect compared to PJR and it was positively correlated to total phenolic contents. In addition, inhibition of PGE_2 was only observed with PJL in UVB irradiated HaCaT keratinocytes, which indicated UV-protection effect of them. However, there was no significant effect in all PJR. We could find that metabolite contents and functional effect vary among each individual and organ. This approach was first attempted in the study of medicinal plant breeding or phytochemical, and it is believed to such a system could introduce new technologies to more easily discover natural materials. This work was carried out with the support of "Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ013238)" Rural Development Administration, Republic of Korea.

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PD-0044

Functionality evaluation and quantification of pharmaceutical compound of *Cynanchum wilfordii* towards breeding of elite cultivars

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Pharmaceutical substances in medicinal plants are popular materials for eco-friendly foods and cosmetics. Many research to develop new natural materials is actively being conducted. *Cynanchum wilfordii* (CW) is a perennial plant of the Asclepiadaceae family, which is a medicinal plant reseed in China, Japan, and Korea. CW contains steroidal glycosides and acetophenone, which can promote immunity, arteriosclerosis and reducing cholesterol levels. In this study, intra-species variation of the secondary metabolite was measured using LC-MS chromatogram. And anti-inflammatory effect in LPS-induced RAW 264.7 cells, DPPH radical scavenging activity, Ultraviolet B (UVB) blocking effect in HaCaT keratinocytes, were evaluated against 10 CW species with morphologically diverse characteristics. HPLC-MS results showed that contents of 8 standard compounds in root extracts of 10 CW (CWR) were highly diverse. CWR reduced Nitric Oxide (NO) production with individual difference and regulated gene expressions on inflammatory response. 10 CWR showed different anti-oxidant activity and positively correlated to total polyphenol contents. In addition, inhibition of Prostaglandin E_2 (PGE_2) production compatible to poitive control was observed with 4 CWR on UVB irradiated HaCaT keratinocytes, which indicated UV-protection effect. This study confirmed that metabolite contents and pharmaceutical effect vary among each individual. Evaluation of functional activities of various CW will strengthen the basis for breeding of optimal cultivars on demand for specific industries such as cosmetics or functional foods.

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PD-0045

Development of a high-efficiency anti-cancer three IgG type fusion vaccine proteins production plant system using Chinese cabbage (*Brassica rapa*)

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Chinese cabbage (*Brassica rapa*) is a most important horticultural crop in East Asia. In order to develop a vaccine against colorectal cancer as an edible vaccine in plant system, *Agrobacterium*-mediated transformation was carried out using vector harboring three types of IgG fusion protein genes. The EpCAM (epithelial cell adhesion molecule) is a tumor-associated antigen (TAA) considered as a target for a tumor vaccine, a cell-surface glycoprotein highly expressed in colorectal cancer. In this study, the EpCAM recombinant protein gene was fused to the gene encoding for the fragment crystallizable (FcK) region of immunoglobulin G (IgG). *Agrobacterium*-mediated transformation was conducted to transfer genes EpCAM-FcK (with KDEL), EpCAM-FcKα (with KDEL and α-tailpiece), and EpCAM-FcKμ (with KDEL and μ-tailpiece) to Chinese cabbage plant. The regenerated T_0 plants were selfed to produce the T_1 plant lines. The genomic PCR confirmed the presence of both T_1 and T_1 transgenic plants in each generation. Also, western blot analysis revealed the variable expression of the three IgG type vaccine proteins in T_0 and T_1 transgenic plants. Thus, the present study will aid the development of vaccines system in horticultural crops. The outcomes of the current experiment is expected to improve the protein expression stability and vaccine function through horticultural crops.

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PE-0001

착즙량과 바이오매스 생산량이 많은 단수수 품종 '초록이'

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'초록이'는 바이오매스 생산량이 많고 착즙하여 시럽을 만드는데 적합한 단수수 신품종으로 2012년에 IS665'을 모본으로 하고 'ISO8001'를 부본으로 인공교배하여 육성하였다. '초록이'의 잎은 연한 녹색이며, 직립성으로 길이가 길며 중륵이 선명하다. 이삭은 밀수형과 산수형의 중간형이며, 이삭이 길고 종실용으로도 활용할 수 있다. '초록이'는 간장이 357 ㎝로 무안재래보다 93 ㎝, 수장도 10 ㎝ 더 길었다. 무안 등 3개 지역 적응성을 검토한 결과, 잎과 줄기 생체중이 10a 당 5,794 ㎏, 착즙량은 무안재래보다 57% 많은 1,395 L였으며 착즙액의 당도는 14.2%였다. '초록이'의 재배적지는 전남, 전북, 경남 및 제주도에 이르는 우리나라의 남부지역이다.

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PE-0002

Genetic analyses in near-isogenic lines of maize using agronomic traits and SSR markers

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In this study, we performed genetic analyses for 10 near-isogenic lines (NILs) and two recurrent inbred lines, HW3 and HW9 to understand the genetic diversity, population structure, and significant marker-trait associations (SMTAs) between agronomic traits and simple sequence repeats (SSRs) markers. Genetic diversity analysis revealed a total of 569 alleles at 200 SSR loci. The mean number of alleles per locus was 2.9. The averages of genetic diversity (GD) and polymorphic information content (PIC) values were 0.538 and 0.456, respectively. The population structure revealed that the 10 NILs and two parental lines were divided into two major groups. Moreover, the UPGMA dendrogram analysis confirmed that the 10 NILs and two parental lines clearly classified into two groups at genetic similarity of 0.64. A result of SMTAs showed that 55 SSR markers were related with eight of ten agronomic traits. Among these SSR markers, 12 SSR markers were associated with two agronomic trait (10 SSR markers with DS and DT, one SSR marker with EL and SEL, one SSR marker with SEL and SC), whereas remain 43 SSR marker were associated with only one agronomic trait. These results will help in optimizing the choice of parents for crossing combinations, as well as in selecting markers for marker-assisted selection (MAS) for maize improvement.

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PE-0003

Effects of Vitamin A enhanced soybean cultivation on insect diversity

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This study was carried out to develop of environmental risk assessments of potential effects on the non-target above-ground insects and spiders within agroecosystems for Vitamin A enhanced soybean with tolerance to the herbicide glufosinate (PPT) at LMO (Living Modified Organism) isolation field. In LMO quarantine areas of Kyungpook National University (Gunwi) and National Institute of Agricultural Sciences (Jeonju), insect species diversities and population densities on vitamin A enhanced soybean and non-GM soybean, Gwangan were investigated. A total of 93,419 individuals of 65 families from 12 orders were collected in LMO isolation field. In Gunwi, total of 17,110 individuals in Vitamin A enhanced soybean and 17,627 individuals in Gwangan were collected, respectively. In Jeonju, total of 28,621 individuals in Vitamin A enhanced soybean and 30,061 individuals in Gwangan were collected, respectively. There was no difference between the population densities of insect pests, natural enemies and other insects on Vitamin A enhanced soybean and Gwangan within same field, while the population densities of insect pests, natural enemies and other insects in Jeonju was higher than those in Gunwi, respectively. Throughout the study, analysis of variance indicated no significant differences ($P<0.05$), and multivariate analysis showed that the abundance and diversity of plant dwelling insects was similar within same filed.

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PE-0004

중북부 고랭지 적응 복합내병성 조생종 벼 '진평'

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최근 우리나라는 기후변화에 따른 폭우, 가뭄, 고온 등 이상기상의 발생 빈도가 높아지고 있어 벼 생육기간 중에 돌발병해충의 발생으로 인한 피해가 우려되고 있다. 따라서 지형이 다양하고 기상 변화가 심한 중북부 산간지 및 고랭지에서 안전하게 재배할 수 있는 고품질 품종 개발이 필요하다. '진평'은 중북부 고랭지에 적응하는 복합내병성 조생 고품질 품종을 육성할 목적으로 2008년에 조생 고품질인 '히토메보레'를 모본으로 내병성이면서 밥맛이 좋은 '신동진'과 '삼광'을 삼원교배한 후대계통에서 선발되었다. 후대 계통 중에서 도열병, 흰잎마름병 및 줄무늬잎마름병 등의 내병성 검정과 저온발아성, 수발아 등 내재해성 및 미질검정을 통해 유망한 계통을 선발하여 생산력검정시험에서 수량성을 검토한 후 '진부63호'로 계통명을 부여하였다. 지역적응시험 3년을 실시한 결과 그 우수성이 인정되어 2019년 농촌진흥청 직무육성 신품종선정위원회에서 신품종으로 선정되었고, '진평'으로 명명하였다. '진평'은 중북부고랭지, 북부평야지 및 중산간지, 남부고랭지, 동북부 해안지 및 냉조풍지 등 지역적응시험 6개소에서 평균 출수기는 7월28일로 '진부벼'보다 3일 늦은 조생종이다. 간장은 75cm로 '진부벼'보다 단간이고, 수장, 수수 및 수당립수는 각각 18cm, 19개, 73개로 '진부벼'와 유사하다. 현미천립중은 20.9g으로 22.5g인 '진부벼'보다 가벼운 단립종으로 등숙률은 81.7%로 '진부벼'와 유사하다. '진평'의 저온발아율, 수발아율 및 불시출수율은 각각 98%, 19.9%, 15.3%로 재해에 대한 안정성을 갖추고 있으며 도열병, 흰잎마름병 및 줄무늬잎마름병에 저항성으로 복합내병성을 갖추고 있다. 또한, 백미완전립률이 95.4%로 높아 도정특성이 우수하고 밥맛이 매우 우수한 품종으로 쌀수량은 지역적응시험 6개소 평균 5.27MT/ha로 '진부벼'와 유사한 수량성을 갖추고 있다. '진평'의 적응지역은 중북부고랭지, 북부평야지 및 중산간지, 남부고랭지, 동북부 해안지이다. 재배상 유의점은 질소질 비료 과용시 도복, 미질 저하 및 병해충 발생이 우려되므로 적정 균형시비를 해야 하고, 흰잎마름병(K3a 균계), 오갈병 및 기타 해충에 저항성이 없으므로 적기 기본방제를 해야 하며 키다리병 방제를 위해 철저한 종자소독을 하여야 한다.

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PE-0005

Transcriptomic analysis of Korean common wheat cultivar 'Keumgang' and wheat-rye translocation recombinant inbred line under salt stress

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Common wheat (*Triticum aestivum*) is a staple crop for human food in the world. Wheat production would be more affected by environmental stresses in many regions as a result of global climate change. Salt stress is one of major environmental stresses to restrain crop production. To surmount this circumstance, 'Keumgang' (Korean common wheat cultivar, salt-susceptible) and '17DSPL371' (1BL.1RS wheat-rye translocation recombinant inbred line, salt-tolerant) were exploited to transcriptome analysis under salt stress. Salt stress was applied for 72 hours of 200 mM NaCl at the fully expanded 3rd leaf stage. Physiological reactions in leaf blade were examined. RNA was extracted from leaf blades and RNA sequencing was conducted using Illumina Hi Seq X10. Function of differentially expressed genes (DEG) were classified with Gene Ontology (GO). 18 items in molecular function, 21 items in biological process, and 14 items in cellular component were 2-fold changed, respectively. Further, Clusters of Orthologous Groups of proteins (COG) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway were analyzed for evaluating comprehensive metabolic pathway. Subsequently, the transcriptomes involved in metabolism such as signal transduction and carbohydrate metabolism were up-regulated whereas those involved in genetic information processing such as translation were down-regulated. These results would be fruitful to proposed project for breeding salt tolerant hexaploid common wheat.

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PE-0006

Effect of cold temperature on the germination and seedlings of yellow, brown and deep purple seed coat color seeds of *Triticum aestivum* L.

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Future agriculture should take in count the actual knowledge and technologies, but also the need to protect the earth and the societal demands. The increasing population and global warming are factors affecting the agricultural production. Plants response under stress by the accumulation of key metabolites produced by enzymatic (e.g. APX, CAT, POD, SOD) and non-enzymatic (e.g. ascorbic acid, carotenoids, tocopherols, and flavonoids) antioxidative components working together with Reactive Oxygen Species (ROS). Due to their antioxidant activity, a possible protective mechanism of flavonoids during freezing may be the scavenging of ROS. We performed genetic analysis of seed color segregation of an F_3 population with parental lines of Yellow and Deep Purple wheat seeds, generating three groups, Yellow, Brown and Deep Purple. Germination of the clustered seeds was performed under cold (» 4°C) and control conditions (18°C) for a week. We hypothesized that colored seeds should germinate faster under cold due to the anthocyanins presented on their seed coat. Additionally, ROS enzymatic activity, as well as gene expression in seedlings of ROS, flavonoid, flavonoid related transcription factors, and cold responsive genes were measured. In general, we conclude that seed coat color in fact, do affect the germination and the cold response in wheat by expressing in various modes on the genes we studied. In the world, cold temperatures have a large impact on the yield of crop plants, thus, the understanding of seed coat colors and their benefits would be useful for the generation of crops with these traits.

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PE-0007

Functional characterization of H2B monoubiquitination enzyme in related to cold requirement in winter wheat (*Triticum aestivum* L.)

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Modification of histone plays a dynamic role in plant growth and development and in response to abiotic stresses such as acetylation, sumoylation, ubiquitination, methylation. We here identified a homolog of *Arabidopsis* HUB2 in wheat. Although HUB2 has been extensively studied in many plants which regulate Histone H2B by monoubiquitinating as substrate but its functional characterization in wheats has been lagged due to huge and complex wheat genomes. Vernalization is one of the most important treatment for floral transition in wheat. In this study, we firstly find 11 *TaHUB2* like genes and chose one TaHUB2 (TraesCS3A02G467300) showing differential gene expression against different vernalization time periods (0, 10, 20, 30, 50 d). Furthermore, protein level of TaHUB2 was more significantly reduced at vernalization for 50 d as compared to 0 d. To study the possible roles TaHUB2 in vernalization, we checked ubiquitination assay and interaction with wheat Histone H2B. The interaction of the TaHUB2 and its interacting protein Histone H2B was verified by yeast two hybrid assay, bimolecular fluorescence complementation assay (BiFC) and in-vitro pull down assay and their subcellular location was detected using GFP-tagged fusion proteins. These results will provide to understand the role of Ring-type E3 ligase and its molecular mechanisms during vernalization for further studies in wheats.

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PE-0008

Role of Sucrose Transporter Genes in the Peduncle of Winter Wheat at the Time of Flowering

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Wheat is one of the highly cultivated and consumed cereal crops in the world. Two common cultivars 'Keumgang' (early) and 'Yeongkwang' (late) whose flowering time difference is about 30 days are incorporated in this experiment. The difference in the timing of flowering between cultivars can be related to the movement of sucrose via the leaf through the peduncle to the spike. Due to sucrose transporter genes being the energy suppliers in the plant, they may be a crucial factor contributing to the plant's transition from the vegetative state to the reproductive stage. Expression of sucrose transporter genes (*SUT1*, *SUT2*, *SUT3*, *SUT4*, *SUT5*) were determined in the peduncle tissues of 'Keumgang' and 'Yeongkwang' during the floret development in the spike till anthesis . Higher expression rates of most *SUT* genes in the late flowering cultivar indicate that late flowering cultivars delay flowering until satisfactory amount of soluble sugar accumulation occurs. Despite many studies that show that sucrose and other soluble sugars have been shown to promote flowering in many other plant species, in the case of wheat cultivars; each variety requires certain level of sucrose and other soluble sugars to meet flowering. Therefore, it can be inferred that peduncle sucrose concentration is one of the factors that control flowering time in wheat.

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PE-0009

분지형 검정색 참깨 '아름'

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참깨는 종피의 색에 따라 흰색, 검정색, 황색, 회색, 갈색 등으로 분류한다. 특히 검정색 참깨는 흑임자라고 하여 노화방지를 갖는 약용 종자로서 취급되어 왔다. 따라서 건강을 중요시하는 소비자 요구에 부응하기 위해서 검정색 참깨 품종 육성이 필요하다. '아름'은 검정색 참깨 품종육성을 목적으로 경상북도농업기술원 생물자원연구소에서 2000년에 '경흑'을 모본으로 하고, '양흑'을 부본으로 하여 인공교배한 후 세대를 양성하였다. 계통육종법에 따라 세대를 진전시키면서 검정색 종피의 분지형 KS0041-B-10-2-6-3을 선발하여 '경북8호'의 계통명을 부여하였다. 본 시험을 수행한 결과 '아름'의 고유 특성은 초형은 분지형이고 꼬투리는 1과성이며 꽃은 흰색, 종피는 검정색이다. 또한 성숙기는 8월 28일로 대조품종인 '양흑'보다 2일 빠르며 경장은 166cm로 크고 주당삭수가 71개로 대조품종 보다 적다. 병해 및 도복저항성은 대조품종인 '양흑'보다 역병 및 도복에 강한 특성을 나타내었다. 종실수량은 '08~'10년 3개년간 전국 6개 지역 평균 96kg/10a으로 대조품종인 '양흑'과 비슷한 수준이었다. 품질분석결과 조지방 함량은 44.9%, 단백질 함량은 24.2%로 '양흑'보다 조지방 함량이 1.3% 높았으며, 리그난 함량은 4.8mg/g로 '양흑'보다 33% 높았다.

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PE-0010

Nitrogen molecular sensors and their use for screening mutants involved in nitrogen use efficiency

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Nitrogen (N) is an essential macronutrient that is required for plant growth and development and has a major impact on crop yield and biomass. However, excessive application of N-based fertilizer results in environmental pollution and increases cultivation cost. A significant target of crop biotechnology is to develop crop varieties with improved N use efficiency (NUE), thereby overcoming these issues. While various aspects of plant N uptake and utilization have been studied, many factors that fundamentally affect NUE remain uncharacterized. For example, much remains to be learnt about the genes that determine NUE. One of the significant barriers to studying NUE is the absence of an *in vivo* N monitoring system. There are currently several methods for measuring plant N status, but they have limitations in terms of screening for NUE mutants and sensitive NUE assessment. Here, we describe strategies for generating and screening mutant pools using N molecular sensors, comprised of the rice genes *OsALN* and *OsUPS1*, the expression of which is sensitive to endogenous N status. Forward and reverse genetic approaches using the molecular N sensors will help identify molecular mechanisms underlying NUE.

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PE-0011

Selection of salt-tolerant breeding materials from soybean mutant lines

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Sea level rise due to climate change and inefficient fertilizer practices cause salinity stress on crops. Cultivated soybeans are susceptible to salt stress that significantly reduces plant growth, seed quality and yield. The purpose of this study is to select a high salt-tolerant line from gamma-irradiated mutant lines and soybean germplasm. The seeds of each line were planted in 50-cell plastic trays in greenhouse. At the V1 stage, 150mM NaCl was treated for 3 weeks, and plant height, shoot and root weight (fresh and dry), and chlorophyll contents were measured. Compared with the control, four mutant lines showing high salt tolerance were selected. These genetic resources identified in this study will be used to create a mapping population and use it to search for salt tolerance genes in soybean.

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PE-0012

Quantitative trait loci (QTL) mapping of high protein content in *Glycine soja*

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Soybeans are one of the most economical crops as a source of protein for livestock feed as well as humans. Therefore, increasing the protein content of soybeans is an important research project for many soybean breeders. Wild soybean has a high genetic diversity, which is an important germplasm resource for the breeding of cultivated soybean. In this study, GWS-1887 (*Glycine soja*) with high protein content was crossed with Daepungkong and 190 F2 population were genotyped using 6K illumina soybean chip. An average of 123.5 SNPs was mapped to 20 soybean chromosomes with an average of 1.1 cM intervals. QTL analysis was performed using protein and oil contents obtained from 190 $F_{2:3}$ individuals. One QTL associated with protein contents (LOD > 9 values and R^2 > 20%) were detected on chr20. Also one QTL associated with oil contents (LOD > 4 4 and R^2 > 10%) were detected on chr15. The results of these studies will help in the search for genes related to protein synthesis in soybeans and provide useful information for the development of new varieties.

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PE-0013

Expression of genes associated starch biosynthesis in high-amylose wheat cultivars

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Wheat is the second largest crop consumed in Korea. High resistant starch (RS) food gets more attention for health purpose recently. RS tends to form the complex of amylose and lipids, which is not easily digested by enzymes. In the current study, we searched public databases and designed 17 RT-PCR primers, to find genes related to the biosynthesis of RS in wheat. The primers were subjected to the analyses of qRT-PCR, estimating the levels of gene expression associated with starch biosynthesis, in order to compare common wheats to high RS wheats. Using these processes, we tried to establish the basis to find high RS lines in wheat cultivars. The seeds of high RS cultivars (UC1495 and UC1836) and common Korean cultivars (Keumgang, Olgreu, and O-free) were used for this study. The levels of gene expression in the high RS cultivars, genes associated with amylose biosynthesis were significantly high whereas those in common wheat was relatively low. In particular, granule-bound starch synthase II (GBSSII) showed dramatic difference in terms of expression levels between high RS cultivars and common cultivars (0.9 and 0.002, respectively). Based on these results, the high RS cultivars have types II and V starch by producing higher amylose. We are planning to develop molecular markers related to starch biosynthesis, enhancing the efficiency of breeding high RS wheats which may be valuable for the materials of many kinds of food, consequently favoring Korean wheat cultivars.

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PE-0014

Mid-late flowering, high biomass yielding whole crop silage rice cultivar ‘Gowoo’ with glabrous leaf and hull

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In 2019, annual domestic rice production was amount to 374.4 million tons but rice consumption has constantly been decreasing, so that per capita rice consumption dropped to 59.2kg, that result in excess supply of rice. Therefore, the government is promoting "paddy field-use alternative crops cultivation support project" from 2018 to control rice supply and demand. Though forage rice is a good way to resolve that instability between supply and demand while keeping features and function of paddy field, at this point, the farmers tend to avoid to plant it without subsidies, as compared to eating rice, due to low income. And so we need to raise economic value and cultivation stability through increasing yielding capacity, disease-insect resistance and livestock palatability, *etc.*. To save working on disease and insect control and to produce the ‘green’ safety forage, ‘Gowoo’ which is resistant to blast, bacterial blight(race K1, K2, K3), rice stripe virus and small brown planthopper was bred. Also, it has glabrous leaf and hull good for livestock. Its average dry matter yield for three years reached 18.2 MT/ha, 21% higher than that of ‘Nokyang’, that means to be able to raise economic value. Furthermore, its feed value is judged high, because its total digestible nutrients(TDN), 68.2%, is equivalent to or more as compared to general forage crops. Due to those usability, ‘Gowoo’ will play an important role in controlling supply and demand through the adjustment of rice production.

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PE-0015

Introgression the *Saltol* QTL into 'Yeongwoo', the elite whole crop silage rice cultivar using marker assisted selection to improve salinity tolerance

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Salinity is the most common abiotic stresses leading to the reduction of rice yield at many rice-growing areas in world wide. Improvement for salt tolerance of rice for target stress regions is one of the important goals in rice breeding program. In this study, we have focused on developing new whole crop silage rice line with salinity tolerance and high biomass by applying marker assisted selection (MAS). A total of 19 primers for detecting the *Saltol* QTLs were applied to the parent varieties to select polymorphic primers for screening the breeding populations. The 'Yeongwoo/IR64-*Saltol*' F_6 lines were analyzed to evaluate the introgression of *Saltol* fragment into 'Yeongwoo' cultivar by 0.6% ($12dSm^{-1}$) salt treatment. After screening and analyzing F_6 population, the best individual salt tolerant *Saltol* QTL homozygote line, SR36122-212-4-2-1 which was similar with level of 'Pokkali' and 'FL478' in salt tolerance, was selected. This line will be useful to be cultivated at about 130 thousand reclaimed areas of Korea.

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PE-0016

Development of genome-wide InDel marker set discriminating CCDD-genome wild rice species and *Oryza sativa* L. and generation of CCDD-genome introgression lines in IR64 background for exploring genetic factors of high biomass and salinity tolerance

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The three CCDD-genome wild rice species (*O. alta*, *O. latifolia*, and *O. grandiglumis*) exhibit the highest biomass and high level salinity tolerance among 24 species in *Oryza* genus. To explore the genetic factors governing the traits, we developed the genome-wide InDel marker set showing polymorphism between the CCDD-genome species and the cultivated rice (AA genome). The genome of three species were sequenced by using Illumina HiSeqX platform (total reads: 50.1~51.7 Gb, >120 x of the reference rice genome) and *de novo* sequences assembly was conducted by using CLC Genomics Workbench (maximum contig size: 158~218 kb). Using the contigs and BLAST tool installed in the CLC Genomics Workbench and NCBI Genome Workbench, the corresponding sequences from three CCDD species and AA genome were extracted and compared to develop InDel markers. In addition, we obtained 10 and 5 F_1s (2n=4x=AACD) from the genome-doubled IR64 (2n=4x=48) × *O. latifolia* (IRGC 100914) cross and IR64 (4x) × *O. grandiglumis* (IRGC 101405), respectively with help of embryo rescue technique. Through backcross and selfing, we obtained BC_1F_1, BC_2F_1, and BC_2F_2s and the presence of the CCDD-genome chromosomes(s) in the developed lines were confirmed by using the newly developed markers. The developed introgression lines (ILs) will be tested for selection of high biomass and salinity tolerant ILs for rice varietal improvement in the future. Furthermore, the newly developed marker set will be useful to develop introgression lines and mapping of other important traits from different accessions of CCDD-genome species.

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PE-0017

올레산 함유량이 높고 도복저항성이 강한 유채 신품종 '유려'

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유채(*Brassica napus* L.)는 채소 및 식용유로 이용하기 위해 재배되고 있다. 유채는 동계 작물이지만 종실수량이 많고 기름 함량이 높아 전 세계 기름작물 중 종실 생산량이 콩 다음으로 많이 생산되며 기름생산량은 팜유, 대두유에 이어 세 번째로 생산량이 많은 작물이다. 우리나라에서는 유채를 주로 경관용으로 재배하고 있으나, 최근 건강한 먹거리에 대한 관심이 높아짐에 따라 국내산 유채유 생산을 목적으로 유채 재배면적이 확대되고 있다. 유채유를 식용유로 이용하기 위해서는 지방산의 조성이 중요하여 에루크산(erucic acid, C22:1)은 없고 단일불포화 지방산인 올레산(oleic acid, C18:1)의 함량이 높은 품종의 육성이 필요하다. '유려'는 2007년에 '한라유채(IT175404)' 종자를 방사선(감마선) 처리한 후 돌연변이 개체를 선발하였고, 2008년부터 2013년 까지 세대를 전개하면서 생육특성이 우수하고 올레산 함유량이 높아 품질이 우수한 계통을 선발하여 '목포123호'로 계통명을 부여하였다. '목포123호'는 2년의 생산력검정시험 (2014~2015)과 3년의 지역적응시험(2016~2018)을 수행한 결과, 이형주의 발생이 없고 대비품종인 '한라유채'에 비하여 내도복성과 내병성(균핵병 저항성)이 강하고 올레산 함유량이 높아 고급 식용유 생산에 적합한 우수한 특성을 가져 '유려(Yuryeo)'로 명명하였다. '유려'의 개화기는 4월9일, 숙기는 6월2일이었으며 종실 수량은 243kg/10a로 대비품종인 '한라유채'와 비슷하였으나, 종자 내의 올레산의 함량이 74.7%로 '한라유채'의 64.7%에 비하여 10%이상 높았으며, 불량지방산인 에루크산은 전혀 검출되지 않았다.

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PE-0018

Daegwang, a High Yielding Potato Variety with Resistance to Late Blight and Tolerance to Drought

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'Daegwang' was released by potato breeding program at the National Institute of Highland Agriculture (NIHA), National Institute of Crop Science, Rural Development Administration. 'Daegwang' was selected from the cross of 'Haryeong' x 'P03404-1' made in 2007. Major agronomic characteristics were evaluated in Gangneung for spring season cultivation and in Pyeongchang for summer season cultivation as clone number 'P07917-4' from 2011 to 2012. 'P07917-4' was renamed as 'Daegwan 1-127' and regional yield trial for this clone was conducted in Cheongju, Naju, Gangneung, and Pyeongchang form 2013 to 2015. Finally, it was registered as a potato cultivar, 'Daegwang', based on key agronomic characteristics including drought tolerance, late blight resistant and high yielding. Its maturity is medium and growth habit is semi-erect type. 'Daegwang' has round to short oval tuber shape, very shallow eye-depth, yellow skin color and white flesh color. Leave color was green and white flowers bloomed abundantly. 'Daegwang' was resistance to potato late blight, however it was susceptible to potato common scab. The incidences of hollow heart and internal brown spot were very low, however the frequency of tuber cracking was high at about 6.0% in summer season cultivation in Pyeongchang. Its average tuber yield in regional yield trial (2013-2015) was 34.1 tons/ha, which was 6.2% higher than that of 'Sumi', and dry matter content was 16.8%. The texture of boiled potatoes of 'Daegwang' was viscous-floury properties and taste was good. 'Daegwang' is expected to be table usage potato. Plant variety protection right of 'Daegwang' was registered in April 2019, and its grant number is 7664.

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PE-0019

Fine mapping of *qSTV11^Z* harboring rice stripe virus resistance gene, *Stv-b*

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Rice stripe virus (RSV) disease is one of the major constraints in rice production, transmitted by the small brown planthopper (SBPH; *Laodelphax striatellus*). Typical symptoms of RSV are chlorosis and weakness of newly emerged leaves, white and yellow spots, stripe on leaves, necrotic and wilting leaves. As a consequence, plant growth is inhibited, and resulting in plant death in severe infection. In this study, we attempted to localize through fine mapping *RSV* resistance gene in the rice variety Zenith, which is known to harbor *Stv-b*. The resistant variety Zenith was crossed with the susceptible variety Ilpum to fine-mapping using 2100 BC_2F_2 plants derived from a backcross between susceptible recurrent parent, Ilpum and resistant donor parent, Zenith. Chromosome segment introgression lines that were heterozygous at a different region were selected, two type of hetero line was displayed a heterozygous genotype between, Sid2 and Sid75 to Indel9 and RM6680. We identified *qSTV11^Z* region harboring *Stv-b* and mapped to 171-kb region between the InDel markers Sid75 and Indel8. The localization of *qSTV11^Z* provides useful information for marker-assisted selection and determination of genetic resources in rice breeding.

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PE-0020

The Prospect of Bentazone tolerance soybean for conventional cultivation

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Soybean is one of the most important crop widely used for human food, animal feed and industrial products. Weeds compete with the crop plant for light, nutrients, water, spaces and other growth requirements that cause an average reduction of 37% on soybean yield. Bentazone (Bentazone 3-Isopropyl-1H-2,1,3-benzothiadiazin-4(3H)-one 2,2-dioxide) is a herbicide that selectively kills broadleaf weeds by competing for the D1 protein binding site causing oxidative stress. We summarize the effects of bentazone, mode and site of action, application, environmental influence, genetic control of resistance and metabolism in soybean plants from previous studies. It does not kill certain genotypes of soybeans able to metabolize the herbicide. The effectiveness of bentazone depends on environmental factors as they influence absorption, translocation and alter metabolism by modifying enzyme activity. Metabolism based resistance of bentazone quickly metabolized into natural plant metabolites in tolerant plants. Bentazone is first hydroxylated at 6 and 8-hydroxy-bentazone then glycosylated in soybean at a position of 6 and 8 of its aromatic ring. Two classes of enzymes, cytochrome P450s and Glutathione S-transferases (GSTs) have already been confirmed as vital candidates for enzymatic detoxification of bentazone. Three cytochrome P-450 genes associated with soybean sensitivity to bentazone have been mapped to chromosome 16, from which a single-base deletion in the cytochrome P-450 hydroxylase encoding gene, CYP81E22, causes the loss of the detoxification function of bentazone. This study will advance our understanding of metabolism, genetic regulation of bentazone resistance as well as to derive us to be sanguine about new possibilities for discovering new mechanism for herbicide action and may include the detection and use of genes that contribute to a soybean competitiveness.

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PE-0021

Screening of drought tolerant and sensitive soybean genotypes with physiological approaches

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Soybean (*Glycine max* [L] Merr) is one of important crops in the world. With many other crops, the sustainability of its production is serious issues in drought-prone area, suppressing yields of up to 40 percent annually. Production of drought-tolerant soybean cultivar is believed to be a successful and efficient way to cope with the water deficient problem. This study was designed to screen drought tolerant soybean for further studies. Although drought is a quantitative trait, many strategies had been applied in the selection of soybean genotypes responsive to drought. Slow wilting under drought is one of important assessments under drought stress. The core set of 1,000 soybean accessions were selected from Korean soybean germplasms in National Agrobiodiversity Center. Of these, 798 soybean accessions were tested under greenhouse condition with and without drought stress. Drought was executed by suppression of irrigation at early vegetative stage (V2) and continued until plants death. Plants were scored for leaf wilting during the stress period. After three successive screenings, eight tolerant and eight susceptible soybean accessions were identified. With selected tolerant and susceptible soybeans, we carried out our greenhouse experiment to identify variations of physiological characteristics such as vegetative indices, chlorophyll content, soil moisture, electrical conductivity, leaf temperature. Of these characteristics, we will determine the most reliable and potentially useful indicators under drought condition. This may be useful in further breeding programs to select for drought tolerance in soybean.

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PE-0022

Identification and map-based cloning of the stunted sterile mutant gene in rice

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Proper organ development is pivotal for normal rice growth and production. Many genes are involved in this process, and these genes provide a basis for rice breeding. The phenotype of a rice mutant, stunted sterile (ss), identified from the japonica rice cultivar Samkwang treated with N-methyl-N-nitrosourea, was characterized, including anatomical and pollen activity analyses. A genetic analysis and fine mapping were performed to identify a candidate locus, followed by a sequence analysis to determine the causal mutation for the phenotype. Compared with wild-type plants, the mutant exhibited a 34% reduction in height, 46% reduction in flag leaf width, and complete panicle sterility. Cell proliferation in the leaf and pollen viability were significantly inhibited in the mutant. The mutant phenotypes were controlled by a single recessive gene that was fine-mapped to an 84 kb region between two SNP markers on the short arm of chromosome 5. A candidate gene analysis determined that the mutant carries an 11 bp insertion in the coding region of LOC_Os05g03550, which encodes a protein containing two SANT domains, resulting in a premature termination codon before the conserved domain. We identified a novel rice gene, Stunted sterile, involved in the regulation of various developmental processes. Our findings improve our understanding of the role of chromatin remodeling in organ development and have implications for breeding owing to the broad effects of the gene on plant growth.

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PE-0023

Identification of novel candidate gene for pod shattering tolerance in soybean

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Pod shattering is an essential mechanism for seed propagation in many wild species. However, the pod shattering at maturing stage can cause a serious yield loss and is a main limiting factor for mechanization in soybean cultivation nowadays. Previously, we could find several QTLs with two RIL populations derived from 'Daewonkong' based on high-density linkage map. The objective of this study was to find novel candidate gene responsible for pod shattering in soybean from the QTL information in previous study and gene expression analysis. Among the QTLs from the previous study, we selected QTLs more than 10% PVE value excluding *pdh1* locus (major QTL) and could find the novel candidate QTL on chromosome 16 (*qPS-DS16-1*) from the allele patterns on QTL region. Out of the 41 genes in the QTL, six genes have SNP/Indel variations in the coding sequence of the parents. *Glyma.16g076600*, one of the six genes, showed a highly different expression level between the parents in growth stages from R3 to R6. *Glyma.16g076600* is a homolog gene of *AT4G19230* in Arabidopsis which is a member of the CYP707A family, is related to ABA catabolism, a known hormone associated with different physiological functions, including pod shattering. The result would provide useful information to understand the genetic mechanism of pod shattering and could be used for improving the efficiency of marker-assisted selection for developing pod shattering tolerant varieties.

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PE-0024

SNP Analysis for Drought Tolerance in Soybean RIL Population Using RNA-Seq and Chip Genotype

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Drought is one of the major abiotic stresses to reduce seed yield in soybean. The drought tolerance of soybean was investigated using 147 F_8 RILs developed from a cross between a tolerant 'PI416937' and a susceptible 'Cheonsang' parents. Further, we conducted an RNA-seq analysis to find the SNPs related to drought tolerance using the transcripts obtained from the parents and the tolerant, susceptible progenies in the RIL population. The RNA samples of plants were trimmed and mapped to a reference genome (Williams82). Only the biallelic 214,638 SNPs were obtained through the variant calling and variant filtering steps. Among them, 1,457 SNPs showed the same patterns in the tolerant progenies and parent as well as in the susceptible progeny and parent each. Chromosomes 3, 4, 7, 8, 12, and 16 had more than 30 SNPs in 0.5Mb region. In Group1 where the tolerant parent and progenies had altered genotypes as compared to the reference genome, 166 out of 944 SNPs make missense or nonsense mutations. In Group2 where the tolerant parent and progeny lines had the same genotypes with that of the reference genome, 101 out of the total 513 SNPs cause missense or nonsense mutation. We also carried out the GO enrichment test of the selected transcripts. Results show that majority of the transcripts are related to membrane component and others are associated with auxin-response factor, leaf and shoot formation, and so on. These results suggest that potential genes for drought tolerance in soybean could be screened through SNP analysis based on RNA-seq.

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PE-0025

Strategies for Introduction Breeding to improve hard wheat adapted in Korea

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Wheat is one of the most important food crops in the world as well as in Korea. The total sales of bread market in Korea has been increased upto 1.8 times and the demand of hard wheat used for bread making is also increasing in the past decade. However, most of hard wheat cultivars in Korea have not have satisfatory protein contents and gluten quality for their end-use quality. Korean wheat cultivars have been developed from limited genetic background, therefore, wheat genetic resources in the world provided by National Agobiodiversiy Center were used for the hard wheat quality improvement. The wheat genetic resources were screened based on high molecular weight-glutenin subunit compositions which play a crucial role in determining the viscoelastic properties of wheat dough. Introduction of wheat genetic resources of diverse glutenin composition and putative hard wheat gemplasms with high protein contents are expected to improve Korean hard wheat breeding, directly and indirectly.

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PE-0026

Selection of hard wheat genetic resources for improvement of Korean hard winter wheat

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As the food consumption pattern in Korea is westernized, the demand of hard wheat flour is increased. However, the self-sufficiency of wheat is only 0.7% due to the relatively low protein contents and unfavorit glutenin compositions, which are frequently present in Korean wheat cultivars. To improve the bread making quality, we introduced hard wheat genetic resources provided by National Agrobiodiversity Center screened by GMS (Genebank Management System). Agronomic traits and quality parameters including heading date, maturity, yield components and seed protein contents of total 200 hard wheat germplasms were evaluated on the different climates and locations (Mid-north: Korea University, Middle: National Institute of Crop Science, South: Gyeongsangnam-do Agricultural Research and Extensive Services) in the year 2018-2019.

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PE-0027

Introduction Breeding: Agronomic traits of pre-evaluated wheat genetic resources

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Hard red winter wheat (HRWW) is utilized for the bread making and its demand is increasing. However, the production base of hard wheat flour in Korea have limitations of low genetic diversity and relatively low quality of gluten proteins. To overcome these limitation, we introduced hard winter wheat genetic resources that are provided by National Agrobiodiversity Center, and evaluated agronomic traits and performances such as winter hardness, heading date, maturity, yield components, and seed protein contents of the 200 germplasms in 2018-2019 at three different locations (mid-north, middle, and south part of Korea). We selected 55 germplasms (genetic resouces) showing superior agronomic performances and suitable protein contents for bread making after agronomic evaluation. Together with the selected germplasms, the agronomic traits and performances of additional 51 hard wheat germplasms newly provided by National Agrobiodiversity Center were evaluated for selection of elite genetic resources in 2019-2020.

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PE-0028

Genotyping of genes related in seed storage protein, and seed traits of hard wheat genetic resources

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Total 200 hard wheat germplasms provided by National Agrobiodiversity Center had been pre-screened using GMS (Genebank Management System) to improve hard wheat breeding program in Korea. To evaluate the genetic traits including seed storage protein compositions, and seed traits of the germplasms, we performed PCR of target genes for genotyping of germplasms. Genotyping of genes that are related in seed storage protein compositions and seed traits was performed, followed by field selection with agronomic traits at three different locations (mid-north, middle, and south part of Korea). Introduction of hard winter wheat genetic resources with superior agronomic performances and useful genes would be an effective strategies for the improvement of Korean hard winter wheat breeding programs.

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PE-0029

A Sesame variety 'KangYou' with Phytophthora blight and Fusarium wilt disease resistance

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Phytophthora blight, caused by pathogen *Phytophthora nicotianae,* and fusarium wilt, caused by pathogen *Fusarium oxysporum f.sp. sesame,* is responsible for a huge reduction in sesame (*Sesamum indicum* L.) crop yields. A sesame variety 'KangYou'(*Sesamum indicum* L.) with phytophthora blight and fusarium wilt disease resistance was developed in 2019. It was crossed between 'China black' and SI982849 in 2006. 'KangYou' has few branch and triple capsule per node and white seed coat color. And maturing date of 'KangYou' is 21st August and height is 163cm and capsule number is 82. Especially 'KangYou' showed phytophthora blight and fusarium wilt disease resistance in the field. And the yield of 'KangYou' was about 1.37ton per hectare, 13% higher than 'Goenbaek'. 'KangYou' showed crude fat content with 53% and crude protein content with 28% and lignan content with 4.8mg/g. Thus 'KangYou' would be suitable for environment-friendly sesame cultivation.

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PE-0030

Characterization of rice gelation using high amylose rice ‘Milyang333’

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Reduction in rice consumption due to recent demographic changes has emerged as an ongoing social problem. Fortunately, various processing varieties are being developed and distributed in accordance with the increase in consumption in the rice processing field, such as home made replcement(HMR), But the range of utilization used is very limited in industry. In order to solve the problem, we examined the gelling properties using high amylose rice and the possibility of using it as a gelling agent for gelled food. The properties of the rice cultivars using rice flour instead of agar were solid in the order of 'Shingil' <'Saegomi' <'Milyang333' <'Dodamssal'. 'Dodamssal' the highest amylose content showed the lowest adhesiveness on the other hand, while 'Milyang333' showed the highest adhesiveness. In addition, as a result of the pudding production, it was found that pudding using 'Milyang333' has the characteristics of high rigidity, low stickiness, and low graininess felt, making it the most suitable as an additive for pudding. In particular, in the case of rice Yanggeng, 'Milyang333' was hard, highly elastic, cohesive, and had relatively little grainy texture felt. Even in the case of pudding, the pudding with 'Milyang333' had a high rigidity, little stickiness, and a little graininess felt by rubbing the palate. Therefore, it was confirmed that 'Milyang333' is the most suitable additive for agar.

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PE-0031

Mapping QTLs for bakanae disease resistance with Korean japonica rice varieties

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Bakanae disease, caused by the fungal pathogen *Fusarium fujikuroi*, has become a serious global threat in majority of the rice-cultivating regions by leading up to high losses in yield. Korean japonica rice varieties showed varying degree of resistance or susceptibility to bakanae disease. We have developed a modified in vitro bakanae disease bioassay method and tested 31 Korean japonica rice varieties. Nampyeong and Samgwang varieties showed highest resistance while 14 varieties including Junam, Hopum and Odae were highly susceptible with 100% mortality rate. We performed mapping QTLs for bakanae disease resistance.with four F2:F3 populations derived from the crosses between Korean japonica rice varieties using the KASP markers developed in our laboratory based on the SNPs detected in Korean japonica rice varieties. Four major QTLs were found on chromosome 1, 4, 6, and 9 with LOD scores of 21.4, 6.9, 6.0, and 60.3, respectively. Fine-mapping of the QTLs on chromosome 1 and 9 which were found with Junam/Nampyeong F2:F3 population and Junam/Samgwang F2:F3 population, respectively, are under progress. These QTLs will be very helpful in developing bakanae disease resistant high quality rice varieties.

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PE-0032

Potential Impact Assessment of Above-Ground Arthropods on Genetically Engineered Soybean

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In order to guarantee the safety of GM soybean crops, it is important to assess the potential toxicity of their expressed insecticidal proteins to non-target organisms. In the present study, the effects of the GM soybean IGF, which is tolerant to the herbicide glufosinate, on plant-dwelling non-target insects and arachnids were evaluated in soybean agroecosystems. In total, 13,031 individual insects and arachnids, representing 64 families in 11 orders, were captured during the study. The results indicate that the GM soybean IGF did not negatively affect plant-dwelling non-target insects and arachnids. The occurrence of insect pests, natural enemies, and other insects differed significantly according to region, region and survey year, and survey year, respectively.

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PE-0033

Genotypic and Environmental Impact on Natural Variation of Proximates, Minerals, and Anti-nutrients in Korean Soybean Varieties and Comparative Compositional Analysis of Transgenic Soybean Overexpressing *Lesquerella FAD3-1*

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Nutritional composition is influenced by genotype, environment, and their interactions. In order to characterize the natural variation in nutritional composition of soybean seeds, thirteen Korean soybean varieties were grown in three locations in South Korea during 2017 and 2018. Statistical analysis of combined data showed significant differences by variety and environment (location and cultivation year) for the measured components. Percent variability analysis demonstrated that environment and the interaction of environment with genotype contributed more to the nutritional contents than genotype. Principal component analysis and orthogonal partial least squares discriminant analysis indicated that significant variance in proximates, minerals, and anti-nutrients was attributable to location and cultivation year. Overall, environment exerted more influence on these components than genotype. In addition, the compositional equivalence of three *PfFAD3* soybean lines expressing omega-3 fatty acid desaturase 3 of *Lesquerella* was assessed. Composition analysis was conducted on eight proximates, nine minerals, and four anti-nutrients of these three *PfFAD3* soybean lines, a nontransgenic commercial comparator (Kwangankong), and three nontransgenic commercial varieties grown at two sites in South Korea. Only the level of calcium significantly differed in *PfFAD3* and Kwangankong, but it was within the range of the nontransgenic commercial varieties. The results indicated that the three *PfFAD3* soybean lines are compositionally equivalent to nontransgenic commercial soybeans in the context of natural variation.

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PE-0034

OsABAR7 유전자 이용 가뭄내성 옥수수 형질전환체 생산 연구

홍준기, 김범기, 김경환, 이강섭, 장희정, 서은정, 이연희*

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옥수수(*Zea mays* L.)는 밀, 벼와 함께 3대 작물 중 하나로 환경 적응 범위가 넓어 세계 다양한 지역에서 재배가 가능하고 식량과 사료로써 널리 이용되고 있다. 생명공학 기술을 적용하여 제초제 및 해충저항성 GM 옥수수가 개발되어 전 세계적으로 공급되고 있으며 최근에는 기후변화에 대응하기 위한 생물학적, 비생물학적 스트레스 내성을 갖는 옥수수 품종이 개발되고 있다. 본 연구는 농과원에서 확립된 옥수수 형질전환 기술을 이용하여 벼에서 가뭄내성 기능이 확인된 *OsABAR7* (ABA receptor *OsPYL/RCAR7*) 유전자를 옥수수에 도입하여 농업적 형질을 개선하고자 하였다. *OsABAR7* 유전자를 *Ubiquitin* 프로모터에 조합하였고 선발마커로 제초제 저항성 유전자 *bar*를 CaMV35S프로모터에 융합하여 제작된 벡터 pPZP를 *Agrobacterium*균주 AGL1에 도입 한 후 옥수수 HiIIA미성숙배에 *Agrobacterium* 공동배양법을 이용하여 형질전환체를 생산하였다. 제초제 bialaphos가 첨가된 배지에서 저항성 캘러스를 형성하는 형질전환 효율은 미성숙배 분리시기에 따라 차이가 있으나 최대 20.8%의 효율을 나타냈다. PAT 단백질 발현 검사와 제초제 Basta 저항성 분석을 통해 형질전환체에 도입된 *bar* 유전자가 안정적으로 발현되는 것을 확인 하였다. 또한 *bar* 및 *Adh* 유전자의 특이 프라이머를 이용하여 Genomic DNA PCR 및 TaqMan 분석법을 통해 형질전환체에 도입된 유전자 유무 및 copy 수를 확인 하였으며 종자를 확보한 상태이다. 금후 계획으로 확보된 *OsABAR7* 형질전환 옥수수 계통들의 가뭄내성 특성을 분석하고 스트레스 관련 유전자의 발현 양성 분석을 통해 안정적으로 가뭄내성 특성이 증가한 계통을 선발하여 후대를 육성할 예정이다.

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PE-0035

Heterologous Expression of Bifunctional Rice Flavonol Synthase in Tobacco Redirects the Metabolic Flux of Flavonoids

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Flavonol synthase (FLS) belongs to the 2-oxoglutarate iron-dependent oxygenase (2-ODD) family and is a key enzyme of the flavonoid biosynthetic pathway, acting at the diverging point separating into the flavonol and anthocyanin subclass branch. We characterized *OsFLS* gene from "Ilmi" rice (*Oryza sativa*) cultivar. OsFLS shared FLS-specific motifs, and the sequence was clustered with other FLSs in the phylogenetic analysis with various 2-ODDs. The *in vivo* substrate-feeding assay demonstrated that recombinant OsFLS exhibited FLS activity showing higher substrate preference for dihydrokaempferol (DHK) than dihydroquercetin (DHQ). Additionally, OsFLS also showed F3H activity that converts flavanones to dihydroflavonols, indicating that OsFLS has bifunctional properties. The expression of *OsFLS* was observed not only in pigmented rice seeds but also in non-pigmented rice seeds. However, the expression of most other flavonoid biosynthetic genes was hardly detected in the non-pigmented rice seeds. Transgenic tobaccos (*Nicotiana tabacum*) expressing *OsFLS* generated pale pink- or white-colored flowers, in which kaempferol significantly increased but anthocyanin dramatically decreased. Additionally, their pod size and weight were reduced compared to wild type. Several early and late flavonoid biosynthetic genes were downregulated in the transgenic flowers. These investigations demonstrated that *OsFLS* plays a functional role in the production of flavonol *in planta*.

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PE-0036

전유전체연관분석(GWAS)을 통한 자포니카 벼 수발아 저항성 관련 유전자위 탐색

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최근 기후변화로 인하여 벼의 등숙기~수확기에 태풍과 강우가 잦아지면서 벼를 수확하기 전에 이삭에서 볍씨가 발아하는 현상인 수발아 발생으로 품질저하 및 수량감소가 심각해지고 있다. 특히 우리나라에서 즐겨 먹는 자포니카 품종은 인디카에 비하여 대부분 수발아 저항성이 매우 약하다. 본 연구에서는 국제벼연구소(IRRI) 보유 유전자원 277점(온대자포니카 156, 열대자포니카 97, 인디카 24점)의 수발아 저항성을 검정하였다. 수발아 저항성은 상대습도 100%, 온도 30℃에서 15일 치상 후 발아하지 않은 종자의 비율로 수치화하였다. 기존에 알려진 바와 같이 수발아 저항성은 온대자포니카와 열대자포니카 그룹이 각각 평균 37.1%, 46.4%로 인디카 그룹의 93.3%에 비하여 훨씬 낮았다. 그러나 온대 및 열대자포니카 자원 중에서도 수발아 저항성이 90%를 상회하는 몇몇 자원이 탐색되었으며, 이들 자원은 추후 자포니카 품종의 수발아 저항성 증진에 유용할 것으로 기대된다. 3,000 Rice Genomes Project로부터 기존에 분석된 4.8백만 여개의 SNP를 이용하여 온대 및 열대자포니카 자원의 수발아 저항성에 대한 전유전체연관분석(genome-wide association study)을 실시하였다. 그 결과 대립인자 효과가 뚜렷한 1번과 4번 염색체 상의 약 180 kb 및 151 kb 부위의 수발아 저항성 유전자위를 선정하였다. 두 개 유전자위에 모두 저항성 대립인자를 보유한 6개 자원의 수발아 저항성은 평균 73%로, 두 개 유전자위에 모두 감수성 대립인자를 보유한 156개 자원의 저항성 수치인 33%에 비하여 월등히 강한 수발아 저항성을 보였다. 추후 탐지된 수발아 저항성 유전자위에 대한 후보유전자 분석을 진행하고 정밀 분자표지 개발을 통해 수발아 저항성 자포니카 육종에 활용할 계획이다.

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PE-0037

벼 종자수명 관련 양적유전자좌(QTL) 탐색

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종자수명은 종자를 장기간 보관한 이후 파종하였을 때도 활력과 발아세를 유지하기 위한 중요한 농업형질이다. 특히 벼를 주식으로 하는 많은 아시아 국가에서 기후변화로 인하여 덥고 습한 환경이 지속되는 기간이 길어지면서 충분한 종자수명을 확보하는 것이 육종적으로 중요한 목표로 부각되고 있다. 본 연구에서는 종자수명이 짧은 열대 자포니카 품종 Azucena와 종자수명이 우수한 인디카 품종 Icta Motagua를 교배하여 육성한 F_2 집단을 활용하여 종자수명을 지배하는 양적유전자좌(QTL)를 탐색하였다. 유전자지도 작성에는 Infinium RiceLD 1K SNP Chip에서 양친간 다형성을 보이는 456개 SNP가 사용되었다. 종자수명은 출수 후 40일에 수확하여 수분함량 10.9%로 즉시 건조시켜 보관한 $F_{2:3}$ 종자를 45℃, 상대습도 60%의 고온다습한 조건에서 급속 노화(accelerated aging)시키면서 매주 발아율 변화를 측정하고, 발아율이 절반으로 감소하는 기간(p_{50})을 수치화하여 결정하였다. 표현형 검정 및 유전분석은 충분한 종자가 확보된 F_2계통들 중 집단 전체의 유전형 분리양상을 비교적 고르게 대표할 수 있는 45계통을 선정하여 진행하였다. QTL 분석 결과 2번 염색체 상에서 표현형 변이 18%를 설명하는 주동 유전자위가 탐지되었고, 해당 위치에서 Icta Motagua 유래 대립인자 보유계통의 p_{50}은 23.2일로 Azucena 유래 대립인자 보유계통의 p_{50}인 12.2일에 비하여 종자수명이 훨씬 오래 유지되었다. 해당 QTL 영역의 크기는 약 2.9 Mb로 주석(annotation) 정보가 있는 232개의 유전자가 위치하고 있으며, gene ontology 분석 결과 이들 중 45개 유전자는 DNA repair, oxidative stress reduction 등 종자수명 관련 메커니즘에 관여할 수 있는 유전자로 분석되었다. 추후 후대분리집단을 이용하여 종자수명 결정 유전자의 보다 정밀한 위치를 구명하고 육종에 활용 가능한 정밀 분자표지를 개발할 계획이다.

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PE-0038

A new hybrid rice cultivar, 'KGHR1' for Southeastern Asia

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Commercial hybrid rice has been cultivated in Asia mostly China since 1976 with more than 20% general yield increment compared to inbred rice in China. In order to develop new hybrid rice cultivar for seed export to Southeastern Asia especially Vietnam, we have bred hybrid rice lines in Cambodia since 2014 and 'KGHR1' was developed in 2019. It demonstrated to be adapted to Northern Vietnam with major disease resistance and high yielding capacity; 'KGHR1' has resistances against Vietnamese blast and bacterial blight and it has rough rice yield of 11.2 MT/ha in Vietnam, 9.0 MT/ha in Korea, same with 'Dasan', high yielding Korean inbred rice. Furthermore, its grain quality is better than that of 'Ⅱ A838', super yielding Chinese hybrid rice. It has 6.6% protein content and 22.7% amylose content lower than those of 'Ⅱ A838' indicating softer texture and better eating quality. As the results of 'Golden Seed Project', 'KGHR1' will play an important role in boosting Korean seed industry as a first commercial hybrid rice in Korea.

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PE-0039

한해에 강한 내도복 다수성 겉보리 '한강'

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최근 월동기 이상기온 현상에 따른 재배 안정성 강화 요구에 의하여 한해(추위)에 강하면서 재배에 안정적인 용도별 적성 품종을 생산자 및 수요자 충족을 위해 내병 내재해 안정성이 높은 고품질 다수성 품종을 육성하기 위해 2007년에 한해에 강한 대립 다수성 등 특성을 가진 '삼광찰보리'을 모본으로, 2조 대립인 'Radiant' 품종을 부본으로 하여 인공교배 하여 출수가 빠르고 한해와 병해 강하면서 수량성이 높은 겉보리 '한강'이 개발하였다. '한강'은 한해에 강한 내도복 다수성 겉보리 품종으로 3년간 전국 5개소 지역적응시험 결과 간장이 81㎝로 올보리 83㎝ 보다 작아 쓰러짐에 잘 견디고, 토양전염병인 보리호위축병 저항성인 품종이다. 특히 연천시험지 내한성 검정포장에서 고사주율은 고휴재배에서 40%로 올보리60.3% 보다 강하였다. 출수기는 4월 22일로 올보리보다 1일 빨랐고, 성숙기는 5월30일로 같았다. 천립중은 33.5g인 대립종으로 항산화 성분인 폴리페놀 함량이 1.69mg/g로 올보리보다 14% 더 높았다. 조곡의 수량성은 ha당 5.67톤으로 올보리보다 15% 더 많은 다수성 품종이다. 재배 적응지역은 1월 최저평균기온이-8℃이상 지역에서 재배가 가능해 광지역 적응성 품종으로 보급이 기대된다.

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PE-0040

Development of Anti-Blast Fungus Rice Plants and Characterization of Molecular Mechanisms underlying Rice-Blast Fungus Interaction Based on HIGS System

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In this study, we established HIGS of rice blast fungus by visualizing silencing of fungal GFP expression in transgenic Arabidopsis as well as rice plants expressing *GFP* siRNAs. All transgenic plants expressing 35S::dsRNAi_*eGFP* showed significant suppression of fungal eGFP expression during invasion, while apparent eGFP signal was observed in all fungal cells propagated on the leaves of control plants. Next, we constructed dsRNAi vectors of fungal pathogenic genes, including *LHS1*, *MgAPT2*, and *RGS1*, which regulate various infection processes and transformed them into rice plants, respectively. Both 35S::dsRNAi_*LHS1* and 35S::dsRNAi_*MgAPT2* transgenic plants showed enhanced resistance to blast fungus, while the 35S::dsRNAi_*RGS1* plants showed hypersensitive phenotype compared to control plants. To dissect the mechanism of these phenotypes cytologically, we analyzed infected transgenic rice plants by using various chemical staining methods visualizing rice cellular resistant responses. While the fungus invading control rice plants showed efficient hemibiotropic development, 35S::dsRNAi_*MgAPT2* and 35S::dsRNAi_*LHS1* plants strongly suppressed fungal infection with the consistent fungal development phenotypes to those of corresponding deletion mutant fungi. Moreover, substantial H_2O_2 accumulated in infected leaves of 35S::dsRNAi_*MgAPT2* and 35S::dsRNAi_*LHS1* plants. In contrast, 35S::dsRNAi_*RGS1* plants were hypersensitive phenotypes to fungal infection. These results provide us not only the evidences of HIGS in rice blast fungus, but also the novel strategy for investigation of rice-blast fungus interaction and development of HIGS-mediated antifungal biotech-crops.

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PE-0041

추위에 강한, 장간, 총체 다수성 귀리 신품종 “신한”

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귀리는 한국의 남부지방에서는 동계 사료맥류로, 중북부 지방에서는 춘파 재배로 이용되며, 남부지방의 3모작 지역에서는 옥수수나, 단기 재배용 벼 수확후에 여름파종의 형태로 이용되는 작물이다. 국립식량과학원에서는 우수한 귀리 품종개발에 대한 농가의 요구에 부응하여, 2004년에 CI7611를 모본으로 하고, CI7604를 부본으로 교배하여 신한을 개발하였다. ‘신한’의 종자의 형태는 겉귀리이면서 이삭형은 산수형이고, 초장은 113cm로 ‘삼한’보다 크다. 출수기는 5월 6일으로 삼한보다는 하루 늦었다. 줄기수는 ㎡당 1,090개로 다얼성이며 삼한보다는 적었다. 내한성은 삼한과 대등하여 추위에 강하였다. 생체수량은 40.0톤/ha로 삼한보다 6% 증수되었으며, 건물수량은 15.3톤/ha로 8% 증수되었다. 조사료 품질은 조단백질 함량이 6.3%였으며, 총가소화영양분(TDN)은 62.1%로 ‘삼한’에 비하여 낮았다. 사일리지 품질은 1등급으로 높았다. ‘신한’의 적응지역은 1월 최저평균기온 -6℃ 이상으로 중산간지 제외하고 재배가 가능하다. ‘신한’은 초장이 크고, 엽신 비율이 높으면서, 조사료 건물수량이 우수하여 금후 축산 농가들로 부터 큰 호응을 얻을 것으로 기대된다.

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PE-0042

A Peanut Variety, 'Gowon' with Early Maturing and High Pod Yield

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A new peanut (*Arachis hypogaea* L.) variety 'Gowon' was developed at the Department of Southern Area Crop Science, National Institute of Crop Science (NICS), Miryang, and approved for release in 2019. For the harvest of vegetable peanut, it is required to have a large pod, and mature comparably earlier with higher fresh-pod yield. 'Gowon' was developed through a pedigree selection from a single cross between the large-grain with short-stem variety 'Pungsan' and 'Miryang47', the early-maturing elite-line. It has 11 branches per plant and its length of main stem and branch was 43cm and 49cm, respectively. Each pod has two grains with brown-color testa and long ellipse-shaped kernel. Among the yield components, 'Gowon' showed 42 pods per plant, 98 g of 100-seed-weight, and 80% of mature pod ratio. The seed contains 30.2% of protein, 47.0% of crude fat, and the composition of oleic acid was 45% among the fatty acids. Average performance during the regional yield trial at four locations (2016-2018), 'Gowon' has demonstrated excellent productivity showing 12.25 MT per ha in fresh pod yield which was 28% higher than reference variety, 'Palkwang'. It showed higher resistance to early and late leaf spot, and lodging compared to the reference at the trials.

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PE-0043

맥주용 원맥 및 맥아 품질 특성이 우수한 내도복, 다수성 맥주보리 '누리맥'

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국내 맥주용 보리는 2003년 육성된 호품보리가 수량성과 품질면에서 우수하여 가장 많이 재배되고 있다. 그러나 호품보리는 내도복성, 흰가루병 저항성, 종실의 대립화, 정립률 증진, 베타글루칸 함량저하 등의 재배적, 품질적 개선이 요구된다. 따라서 고품질 내재해성 맥주보리 품종을 육성하기 위해 2004년도 다수성인 '밀양127호'와 도복과 바이러스병에 강한 'Miharu gold'를 인공교배하여 F_2는 집단으로, F_3 이후는 계통으로 키가 작으면서 도복에 강하고, 수량이 많은 계통을 선발하였다. 그리고 2014년부터 2016년까지 '익산 175호' 계통명을 부여하여 전북, 전남, 경남, 제주 4개지역에서 지역적응시험을 수행하였다. '익산175'는 간장이 77cm로 호품(84cm)보다 작아 쓰러짐에 잘 견디고, 호위축병과 흰가루병에도 저항성을 보였다. 출수기는 4월 12일로 호품과 같았고, 성숙기는 5월 21일로 호품 보다 하루 늦었다. 천립중은 42.9g으로 호품보리(42.1g)와 비슷했으며, 수량성은 전작에서 495kg/10a, 답리작 379kg/10a로 호품보리보다 각각 21%, 17% 증수한 다수성을 보였다. 맥주용 원맥 및 맥아 품질에서 정립률 90%(호품 90%), 베타글루칸 3.3%(4.1%), 단백질 10.8%(11.3%), Friability 81.5%(69.1%), 가용성 단백질 4.2%(3.8%), 효소역가 243WK(294WK) 등으로 우수한 품질 특성을 보여, 2016년 신품종으로 선정되어 '누리맥'으로 명명되었다. 누리맥은 내한성이 약하므로 한해 피해에 안전한 남부지역 맥주보리 재배지에 적합하다.

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PE-0044

Development of New Perilla Cultivar 'Nulsaemi' with Large Seeds and Tender Coat for Edible Seed

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The Perilla oil and powder extracted from perilla seeds. Rosmarinic acid found in perilla seeds and leaves is known to be effective for antioxidant and dementia prevention, and perilla oil is known to be effective in improving thinking skills and memory, causing perilla consumption prices to increase, making it a cash cow crop among farms. A new perilla cultivar 'Miryang73' was developed at the National Institute of Crop Science from the cross between the 'Daesildeulkkae' which is high in crude fat and has a tender coat and the 'K015412' with large seeds and hard coat, and has been called 'Nulsaemi,' a new perilla cultivar. The backcross performed in the year 2008, and via pedigree process their progenies were selected from generations F3 to F6. From 2017 to 2019 regional yield trials (RYTs) were carried out in four regions. The 'Nulsaemi' is brown-coated, as heavy as 5.2 g per 1,000 seeds, with a rich content of 45% crude fat. Its tender coat makes it suitable for the production of oil and flour, and the seeds contain 2,130,6 μ g/g rosemary acid, which is 18% higher than the normal cultivar 'Dayu'. The yield is 1.25MT per ha, 3% higher than 'Dayu.' The possible cultivar source for the production of good quality perilla oil is considered to be 'Nulsaemi.'

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PE-0045

Development of Vegetable Perilla Cultivar ‘Somirang’ with Heart-shaped and Thick leaves

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The seeds of perilla are used as perilla oil or seasoning powder, and the leaves are beloved as fresh vegetables or pickles. In the National Institute of Crop Science, ‘Somirang (Milyang80)’ was developed as a new vegetable perilla cultivar from the cross between the 'YPL32'97Acp-B-1-47-1-11', which is heart-shaped and thick leaves, and the ‘Saebora’ with excellent purple color on both sides of leaf. The parents were crossed in 2004, and their progenies were selected from F_3 to F_{11} generations through pedigree method. Advanced yield trials (AYTs) were conducted in Miryang from 2016 to 2018. 'Somirang' has a maximum leaf length of 14.2cm, which increases its commercial value, and has a high rate of 59.9% of inner leaves per product leaf. According to the thick of leaves, ’Somirang’ is more efficient to long term storage, and the leaf yield was excellent at 56.20 MT per ha. The new cultivar with better qualities and high yield are expected to contribute to the increase of farm incomes.

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PE-0046

국내 잡초벼(완도앵미6) 유래 재조합자식집단의 발아 관련 특성 분석

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잡초벼 완도앵미6에서 유래된 재조합자식집단(RILs)을 이용하여 저온발아, 저산소, 수발아 등에 대한 육성집단의 발아 관련 특성을 분석하였다. 양친인 화영과 완도앵미6은 30℃ 발아율이 모두96 %이상으로 정상적으로 발아하였다. 저온 조건(13℃), 저산소(온실, 포장), 수발아 처리 조건 등에서 화영은 각각 72 %, 82 %, 34 %, 완도앵미6은 42 %, 32.5 %, 0.5 %로 처리 환경에 따라 발아율 차이를 보였다. RIL 집단의 저온 발아율은 평균40 %로0~88 % 범위에서 정규분포 하였다. 온실 혐기 조건에서 계통들의 토중출아율과 생존율을 조사한 결과, 파종 후 14일경에는 평균 50 %, 10 %이었고 21일경에는 각각 65 %, 32 %였다. 집단의 수발아율은 평균 66 %로 0~76 % 범위에서 분포하였며 오른쪽 꼬리 분포의 형태를 보였다. 포장 담수 조건의 경우 화영은 파종립의 약 60 %정도가 발아 하였지만 완도앵미6은 거의 발아하지 않았다. 화영의 발아율은 담수조건에서 체크품종으로 사용한 KHO와 비슷하였다. 재조합자식집단의 포장에서 저산소 발아율은 파종 후 12~14일경에 평균 7 % 수준에서0~40 % 범위에서, 16일경에는 평균 14 %와0~63 % 범위에서 분포하였다. 각 처리환경에서 조사된 발아율을 상관분석한 결과 종자의 상온(30℃) 발아율은 온실 저산소 발아율과 비교적 높은 상관(0.69)을 보였지만 수발아율과 저온발아율, 포장 저산소 발아율과 낮은 상관을 보였다. 수발아율은 저온발아율과 저산소 발아율과 매우 낮은 상관을 보였으며 저온발아율도 저산소 발아율과 낮은 양의 상관을 보였다. 온실에서 조사된 저산소 발아율과 생존율은 포장 저산소 발아율과 비교적 높은 상관을 보였다.

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PE-0047

Molecular characterization of Mother of FT and TFL1 (*MFT*) gene under Pre-harvest Sprouting (PHS) stress in Korean Wheat (*Triticum aestivum*)

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PHS is an early germination in wheat spikes when excessive moisture and low temperature conditions are maintained before harvesting. Because PHS in wheat drastically reduced the quality and economic value of wheat grain, the improving PHS wheat is one of the most important breeding goal in Korean wheat breeding program. Mother of FT and TFL1 (*MFT*) gene is known to be a very important gene for seed dormancy and has been shown to be highly expressed in mature wheat seeds placed in low temperature environment. A total of 22 Korean cultivars of common wheat including 'Keumgang' and 'Woori' were used in this study. The germination experiment was conducted using the sandbury method. Phylogenetic analysis was performed for *MFT* gene and created the neighbor-joining tree. The qRT-PCR was carried out at 35 Day After Fertilization (DAF) wheat grain and accordance with germination stage (0, 1, 7, and 14 days). These PHS induction experiments showed that there was a difference in germination between the cultivars. Woori, Chunggye, Joeun, Koso and Dajoong were determined as PHS resistant wheat cultivars but Keumgang, Olmil, Baekjoong and Jeokjoong as susceptible cultivars. We isolated *MFT* genes from 22 Korean wheat cultivar and identified an InDel sequence (TATG) in the exon region and classified two groups according to possess of InDel sequence. After qRT-PCR analysis, *MFT* transcript from 'Woori' has been confirmed to have a higher level gene expression than Keumgang. That was caused from the germination stage. The *MFT* gene might increase the expression level until immediately before germination in wheat. After yeast two-hybrid assay was conducted to find out the binding subunits with *MFT* genes, *SUT1* (Sucrose Transporter 1) was identified as an interacting gene. The subcellular localizations were revealed *MFT* is target to the cytosol and *SUT1* to cytosol and nuclear. These results may be helpful to understand the germination mechanism in wheat.

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PE-0048

Breeding hybrid rice with genes resistant to diseases and insects using marker-assisted selection and evaluation of biological assay

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Hybrid rice (F1) is the product by crossing with two different varieties; most of them have to be high yield at least 20% more than regular ones and resistance to diseases and insects. Crop yield losses are caused by diseases and insect pests of tropical and temperate rice cultivation area in Asia. The objective of this study is to identify F1 hybrid rice with hybrid traits and genes related to disease/insect resistance using MAS and phenotypic selection for improving grain yield of F1 hybrid rice and developing excellent variety of hybrid rice for export. Two hundred forty genetic resources and F1 of hybrid rice combinations were analyzed by using PCR-based markers related to disease/insect resistance genes and hybrid traits. The restorer of fertility gene Rf3 was detected in 176 and 216 hybrid lines using microsatellite marker RF3-5 and RF3-10, respectively. The primary gene Rf4 was amplified in 96 and 125 hybrid lines using RF4-14 and M19280. Bacterial blight genes Xa3, Xa4, xa5, Xa7, xa13, and Xa21 were detected in 20, 32, 36, 10, 3, and 4 F1 hybrid combinations, respectively. Seven resistance genes combination (Xa4 Xa5, Pi-ta, Pib, Pi5, Bph18(t), and tsv1) identified in indica variety 'Rumpe'. Eleven of F1 hybrid combinations and two control varieties were conducted biological assay at the Red River Delta region in Vietnam. Eight F1 hybrid combinations showed resistance to bacterial blight, meanwhile, in ten F1 hybrid combinations excluding KR1487H, blast resistance. KR0695H showed the highest yield(11.8 Ton/ha) among the eight F1 hybrid combinations.

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PE-0049

QTL analysis for improving and diversifying the grain shape of rice cultivars in Korea

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Rice grain shape is one of the key components of grain yield and market values. Understanding the genetic basis of variations in grain shape could be used effectively to improve grain shape. In this study we developed a total of 265 F_2 individuals derived from a cross between japonica cultivars (Josaeng-jado and Langi) and used the population for quantitative trait locus (QLT) analysis.

To explain the relationship among the grain traits (GL: grain length, GW: grain width, L/W: ratio of length for width, TGW: 1000 grain weight) correlation analysis was performed. The grain shape was positively correlated with GL and TGW, and negatively correlated with GW. In QTL analysis associated with grain shape, one QTL qGL5 for GL were detected on chromosome 5, explaining 20.3% of phenotypic variation (PV), and two QTL, *qGW5* (PV=36.1) and *qGW7* (PV=26.1) for GW were identified on chromosome 5 and 7, respectively. In the evaluation of the QTL's effect for the grain shape lines with each QTL on grain shape in the population showed significant difference in the grain size comparing lines without the QTL. According to the QTL combination of the allelic type grain shape of tested lines was presented variously from semi-round type to long spindle-shaped type.

Acknowledgement: The results in this study would be used to extend genetic pool for diversity of grain shape in japonica cultivars and could be facilitated on the improvement of the grain shape through marker-assisted selection breeding in Korea

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PE-0050

Characterization of Yield and Panicle-related Traits of Early Maturing Rice Varieties by Cultivation Times in the Honam Plain Area of Korea

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The cultivation of early maturing rice in the Honam plain area of Korea is increasing to diversify the cropping systems. The cropping systems of this rice are usually classified as early, ordinary, and late cultivations based on transplanting time. The characteristics of varieties vary depending on the cultivations. To evaluate the performance of varieties and interpret the relationships between genotype and environment, nine yield and 17 panicle-related traits of six early maturing rice varieties (Jopyeong, Odae, Unkwang, Haedamssal, Jinkwang, and Haedeul) were characterized on early, ordinary, and late cultivations. Heading date was longer in order of early, ordinary, and late cultivations. The cumulative mean temperature of growth stage was similar for all cultivations. The variation in the number of spikelets per panicle (NS) was mainly due to the variety and the traits related with secondary rachis-branch were affected more by variety than the traits related to primary rachis-branch. The varieties with the highest yield were Haedamssal on early maturing cultivation and Unkwang on ordinary and late cultivations. Haedamssal displayed a panicle-number type plant architecture with relatively higher number of panicles per hill (PN) and average NS. Unkwang exhibited panicle-weight type with many NS and less PN. Additive main effects and multiplicative interaction) analysis revealed that, NS and HD were mostly affected by genotype and environment, respectively. Among yield-related traits, NS contributed the most to enhanced yield of varieties in all cultivations. NS could be the target trait of breeding programs intended to improve the yield potential of early maturing rice adaptable to the Honam plain area. However, proper PN should be considered because PN, which was negatively correlated with NS, also affected the yield.

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PE-0051

Development of biotic-abiotic stress tolerant rice by Pi9 introgression into Ciherang-Sub1-AG1

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Rice blast, caused by *Magnaporthe oryzae*, is one of the limiting factors reducing 30% of yield. Against to blast, broad-spectrum rice blast genes were cloned and *Pi9* is particularly effective in South and Southeast Asia, the biggest rice producing region. In many Asian countries, abiotic stresses such as flooding are additional factor to yield loss. In this study, *Pi9* was introgressed into Ciherang-Sub1-AG1 (CSA), which has tolerance to submerged and anaerobic germination conditions with *Sub1* and *AG1*, to deal with biotic and abiotic stresses. Using developed functional NBS2-Pi9 allele-specific marker and rice blast test, Ciherang-Sub1-AG1-Pi9 (CSAP), which has tolerance to abiotic stress conditions and carries functional NBS2-Pi9 allele was selected and characterized in BC_2F_8. Background similarity of CSAP was 99.2% and 87.4% to CSA with chip set markers designed with IRGSP and MH63. CSAP showed tolerance phenotype under submerged and anaerobic germinative conditions. The RNA expressional levels of *Sub1A* and *OsTPP7*, which are the major genes of *Sub1* and *AG1*, didn't show any differences with positive controls under corresponding stress conditions. When CSAP was inoculated with PO6-6 carrying AvrPi9 and R01-1 lacking AvrPi9, lesion of CSAP was decreased in PO6-6 inoculated. In terms of agronomic traits, 100 grains weight were decreased in CSAP, however, yield was not decreased because of increased spikelet number per panicle. The seed size is smaller than CSA, chalk was also decreased in CSAP. Based on these results, the newly developed biotic-abiotic stress tolerant CSAP can be useful materials to climate resilient rice cropping system.

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PE-0052

Genetic and Phenotypic characterization of salinity tolerant temperate rice variety, 'Seso' utilizing *Saltol* QTL

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Global food production has new levels of uncertainty. Salinity in soil affects almost all aspects of plant development. Several QTLs and genes have been reported on salinity tolerance. Saltol is one of the most well-known quantitative loci (QTLs) for salinity tolerance in rice. It has been used to develop highly tolerant rice varieties in saline and coastal areas in Southeast Asia, South Asia, and Africa. However, the functional activity of Saltol is not well known, and the molecular marker application of readily developed linked markers in Saltol has not always been successful in the rice breeding programs for salinity tolerance improvement. Interestingly, two BC2F9 sister backcrossed inbred lines (BILs), which have been developed by marker-assisted backcrossing utilized the linked markers of Saltol to improve the salinity tolerance of MS11 (a temperate japonica growing in tropical condition). The BILs showed very different phenotypic and stress tolerance, although both contained the Saltol QTL. The genomic similarity of the two BILs was 73%, and we have identified the genomic sites of different genic constitutions between the lines utilizing background genotyping. The stress response of the two BILs showed difference in survival rate, grain yield under highly saline field condition, and SPAD, SES in hydroponic conditions. MS11-SaltolA showed salinity tolerance through Na+/K+ homeostasis with relatively high K+ ion uptake and low Na+ ion uptake in the seedling stage. Further genomic analyses with whole genome resequencing is ongoing to study on gene interactions. The developed highly tolerant MS11-SaltolA can be used as an improved donor in rice molecular breeding for high salinity tolerance.
one of sthe ptionfrom different or sequentially under unfavorable conditions, the breeding multiple-stress tolerant rice should be developed. have analyses are being conducted

Keywords: Rice, Salinity, Saltol, Backcross inbred lines, SNP markers, Molecular breeding

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PE-0053

소립 적립계 조숙 내한성 국수용 밀 '조한'의 주요 특성

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국내 밀 품종개발은 1970년 이후 금강밀 등 40개 품종이 개발되었으며, 주로 숙기 단축과 수량증대를 목표로 진행되었다. 그러나 숙기가 빠른 조숙성 품종은 내한성이 약하고, 수량이 적은 단점이 있어 개선이 요구되었다. 이에 농촌진흥청에서는 숙기가 빠르면서 이모작에 적합하면서 수량이 많고, 추위와 도복에 강할 뿐만 아니라, 국수용에 적합한 '조한'을 개발하였기에 주요 특성을 소개하고자 한다. '조한'의 이삭은 방추형이며, 종실의 크기가 작고 색은 적색을 나타낸다. 출수기는 전작과 답리작에서 4월 17일로 대조품종인 금강보다 2~3일 빠르게 나타났다. 성숙기는 전작과 답리작에서 각각 6월 1일과 5월 27일로 금강보다 빠르게 평가되었다. '조한'의 간장과 수장은 각각 74㎝와 7.1㎝로 준단간형이며, 이삭은 금강과 비슷하게 나타났다. 단위면적당 수수, 1수립수, 용적중과 천립중은 각각 785개, 35립, 806g, 38.7g으로 금강에 비해 단위면적당 수수와 1수립수는 많고, 리터중과 천립중은 가볍고 소립종인 것으로 평가되었다. 지역별 수량은 전작에서 556㎏/10a으로 금강보다 24%, 답리작에서 517㎏/10a으로 금강보다 22% 많게 나타났다. '조한'의 겨울철 고휴에서 동사율은 4.8%로 금강(32.6%)보다 강하게 나타났으며, 도복도 금강에 비해 저항성인 것으로 나타났다. 밀 품질 조사결과, 단백질의 함량(10.0%)과 글루텐(7.3%)은 금강에 비해 낮은 중력분의 특성을 나타냈으며, 밀가루 밝기는(L*)는 92.18로 금강보다 밝게 나타났다. 국수면대의 밝기는 83.75로 밝고, 삶은 국수의 경도는 4.25로 약간 낮고, 점성과 탄성이 높게 나타나 국수용에 적합한 것으로 판단되었다.

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PE-0054

국내산 밀 품종의 천연 발효빵 특성 평가

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국내에서도 식사대용으로 빵을 섭취하는 소비자가 늘어나면서 건강에 도움이 되는 천연 발효빵에 대한 연구와 관심이 높아지고 있다. 본 연구는 국내 빵용 밀 품종의 밀가루 특성이 천연발효빵인 깜빠뉴의 제빵 품질에 미치는 영향을 분석하고자 수행되었다. 연구 시료로는 고분자 글루테닌의 유전조성 중 *Glu-D1d* 를 지니고 있어 빵용으로 적합한 국내 5 품종(백강, 황금, 조경, 중모2008, 금강)과 수입산 원맥(Hard Red Winter Wheat, HRW), 수입 밀가루 (Rarine Francaise French Wheat Flour T55)등 총 7개를 사용하였다. 밀가루 품질 특성은 회분(%), 백색도, 입자크기(μm), 단백질(%), 글루텐(%), 침전가(mL)를 측정하였고, 호화 및 반죽 특성은 믹소랩을 이용하여 분석하였으며, 최종적으로 깜빠뉴를 제조하여 빵의 품질을 평가하였다. 반죽의 수분 흡수율, 반죽시간, 안정도, 점성, 노화 특성 분석 결과, 중모2008은 HRW과 유사한 반죽 특성을 나타내었고, 백강과 황금은 T55와 유사하였다. 깜빠뉴의 제빵 특성 분석 결과 국산밀의 평균 빵 부피와 속질 경도는 553.76 mL, 5.58 N였으며 특히 중모 2008의 경우, 부피는 602.16 mL, 비용적 2.47 N 로 가장 우수한 발효 부품성을 나타내었다. 본 연구는 향후 천연 발효빵에 적합한 국산밀 품종 선발 및 블렌딩 비율 설정과 소비자가 선호하는 다양한 제품 개발의 기초자료로 활용될 것으로 기대된다.

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PE-0055

Development of PCR markers for primary screening and safety management of GM rice plants

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Since the first commercialization of genetically modified (GM) tomato, GM rice plants with a trait of resveratrol biosynthesis, insect-resistance, or herbicide-tolerance were developed and intensively studied for environmental risk assessments in Korea. Other many rice plants carrying diverse traits of biotic/abiotic stress-tolerance, bio-pharming, or composition change were developed and studied domestically. In this study, we collected and extracted information from over a hundred GM rice plants including 100 of domestically developed lines, 8 of commercial events, and several other from websites. Functional components of introduced T-DNA(s) such as promoters and terminators were categorized. Based on these data, we confirmed 7 sets of PCR primers, 2 new primer sets, which can be used for the primary screening of GM rice plants. Several GM rice plants were used to prove efficiencies of these primers and qualitative PCR analysis. In this respect, these PCR primer sets would be a reliable tool to detect transgenes from GM rice plants, and could be used for the safety management of rice food chains in Korea.

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PE-0056

RNA-seq analysis of intergenic *PsGPD* transformation with improved drought tolerance in rice

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Plants are often exposed to biotic and abiotic stressor that affects plant growth, development, and productivity. Drought is an important abiotic stress that has a particularly serious impact on plant growth and development. We transformed rice with *PsGPD* using Agrobacterium-mediated transformation. We generated independent *PsGPD*-homozygous transgenic rice plants selected as single copy/intergenic lines by the TaqMan copy number assay and by T-DNA flanking sequences. These transgenic rice plants showed improvement of drought tolerance compared to wild-type plants under drought condition. RNA sequencing analysis showed that 2,992 genes were transcriptionally affected by the *PsGPD* transgene or drought treatment. In total, 145 genes were modulated by the *PsGPD* transgene before and after drought treatment. Among these candidate genes, 4 were up- and downregulated in all four comparisons. Several genes, including Os04t0576900, Os03t0629800, and Os04t0518400 (OsPAL7), were involved in tetrapyrrole synthesis. Os09t0522200 (DREB1A), an important component in hormone signal transduction, is a transcription factor (TF) gene that plays vital roles instress response. We partially characterized the functions of *PsGPD* in the drought stress response and the role of major TFs in the drought tolerance mechanism. These genes will be useful targets for both future research and the breeding of drought tolerance in rice.

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PE-0057

Comparison of radiosensitivity response to acute and chronic γ-irradiation in rice

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Biological responses of plants to radiation vary, affected by the total dose as well as irradiation rates. This study was performed to compare physiological and growth responses between acute and chronic irradiation with different doses. Rice plants were exposed to gamma rays with doses of 100, 200, and 300 Gy, 8 hours for acute irradiation and 10 days chronic irradiation, respectively. Analyses of DNA damage, oxidative stress including free radicals and lipid peroxidation, radical scavenging and antioxidant activities showed that all indices increased immediately after irradiation by both acute and chronic irradiation in a dose dependent manner. Overall, irradiation effect seemed to be greater in acutely irradiated plants. Photosynthesis efficiency and growth measured 10, 20, 30 days after irradiation showed decrease in irradiated plants, similarly plants were affected more severely by acute irradiation than by chronic irradiation. On the other hand, acutely irradiated plants produced seed progenies with dramatically decreased fertility rate but chronically irradiated plants could not produce fertile seeds. These results suggest that acute irradiation instantly causes more damage physiologically, whereas chronic irradiation causes substantial damage that make reproduction impossible.

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PE-0058

A Study on the Association of Endogenous Gibberellic Acid with Voltage-Dependent Anion Channels (VDAC) in Seed Germination through CRISPR/Cas9-Mediated Targeting Mutagenesis

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Anion channel is one kind of membrane transporters and ubiquitously distributed in plant membranes. The voltage-dependent anion channels (VDACs) are found on the outer mitochondrial membrane of all organisms. VDAC has been isolated from mitochondria of all eukaryotic kingdoms and forms large voltage-gated pores when incorporated into the plasma lipid bilayers. VDAC is permeable to molecules with a molecular mass smaller than a 6 kDa which freely pass through the channels in their open state. In the previous study, we isolated the TaVDAC gene by transcriptome analysis under pre-harvest sprouting (PHS) treatment as a down-regulated transcript in Korean wheat. To identify the physiological mechanism under PHS stress, we conducted on generating targeted mutagenesis plants using CRISPR/Cas9 technology in Brachypodium distachyon. Two T3 homozygous mutant seeds were evaluated for seed germination under hormone treatment. The VDAC knockout mutants were less germination on normal medium and hardly germinated on PAC medium compared to WT. The expression analysis in the GA biosynthesis pathway using qRT-PCR showed the opposite expression pattern for the KS gene in knockout mutant lines. These results revealed that the VDAC gene may be involved in GA biosynthesis or signaling. Further, experiments will be discussed.

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PE-0059

Analysis of KIX and PPD genes related to organs size regulation in Soybean

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Soybean (*Glycine max* L.) is one of the most important crops worldwide used as food and forage. With the completion of the soybean genome sequence, extensive functional genomics becomes possible for the genetic improvement of soybean. One of the most important agronomic traits in soybean is yield, which includes increased seed size as grain and leaf biomass as forage crops. Studies for regulation of plant organs size were performed mainly in Arabidopsis and the KIX-PPD complex were recently reported to influences organs size by regulating cell proliferation and growth. We identified the genes in soybean genome using the database of KIX base and soybase. Three paralogs of KIX8, two paralogs of KIX9 and two parologs of PPD were isolated to from cDNA of six soybean cultivars. An analysis of the deduced amino acid sequences indicated that paralogs of GmKIX8 and GmKIX9 conserved KIX domain that share high amino acid sequence similarities. Two members of PPD genes also showed the similarly structured containing eight introns and nine exons, although the lengths of each intron and exon size differ among two genes. To better understand of KIX-PPD complex related to organs size of soybean, we are doing on functional analysis of these genes using soybean accessions with various seed size.

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PE-0060

Molecular characterization of genes related to soyasaponins biosynthesis pathway in Soybean

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Soybean (*Glycine max* L.) is one of the most economically valuable crops, because its seeds contain high-quality protein and abundant lipids. Furthermore, soybean seeds contains various secondary metabolites, such as soyasaponins, lutein and isoflavone. Soyasaponins have recently attracted attention because its various health benefits, including the prevention of dietary hypercholesterolaemia, antioxidant and anticarcinogenic activity. Understanding the biosynthetic genes of soyasaponins will provide new approaches to control the pathway for valuable seed production. Some genes were reported by the genetic and functional studies using the soybean mutant population. CYP72A69 gene were known as a regulators of GroupA and DDMP saponins. We isolated four CYP72A69 paralogs from cDNA of six soybean cultivars for regulation of soyasaponins pathway by genome editing. To better understand the regulation and function of GmCYP72A69 genes, we currently are being analyzed the molecular characterization of GmCYP72A69 genes.

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PE-0061

중만생 고품질 복합내병성 벼 '새봉황'

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'새봉황'은 직파적응성이며 외관 미질이 깨끗하며 병에 강해 재배안정성이 높은 남부지역 적응 중만생 고품질 품종개발을 목적으로 국립식량과학원에서 2009/2010년 동계에 밥맛이 좋고 수량성이 높으며 단간인 복합내병성 품종 호품을 모본으로 하고 중생종으로 쌀이 깨끗하며 간장이 중간인 히토메보레를 부본으로 3번 여교잡 교배하여 육성하였다. 인공교배로 교배립 25립을 수확하였고 이 교배립은 세대진전을 위하여 2010년 하계에 국립식량과학원 벼육종포장에서 F1 20개체를 재배하였다. 우량품종을 조기 육성하기 위하여 F2 1,200개체를 양성하였고 이후 계통육종법으로 육성하였다. 2012년 F3이후부터는 초형과 수량성, 미질, 잎도열병검정, 흰잎마름병검정을 실시하여 F3에서 73계통, F4에서 120계통, F5에서 70계통을 선발하였고, 2015년과 2016년에 우수계통인 HR28694-19-2-5에 대하여 계통육성과 동시에 생산력검정을 실시하였고 생육특성, 수량성, 내병성(도열병, 흰잎마름병, 줄무늬잎마름병), 미질, 밥맛 등과 토중출아성이 우수하고 흰잎마름병 및 줄무늬잎마름병에 저항성이고 쌀 외관 품위가 우수한 HR28694-19-2-5-4-1 계통을 선발 '전주610호'로 계통명을 부여하였다. '전주610호'는 2017~2019년 직파재배 5개소, 보통기 재배 전국 8개소, 이모작재배 2개소에서 지역적응시험을 실시한 결과 호품벼의 간장, 외관미질과 수발아성이 개선되고 수량성, 내병성(흰잎마름병, 줄무늬잎마름병)이 강하고 쌀 외관품위와 밥맛이 좋은 계통으로 2019년 12월 농촌진흥청 농작물직무육성 신품종선정심의회에서 그 우수성이 인정되어 품종명을 '새봉황'으로 명명하였고 충남이남평야지 및 서남부해안지(충남, 전남북, 경남)에 적응하는 품종으로 보급하게 되었다.

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PE-0062

지역에 따른 소립 나물용 콩의 종자 및 콩나물 특성 변이

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콩나물용 콩은 재배적 특성뿐만 아니라 종자의 품질과 콩나물 특성 또한 매우 중요하다. 재배 지역에 따른 종자 및 콩나물 특성을 분석하여 지역별 영향과 유전형별 반응을 통해 품종개발 및 적응지 선택을 위한 기초자료로 사용하기 위해 본 실험을 수행하였다. 2년간(2018~2019년) 4지역(경기 수원, 전남 나주, 대구 달성, 제주)에서 생산된 4 품종 및 계통(풍산나물콩, 밀양341호, 밀양356호, 밀양358호)을 이용하여, 100립중, 균일도(6.3 - 5.6 - 4.0mm), 콩나물 특성을 조사하였다. 콩나물 재배는 300립을 4시간 침종 후 암실 내 20±1℃ 기온 및 수온에서 매 4시간 관수하여 5일간 재배하고 평가하였다. 평가 항목은 콩나물 전장, 배축장, 배축굵기, 발아특성(부패립, 경실립, 미발아립), 수율이다. 지역별 100립중 조사 결과 품종 및 계통별로 지역별 무게의 순서는 차이가 있었으나, 평균 달성에서 12.0g, 나주에서 11.5g, 수원에서 11.4g이었으며, 특히 제주에서 9.6g으로 가벼운 것으로 나타났다. 지역별 균일도 조사 결과 평균적으로 내륙지역에서는 5.6mm 비율이 가장 높았으며 수원 54.3%, 달성 62.2%, 나주 58.7%로 나타났으며 제주에서는 4.0mm 비율이 75.5%로 가장 높아 제주에서 콩 100립중과 알멩이 크기가 가장 작아지는 것으로 나타났다. 지역별 콩나물 재배특성을 조사한 결과 품종간 반응 차이는 있었으나 대체로 달성에서 콩나물 전체 길이가 긴 것으로 나타났다. 수율은 4 지역간 통계적 차이는 없었으나 제주가 평균 597%로 가장 높았다. 주요 품종(풍산나물콩, 아람, 해원)으로 종자 크기에 따라 콩나물 특성을 조사한 결과 6.3mm 종자가 콩나물 전체길이, 배축길이, 뿌리길이가 가장 긴 것으로 나타났으며, 미발아율과 경실율은 4.0mm에서 비교적 높았다. 수율은 알이 비교적 큰 풍산나물콩은 5.6mm에서 가장 높았으나, 알이 작은 아람과 해원은 6.5mm에서 높았다. 지역에 따라 종자 무게와 크기 및 균일도가 달라지며, 품종에 따른 종자 크기별 콩나물 품질도 달라질 수 있음으로 최적 규격 조사방법 및 설정에 대한 연구가 필요할 것으로 생각된다.

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PE-0063

‘오대’ 쌀 외관특성 및 재배안전성이 개선된 ‘철원104호’ 특성

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우리나라 조생 대표 벼 품종인 ‘오대’는 중북부지역에서 일교차가 크고 일장이 길어 쌀알이 굵어도 등숙이 양호하지만, 쌀에 심복백이 있고 단백질함량이 다소 높으며 내병성이 없는 단점이 있다. 본 연구는 ‘오대’의 쌀 외관, 미질특성 및 내병성이 개선된 ‘철원104호’를 육성하여 그 특성을 밝히고자 하였다. ‘철원104호’는 ‘오대’를 모본, 중만생 중립 내병성 ‘다미’를 부본으로 교배하여 중립이면서 내병성, 내수발아성 등 재배안전성이 높고 심복백이 감소된 고품질 계통이다. ‘철원104호’의 출수기는 7월 25일로 ‘오대’와 같다. 간장은 69㎝로 ‘오대’보다 약 5㎝ 작고, 현미천립중은 24.4g으로 비슷하다. 쌀 수량성은 583kg/10a 로 ‘오대’와 같은 수준이다. 쓰러짐에 강하고 도열병, 흰잎마름병에 강하며, 수발아는 14.1%로 중강 정도의 반응을 보였다. 쌀알 외관이 깨끗하고 단백질함량이 낮으며 윤기치가 ‘오대’보다 높다. ‘철원104호’는 밥 냄새와 밥맛이 ‘오대’와 비슷하여 향후 쌀 외관특성과 내병성이 개선된 ‘오대’ 대체 품종으로 활용이 가능할 것으로 기대된다.

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PE-0064

Construction and Analysis of wheat core collection using wheat SNP chip

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Wheat is one of major crops for mankind in the world and plenty of breeding materials are developed to improve genetic background. However, a huge genome size of wheat, 17G, provide several obstacle in the wheat breeding. The draft sequence of Chinese spring, a representative variety of wheat, was identify in 2018, but it is still difficult to apply it to Korean wheat. In this study, we collected the Korean wheat and various foreign varieties to construct a core collection suitable for the Korean cultivation environment. A total of 1,969 accession were performed 73,000 PCR with 37 allele specific SSR markers to select specific polymorphism and then analyzed with Genecore and Corehunter for primary core collection. After selection of 614 accession for primary core collection, that was performed to genotyping analysis using Axiom 384 wheat SNP chip for core collection. A total of 19 agricultural traits were analyzed with SNP genotyping data to execute Genome Wide Associated Study (GWAS).

We selected several SNPs that are thought to be closely related to the heading date (AX-95112052, AX-94848813_Pyuvate decarboxylase related), ripening period (AX-94911569, AX-95140058, AX-94950266_Inodle-3- Acetic Acid related), loading (AX-94489976_reticulon-like protein related), culm length, seed coat color and cold damage (AX-95188125_auxin response factor related, AX-94517396). After evaluation SNPs to domestic varieties and core collection, SNP markers may be developed for Korean wheat agricultural traits from core collection.

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PE-0065

두부특성 간이검정법 개발과 RIL계통을 활용한 QTL 탐색

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콩은 주로 식물성 단백질과 지방으로 이루어져 있어 영양상 동물성 단백질의 대체 식품으로 많이 사용되고 있다. 국내에서 콩을 이용한 두유, 두부, 된장, 간장, 콩나물 등의 다양한 식품이 소비되고 있으며 이중에서 두부는 콩으로 만든 식품 중에서 가장 대중적이며 전통적인 가공식품이다. 두부는 대두의 수용성 단백질을 용출하여 칼슘이나 마그네슘을 함유한 염에 의해 압식 제조하는 것으로 두유에 존재하는 지방, 탄수화물, 비타민 등 다양한 영양성분이 함께 존재하는 영양가가 우수한 식품이다. 콩에 대한 연구동향이 과거에는 수량에 관련한 연구가 중점적으로 추진되어졌다면 최근에는 콩의 용도에 따른 맞춤형 및 각종 기능성이 강화된 신품종의 개발로 관심이 집중되고 있다. 본 연구는 고수율의 두부 및 두유용 콩 품종의 개발을 위해 대량의 시료를 효율적으로 검정할 수 있는 간이검정법을 개발하고, 나아가 RIL집단에 간이검정법을 적용하여 두부 가공적성과 연관된 QTL 탐색 하기위해 수행하였다. 먼저 국내 콩 20품종을 이용하여 두부 제조 일반검정법과 높은 상관관계를 보이는 두부 제조 간이 검정법을 탐색하였다. 두부 제조 간이 검정법은 15g의 콩을 사용하여 마쇄 및 가열 후 두유로 거르는 단계에서 자연여과법(필터), 가중압착법(면포), 압착법(짤순이), 원심분리법(탈수기)의 네가지 방법으로 두부를 제조하였으며 100g의 콩을 사용한 일반검정법의 두부 수율과 상관관계를 분석하였다. 두부 가공적성과 연관된 QTL 탐색을 위해 대풍 x 새단백 RIL(Recombinant Inbred Line)집단에 개발한 간이검정법을 적용하여 표현형을 탐색하였고 180k soya SNP array을 활용하여 Genotyping 결과를 확보하였다. 이후 QTL ICIMapping V4.1 프로그램을 사용해 유전자 지도 작성 및 QTL를 탐색하였다. 그 결과 두부 제조 간이검정법은 네가지 방법 중에서 탈수기를 활용한 원심분리법이 가장 효율적이며 높은 상관관계를 보였다. 대풍 x 새단백 RIL의 QTL탐색 결과 3번 염색에서 의미 있는 영역을 탐색하였다.

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PE-0066

Evaluation of drought resistance of potato breeding lines by water stress for selection good potato line

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Potato production has recently been going down because high temperature drying environment was made by climate change. We need to make good cultivar that have drought resistance. Potato lines that selected by drought resistance test *in vitro* were planted on plastic box. We evaluated shoot, root, yield characteristics by water stresses that normal, dry and over-dry. Shoot characteristics in dry and over-dry was worse than in normal. Stem length and weight of control cultivar were 27.4 cm, 99.6g in over-dry environment and shoot potato lines were 12.3~57.6 cm, 20~202.6g. Although root weight did not showed difference, root length in dry was longer than normal. Root length and weight of control cultivar that were 8.1 cm, 1.5g in over-dry and potato lines were 10.8~24.2cm, 1.0~6.6g. Yield characteristics that were the number of tubers was 19.6, weight was 382.7g in over-dry were worse than normal. Yield characteristics of control cultivar in over-dry were that the number of tubers was 19.6, total weight was 344g. Potato lines were that the number was 4~33, total tuber weight was 12-568.7g and average weight per tuber was 3~26g.The result in compare characteristics by water stresses was that of BE lines were worse than control cultivar in over-dry. On the other hand, LF lines were excellent in over-dry. We will check characteristics related drought resistance of main potato lines once more in this year and on field in next year. So, we will select good potato line that was strong in drought environment and develop selection technology.

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PE-0067

Participatory varietal development: A premium rice variety, ‘Alchanmi’, for local rice brand in Gyeonggi province, Korea

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Participatory rice breeding has been implemented only recently in Korea to address problems of replacing foreign varieties which have long been adopted and grown by some of local rice processors or rice businesses. These foreign varieties are quite old varieties which are easy to lodge and susceptible to disease and insect. A premium quality medium-maturing rice, ‘Alchanmi’ was developed and released in 2018 by collaboration among various stakeholders; rice breeders of NICS, Icheon City, rice processing center and farmers of the Icheon rice area of Gyeonggi province. This participatory breeding required series of activities including elite line selections, participatory testing, demonstrations, seed productions, sensitization of farmers by education and training, and propaganda etc. ‘Alchanmi’ was mated in 2008 with ‘Junam’ and ‘Chilbo’ as the parent. To shorten the generation, at the F_3 generation it was advanced in the winter green house and a SR32451-GHB-135-1 which showed excellent rice quality and resistance to blast, bacterial blight(race K1, K2, K3) and rice strip virus was selected in fixed generation and given the name of Suwon 600. 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. 'Alchanmi' is middle maturing variety with excellent taste and multiple disease resistance, so it can be satisfied from farmers to consumers and is expected to play a role as a variety that can replace the old foreign variety in Gyeonggi province.

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PE-0068

An Early Maturing Glutinous Rice Variety, 『Gawihyangchal』 with a Savory Aroma

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'Gawihyangchal' is an early maturing glutinous rice variety with a savory aroma developed in 2019. 'Gawihyangchal' was derived from a cross between 'Sheolhyangchal' and 'Samgwang' in 2009. This variety had heading date of August 2 in Gyeonggi Province. Its culm length was 77 cm. This variety had 14 tillers per hill and 95 spikelets per panicle. It was medium-small grain variety that 1,000 grain weight of brown rice was 21.7g. Its protein contents of milled rice was 6.7% and milling ratio was 75.3%. The yield of milled rice was 4.53 MT/ha under the ordinary culture of the local adaptability test in 3 areas of Gyeonggi Province for three years. 'Gawihyangchal' would be adaptable to Gyeonggi Province.

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PE-0069

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

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A new waxy corn hybrid 'Seamichal' is a single cross hybrid developed by Gyeonggi-do Agricultural Research & Extension Services(GARES), Hwaseong, Korea in 2017. This hybrid was made by crossing between seed parent GMW0039 and pollen parent GMW0082. 'Seamichal' which showed good growth and eating quality, had 65 days of growth duration from seeding to silking, 6 days faster than Ilmichal, ear length of 19.3 cm and ear diameter of 40.6 mm, and ratio of kernel set length to ear length of 96.2%. The number of fresh ears harvested per unit area was larger than Ilmichal but the weight of fresh ears per unit area was lower than Ilmichal in regional yield trials(RYT) from 2015 to 2017. This cultivar would be well adaptable to the Gyenonggi province.

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PE-0070

Probable L-ascorbate peroxidase 4 gene from an interspecific cross show enhanced yield and antioxidant activity

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We previously identified a yield-related QTL including plant height and grain weight in a near-isogenic line (NIL) derived from an interspecific cross between *Oryza sativa* and *O. rufipogon*. Map-based cloning approaches revealed that probable L-ascorbate peroxidase 4 (APX) is associated with the yield QTL cluster. To predict the candidate gene responsible for the QTL cluster, we carried out gene expression analysis using various tissues between Hwaseong and NIL. Sequence differences of probable L-ascorbate peroxidase 4 gene were observed in the coding region between two parental lines including a 3-bp InDel in the exon. In order to demonstrate the role of gene in abiotic stresses tolerance, we compared the growth of Hwaseong and NIL plants under drought, cold (10℃), salt (200mM NaCl) and oxidative stress (5mM H_2O_2) treatment, respectively. Also, whether APX gene is involved in the ROS-scavenging metabolism, we used DAB staining, DPPH assay and measured the APX activity in Hwaseong and NIL plants. To know the subcellular localization of APX protein, it was constructed to the C-terminal site of the GFP vector. We generated probable L-ascorbate peroxidase 4 gene over-expression (OE) transgenic plants in Hwaseong background. APX-OE lines had increased gain size and weight than Hwaseong plants whereas APX T-DNA knock-out (KO) mutant lines showed reduced grain size and grain weight.

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PE-0071

qLTG1 reveals the grain size, abiotic stress resistance and low-temperature germination in rice

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Seed germination is being delayed or inhibited under several kinds of stress such as temperature, salt, and osmotic pressure. The high germination rate for low-temperature is an important factor in growing rice. In the direct-seeded method in rice, low-temperature germinability is considered as one of the factors for stable plant stand establishment in temperate regions and high altitude areas. Previously, the *qLTG1* was detected and located between RM10313 and CRM37 on chromosome 1 within 32.1 kb region harboring 7 genes. Also, we detected the *qLTG1* as the quantitative trait locus (QTL) that plays a vital role in controlling tolerance to a low temperature in seed germination stage and tolerance for several abiotic stresses using progenies derived from a cross between *Oryza sativa* (cv. Hwaseong) and *Oryza rufipogon* (IRGC 105491). To identify the genes targeted by *qLTG1*, the expression profiles of the identified candidate genes and germination behavior of qLTG1 under different low-temperature conditions were investigated and compared to HS, Rufi, and TR5 (BC_3F_7). These results indicated that *qLTG1* showed tolerance for several abiotic stresses such as salt, drought, and low temperature. The *qLTG1* for low-temperature germinability would be useful in rice breeding programs especially in the development of lines possessing low-temperature germinability.

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PE-0072

Fine mapping and association with dark-tip embryo using transgenic plants and NILs from a cross between *Oryza sativa* and *Oryza rufipogon*

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Hybrid weakness, a form of hybrid incompatibility that appears at the post-embryonic stage during plant development, is frequently observed throughout plant taxa. Hybrid weakness establishes itself through characteristic dwarfing of the F_1 plants, chlorotic phenotype, stunted growth, necrotic tissues, defective root development, and partial or complete sterility. This phenomenon can be regarded as the opposite of hybrid vigor that is believed to be controlled by the interaction of genes from both parents. A novel dark tip embryo phenotype (*DTE*) was observed in an introgression line, derived from a cross between *Oryza sativa* spp. *japonica* cultivar 'Hwayeong' (HY) and *O. rufipogon* accession, W1944. The DTE-NIL plant had protruding embryos and also showed alterations on the inner floral organs such as several stigmas and carpels. The gene responsible for this phenotype was mapped within 28.8-kb region on chromosome 9 with three candidate genes. The DTE phenotype is a new trait not seen in the parent generation and appears to be a result of hybrid weakness. These results will contribute to an understanding of the molecular mechanism causing hybrid weakness and rice breeding program.

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PE-0073

Characterization of QTL for Spikelet Number per Panicle Using a Nearly Isogenic Line Derived from an Interspecific Cross in Rice

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Previously, we mapped the qSPP7 QTL affecting the number of spikelets per panicle (SPP) on rice chromosome 7 using near-isogenic line (NIL WH29001) derived from an interspecific cross between the *japonica* 'Hwaseong' and Oryza minuta. In the present study, we confirmed this QTL using progeny derived from a cross between IL102, a WH29001 sister line and Hwaseong. Genetic analysis determined that qSPP7 was located between a KASP marker KJ07-049 and RM21605. The *O. minuta* segment on chromosome 7 introgressed into the Hwaseong background was associated with an increase in SPP. The panicle structure of IL102 revealed that not only the number of SPP increased significantly, but also the number of branches per panicle increased as compared to Hwaseong suggesting that the donor allele of qSPP7 promotes branching in the genetic background of Hwaseong. Linkage analysis indicated that *qEhd1* on chromosome 10 is involved in the difference in heading date of IL102 and Hwaseong. Experiments under 3 different day length conditions revealed that IL102 always showed earlier heading and higher SPP as compared to Hwaseong indicating that the effect of *qSPP7* in the Hwaseong background was not dependent on photoperiod, and SPP increased in proportion to the number of days to heading.

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PE-0074

QTL mapping for starch-related traits in rice using recombinant inbred lines derived from a cross between *japonica* cultivars

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Quantitative trait loci (QTLs) for starch-related traits such as amylose content (AC) and resistant starch (RS) have received much research attention in recent years due to the potential health benefits of cereals high in AC and RS. In this study, QTLs associated with AC and RS were identified using 92 recombinant inbred lines (RILs) developed from a cross between two closely-related *japonica* cultivars 'Dodam' (DD) and 'Hwayeong' (HY) in a two-year field experiment. 210 F_2 plants derived from a cross between Hwayeong and two selected RILs were used to analyze the possible interaction between starch branching enzyme 3 (*SBE3*) and granule-bound starch synthase 1 (*GBSS1*). One QTL on chromosome 2 for RS and 5 QTLs for AC on chromosomes 1, 2, 5, 6, and 11 were detected in RIL, respectively. Among 5 QTLs for AC, two major QTLs on chromosomes 2 and 6 allelic to *SBE3* and *GBSS1*, respectively explained 34.1% and 23.8% (2017) and 17.3% and 55.4% (2018) phenotypic variation and the Dodam alleles increased the AC. The concerted effect of *SBE3* and *GBSS1* in the F_2 population suggested that both genes act in an additive manner functionally complementing each other as AC between HY homozygous F_2 plants (14.51%) and DD homozygous F_2 plants at *SBE3* and *GBSS1* (34.76%) was significantly different. Preliminary findings on the joint effect of *SBE3* and *GBSS1* imply that gene interaction possibly exists and may play a part to regulate the starch-related properties of rice.

Keywords: recombinant inbred lines, amylose content, resistant starch content

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PE-0075

Quantitative trait loci analysis for germination and coleoptile length under low- temperature condition using introgression lines derived from an interspecific cross in rice

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Previously, five putative QTLs for LTG were detected using 96 BC_3F_8 lines derived from an interspecific cross between the Korean *japonica* cultivar "Hwaseongbyeo" and *O. rufipogon*. In this study, we used two introgression lines CR1517 and CR1518 as parents to detect additional QTLs and analyze interactions among QTLs for LTG. The F_2 population (154 plants) along with parental lines, Hwaseong and *O. rufipogon*, were evaluated for LTG and coleoptile length under low-temperature condition (13℃). A total of 4 QTLs for LTG were detected and these QTLs explained 3.2-23.8% of the total phenotypic variance at 6 DAI and 5.4-22.1 % at 7 DAI. Among them, 2 major QTLs *qLTG1* and *qLTG3* were consistently detected at 6 and 7 DAI. Two minor QTLs were detected on chromosomes 8 and 10. Interestingly, the Hwaseong allele at *qLTG10* on chromosome 10 increased LTG whereas the *O. rufipogon* alleles at the other loci increased LTG. Based on the location on chromosome 8, *qLTG8* appears to be a new QTL for LTG. Two-way ANOVA analysis indicated that interaction between *qLTG1* and *qLTG8*, and *qLTG3* and *qLTG8* were not significant, implying that these QTLs act in an additive manner. Accordingly, the F_2 plants with the combination of *O. rufipogon* alleles at *qLTG1*, *qLTG3* and *qLTG8* and Hwaseong allele at *qLTG10* showed higher LTG than CR1518 harboring *O. rufipogon* alleles at 4 QTL. For coleoptile length, 3 QTLs on chromosomes 1, 3 and 8 were observed and they were colocalized with LTG QTLs suggesting the pleiotropy of the single gene at each locus.

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PE-0076

Development and characterization of EMS-induced salt-tolerance silage maize mutant

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Maize (*Zea mays* L.) is one of the most valuable agricultural crops and grown under a wide spectrum of environmental conditions. However, maize is due to moderately sensitive to salt stress, soil salinity is a serious threat to its production worldwide. In this study, we used ethyl methanesulfonate (EMS) for generate the salt-tolerant silage maize mutants. We screened salt-tolerant lines from 203 M_3 mutant populations by evaluating the morphological phenotype after salt stress treatment and selected 140ES91 line. The 140ES mutant shows improved plant growth, higher proline contents and leaf photosynthetic capacity compared with wild-type under salt stress conditions. Furthermore, the expression pattern of three genes involved in salt stress response was increased in the 140ES91 mutant by salt stress. In whole-genome re-sequencing analysis, 1,103 single nucleotide polymorphisms (SNPs) and 71 insertions or deletions (InDels) identified as common variants between KS140 and 140ES91 against reference genome. The mutant line identified in our study could be used as an improved breeding materials for transfering salt tolerance traits in maize variety.

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PE-0077

Development and characterization of gamma radiation-induced mutants with salt tolerance in silage maize

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Salt stress is a significant factor limiting growth and productivity in crops. However, little is known about the response and resistance mechanism to salt stress in maize. The objective of this research was to develop an enhanced salt-tolerant silage maize by mutagenesis with gamma radiation. To generate gamma radiation-induced salt-tolerant silage maize, we irradiated a KS140 inbred line with 100 Gy gamma rays. Salt tolerance was determined by evaluating plant growth, morphological changes, and gene expression under NaCl stress. We screened 10 salt-tolerant maize inbred lines from 2,248 M2 mutant populations and selected a line showing better growth under salt stress conditions. The selected 140RS516 mutant exhibited improved seed germination and plant growth when compared with the wild-type under salt stress conditions. Enhanced salt tolerance of the 140RS516 mutant was attributed to higher stomatal conductance and proline content. Using whole-genome re-sequencing analysis, a total of 328 single nucleotide polymorphisms and insertions or deletions were identified in the 140RS516 mutant. We found that the expression of the genes involved in salt stress tolerance, ABP9, CIPK21, and CIPK31, was increased by salt stress in the 140RS516 mutant. Our results suggest that the 140RS516 mutant induced by gamma rays could be a good material for developing cultivars with salt tolerance in maize.

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PE-0078

In vitro selection and characterization of salt stress tolerant cultivars in silage rice

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Salinity is one of the major abiotic stress that inhibit growth, yield and productivity of crop plants. Therefore, it is necessary to develop an increased salt tolerance crops for the cultivation in saline soil such as reclaimed land. The objective of this study is to develop a salt-tolerant silage rice lines that grow on reclaimed lands. In order to develop a salt-tolerant silage rice, we carried out to transfer Saltol, a major QTL associated with salt tolerance, from IR64-Saltol, a salt-tolerant indica variety, into Mogyang, a susceptible elite japonica variety. To determine the effect of salt stress, Mogyang and IR64-Saltol cultivars were grown on medium containing various concentrations of NaCl in in vitro condition. The shoot length was decrease with increasing salt concentration and roots growth was almost arrested at over 50 mM NaCl concentration in Mogyang cultivar. Based on the preliminary results, we screened 5 salt-tolerant lines showing better growth under salt stress conditions. PCR and sequencing results showed that the introgression type of Saltol QTL in almost of selected lines were derived from IR64-Saltol cultivar. Based on the growth and physiological conditions, the new Saltol introgression lines showed higher salt tolerance compared to the parental cultivar Mogyang. The salt-tolerant lines identified in this study could be used as a genetic resource to improve salt tolerance.

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PE-0079

Isolation and molecular characterization of the FLC homologs for early- and late-flowering Brassica genotypes

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Flowering repressor called *FLOWERING LOCUS C* or *FLC* is found to influence the optimum flowering time in the Cabbages (*Brassica oleracea* L.), an important vegetable crop. *B. oleracea* genome contains four *FLC* homolog genes (*BoFLC1*, *BoFLC.C2/4*, *BoFLC3*, *BoFLC5*) which have been characterized already for premature flowering under verbalization or low temperature. Here, we describe the molecular characterization of *FLC* homologs between early- and late-flowering Brassica cultivars. Through allele-specific polymerase chain reaction (ASPCR) amplification and cloning, a total of 10 *BoFLC* encoding genes from early- and late-flowering cultivars of green Cabbage (*B. oleracea* var. *capitata*) (*BoFLC1*, *FLC2/4*, and *FLC3*), Broccoli (*B. oleracea* var. *italica*) (*BoFLC1*) and Kohlrabi (*B. oleracea* var. *gongylodes*) (*BoFLC1*) were obtained, all of them had typical structural features of *FLC* orthologs from Brassica and related species. The identified sequence variations result from cis polymorphism at *BoFLC* homologs, which might be critical for *FLC* transcription and possibly contributed in flowering time variation between the early- and late-flowering cultivars. *BoFLC1* showed a stronger transcript accumulation than *BoFLC2/4* or *BoFLC3*. Further, the mRNA expression levels of *BoFLC1* genes were higher in late-flowering cultivars of green Cabbage, Broccoli and Kohlrabi under field conditions, indicating that the *BoFLC1* transcript levels possibly could be associated with flowering time variation. The genetic improvement of late-flowering is a major objective of the cabbage breeding industry. Therefore, the identified *BoFLC* allelic variants in this study will facilitate the breeding of cabbage varieties with late-flowering through targeted genome editing technology using engineered nucleases such as CRISPR-CAS9.

Keywords: *Brassica oleracea*, Cabbage, FLC, vernalization, AS-PCR, Early- and late-flowering

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PE-0080

Sweetpotato variety 'Bodeuremi' with high yield and moist texture

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Domestic sweetpotato production per unit area decreased 31.8% from 21.4 MT/ha in 2000 to 14.6 MT/ha in 2018 due to the cultivation of varieties vulnerable to pests and diseases. To improve the productivity of sweetpotatoes, it is necessary to develop sweetpotato varieties that are resistant to Fusarium wilt and root-knot nematode. 'Bodeuremi' has storage roots with elliptic shape, red skin, and light orange flesh. 'Bodeuremi' took 17 days to be sprouted 50% of storage roots transplanted, and it was two days earlier than that of 'Pungwonmi' variety. 'Bodeuremi' was suitable for early-season culture because the amount of product of storage roots under early-season culture was 30.3 MT/ha, which is 4% higher than 'Pungwonmi'. The number of marketable storage roots was 2.5, and the average weight of the storage roots was 214 g under normal-season culture in 'Bodeuremi'. The amount of product of storage roots in 'Bodeuremi' was 31.2 MT/ha, which is 2% higher than that in 'Pungwonmi' under normal-season culture. 'Bodeuremi' has cultivation stability, because it is moderately resistant to Fusarium wilt and resistant to root-knot nematode. The texture of the steamed storage root of 'Bodeuremi' is moist, and the palatability of steamed storage roots of 'Bodeuremi' was similar to that of 'Pungwonmi'. The β-carotene content of storage roots of 'Bodeuremi' is 6.1mg/100g dry weight basis. 'Bodeuremi' is expected to contribute to improving the share and productivity of domestic sweetpotato varieties because it has a large number of storage roots under early-season and normal-season culture, and has cultivation stability.

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PE-0081

GORI encoding the WD40 domain protein is required for pollen tube germination and elongation in rice

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Successful sperm cell delivery to the embryo sac is mediated by pollen tube growth in higher plants. The molecular mechanisms underlying pollen germination and tube growth in crop plants remain highly unclear, although these mechanisms are crucial to plant reproduction and seed formation. By screening pollen-specific gene mutants in rice (*Oryza sativa*), we identified a T-DNA insertional mutant of *Germinating modulator of rice pollen* (*GORI*) that showed one-to-one segregation ratio for wild type (WT) to heterozygotes. *GORI* encodes a seven-WD40 motif protein that is homologous to *JINGUBANG/REN4* in *Arabidopsis*. *GORI* is specifically expressed in rice pollen, and its protein is localized in the nucleus, cytosol, and plasma membrane. Furthermore, a homozygous mutant, *gori-2*, created through CRISPR-Cas9 clearly exhibited male sterility with disruption of pollen tube germination and elongation. The germinated pollen tube of *gori-2* exhibited decreased actin filament and altered pectin distribution. Transcriptome analysis revealed that 852 pollen-specific genes were downregulated in *gori-2* compared with the WT, and gene ontology enrichment analysis indicated that these genes are strongly associated with cell wall modification and clathrin coat assembly. Based on the molecular features of GORI, phenotypical observation of the *gori* mutant, and its interaction with endocytic proteins and Rac GTPase (ROP), we propose that GORI plays key roles in forming endo/exocytosis complexes that could mediate pollen tube growth in rice.

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PE-0082

Overexpression of *CBF1* confers heat tolerance in *Arabidopsis thaliana*

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Plants are sessile organisms, and so they commonly subjected to a combination of different abiotic stress. Especially, abiotic stress such as drought, salinity and extreme temperature is the primary cause of crop loss worldwide, reducing crop productivity by an estimated 50% annually. High temperature can directly affect the attribute of diverse cellular components and disrupt metabolic equilibrium, causing cellular malfunction, which eventually leads to cell death. CBFs, also called DREB (dehydration responsive element binding), encode AP2/ERF (APETALA2/ethylene-responsive factor)-type transcription factors. There have been reports that overexpression of CBFs (C-repeat-binding factors)/DREB1s (dehydration-responsive element-binding protein 1) increases freezing tolerance by inducing expression of cold-responsive genes (*COR*) in Arabidopsis. To study the roles of several abiotic stress-responsive genes during heat stress, Arabidopsis plants overexpressing candidate genes such as *HSP101, CBF1, GolS1, NDPK2, YUCCA6, and PRE1* were generated. 10-day-old Arabidopsis seedlings were subjected to the heat tolerance test and overexpression lines of *HSP101* and *CBF1* had an improved tolerance to heat stress. Heat stress also induced expression of HSPs and ROS accumulation. We further analyzed transcripts level of HSPs and ROS scavenging enzymes. As heat treatment time increased, *CBF1-OX* plants showed higher expression levels of HSPs and ROS scavenging enzymes transcripts compared to WT plant. Our results suggest that overexpression of *CBF1* gene confers enhanced heat tolerance in Arabidopsis seedling stages. Based on this result we will continue to investigate whether *CBF1* gene also plays a crucial role for heat tolerance during reproductive stages.

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PE-0083

OsDREB1s gene expression profiles of heat stress response in rice (*Oryza sativa* L.) cultivar Nipponbare (Japonica)

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Plants have evolved the adaptive response to adverse environment, such as drought, cold, salinity, and heat. Understanding the molecular mechanisms of plant response to abiotic stress is a prerequisite for the manipulation of plants to improve stress tolerance and productivity. The DREB transcription factors play an important role in plant abiotic stress tolerance by regulating the expression of many cold or/and drought-inducible genes in an ABA-independent pathway. However, little has been known about heat-related roles of *dehydration-responsive element binding protein 1* (*OsDREB1*) genes in rice. Real-time PCR analysis revealed that the expression levels of *OsDREB1* family genes, which functions in the cold stress response in rice, were increased in Nipponbare under heat stress conditions. Our results suggest that *OsDREB1s* have been shown to be novel factors in transcriptional regulation of heat-responsive gene expression, contributing improved heat tolerance in rice.

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PE-0084

가공용 초다수성 복합내병성 찰벼 신품종 “미르찰”

이지윤*, 조준현, 박동수, 송유천, 이종희, 조수민, 권영호, 이소명, 고종민

경남 밀양시 점필재로 20 국립식량과학원 남부작물부

“미르찰”은 수량성과 재배안정성이 높은 초다수성 찰벼를 개발하기 위하여 2010/2011년 동계 1차에 복합내병성이며 수량성이 높은 밀양240호, 통일형 찰벼인 한강찰1호, 수량성이 높은 한아름이 삼원교배된 F1에 밀양240호를 부본으로 인공교배하여, 2010/2011년 동계 2차에 F1을 양성하였다. 2011년 하계에 F2 집단을 전개하여 1,400개체에서 1립씩 종자를 채종하여 2011/2012년 동계1차부터 2012/2013년 동계 1차까지 3세대를 1개체 1육종법 진전시킨 후 2013년부터 2014년까지 2년간 계통육종법에 따라 세대를 진전시켰다. 이 후 2015년부터 2년간의 생산력검정시험을 거쳐 2016년 밀양328호의 계통명이 부여되었고, 2017년부터 2019년까지 3년간의 지역적응시험 결과, 수량성이 높고 도열병, 흰잎마름병(K1~K3a), 줄무늬잎마름병 및 도열병저항성 등의 우수성이 인정되어 2019년 농작물 직무육성 신품종선정위원회에서 “미르찰”로 명명되었다. ‘미르찰’은 중부, 호남 및 영남 4개 지역에서 출수기가 8월 10일로 일반 중생종보다 4일 정도 늦은 편이다. 벼키는 90㎝로 큰 편이나 줄기의 강도가 강하여 잘 쓰러지지 않으며, 이삭의 길이와 낟알 수는 각각 23㎝와 111개로 보통 수준이다. 벼 포기당 가지수가 많고 현미의 천립무게가 24.7g으로 무겁고 벼알이 잘 여물어 1,000㎡당 평균 쌀수량이 739㎏이다. 도열병에 강하고, 흰잎마름병(K3a) 및 줄무늬잎마름병에 강하여 재배 안정성이 우수하다. ‘미르찰’은 찹쌀가루용으로 이용이 가능하며, 특히 삭힌 찹쌀가루의 입자크기가 일반 찰벼보다 작아 유과 가공 적성이 우수하다.

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PE-0085

Identification of QTL for seedling traits from weedy rice

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The Korean weedy rice, PBR (photoblastic rice) was reported to have light-inducible seed germination (photoblastism) and long mesocotyl than that of cultivar rice. Light-induced effect on germination of seeds was compared among three accessions (Oryza sativa L.), PBR, Milyang 23 and Ilpum. Two QTL for photoblastism were identified on chromosomes 1 and 12 explaining 11.2 and 12.8% of the phenotypic variance, respectively. Moreover, using 120 F8 lines, we identified two QTL controlling mesocotyl lengths on chromosome 1 and 3. The QTL for photoblastism was co-localized with the QTL for mesocotyl length near the SSR markers RM8260-RM246 on chromosome 1. To confirm the co-localization of QTL on chromosome 1, 95 F3 lines were developed from a cross between Ilpumbyeo and CR7124. The CR7124 having photoblastism and long mesocotyl length was selected in 120 F8 lines from a cross between Ilpumbyeo and PBR. The germination rate of Ilpumbyeo in dark (100%) was significantly higher than PBR (13%). The germination rate ranged from 29% to 100% of the 110 F3 lines in dark conditions. The mesocotyl length ranged from 0.9 mm to 16.3 mm of the 110 F3 lines. The mesocotyl length of F3 lines showed significant correlations with germination rate in dark condition ($r = 0.7$, $P < 0.0001$). Using 95 F3 lines the linkage of two QTL for photoblastism and mesocotyl length on chromosome 1 was confirmed. This work was carried out with the support of “Cooperative Research Program for Agriculture Science and Technology Development (Project No. PJ01321401)”, Rural Development Administration.

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PE-0086

고시히카리 줄무늬잎마름병 저항성 근동질 계통 육성

박소연, 강주원, 이지윤, 권영호, 이소명, 신동진, 송유천, 이종희*

경상남도 밀양시 점필재로 20 국립식량과학원 남부작물부 논이용작물과

최근 한반도 기후변화에 따른 병해충 발생 등으로 농작물 재해 발생이 계속 증가되고 있고, 특히 바이러스병의 발생도 증가되고 있는 실정이다. 반면, 소비자의 쌀 소비 트랜드 변화는 고 품질을 선호하는 추세로 고급화 되고 있고, 벼 품종도 이에 발맞추어 오대벼, 일품벼, 신동진벼 등 브랜드쌀 품종의 재배면적이 증가되고 있으며, 외래품종인 고시히카리의 재배면적 또한 지속적으로 증가하고 있다. 그러나 이들 품종은 병해충 저항성이 약하여 피해농가의 발생이 증가 될 우려가 있다. 따라서 본 연구에서는 최근 지속적으로 재배면적이 증가되고 있는 일본 품종인 고시히카리의 줄무늬잎마름병 단점을 개량하고, 외래품종을 대체할 수 있는 근동질계통을 육성하고자 본 연구를 수행하였다. 2016년도 해담쌀과 고시히카리를 교배하여 동계에 F1 종자를 얻었으며, 여교배를 수행하여 얻어진 식물체들에 RSV 저항성마커와 이삭도열병 저항성 마커를 이용하여 헤테로를 선발하였다. 선발된 개체들은 여교배에 이용되었고, BC2F1식물체 8개중 2개를 MAS로 선발하였다. 이후 Background selection을 위해 다형성을 가지는 133개의 KASP를 선발하여 이용한 결과 반복친에 대한 회복율은 평균 61.8%이었고, 자식 후 채종된 세대 각각에 대하여 RSV와 도열병 마커를 이용하여 저항성을 모두 가지고 있는 개체들을 선발하였다. 2차 Background Selection에서 해담쌀 평균 이입 단편수가 적고 반복친의 회복률이 높은 계통들을 선발하여 초장 및 경수, 엽록소 함량에 대한 생육특성을 조사 하였다.

사사: 본 연구는 농촌진흥청 아젠다 사업(과제번호: PJ0142822020)의 지원에 의해 수행되었다.

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PE-0087

직무육성 벼 핵심품종 기반의 NAM 집단 변이다양성 탐색을 위한 표본분석

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우리나라 직무육성 벼 핵심 품종 46종을 모본으로, 화영벼를 부본으로 NAM(nested association mapping) 집단을 구축(46 species * 200 RILs = 총 9,200 plants)하여 세대진전(F6)된 집단 대상으로 유전체 분석 타당성 검토를 위하여 본 실험을 수행하였다. 표본샘플 96종(16조합 * 6개체)의 genomic DNA를 분리하여 GBS 기반의 NGS분석을 실시하고 structure, phylogenetic tree 등 비교분석을 통해 전체 NAM 집단의 전장유전체 연관분석 가능성을 분석하였다. 16개의 subgroup의 QTL 분석 가능성을 검토한 결과 6개의 subset에서 SNP 개수가 540~12,745개로 다양하였고, 전 염색체별로 고르게 분포하여 전체 유전체를 커버할 수 있는 QTL 분석이 가능할 것으로 판단되었다. 전체 NAM 집단 대상 전장 유전체 연관분석 가능성을 분석하기 위하여 주성분 분석결과 96개 샘플의 분포가 두 가지 방법으로 분석한 phylogenetic tree와 일치하였으며, STRUCTURE를 통한 집단구조 분석 결과와 일치하는 것으로 나타났다. 또한, NAM 집단의 이질접합성 인자 비율이 0.007로 매우 낮아 동형접합성 유효성이 인정되어 집단이 충실하게 만들어지고 유지된 것으로 판단되었다. 따라서 본 NAM 집단을 활용하여 목표형질별, 조합별 표현형과 전장유전체 연관분석을 통해 정밀육종이 가능할 것으로 기대된다.

사사: 본 연구는 농촌진흥청 연구사업(세부과제명: 중부지역에서 국내 육성 벼 품종별 작물학적 특성평가, 세부과제번호: PJ013572012020)의 지원에 의해 이루어진 결과임.

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PE-0088

Production of transgenic overexpression population to discover genes related grain size in rice

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The growing population has put more pressure on maintaining food security worldwide. As rice is a staple crop, the increase of rice yield by genetic improvement is indispensable. There are various agronomical traits affecting rice productivity, which include morphological and yield phenotypes of seed and plant. Here, we focus on seed size - a primary trait of the important determinants in crop yield. To discover novel genes regulating seed size, the gene-overexpression pool has been utilized for the screening.

To elucidate novel functions of crop genes, there have been numerous efforts to generate a lot of loss-of-function resources by mutagenesis with chemicals, insertions of transposable elements or T-DNA. Also, activation-tagging lines have been developed using random insertion of enhancers. Recent progress in DNA sequencing technology has enabled the collection of full-length cDNAs with ease and at a cheap price. We have generated genome-wide transgenic pool overexpressing endogenous genes in rice. Unlike loss-of-function resources or activation tagging lines, it is more likely that a mutant phenotype could be conferred on the overexpressed full-length cDNA. Full-length insertion fragments of the constructed cDNA library were selected and the clones were transformed into rice (*Oryza sativa* cv. Dongjin). After the mass transformation into rice through *Agrobacterium* mediated co-cultivation, we obtained T0 transgenic seedlings and also harvested their seeds. To check the difference of seed size, the seeds of T2 generation were utilized. The selection strategy based on the transgenic overexpression pool has been demonstrated as a useful tool in identifying genes and phenotypes for application in crop breeding.

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PE-0089

Rice ETHYLENE RESPONSE FACTOR 101 Promotes Leaf Senescence Through Jasmonic Acid-Mediated Regulation of OsNAP and OsMYC2

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Leaf senescence is the final stage of leaf development and an important step that relocates nutrients for grain filling in cereal crops. Senescence occurs in an age-dependent manner and under unfavorable environmental conditions such as deep shade, water deficit, and high salinity stresses. Although many transcription factors that modulate leaf senescence have been identified, the mechanisms that regulate leaf senescence in response to environmental conditions remain elusive. Here, we show that rice (Oryza sativa) ETHYLENE RESPONSE FACTOR 101 (OsERF101) promotes the onset and progression of leaf senescence. OsERF101 encodes a predicted transcription factor and OsERF101 transcript levels rapidly increased in rice leaves during dark-induced senescence (DIS), indicating that OsERF101 is a senescence-associated transcription factor. Compared with wild type, the oserf101 T-DNA knockout mutant showed delayed leaf yellowing and higher chlorophyll contents during DIS and natural senescence. Consistent with its delayed-yellowing phenotype, the oserf101 mutant exhibited downregulation of genes involved in chlorophyll degradation, including rice NAM, ATAF1/2, and CUC2 (OsNAP), STAY-GREEN (SGR), NON-YELLOW COLORING 1 (NYC1), and NYC3 during DIS. After methyl jasmonate treatment to induce rapid leaf de-greening, the oserf101 leaves retained more chlorophyll compared with wild type, indicating that OsERF101 is involved in promoting jasmonic acid (JA)-induced leaf senescence. Consistent with the involvement of JA, the expression of the JA signaling genes OsMYC2/JA INSENSITIVE 1 (OsJAI1) and CORONATINE INSENSITIVE 1a (OsCOI1a), was downregulated in the oserf101 leaves during DIS. Transient transactivation and chromatin immunoprecipitation assays revealed that OsERF101 directly binds to the promoter regions of OsNAP and OsMYC2, which activate genes involved in chlorophyll degradation and JA signaling-mediated leaf senescence. These results demonstrate that OsERF101 promotes the onset and progression of leaf senescence through a JA-mediated signaling pathway.

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PF-0001

방울토마토에 있어서 대목이용에 따른 생육상황의 변화

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토마토는 재배형태가 장기재배 형태로 바뀌고 있으며, 재배기간 동안 다양한 불량환경 및 병해충을 견디고 재배 후기까지 초세를 유지하는 대목의 필요성이 증가되고 있다. 또한 기존에 개발된 대목들이 풋마름병의 새로운 병원균 레이스가 출현하면서 감수성으로 바뀌고 있어서 저항성 대목 개발이 필요한 실정이다. 본 연구는 방울토마토에 있어서 대목 사용시 생육기간에 따라 생육변화을 조사하여 대목의 활용, 온실 환경 조절 및 양 수분 공급의 자료로 활용하기 위하여 수행되었다. 토마토 대목 4종류와 접수를 활용하여 실험한 결과 생육 초기에 개화위치를 조사한 결과 대목과 접수에 관계없이 영양생장 형태를 보였으며, 일부 대목의 경우 영양생장의 정도가 강한 모습을 보였다. 대목사용의 모든 처리구가 생육후반으로 갈수록 생식생장으로 변환되는 모습을 보였고, 대목을 사용하지 않은 처리 구는 생식생장이 강한 것을 보여서 대목을 사용할 경우 생육후반기에 있어서도 식물체의 초세가 계속 유지되는 현상을 보였다. 생장강도에 있어서도 대목별 초기 생장강도는 차이가 없었지만 생육후기에 있어서는 대목과 접수 간 차이가 있었으며 일부대목의 경우 생육후반기에도 강한 생장강도를 보였다. 이상의 결과를 볼 때 토마토에 있어서 대목을 사용하는 것이 토마토 생산량 증가에 도움을 줄 것으로 판단된다.

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PF-0002

완숙토마토에 있어서 대목이용에 따른 수확량 변화

안율균[1*], 이혜원[1], 홍규현[1], 권덕호[1], 조명철[2], 이준구[3], 황인덕[4]

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풋마름병은 *Ralstonia solanacearum*으로 토마토 재배 시 가장 문제시 되는 병 중 하나이다. 토마토 시설재배에 있어서 토경재배를 하는 경우 연작에 의한 피해가 늘어가고 있으며 풋마름병의 피해도 증가하고 있는 추세에 있다. 현재 풋마름병에 대한 대책으로 대목을 사용하고 있으며, 토마토 접목재배가 점차적으로 늘어나는 추세에 있다. 또한 토마토의 재배형태가 단기재배에서 장기재배로 바뀌고 있다. 다양한 불량환경 및 병해충을 견디고 재배 후기까지 초세를 유지하는 대목의 개발과 기존에 개발된 대목들이 풋마름병에 감수성으로 바뀌고 있어서 저항성 대목 개발이 필요한 실정이다. 본 연구는 토마토 대목을 사용한 접목묘와 접목을 하지 않은 묘를 정식하여 수확기간 동안 수량변화를 관찰하여 대목을 이용할 때 수량증가를 보이는 시기를 조사함으로써 대목사용이 토마토 정밀 생육관리의 자료로 활용하기 위해서 수행되었다. 완숙 토마토에 있어서 생육초기에는 대목을 사용하지 않은 처리 구가 대목을 사용한 처리 구 보다 수량이 많았다. 이는 대목을 이용한 처리 구가 첫 개화일이 늦어서 나타나는 현상이다. 월 별로 수확량의 변화를 살펴보면 광 환경이 좋지 않은 1월과 2월에 수확량이 떨어졌으며, 이후 수확량이 증가하는 경향을 보였다. 대목을 이용한 완숙토마토의 수확량은 1월의 수확량을 제외하면 전체 재배기간 동안 수량이 높은 것을 확인할 수 있었다. 완숙 토마토 재배기간 후반기로 갈수록 접목한 처리 구와 하지않은 처리 구 사이에 수확량 차이는 더 벌어지는 것을 관찰할 수 있어서 토마토 장기재배에 있어서는 대목을 사용하는 것이 높은 수량을 얻을 수 있는 것으로 판단된다.

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PF-0003

Ploidy Level Determination in Several *Phalaenopsis* Species Using Chromosome Counting

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Phalaenopsis, commonly called as moth orchids, is a genus in the family Orchidaceae which comprises of more than seventy species widely distributed in the subtropical and tropical Asia, and northern Australia. It is one of the most popular cultivated orchids worldwide due to its beautiful and long-lasting flowers. Interspecific and intergeneric hybridization have long been used in producing novel cultivars in *Phalaenopsis* orchids however, cytogenetic reports on this genus are very limited. The basic chromosome number of most *Phalaenopsis* species is n = 9, and variations in the chromosome numbers in some *Phalaenopsis* cultivars have been observed which suggest the frequent occurrence of polyploidy in these cultivars. Hence, chromosomal information is essential and crucial in the breeding of orchids. This study on the chromosome numbers of *Phalaenopsis* species has been conducted to determine their genetic characteristics and variations. Somatic metaphase chromosome spread has been used for chromosome counting. Results showed triploid (2n = 3x = 57) in *P.* 'Princess' and tetraploid (2n = 4x = 76) in *P.* 'White Smile' and *P.* 'KS Littlegem' cultivars. Aneuploidy with 2n = 56, 77, and 78 were observed in five *Phalaenopsis* cultivars (*P.* 'Yellow Star', *P.* 'Pink Dream', *P.* 'White Pearl', *P.* 'Pinky', and *P.* 'Sweet Orange'). These findings on the chromosome numbers of selected *Phalaenopsis* species will provide valuable information to orchid breeders in relation to selecting the right variety for cultivation..

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PF-0004

Bacterial wilt resistance bioassay using two different isolates of *Ralstonia solanacearum* in domestic commercial varieties of chili pepper (*Capsicum annuum* L.)

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Bacterial wilt caused by *Ralstonia solanacearum* is one of the most destructive soil-borne pathogens worldwide. The pathogen infects more than 450 plant species, mainly causing damages to the Solanaceous crops such as pepper, tomato, potato, tobacco and so on. As the average summer temperature in Korea is continuously rising amid global warming, the frequency of bacterial wilt disease is on rise. Accordingly, various strategies for controlling bacterial wilt have been developed, but the most desirable to control the disease is the development of new varieties resistant to bacterial wilt. So far, a few resistant varieties to bacterial wilt disease have been reported, including a commercial variety 'Muhanjilju'. In this study, we attempted to determine the degree of bacterial wilt resistance using isolates from major cultivated areas of chili pepper in Korea. Inocula of two different isolates of *R. solanacearum*, moderately pathogenic isolate 'HS' and highly pathogenic isolate 'HWA', were used as pathogens. A total of 16 commercial varieties, mainly cultivated in Korea, were used as plant materials. The degree of disease resistance was evaluated at every seventh day after inoculation for six weeks and based on the disease index (DI). The symptoms of the disease were scored 0 (resistance, no symptom) to 3 (susceptible, plant death). The resistance was classified as resistant (R), moderate resistant (MR), and susceptible (S). As a result, depending on the isolates, the degree of resistance was different. Overall, the HWA isolate was more virulent to the 16 commercial pepper cultivars than the HS isolate. Four commercial cultivars, 'Titandaebak', 'Bulcolor', 'Colorzzang', and 'Kibantantan', were resistant to the HS isolate and more resistant than the cultivar 'Muhanjilju'. However, no cultivars and only control resistant variety 'Konesian Hot' were resistant to the HWA isolate.

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PF-0005

Development of SNP-based HRM markers linked to QTLs controlling anthocyanin synthesis and content in bulb onion (*Allium cepa* L.)

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Bulb onion (*Allium cepa* L.), one of the most important vegetables worldwide, abundantly contains various functional compounds such as quercetin, allicin, and flavonoids. Flavonoids, which act as pigments in plants, were reported to improve blood circulation in human and have antioxidant activity. Red onion contains anthocyanins, a member of flavonoids, which are biologically functional compounds to have anti-cancer and antioxidant activity. Therefore, red onion is highly preferred recently. In the previous study, one QTL (*qAS7.1*) for anthocyanin synthesis and two QTLs (*qAC4.1* and *qAC4.2*) for anthocyanin content were identified in a segregating F_2 population derived from 'SP3B' (yellow) and 'H6' (red) using genotyping-by-sequencing (GBS) analysis with a reference gene set. The major QTL *qAS7.1*, located on chromosome 7, might be associated with a dihydroflavonol 4-reductase (*DFR*) gene. In this study, we aimed to develop SNP-based high-resolution melting (HRM) markers closely linked to the QTLs. A total of 38 primer sets were designed for the development of HRM markers. As a result, two HRM markers (AC4.1_57513.1_394-HRM and AC4.1_53764.1_356-HRM) were developed for the identification of QTL *qAC4.1*, and four HRM markers (AC4.2_65336.1_1123-HRM, AC4.2_53230.3_454-HRM, AC4.2_11999.7_756-HRM, and AC4.2_14596.1_345-HRM) were developed for the identification of QTL *qAC4.2*. In addition, six HRM markers (AC7_25488.1-1,4,5,6-HRM and AC7_48105.1-1,2-HRM) were developed for the identification of QTL *qAS7.1*, by which yellow and red onions were distinguished. The developed HRM markers are expected to be helpful for the development of red onion varieties with high anthocyanin content.

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PF-0006

Phenotype and Anatomical Evaluation of 10 *Echeveria* Species

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Succulents are recently gained popularity as house plants for decoration or landscape because of their peculiar shape and attractive colors. With high demand prices, breeders and growers put efforts in exploring differences in their morphologies, including developing new cultivars and varieties. However, identification of succulent plants is often difficult because they share the similarities in phenotype, particularly, those belong to *Echeveria* genus. In this study, we combined anatomical analysis and morphological evaluation of ten plants, namely: *E. cante*, *E.* 'Heart's Delight', *E.* 'Snow Bunny' (*E. elegans* × *E. lauii*), *E.* 'Monroe', *E. lauii, E.* 'Brink's Blue' (*E. lauii* × *E. cante*), *E.* 'Domingo' (*E. cante* × *E. runyonii*), *E. ebony*, *E.* 'Moonshine', and *E.* 'Glam Pink' in order to provide reference for identification species of *Echeveria* genus. Phenotype evaluation included plant parameters and leaf morphologies showed they are sharing entire leaf margin but variation in leaf morphology ranging from elliptical, obovate, rhomboid, spathulate to oblanceolate which helps to distinguish each species. In addition, variation in colors ranging from purple to green and red also aids for classification. Anatomical evaluation revealed ten plants having the similarities of anisocytic stomata structure, amphistomatic leaves, uniseriate epidermises. Two type of cell arrangement were observed in which *E. cante, E.* 'Domingo', *E. lauii*, *E.* 'Monroe', and *E.* 'Moonshine' are classified as all-cell succulents, while *E.* 'Brink's Blue', *E. ebony*, *E.* 'Glam Pink', *E.* 'Heart's Delight', and *E.* 'Snow Bunny' are storage succulence type. Hence, this study is highly beneficial for building an identification reference of species belonging to *Echeveria* genus.

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PF-0007

Determination of LD_{50} of Colchicine and Oryzalin for Inducing Mutation among *Echeveria* Cultivars

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Due to its effectiveness and ease of handling, chemical mutagenesis has been preferred for producing mutant crops to improve conditional traits, increase crop quality, and maximize yield. Anti-microtubule agents are commonly used in plant mutagenesis to induce chromosome doubling which is observed to create miniatures, chimera, and variegation. These changes are found to be the aim of plant breeders and propagators for foliage ornamental plants like that of succulents. A previous study on chemical mutagenesis of succulents suggests that between alkylating agents, anti-microtube agents, and sodium azide, colchicine has produced the highest number of mutation rates. In this study, the use of anti-microtubule agents, colchicine and oryzalin, are investigated to determine the Lethal Dose 50 (LD_{50}) of five *Echeveria* cultivars namely: 'Brave', 'Glam Pink', 'Liliacina', 'Momotarou' and 'Sistar'. A range of doses is tested at different treatment times to determine which concentration would enable regeneration survival by 50%. The results of the study revealed that colchicine had a higher survival rate compared to those of oryzalin regardless of species. 'Brave' species had the highest number of mutants. For 'Brave' cultivars, the use of colchicine exceeded more than 50% survival rate, however, the use of 1.00% + 12 h gave the highest number of mutants with 9.26%. The use of oryzalin provided only three treatments having a 50% survival rate and the highest number of mutants were observed from those treated with 1.00% + 3 h with 25%. Among 'Momotarou' species, only those of oryzalin treatments produced mutants. On the other hand, the use of colchicine treatments produced mutants for 'Liliacina and 'Glamp pink'. The use of colchicine for 'Sistar' provided survival rates below half of the population. However, the use of 0.80% + 3 h produced the highest rate of mutation of 6.25%. Oryzalin treatment for the said species had 2 treatments that had a survival rate higher than 50%. The use of 0.8% of +3 h had the highest mutant rate of 7.14%. In summary, the use of colchicine and oryzalin varies per mutagen, and their concentration and soaking time does as well. Further studies will be done by the proponents to identify the changes in the phenotypic and genetic levels of mutagens.

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PF-0008

가지과 채소 내서성 우량계통 육성 전략

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전라북도 완주군 이서면 농생명로 100 국립원예특작과학원 원예작물부 채소과

파프리카, 토마토 등의 가지과 채소는 생육적온이 높은 호온성 작물이지만 30℃ 이상의 고온에서는 화분활력이 감소하여 정상적인 수정이 제한된다. 이러한 이유로 시설 내 환경을 개선하여 고온을 극복하려는 시도(포그냉방, 도포제처리, 차광)들이 진행되어 왔으나, 기후 온난화에 따른 이상고온 현상이 심화되면서 완벽한 대응이 쉽지 않은 상황이다. 따라서 위 재배적 조치들과 함께 고온에서도 안정적으로 착과가 되는 품종을 활용해야만 비로소 효율적인 대응이 가능해질 것으로 보인다. 한편, 품종 육성을 위해서는 내서성 자원을 확보해야 하는데, 착과의 경우 관여하는 환경적, 유전적 요인이 많기 때문에 자원선발을 위한 전략이 필요하다. 본 연구에서는 고온 관리구(35℃)와 일반 관리구(<30℃)를 별도로 운영하여 착과율 및 과실 관련 형질 특성평가를 진행한 뒤 고온에서도 우수한 성능을 유지하는 자원을 선발하고자 한다. 또한 1차적으로 선발한 자원은 온도 이외의 조건이 통제된 조건에서 유묘기 검정을 시행하여 재현성 있는 결과를 나타내는지 검증하고자 한다. 현재 파프리카 76점과 토마토 52점 대상 특성평가를 진행하고 있으며, 측창 개폐온도 조절 및 포그냉방 등을 통해 관리구별 온도 차이를 조성하고 있다. 향후 2~4마디(또는 화방) 기준, 일반 관리구 대비 고온 관리구에서의 착과율이 70% 이상인 자원을 선발하고자 하며, 해당 자원들의 개화기 직전 유묘를 국립원예특작과학원 이상기상연구동 내에서 고온처리하여 정상적으로 착과가 이루어지는지 검정할 예정이다. 이를 통해 최종 선발된 자원은 형질고정 및 교배조합 작성 등을 통해 내서성 우량계통 육성에 활용하고자 한다.

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PF-0009

Whole genome resequencing of *Capsicum annuum* to discover genetic variants related to bacterial wilt resistance

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Bacterial wilt disease (BW) by *Ralstonia solanacearum* caused serious yield loss in pepper. The primary strategy for controlling BW is known as breeding of resistant varieties. However, genetic variations have not sufficiently studied in pepper. Here, we re-sequenced two pepper inbred lines, resistant(R) and susceptible(S) to *R. solanacearum.* An average of 139 billion sequences (R for 141,329,789,370 and S for 137,696,065,574) were produced with a coverage ranging from 46.13X (R) and 44.94X (S) through Illumina HiSeq X Ten platform. And then, we identified genomic variations between the reference genome and each line. A total of 26,145,264 and 2,338,147 of genetic variants including SNPs and InDels were founded in R and S line, respectively. In genic region, genetic variants showed 3,093,513 and 489,135 for each line. Further, 1,640,614 non-synonymous SNPs were identified in R line but 1,391,665 non-synonymous SNPs in S line. Comparison between R and S pepper to cover informative SNPs responsible for BW resistance is being underway. This study could provide a useful information for markers development to improve BW resistance in pepper varieties.

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PF-0010

Establishment of a novel bioassay in *Capsicum annuum* leaves against *Ralstonia solanacearum*

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Bacterial wilt disease (BW) by *Ralstonia solanacearum* is a serious disease and cause severe yield losses in chili pepper worldwide. Resistant cultivar breeding is the most effective to control BW. For this, a simple and reliable evaluation method is required to determine resistance response and assess of disease severity in pepper germplasm. Although drenching and root-dipping methods have been widely used screening of BW resistance in pepper, the limitation is low uniformity and difficult to confirm disease symptom or resistance response. Here, we developed a novel and reliable evaluation method of BW resistance in pepper. Leaf-inoculated resistance pepper showed high resistance compared to that of susceptible cultivar. The susceptible cultivar represented spreading disease symptom from leaf to a whole plant that denoted similar result compared to drenching method. We determined scoring value for disease severity index from 0 to 4 based on leaf wilting and abscission severity. The inoculum concentration was optimized showing fastest and uniform phenotypic differences between resistant and susceptible cultivars. Now, the study is underway for comparison between leaf injection and the drenching method to pepper germplasm. This bioassay will provide an accurate and reliable evaluation to pepper resistant breeding against BW.

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PF-0011

An Early-ripening Large Sized Sweet Persimmon (*Diospyros kaki* Thunb.) Cultivar, 'Olnuri'

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'Olnuri' is an early-ripening large sized new persimmon cultivar. It has been bred in 2019 by Sweet Persimmon Research Institute from a crossing between 'Shinshu' and 'Taishu'. Fruits ripen around September 24 in Gimhae, which is 25 days faster than those of 'Uenishwase' (control cultivar), and their average weight is 280g, 47% larger than that of 'Uenishwase'. Fruit shape index (diameter/length) is lower than the control cultivar. De-astringency character of the flesh shows pollination constant non-astringent type. This cultivar is characterized by high sugar content of 17.0°Brix in the flesh, about 1.2°Brix higher than that of 'Uenishwase'. The flesh tends to fast soften after harvest, compared with 'Uenishwase'. Although 'Taishu', having a lot of stain in the skin, was crossed for this cultivar, the occurrence of stains is rare in 'Olnuri'. The fruit contains 2 seeds in average, reflecting higher eating convenience than 'Uenishwase' fruit (4 seeds/fruit). Since the tree bears large sized fruits in general, adjusting leaf-to-fruit ratio to 15-20 by flower bud and fruitlet thinning is required to prevent the tree vigor from weakness.

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PF-0012

Interrelation between Proline and Leaf Heat Damage in Tomato Seedlings with Different Growth Stages under Short-Term Heat Stress

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Heat stress leads to an array of physiological, biochemical, and molecular changes in plants affecting its growth and development. In response to different stresses plants accumulate large quantities of different types of compatible solutes. One of them is proline, which accumulates in many plant species under a broad range of stress conditions such as water shortage, salinity, extreme temperatures, and high light intensity. High proline content might contribute toward greater heat tolerance. However, the exact physiological function of proline is still controversial, and several researchers have attributed its beneficial function to the process of proline metabolism rather than to the proline molecule itself. Despite the beneficial effects of exogenous proline application, it imparts toxic effects as well if over-accumulated or applied at excessive concentrations. Such negative effects of exogenous proline were observed in tomato, where an imbalance in inorganic ions was determined. The aim of this study was to investigate of effect of short-term heat stress on proline content in two commercial cultivars of tomato seedlings with different growth stages. Two commercial tomato cultivars 'Minichal' and 'Dafinis' were sown in 15 May of 2020 in plastic trays containing 1:1 sand: peat by volume and grown in a glass greenhouse (26/18°C D/N). Tomato seedlings with 4-5 true leaf stage (LS) 30 days and with 5-6 LS 45 days after sowing were transferred on 16 and 28 June 2020 into growth chamber, respectively, where day and night temperatures were maintained at 40°C, light intensity 600 μmol $m^{-2}s^{-1}$ (16/8h) and relatively humidity was within 60-70%. Leaf heat damages (LHD) of tomato leaves were measured visual, where injured leaf part was calculated in % and divided on 5 grades: 1- normal growth- no damage; 2- fewer than 1/10 damage of the leaves (>10%) become lightly yellowed-whited or desiccated-dried; 3- damages of the leaves from 11-25%, become lightly yellowed-whited or desiccated-dried; 4- damages 1/4 to 1/2 of the leaves (from 25 to 50%) become lightly yellowed-whited or desiccated-dried; 5- damage 1/2 to 3/4 of the leaves (from 50 to 75%) become yellowed-whited or desiccated-dried; 6- damage more than 3/4 of the leaves (>75%) become severely yellowed-whited or the whole plant dies. Free total proline in leaves extracted using colorimetric assayed by method Claussen. Statistical analysis was done with EXCEL 2016 (Microsoft, WA, USA). Proline measurements were done on 0 (CT-control), 1st, 3rd and 7th days of heat stress treatment. According to results were identified that in heat susceptible tomato cultivar 'Dafinis' was revealed high accumulation of proline content during short-term heat stress treatment period regardless of tomato seedlings growth stages. In heat tolerant cultivar 'Minichal' seedlings with 4-5 and 5-6 LS were revealed low content of proline in comparison with heat susceptible cultivar 'Dafinis'. Decreasing of proline in seedlings of cultivar 'Dafinis' with 4-5 LS on 7th day of heat treatment can be explained that 7 day was critical for thermotolerance, where was determined of increasing the leaf heat damage level (in seedlings were detected the yellowed-whited or desiccated-dried leaves), destroying of metabolism and toxic effects of exogenous proline. Heat tolerance of seedlings in cultivar 'Dafinis' were increased in 5-6 LS than 4-5 LS, while in cultivar 'Minichal' was identified opposite pattern, where seedlings with 4-5 LS were tolerant in comparison with 5-6 LS.

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PF-0013

Physiological and Biochemical Response of Hot Pepper Seedlings on Heat Stress

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Heat stress caused by elevated temperatures induces morphological, anatomical, physiological, biochemical and genetic responses in plants. Hot pepper cultivars differ in their sensitivity to heat stress, and the sensitivity depends on the developmental stage of the plants. To secure high-temperature tolerant pepper lines for improved production, a good understanding of the physiological and agronomical responses to high-temperature stress in peppers is imperative. Therefore, evaluation of physiological and biochemical response of hot pepper seedlings on heat stress during the vegetative are playing a vital role in the formation of generative organs and thus the final yield.

The aim of this study was to investigate of photosynthetic parameters, electrical conductivity, chlorophyll and proline content during heat stress in seedling stage of pepper cultivars.

Pepper commercial cultivars 'Chyung Yang' and 'New Bigarim' were sown in 31 March of 2020 in plastic trays containing 1:1 sand: peat by volume and grown in a glass greenhouse (26/18°C D/N). Pepper seedlings with 8-10 true leaf stage (LS) 40 days after sowing were transferred on 11 May 2020 into growth chamber, where day and night temperatures were maintained at 42°C, light intensity 600 μmol m^{-2} s^{-1} (16/8h) and relatively humidity was within 60-70%. The Photosynthesis rate (μ mol CO_2 m^{-2} s^{-1}), Stomatal conductance (mol H_2O m^{-2} s^{-1}), Intercellular CO_2 concentration (μ mol CO_2 mol^{-1}), and Transpiration rate (mmol H_2O m^{-2} s^{-1}) measured using a portable photosynthesis measurement system (LI-6400, LI-COR Bioscience, Lincoln, NE, USA). Electrolyte conductivity was measured according to the method of Bajji et al. [2002]. Chlorophyll content (CHL) in leaves of pepper plants were measured by SPAD meter (Konica Minolta, Japan). Free total proline in leaves extracted using colorimetric assayed by method Claussen [2005]. Statistical analysis was done with EXCEL 2016 (Microsoft, WA, USA). Measurement were done on 0 (CT-control), 2^{nd} and 7^{th} days of heat stress treatment.

Heat stress significantly increased the photosynthetic rate during 2 days of treatment than initial rate (control) and on the 7^{th} days was determined reducing it in both cultivars. It was revealed significantly increasing the stomatal conductance, intercellular CO_2 concentration and transpiration values at heat stress condition compared to control. Electrical conductivity rate ranged depends on cultivars, where in cultivar 'New Bigarim' it decreased during all heat stress treatment, while in 'Chyung Yang' it increased for 2 days and then again increased. There were detected the degradation of chlorophyll content in leaf during heat stress. Total free proline content increased in cultivar 'New Bigarim' during heat stress, whereas in 'Chyung Yang' it reduced in 2^{nd} days and again determined its increasing in 7^{th} days of treatment. According to this study, we can conclude that continuously treatment of seedlings at high temperature condition may reduce photosynthetic activity and chlorophyll content in leaves. There were identified interrelation between the stomatal, intercellular CO_2 concentration and transpiration values, however there no revealed any relation between photosynthesis, electrical conductivity and proline content.

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PF-0014

A transcriptional network of anthocyanin biosynthesis in Chinese cabbages leaves

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Anthocyanins, belong to the flavonoid group, have diverse biological functions in plants and are play beneficial roles in human health. Due to the health-promoting properties, enhancing anthocyanins in crops is interesting project for breeders and researchers. Anthocyanins biosynthetic genes is regulated by the activity of MYB-bHLH-WD repeat (MBW) complexes. Recent studies reported the active MBW complexes is disrupted by repressor regulatory genes. To elucidate the anthocyanin biosynthetic mechanisms in *Brassica rapa*, we analyzed differentially expressed anthocyanin biosynthetic genes between different colored Chinese cabbages. As like a visible appearance in leaves, the transcript levels of active MBW regulators were higher in purple leaves than in green leaves, resulting that the transcript levels of all structural genes were higher in purple leaves than in green leaves. Interestingly, the expression pattern of candidate repressors was negatively correlated with anthocyanin accumulation. We found that green colored Chinese cabbage contain the nonfunctional version of active anthocyanin regulator and functional repressor regulators. Through the further study, we are going to confirm the role of activator or repressor in anthocyanin biosynthesis in Chinese cabbage.

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PF-0015

Breeding of Pink Colored Multi Floral *Phalaenopsis* 'Tiny Bell'

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A new small-type pink colored *Phalaenopsis* cultivar, 'Tiny Bell', was released by the National Institute of Horticultural and Herbal Science, Rural Development Administration (Korea) in 2018. The 'Tiny Bell' was derived from crossing between *P*. D07PN16, small type cultivar with pink colored flowers, and *P*. D03PN22 small type cultivar with light pink colored flowers in 2010. Preliminary selection was conducted as '10531-53' among 100 individual progenies in 2014 according to phenotypic standards such as flower color and shape, inflorescence number, and leaf attitude. The stability and uniformity of the cultivar was confirmed through the first and second characteristics tests from 2014 to 2018, and named thereafter as 'Tiny Bell'. 'Tiny Bell' has deep pink (RHS, PVGN80A) flowers with white edge. The mini sized florets measure 3.9 and 4.0 cm in length and width, respectively. 'Tiny Bell' is regarded as raceme flower type with many florets. The number of florets per inflorescence was 19.7, which was suitably large and abundant. The leaves of 'Tiny Bell' grow horizontally and are 13.1 cm in length and 5.3 cm in width. 'Tiny Bell' can be mainly available for small-type potted flowers.

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PF-0016

Assessment of substantial equivalence of useful biotechnological Chinese cabbage line for agricultural problem

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Breeding technology of Chinese cabbage in Korea is superior to other countries, and various varieties have been exported to Japan, China, and Southeast Asia. By combining traditional breeding with biotechnological breeding, the useful varieties could be developed. In this study, inbred line and advancement of developed transgenic lines were cultivated and these transgenic lines have shown beneficial characteristics such as *Tetranychus urticae* resistance, drought stress resistance or self-compatibility. Generation progress of developed transgenic lines is being made to fix the acquired traits. Comparison of 26 characteristics including height of plants, size of outer leaves, and shape of leaves between non-transgenic and transgenic lines was investigated according to the guidelines issued by the Korea Seed & Variety Service. As the result of observation, no difference was found in 26 characteristics between non-transgenic and transgenic lines.

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PF-0017

양파 조생계 신품종 '메이풀리'

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신품종 '메이풀리'는 조생계 F1 품종을 육성하기 위해 'MMS175'를 종자친으로 하고, 'MSC231'을 교배하였다. 2014~15년에 조합능력 검정을 하여 그 결과가 우수하였고, 2015년에 생산력 검정을 실시하였다. 2016년 '목포30호'로 명명하여 2018년까지 3년 동안 무안, 고흥, 제주 2지역에서 지역적응검정 시험을 수행하였다. 초형, 구형, 구중 등의 균일도가 높고 저장성이 우수하여 2018년 직무육성심의회에 상정하여 보호 출원 하였다. 도복기는 5월 1일로 대비품종(로망)에 비해 3일 빠르다. 구중은 333g으로 대비품종보다 무거우며 초장, 엽초경, 엽초장은 대비품종보다 적은 경향을 보인다. 품질 특성인 당도는 7.9°Brix로 대비품종(7.3°Brix)보다 높다. 평균상품수량은 6,194kg/10a로 대비품종(6,116kg/10a) 보다 4% 증수되었으나 2년차를 제외하고 1년차와 3년차에 각각 25%, 10% 증수되었다. 저장성은 부패율 15.4%로 대비품종(16.3%)와 큰 차이가 없었으나, 맹아율은 15.6%로 대비품종(8.7%)에 비해 맹아율이 높았다.

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PF-0018

양파 F1 종자생산용 중만생계 웅성불임계통 '원예30015' 육성

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극조생계를 제외하고 대부분의 양파 품종은 F1품종이 보급되고 있다. 양파의 웅성불임계통(A-line)은 F1 종자생산에 필수적인 교배모본이며 화분친(C-line)과 더불어 F1 품종의 특성을 결정한다. '원예30015'는 중만생계통으로서 웅성불임개체 'LMS205-2'와 'MSC144'를 교배하여 유지계통(B-line) 'MSB53-2'를 선발하였다. 웅성불임계통 육성을 위해 2007년부터 2011년까지 3세대 동안 자식과 여교배를하여 모구를 선발하였으며 2013년부터 2018년까지 4세대 동안 집단선발과 여교배로 형질을 고정하였다. 2017~2018년에는 화분친계통들(C-line)과 교배하여 F1종자를 채종하고 그 계통들의 조합능력을 검정한 결과 우수한 원예적인 특성과 수량성이 확인되어 2018년 직무육성신품종선정심의 결과 '원예30015'로 명명되었으며 2019년에 품종보호출원 하였다. '원예30015'의 도복기는 5월 19일로 대조품종과 같으며 초형은 잎 자세가 곧추선 직립형이다. 웅성불임계통과 유지계통의 구형지수는 각각 0.94, 0.87로 원형에 가까우며 구중과 당도는 각각 191.6g, 7.3°Brix로 대비품종에 비해 구중(278.4g)은 낮았으나 당도는 대비품종(7.1 °Brix)보다 높았다. '원예30015'와 화분친 5계통을 교배하여 F1 조합능력을 검정한 결과 모든 교배조합에서 수량성이 대비품종보다 높은 것으로 나타났다. '원예30015'는 중만생계 웅성불임계통으로 중만생계 또는 중생계통의 F1 품종육성에 유용한 중간모본으로 활용될 것으로 기대된다.

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PF-0019

The Calcium Signaling Pathway mediated by SlCBL4 and SlCIPK24 Complex Plays a Critical Role in Salt Tolerance in *Solanum lycopersicum*

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Soil salinity is one of the major environmental stresses that restrict the growth and productivity of tomato (*Solanum lycopersicum* L.) worldwide. It has been well studied in Arabidopsis that the calcium signaling pathway mediated by calcineurin B-like protein 4 (CBL4) and CBL-interacting protein kinase 24 (CIPK24) plays a critical role in salt response. In this study, we have isolated two full-length cDNAs for the tomato homolog genes designated as SlCBL4 and SlCIPK24, respectively. Bimolecular fluorescence complementation (BiFC) and pull-down assays indicated that SlCBL4 can physically interact with SlCIPK24 at the plasma membrane of plant cells in a Ca^{2+}-dependent manner. Overexpression of *SlCBL4* or superactive *SlCIPK24* mutant (SlCIPK24M) conferred salt tolerance to transgenic tomato plants (cv. Moneymaker). In particular, the SlCIPK24M-overexpression lines displayed dramatically increased tolerance to high salinity, which is associated with higher contents of Na^+ and K^+ in the roots compared to the wild-type tomato plants. Taken together, our findings clearly suggest that SlCBL4 and SlCIPK24 are functional tomato orthologs of the Arabidopsis counterpart genes, and they can be utilized to produce enhanced salt-tolerant tomato plants.

Keywords: Solanum lycopersicum, calcium signaling, CBL4, CIPK24, salt tolerance

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PF-0020

배추 *SHORT VEGETATIVE PHASE* 유전자를 활용한 배추 개화시기 조절 연구

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배추는 우리나라 주요 3대 작물 중의 하나로 개화를 하기 위해서는 일정기간 이상의 저온처리(vernalization)를 필요로 하며 서늘한 기후에서 재배하기 적합한 작물이다. 우리나라에서는 급작스런 온도 변화로 저온에 감응하여 일찍 추대 현상이 일어나면서 배추의 상품성을 크게 떨어뜨린다. 따라서 이러한 문제를 해결하기 위하여 식물체에서 개화시기를 조절하는 중요한 유전자인 *SHORT VEGETATIVE PHASE* (*SVP*)를 활용하여 배추의 농업적 형질을 개선하고자 하였다. SVP는 MADS-box를 갖고 있는 식물 전사조절인자로 *FLC*와 상호작용에 의하여 개화 억제자로서 역할을 하고 있다. 배추로부터 분리된 *BrSVP* 유전자를 35S 프로모터에 결합시켜 식물 형질전환 벡터를 제작한 후 아그로박테리움을 이용하여 배추에 형질전환하였다. 선발된 형질전환체의 특성을 분석한 결과 비형질전환 배추는 저온 처리 40일 후 16일째 모든 개체에서 꽃봉오리가 관찰되었으나 형질전환 배추는 평균 21-24일이 소요되었으며 모든 계통들에서 개화시기가 지연된 것을 확인 하였다. RT-PCR로 유전자 발현을 분석한 결과 *BrSVP*유전자는 floral integrator *AGL20*, *AGL24*, *FT* 유전자의 발현을 억제시킴으로써 배추의 개화 및 추대시기를 지연시키는 효과를 나타낸 것으로 사료된다. 따라서 본 연구 결과로부터 배추 *SVP* 유전자는 배추에서 춘화처리 동안 floral integrator 유전자들의 발현에 영향을 주어 개화시기를 조절 할 수 있는 유용 유전자로서의 기능을 할 수 있을 것으로 사료된다.

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PF-0021

Application of pepper Fluidigm SNP markers in paprika (*Capsicum annuum* L.) accessions and cultivars

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Paprika (*Capsicum annuum* L.), a colored bell-typed sweet pepper, is one of the most important fruit vegetables in Korea. Therefore, disease resistance to powdery mildew (*Leveillula taurica*), pepper mottle virus (PepMoV), pepper mild mottle virus (PMMoV), and bacterial spot (*Xanthomonas campestris* pv. *vesicatoria*, Xcv) is generally required for paprika breeding. In light of the advances in molecular breeding, SNP marker-based multiplexed analyzing systems will be helpful for the development of new paprika cultivars with multiple disease resistance. In this study, we performed validation test of the previously developed pepper Fluidigm SNP markers using 136 accessions (408 plants) and 32 cultivars of paprika. The traits targeted and the 24 SNP markers linked with are as follows: bacterial spot resistance (Bs2, Bs3-1, and Bs3-2), anthracnose resistance (CA09g12180, CA09g19170, CA12g17210, CA12g19240, and CcR9), CMV resistance (Cmr1-2), genic-male sterility (GMSK2, GMSK3, and MS1), TMV resistance (L1-3K and L4), powdery mildew resistance (Ltr4.1-40344, Ltr4.2-56301, and Ltr4.2-585119), phytophthora resistance (M3-2 and M3-3), potyvirus resistance (pvr1, pvr2-123457, pvr2-689, and Pvr4-1072-2), and TSWV resistance (TSW1-4). From the results of 440 plants tested, there were no resistant lines with the SNP markers linked to anthracnose resistance (CA09g12180, CA09g19170, CA12g17210, CA12g19240, and CcR9), powdery mildew resistance (Ltr4.1-40344, Ltr4.2-56301, and Ltr4.2-585119), and potyvirus resistance (pvr1). This might be due to the origin of resistant alleles: anthracnose and powdery mildew resistant alleles originated from *C. baccatum* species, and *pvr1* resistance allele from *C. chinense*. For the other markers, at least one plant has resistant alleles. Consequently, we consider that the Fluidigm SNP marker assay is an efficient and fast multiplexed analyzing system. Therefore, we pursue the development of more SNP markers linked to important traits for paprika breeding.

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PF-0022

AcFLS Expression in Tobacco Leads to Changes in Flower Color and Root Growth

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Recently, *AcFLS-HRB*, encoding flavonol synthase, was identified from yellow onion 'Hwangryongball'. In this study, AcFLS-HRB was expressed in bacteria and its enzymatic properties were examined by *in vivo* feeding assays. Recombinant AcFLS-HRB exhibited both flavanone 3-hydroxylase (F3H) and FLS activity. Transgenic tobacco (*Nicotiana tabacum*) expressing *AcFLS-HRB* produced lighter-pink flowers compared to wild-type plants. In transgenic petals, *AcFLS-HRB* was highly expressed at the mRNA and protein levels, and most AcFLS-HRB protein accumulated in the insoluble microsomal fractions. High-performance liquid chromatography (HPLC) analysis showed that flavonol levels increased but anthocyanin levels decreased in transgenic petals, indicating that AcFLS-HRB is a functional gene in planta. Gene expression analysis showed the reduced transcript levels of general phenylpropanoid biosynthetic genes and flavonoid biosynthetic genes in *AcFLS-HRB* overexpressed tobacco petals. Additionally, transgenic tobacco plants at the seedling stages showed increased primary root and root hair length and enhanced quercetin signals in roots. Exogenous supplementation with quercetin 3-*O*-rutinoside (rutin) led to the same phenotypic changes in root growth, suggesting that rutin is the causal compound that promotes root growth in tobacco. Therefore, augmenting flavonol levels affects both flower color and root growth in tobacco.

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PF-0023

고품질 소형과 수박 대량생산을 위한 품종별 수직재배 적응 특성 평가

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핵가족화와 소득수준 향상으로 수박 소비 형태도 큰 수박에서 특색 있는 고당도 작은 수박으로 변화하고 있다. 그러나 소형과 수박을 재배 할 경우 생산량 감소에 따른 소득 감소, 중소형 수박 재배법 미확립에 따른 품질저하 등의 문제를 재배와 유통과정 모두에서 직면하게 된다. 본 연구에서는 소형과 수박 재배 농업인의 소득 안전성을 높이고자 다양한 칼라 수박 품종별 수직밀식재배 적응성을 분석하였다. 수박 품종의 과피와 과육색을 기준으로 호피적색과육, 호피황색과육, 황피적색과육, 흑피적색과육, 흑피황색과육으로 분류하여 총 28품종(계통)을 대상으로 적응특성과 수량성을 조사하였다. 재배방법은 수박연구소에서 개발한 I자형 수직재배 장치를 이용하여 재식거리 20cm 간격으로 정식하고, 2줄기를 수직 유인 하였고, 벌을 활용해 수정하였다. 다착과성을 검증하기 위해 2번 자화부터 수정시켜 적과를 하지 않고 재배하였다. 수정 후 15일에는 모든 품종(계통)에서 1주에 평균 2.6개가 착과되었으나, 2번째 이후 착과된 과실의 경우 생육정지 및 자연낙과 발생률이 평균 74% 정도로 높았고, 4번과 이상 착과시 상품성이 없었다. 수확기 수박 착과수 조사결과 1주에 2개의 과실이 안정적으로 착과되는 품종은 미니수박인 애플미니나이스샷과 대과종인 블랙위너 품종이었고, 나머지 품종(계통)들은 1.0~1.8개의 착과율을 나타내었다. 당도가 11°Bx이상 되는 품종은 호피적색과육인 포미나, 뉴꼬꼬마, 씨자근, 달코미미니와 흑피황색과육 품종인 로얄블랙, 깜놀이었다. 과중은 애플미니나이스샷이 1kg 내외로 가장 작았으며, 나머지 품종(계통)의 경우 평균 2.3kg 내외였다. 상품수량 분석결과 10a당 평균 7,032kg으로 일반 대형과 수박에 비해 1.5배 정도 증수되었다. 소형과 수박 재배의 경우 다착과시 과중과 숙기가 균일하지 못해 품질이 낮아지는 문제가 있으므로, 10a에 3,000주 재식을 목표로 1주 1과를 동시 착과시켜 대량 일시 수확하여야 할 것으로 판단되었다.

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PF-0024

Breeding of Bright Pink *Cymbidium* 'Aria' with Multi-flower

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Cymbidium 'Aria' was developed as a hybrid by the National Institute of Horticultural & Herbal Science, Rural Development Administration in 2017. The hybrid was made from a cross between 'Haruka' with white colored flower and pink lips and Lucky Rainbow 'Lapin Hot' with light pink colored flower and red lips in 2000. After the cross, 125 seedlings were obtained through planting and acclimatization in a greenhouse. Based on flower color, leaf shape, flower stalk, and vigorous growth, the first selection were conducted from 2001 to 2008. Among three selected lines, the stability and uniformity of the lines were confirmed through characteristics test from 2009 to 2014 and the final line was selected. The line with the code '00-1174-77' was named as 'Wongyuo F1-63'. After the evaluation of secondary characteristics in 2014, it was named as 'Aria'. It has bright pink colored petals (RP69D, RP62C) and dark pink lips (RP58A). Flower and plant size of 'Aria' are medium and it has approximately 17.4 flowers per peduncle, which can be considered as good spike habit. The petals and sepals show in the middle of incurved and spreading shape. The peduncle is erect with vigorous growth. Under optimum cultural conditions, it starts to blooming in middle of December (PBR Registration No. 7876).

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PF-0025

Breeding of Large White *Cymbidium* 'Super Star' for Cut Flower

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Cymbidium 'Super Star' was bred by the National Institute of Horticultural & Herbal Science, Rural Development Administration in 2018. The hybrid was derived from cross between *C.* 'Grace Kelly' and *C.* 'Jung Frau' in 1997. After the cross, 97 seedlings were obtained through planting and acclimatization in a greenhouse. From 1998 to 2010, the first selection was conducted in basis of the characteristics such as flower color, leaf shape and vigorous growth. Then after the stability and uniformity of the lines were confirmed through characteristics test from 2011 to 2017 and the final line was selected. The line with the code '97-0608-14' was named as 'Wongyuo F1-67' having uniformity and distinguishing characteristics. 'Super Star' has a white colored petals (GW157D) and light green lip(YG144C) giving overall bright look. It has big size of flower with 8.2cm of length and 10.5cm of width with strong spike habit. The peduncle is long and erect that is 87.6cm of height, which can be considered as proper characteristics for cut flower. It starts to bloom between February to March under optimum cultural conditions. During flowering season, low temperature may cause the flower greenish.

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PF-0026

Development of optimal water management system for cultivation of high cost in reclaimed farmland

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In this study, we proposed a basic production base for the cultivation of various crops other than rice on large reclaimed land in order to solve disparity in rice supply and demand and realization of high value of agriculture. Soil characteristics, climatic and water resources, and proposed a suitable soil improvement plan for reclaimed land. It is also possible to provide manuals for the cultivation of reclaimed land. It is also possible to provide basic data on investment decision making by presenting proper and appropriate criteria of production infrastructure cost to be invested in reclamation of farmland by estimating appropriate quantity and presenting soil management method. With the development of irrigation system in reclaimed land, precise irrigation planning and scientific water management will be implemented and water loss can be minimized. It is expected to be applied to basic planning, design, construction, and maintenance so that optimum performance and functions can be demonstrated through the presentation of irrigation technology guidelines for field irrigation facilities.

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PF-0027

꽃가루양 많은 수분수용 꽃사과 '버디벨' 육성

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사과는 타가수정 작물로 자가불화합 유전자형이 다른 품종이나, 꽃사과 2~3품종을 섞어 심어야 안정적인 결실이 가능하다. 여러 품종을 혼식하면 일괄적인 재배관리가 어렵지만 꽃사과를 수분수로 이용하면 재배관리의 효율을 향상할 수 있다. 또한 꽃사과는 주로 병해충에 강하며 1년생 가지에서도 꽃눈형성이 잘되는 특성이 있기 때문에 수분수로 개발하여 보급할 필요성이 있다. 따라서, 2019년 농촌진흥청 국립원예특작과학원 사과연구소에서 꽃가루 생산이 많고 주품종 보다 개화시기가 약간 빠른 꽃사과 '버디벨' 품종을 개발하였다. '버디벨'의 육성내력은 다음과 같다. 2003년 강원도 인제군 점봉산에서 야광나무(*Malus baccata*.)의 가지를 수집하여 2004~2008년 실생대목에 접목 증식 후 사과연구소 포장에 재식하여 모수를 관리하였다. 2008년 자연방임수분으로 획득한 종자를 채종하고 2009년 파종 및 실생 양성 후 2010~2019년 생육관찰 및 특성검정을 통해 최종선발하였다. 2020년 '버디벨'로 명명하여 국립종자원에 품종보호출원 하였다. '버디벨'의 개화시는 4월 16일, 중심화 만개기는 4월 17일로 빠른 편이며 대조품종 '만추리안'에 비해 비슷하거나 1일 느리다. 개화기간은 약 9일로 대조품종과 같다. 과일은 약 1g으로 대조품종(6.9g)에 비해 작다. 적색인 과일의 관상가능기간은 약 120일로 대조품종(40일)에 비해 더 길다. 주요 재배품종 '후지', '홍로', '쓰가루'를 모본으로 '버디벨'을 부본으로 하여 꽃가루친화성을 확인한 결과 착과율이 각각 67, 87, 93%로 친화성이 있는 것으로 확인되었다. 꽃 1000화 당 화분양은 '버디벨'이 1,120mg이었고 '메이폴'은 446mg으로 '버디벨'이 2.5배 더 많았다. 또한 '버디벨'은 주요 사과 병해충에도 강하며 해거리 없이 매년 개화량이 많고 수체가 크게 자라지 않는 특성이 있다.

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PF-0028

꽃향기가 진한 조경용 꽃사과 '차밍벨' 육성

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꽃이 화려하며 관상가치가 높은 꽃사과는 가로수, 골프장, 공원 등 조경용에 대한 지속적인 수요가 있으나 품종 구분 없이 '꽃사과'로 통칭되어 판매 되고 있다. 이에 대응하기 위하여 2019년 농촌진흥청 국립원예특작과학원 사과연구소에서 개화기 꽃의 관상가치가 높고 꽃향기가 진한 조경용 꽃사과 '차밍벨'을 개발하였다. '차밍벨'의 육성내력은 다음과 같다. 2002년 경북 군위군 팔공산에서 야광나무(*Malus baccata*.)의 가지를 수집하여 2003~2008년 실생대목에 접목 증식 후 사과연구소 포장에 재식하여 모수를 관리하였다. 2008년 자연방임수분으로 획득한 종자를 채종하고 2009년 파종 및 실생 양성 후 2010~2019년 생육관찰 및 특성검정을 통해 최종선발 하였다. 2020년 '차밍벨'로 명명하여 국립종자원에 품종보호출원 하였다. '차밍벨'의 개화시는 4월 18일로 대조품종 '만추리안'에 비해 3일 느리고 개화기간은 약 10일 정도로 대조품종에 비해 1~2일 길다. 흰색인 꽃의 크기는 5.3cm로 대조품종에 비해 약 1.5cm 더 크고 과일은 약 1g으로 대조품종(6.9g)에 비해 작다. 적색인 과일의 관상가능기간은 약 120일로 대조품종(40일)에 비해 더 길다. 또한 '차밍벨'은 주요 사과 병해충에 강하고 수체가 크게 자라지 않는 편이며 꽃가루양이 적기 때문에 수분수용으로는 적합하지 않은 특성이 있다. 달콤하고 상쾌한 향기가 진하게 풍기는 '차밍벨' 꽃의 향기성분 분석을 실시한 결과 자스민, 일랑일랑 등의 에센셜오일 성분이며 꿀벌을 유인하는 물질인 벤질아세테이트($C_9H_{10}O_2$)가 다량 포함되어 있음을 확인하였다. 개화기간 동안 좋은 향기를 풍기며 꽃의 모양이 우아하고 아름다워 관상가치가 높은 꽃사과 '차밍벨' 품종은 조경용으로 유망할 것이다.

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PF-0029

무 육성 계통종자의 기내파종을 위한 종자소독 최적 조건 규명

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최근 품종 육성 과정에서 조직배양을 통한 계통의 대량 증식이 주목받고 있다. 계통 육성 후 무소독 종자에는 다양한 곰팡이, 박테리아 등이 존재하기 때문에 일반 소독 방법을 이용하여 기내에 파종할 경우 많은 오염으로 인한 종자 손실이 크게 증가한다. 그러므로 종자의 기내 파종을 위해 효과적인 종자 소독 방법이 요구된다. 본 연구에서는 무 계통 종자 소독 시에 보편적으로 사용되고 있는 차아염소산나트륨(NaOCl)의 전처리와 후처리의 농도와 시간, 소독처리시 진공처리 유무, 소독 후 멸균수 침지 시간의 효과 등을 비교하여 기내 파종의 효율을 높일 수 있는 최적 종자 소독 방법을 규명하고자 하였다. 본 실험에 사용된 무 종자는 다쿠요우, 겐까,3403개 계통을 사용하였고 전처리는 시판중인 락스(NaOCl) 원액을 농도별(0.1%, 0.2%), 시간별(0분, 15분, 30분)로 처리하고 후처리는 농도별(1%, 1.5%, 2%, 2.5%, 3%), 시간별(10분, 15분, 20분), 진공펌프 사용 여부(有, 無)로 처리하였다. 후처리 후 침지 효과는 멸균수로 세척 후 멸균수 침지시간별(0분, 30분, 1시간)로 하였다. 소독 후 종자는 식물생장조절제를 첨가하지 않은 0.75% 반고체 설탕배지(pH 5.8)에 파종하여 4일 후 발아세와 오염률을 조사하였다. 전처리 결과 NaOCl 0.2%를 15분 동안 처리했을 때 발아세가 가장 높았고 오염률이 가장 낮은 것으로 나타났다. 후처리 결과 NaOCl 1%로 10분, 1.5%로 15분 처리했을 때 유의성 있게 발아세가 가장 높았고, 1%로 10분 처리했을 때 오염률이 더 낮게 나타났다. 또한 진공 처리로 소독했을 때 대체로 발아율이 높고 오염률이 낮은 것으로 나타나 후처리시 진공을 하여 소독하는 것이 효과적인 것으로 나타났다. 마지막으로, 5회 세척 후 멸균수에 30분간 침지했을 때 발아율이 가장 높았고 오염률은 가장 낮은 것으로 나타났다. 또한 후처리시 소독액의 농도가 높다고 오염률이 낮아지는 것이 아님을 알 수 있었다. 소량의 종자를 획득하는 무 계통을 기내에서 대량번식을 해야 하는 경우에 이 소독 방법을 적용한다면 조직배양을 통한 효율적인 대량 증식에 도움이 될 것으로 기대된다. 본 결과물은 농촌진흥청 차세대 농작물 신육종 기술개발사업(세부과제번호: PJ014873012020)의 지원에 의해 이루어진 것임.

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PF-0030

Overexpression of *AHL23* and *AHL20*, *Arabidopsis AT-hook motif nuclear-localized* genes, confers salt tolerance in transgenic zoysiagrass

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Zoysia japonica is a warm season turfgrass and used in Korea popularly as well as all over the world. Soil salinity inhibits plant growth and affects adversely the quality of the turfgrass. AT-hook motif nuclear-localized (AHL) family proteins known to co-regulate the transcription of genes as a chromatin remodeling factor play a role in plant developmental processes and stress responses. In this study, *AHL20* and *AHL23*, two *AHL* genes from *A. thaliana*, were transformed into *Z. japonica* under the control of a constitutive ubiquitin promoter. Southern blot analysis proved that *AHL20* and *AHL23* were introduced into the *AHL20*-transgenic plants and *AHL23*-transgenic plants, respectively. Overexpression of each *AHL20* and *AHL23* in all of the transgenic plants was confirmed by qRT-PCR. To evaluate a tolerant response to salt stress of the transgenic plants, 4 transgenic plants including *AHL20*-OX1 and *AHL20*-OX2, and *AHL23*-OX1 and *AHL23*-OX2 were selected, respectively. All the transgenic plants showed higher salt tolerant phenotype with higher chlorophyll content and lower malondialdehyde (MDA) content under salt treatment, compared to wild type. Also, under salt treatment, the transgenic plants revealed higher activities of catalase (CAT) and peroxidase (POD), reactive oxygen species (ROS)-scavenging enzymes, than the wild type plant. These results indicate that overexpression of *AHL20* or *AHL23* belonging to *AHL* gene family confers salt tolerance to the transgenic zoysiagrass plants.

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PF-0031

Genetic mapping of the *Up* gene controlling fruit orientation in pepper (*Capsicum* spp.)

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The orientation of fruits is one of the distinguishing morphological features of *Capsicum* varieties. The downward curved growth of fruit stalks is highly correlated with fruit weight and pedicel length. Genetic analysis revealed that the pendant fruit orientation is governed by one dominant gene while incomplete inheritance is also observed in some *Capsicum* accessions. To identify and localize the fruit orientation controlling gene, a single trait locus analysis involving one F_2 and two recombinant inbred line (RIL) populations following the procedure of quantitative trait loci (QTL) mapping, and a genome-wide association study (GWAS) using core collection were performed. From the QTL mapping and GWAS results, the candidate locus, *Up* was co-localized to a 200-250 Mb region on chromosome 12. In the candidate region, a total of six markers were developed including two completely-linked (0 cM) markers with the orientation of fruits using an F_2 segregating population. In this candidate region, thirteen genes were functionally annotated among 81 structually annotated genes. To isolate the *Up* gene in pepper, functional study of the thirteen candidate genes have to be performed.

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PF-0032

Genetic mapping of the *c1* locus by GBS-based BSA-seq revealed *Pseudo-Response Regulator 2* as a candidate gene controlling pepper fruit color

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The loci *c1*, *c2,* and *y* have been widely reported as genetic determinants of various ripe fruit colors in pepper. However, *c1*, which may impact reduced pigmentation in red, orange, and yellow fruits, is not well understood. Two cultivars showing peach or orange fruit in *Capsicum chinense* 'Habanero' were found to have *c2* mutation and were hypothesized to segregate *c1* locus in the F_2 population. Habanero peach (HP) showed a reduced level of chlorophylls, carotenoids and total soluble solids in immature and ripe fruit. A microscopic examination of the fruit pericarps revealed smaller chloroplasts and less stacked thylakoid grana in HP. The expression of many genes related to chlorophyll and carotenoid biosynthetic pathways were reduced in HP. To identify the genomic region of the *c1* locus, bulked segregant analysis combined with genotyping-by-sequencing was employed on an F_2 population derived from a cross between Habanero orange and HP. One SNP at chromosome 1 was strongly associated with the peach fruit color. Pepper *Pseudo-Response Regulator 2* (*PRR2*) was located close to the SNP and cosegregated with the peach fruit color. A 41 bp deletion at the third exon-intron junction region of *CcPRR2* in HP resulted in a premature termination codon. A nonsense mutation of *CaPRR2* was found in *C. annuum* 'IT158782' which had white ripe fruit coupled with null mutations of *capsanthin-capsorubin synthase* (*y*) and *phytoene synthase 1* (*c2*). These results will be useful for the genetic improvement of fruit color and nutritional quality in pepper.

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PF-0033

토마토 대목 육성을 위한 우량계통 특성평가 및 선발 결과

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최근 토마토 장기재배 및 연작시 안정 생산을 위해서는 우수한 대목용 품종의 개발이 요구된다. 현재는 대부분의 대목용 토마토 품종들은 외국에서 육성된 품종들을 활용하고 있어 국내에서 적응성이 우수한 대목 개발의 필요성이 강조되고 있다. 이를 위해 국립원예특작과학원 채소과에서는 대목으로 활용 가능한 다양한 유전자원을 수집, 평가하여, 활용 가능성이 높은 자원들을 선발하기 위해 풋마름병 저항성 생물 검정, 원예적 특성 평가 및 기 개발된 병 저항성 마커를 활용한 우수 자원 선발을 수행하였다. 수집, 선발된 유전자원 35점 및 시판종 등 51점을 대상으로 평가하여 풋마름병에 저항성이면서 복합저항성인 자원으로 15계통을 선발하였다. 풋마름병 생물검정 결과 TRS 2, 3, 4, 9 등 13계통을 선발하고, 선발된 계통들에 대해서는 풋마름병 저항성 마커 등 15개의 저항성 마커 검정을 실시하였다. 복합병 저항성 계통 선발을 위해 Ty1, Ty3 등 13종의 알려진 마커를 이용한 검정 결과 9개의 마커에 저항성 호모 또는 헤테로인 TRS 6, 7, 2계통과 8개의 마커를 보유한 TRS 20, 26, 30, 32 4계통을 선발하였다. 선발된 계통들에 대해서는 자식 및 원예적 특성 평가를 통해 우수한 토마토 대목용 품종 육성에 활용하고자 한다.

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PF-0034

상업품종의 적색 고추에서 비타민 함량에 대한 변이요인 분석

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홍고추는 사람의 식이에서 주요 비타민 공급원이며, 우리나라 사람들은 홍고추를 많이 섭취하고 있다. 국내 상업품종 홍고추의 비타민 함량 분석에 대한 연구는 많이 수행되고 있으나 비타민 함량에 대한 품종, 재배지역 및 재배연도에 의한 성분의 자연변이 연구는 국내에서 거의 수행되지 않았다. 이를 위하여 본 연구에서는 12개 상업품종을 대상으로 2016년도와 2017년도 2년간, 2개지역(4개의 재배환경)에서 재배 및 수확하여 홍고추 과육에서 비타민 A, 비타민 B1, B2, B3, B6, E 함량을 비교 분석하였다.

또한 고추 과육에서 분석한 비타민 함량을 통합하여 재배환경에 대한 자연변이를 비교하기 위해 연구실에서 자체 개발한 통계 알고리즘에 적용한 결과, 비타민의 성분은 품종별, 지역별, 연도별로 자연변동성에 유의미한 차이를 보였다. 다변량 통계분석(PLS-DA)를 이용한 주성분 분석과 더불어 R 통계 기법을 이용한 변동성(% variability) 분석을 실시한 결과, 비타민 성분의 자연변동성은 품종 요인보다는 재배지역이나 재배연도 또는 세 가지 통합 요인의 교호작용에 의해 더 많은 영향을 받는 것으로 확인되었다. 특히 비타민 C와 비타민 B2, B3, γ -tocopherol은 주로 재배연도에 의해 성분변이가 큰 것으로 분석되었다. 더불어 비타민 분석 결과에 대해 품종별, 지역별, 연도별로 PLS-DA분석을 실시한 결과, 재배지역과 재배연도 요인에 의한 데이터 클러스터가 가시적으로는 뚜렷하게 구분되었으나, PC1과 PC2의 합산 분산력이 60% 미만으로 2차원의 주성분으로 전체 데이터의 분산을 설명하기에는 약간 부족한 것으로 확인되었다.

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PF-0035

Characteristics of Growth and Fruit Quality by the Heating Green House in the Domestic Breeding variety 'Haraejosaeng(*Citrus unshiu*)' in Jeju

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'Haraejosaeng' is a kind of *Citrus unshiu* that was bred by the Citrus Research Institute of the Rural Development Administration. It is a domestic variety that was bred by nucellar embryonic and was cross *C. unshiu* 'Tachima wase' and *C. natsudaidai* in 1992. The planted area of 'Haraejosaeng' began to expand by Golden Seed Project(GSP) which started in 2013. It replaces the previously grown cultivated of old or mixed varieties of *C. unshiu* of the open field in Jeju. In recent years, cultivation with heating(keep at least 17℃ from Dec.) using 'Haraejosaeng' has also increased.

This study was conducted to find superiority or differentiation while examining various cultivation types of citrus domestic variety 'Haraejosaeng'. It was found that 'Haraejosaeng' was colored faster 3 days and harvested earlier 7 days than previously grown variety *C. unshiu* 'Miyagawa Wase'. The peel color(a*) of 'Haraejosaeng' is rapidly colored compared to C. unshiu 'Miyagawa Wase' in mid-May. In June of harvest, the peel color(a*) is about 3 to 14 higher than the *C. unshiu* 'Miyakawa Wase', resulting in a dark red color. Therefore, the domestically *C. unshiu* 'Haraejosaeng' has a higher soluble solid content, a similar acidity, darker red peel color than the *C. unshiu* 'Miyagawa Wase'.

In the future, it is necessary to continuously discover and promote excellence in order to expand the distribution of *C. unshiu* 'Haraejosaeng' of the domestic variety.

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PF-0036

Natural variation in phenolic acid profiles of Korean red pepper (*Capsicum annum* L.) varieties

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Phenolic acids play significant role in plants and human health as antioxidants. This study was conducted to determine the content of phenolic acids in Korean red pepper cultivars. Although phenolic acids are an important antioxidants found in edible plants, to the best of our knowledge, phenolic acid concentrations in Korean red pepper fruits from various cultivars had not been reported. Moreover, to evaluate the impact of genotype versus environmental influence on the phenolic acid profiles of red pepper fruits, phenolic acids were investigated in samples of eleven Korean red pepper (Capsicum annum L.) grown simultaneously at Imsil and Youngyang for three years. Five different phenolic acids (*p*-hydroxybenzoic, vanillic, syringic, ferulic, and sinapic acids) were identified by GC-TOFMS including *tert*-butyldimethylsilyl derivatization. All data were subjected to principal component analysis (PCA) to identify the specific chemical composition of red pepper samples attributable to location, cultivation year, or genotype. The PCA analysis showed no clear separation among the eleven cultivars and by two cultivation regions. However, small but some extent of separation was observed according to cultivation year. Further studies using several statistical methods are planned in order to assess natural variation in phenolic acid composition of red peppers.

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PF-0037

Assessment of seed oil composition of rapeseed mutant lines derived from gamma-ray

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Rapeseed are the most important oil crop used in food and biodiesel industries. Recently, several rapeseed mutant lines with improved flowering, crude fat and fatty acid traits have been developed using gamma irradiation. The 47 rapeseed lines were divided in to three categories; early flowering (160 to 169 day after sowing) with 15 mutant lines, middle flowering (170 to 179 day after sowing) with original cultivar and 26 mutant lines and late flowering (180 to 189 day after sowing) with 6 mutant lines. The crude fat content of original cultivar was 33.9 mg/100 g. The crude fat content for all mutant lines ranged from 26.9 to 42.3 mg/100 g with an average 34.4 mg/100 g. Oleic, linoleic, linolenic, eurcic acid were principal fatty acid presented in the rapeseed lines. The oleic acid compositions from all the mutant lines ranged from 35.3% to 76.7%. The erucic acid content observed in 10 mutant lines with composition range of 0.1% to 21.6%. The hierarchical cluster analysis divided the flowering time, crude fat content and six fatty acid compounds into two clusters and two independent group. Overall results could be applied to breeding programs to develop rapeseed cultivars with improved flowering time and fatty acid compounds.

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PF-0038

Comparative analysis of oil yield and aroma compound compositions of *Veronica* genotypes

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The genus *Veronica* have been used as ornamental and traditional folk medicines in Korean. In this study, we investigated the volatile compound compositions of aroma oil in twelve speedwell genotypes. Aroma oils from the whole plant with flower of these accessions were analyzed by gas chromatography-mass spectrometry (GC-MS). The highest total oil yield was observed in the 'VA168' genotype and the lowest content in 'Kinsan'. Thirty-four aroma compounds were detected and the abundant volatiles were organic acid, hydrocarbons and fatty acid in the all accessions. A significant difference in the volatiles compound contents was observed among the accessions. The Guwa and Dungkunsa showed higher contents of benzoic acid compounds than did the other spices. The highest hexacosane content was observed in Busan. The hierarchical cluster analysis of the 12 genotypes showed that they formed two groups according to their aroma compound content. These findings suggested the potentials of using the selected breeding materials as a functional source, related to the abundant of aroma beneficial components.

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PF-0039

Phytochemical compounds in the flower aroma oil of rose mutant derived from gamma-irradiation

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Roses are one of the most important industrials crop, and their aroma oils have long been used for cosmetics and aromatherapy. We investigated the aroma compounds of 12 flower-color mutant variants and their original cultivars. Twelve rose mutant genotypes were developed by treatment with 70 Gy of ^{60}Co gamma irradiation of six commercial rose cultivars. Aroma oils from the flowers of the 18 genotypes were analyzed by gas chromatography-mass spectrometry (GC-MS). Seventy-seven volatile compounds were detected, which were categorized into five classes: hydrocarbons, terpenoids, alcohols, esters, and others. Hydrocarbons, alcohols, and esters were major components in rose gemplasms. Two mutant genotypes (CR-S8 and CR-S9) showed higher contents of hydrocarbons than the original cultivar. Furthermore, CR-S1, CR-S3, and CR-S4 mutant genotypes showed higher ester contents than their original cultivar. Nonacosane, 2-methylhexacosane, and 2-methyltricosane were major aroma compounds among rose genotypes. Hierarchical cluster analysis of the rose genotypes gave four groups according to grouping among the 77 volatile compound similarities. These findings will be useful for the selection of rose genotypes with improved aroma compounds.

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PF-0040

Discovery of novel SNP associated with flowering in *Raphanus sativus* in-bred lines using transciptome sequencing for marker-assisted backcross breeding

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To accelerate the genomics assisted breeding and genetic selection in *Raphanus sativus*, transcriptomes of 33 radish inbred lines with diverse traits were sequenced for the development of single nucleotide polymorphic (SNP) markers. The sequence reads ranged from 2,560,543,741 bp to 20,039,688,139 bp with the GC (%) of 47.80 - 49.34 and phred quality score (Q30) of 96.47 - 97.54%. A total of 4951 polymorphic SNPs have been identified among the accessions after stringent filtering and 298 SNPs with efficient marker assisted backcross breeding (MAB) markers were generated from the polymorphic SNPs. Further, functional annotations of SNPs revealed the effects and importance of the SNPs identified in the flowering process. The SNPs were predominantly associated with the four major flowering related transcription factors such as MYB, MADS box (AG), AP2/EREB, and bHLH. In addition, SNPs in the vital flowering integrator gene (FT) and floral repressors (EMBRYONIC FLOWER 1, 2, and FIRGIDA) have been identified among the radish inbred lines. Further, 50 SNPs were randomly selected from 298 SNPs and validated using Kompetitive Allele Specific PCR genotyping system (KASP) in 102 radish inbred lines. The homozygosity of the inbred lines varied from 56%~96% and the phylogenetic analysis resulted in the clustering of inbred lines into three subgroups. Taken together, the SNP markers identified in the present study can be utilized for the discrimination, seed purity test, and adjusting parental combinations for breeding in radish.

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PF-0041

Characterization of gamma-irradiation generated orchid mutants altered in anthocyanin biosynthesis

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Orchids with colorful leaves and flowers have significant ornamental value. Here, we used γ - irradiation based mutagenesis to produce a *Dendrobium bigibbum* mutant that developed purple, instead of the normal green, leaves. RNA sequencing of the mutant plant identified 2,513 differentially expressed genes, including 1,870 up- and 706 downregulated genes. Genes that encoded key biosynthetic enzymes in the anthocyanin biosynthetic pathway and transcription factors (MYBs, basic helix-loop-helixes, WD40 classes, and WRKYs) that regulate anthocyanin biosynthesis were upregulated in the mutant. Additionally, the expression levels of these differentially expressed genes correlated well with higher anthocyanin levels in the mutant. Thus, the purple coloration of orchid leaves may result from the altered expression levels of regulatory genes participating in anthocyanin biosynthesis.

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PF-0042

Estimation of Heritability for Fruit Size Related Traits in Progenies Derived from a Cross Between 'Manpungbae' and 'Ooharabeni' (*Pyrus* spp.)

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Fruit size is one of the most important quality trait in commercial fruit crops. Fruit size is usually quantified by fruit weight (FW) and determined by fruit length (FL) and diameter (FD). To estimate the heritability for fruit size of pear fruits, quantitative traits (FW, FL, and FD) were identified in a hybrid population derived from a cross between 'Manpungbae' and 'Ooharabeni' (*Pyrus* spp.) for 3 consecutive years from 2016 to 2018. FW, FL, and FD followed a normal distribution. The average phenotypic values of FW, FL, and FD were 228.8 g (range 26.9-721.5 g), 67.86 mm (range 34.3-99.0 mm), and 76.05 mm (range 38.1-118.8 mm), respectively. Pearson's phenotypic correlation coefficients between the three years were highly significant for all three traits, ranging from r = 0.59 between FL in 2017 and FD in 2018 to r = 0.95 between FW in 2017 and FD in 2017. The values of broad-sense heritability (H^2) of FW, FL, and FD were 82.42, 79.23, and 77.11%, respectively, suggesting that these three traits are stably inherited. These results will be useful for the application breeding program for fruit size in pear.

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PF-0043

Linkage Analysis for Fruit Quality Traits in Apple (*Malus* × *domestica*)

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Apple is one of the important temperate Rosaceae fruit trees. An apple cultivar 'Gala' displays pink red fruit color and low titratable acidity. Whereas, 'Jonathan' has red fruit color and high titratable acidity. A cross population of 'Gala' × 'Jonathan' is a suitable material for identification of genetic loci associated with interest fruit traits in apple. Thus, the present study was performed to identify genetic loci associated with fruit color and titratable acidity using 'Gala' × 'Jonathan'. Genetic linkage maps for the parents were constructed using GBS-SNPs and SSRs derived from apple and pear. The genetic linkage maps of 'Gala' and 'Jonathan' covered ~85% of pseudo-chromosomes. As a result of QTL analysis, significant QTL regions related to titratable acidity and Hunter a* were detected in the linkage group 13 and 15, respectively in 'Jonathan' map. A SNP marker, chr13_12135410, were closely linked with QTL controlling titratable acidity. In addition, a SNP marker (chr15_11310163) and a SSR (CH01d08) were linked with QTL affecting Hunter a*. These results will facilitate development of molecular markers that can distinguish red color and high titratable acidity in apple breeding.

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PF-0044

Insertion-Deletion (InDel) Marker Development for Marker-Assisted Selection of Pollen Fertility in Pears (*Pyrus* spp.)

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Insertion and deletions (InDels) refer to insertion or deletion of genomic sequences in the DNA. Because InDels are preferred ideal sequence-based, it is easily detected by comparing genomic sequences between two individuals. Polymorphisms can be confirmed with PCR amplification followed by agarose gel electrophoresis. In our preceding work, a genomic region associated with pollen fertility was identified via the genetic linkage mapping in the F_1 population of 'Whangkeumbae' (*Pyrus pyrifolia*) and 'Minibae' ((*P. pyrifolia* × *P. ussuriensis*) × *P. pyrifolia*). After detecting InDel structures in the vicinity of SNP loci where the pollen fertility is associated with, five pairs of primers were designed to amplify 200-300 bp of PCR amplicon. CBp11id01 was polymorphic in parents ('Whangkeumbae' and 'Minibae'). Phenotypes for 71 out of 88 F_1 individuals were successfully predicted by the marker genotype of CBp11id01. It is anticipated that CBp11id01 can be utilized for marker-assisted selection of pollen fertility in pear breeding program.

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PF-0045

Identification of QTLs Linked with Exocarp Russet Formation in Asian Pear (*Pyrus* spp.)

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Russet is an interesting trait in pear breeding because it influences on commercial value. The present study was performed QTL identification, which controls russet formation in exocarp of Asian pear. As a foundation work of QTL analysis, array-SNPs were anchored to previously constructed genetic linkage map of 'Whangkeumbae' × 'Minibae'. Russet was evaluated as visual estimation, Hunter a*, and image analysis. The positive correlation between Hunter a* and russet coverage calculated using image analysis indicated that the image analysis is a promising phenotyping method for evaluation of fruit skin color. QTL controlling russet formation was identified in linkage group 8 of 'Whangkeumbae' × 'Minibae'. In addition, there were candidate genes affecting russet formation in the QTL region. The candidate genes have been known to response to environmental stresses and pathogen invasion. Therefore, the russet in exocarp of Asian pear seems to be represented by expression of stress responsive genes. These results could help in development of molecular markers that could distinguish russet and non-russet exocarps.

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PF-0046

Comparison of Phenotypic Distribution and Heritability According to Fruit Indices in Interspecific Pears (*Pyrus* spp.)

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European pears generally have pyriform shape, whereas, Asian pears have from round to pyriform shapes. Until now, fruit shape has been usually evaluated L/D ratio, that could not correctly reflect fruit shapes. This study compared phenotypic distributions and heritability for two fruit shape indices between two interspecific populations that are 'Whangkeumbae' × 'Yali' (WY) and 'Whangkeumbae' × 'Bartlett' (WB). L/D ratio represented as ratio of longitudinal diameter (L) to maximum diameter (D). A/A' ratio, the other fruit shape index, means ratio of length from fruit stalk to the middle of fruit diameter (A) to from fruit apex to the middle of fruit diameter (A'). L/D ratios for 'Whangkeumbae' (round), 'Yali' (pyriform), and 'Bartlett' (pyriform) were 1.00, 1.15, and 1.17, and A/A' ratio were 1.04, 2.48, and 2.34, respectively. L/D ratios for F_1 progenies of WY and WB ranged from 0.83 to 1.16, and from 0.83 to 1.22, respectively. A/A' ratios for F_1 progenies ranged from 0.94 to 4.4 in WY, and from 1.06 to 2.12 in WB. Phenotypic distributions for fruit shape indices were similar to normal distribution and biased towards 'Whangkeumbae'. The heritabilities of L/D and A/A' ratio were 0.74 and 0.84 in WY, and were 0.88 and 0.83 in WB, respectively. Although fruit shape has been known as quantitative trait, we thought that fruit shape could be influenced by genetic factors rather than environmental factors. Based on these results, it will be possible to develop molecular markers related to fruit shape by performing quantitative trait loci mapping.

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PF-0047

Transcriptome Analysis Associated with Exocarp Russet Formation in Asian Pear (*Pyrus* spp.)

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The russet, one of the skin colors in Asian pear, consists of suberin, lignin, cellulose, and hemicellulose. Expression of genes involved in russet formation could support understanding the expression of fruit skin color. The present study was performed RNA-sequencing (RNA-seq) using exocarp of 'Minibae' ((*P. pyrifolia* × *P. ussuriensis*) × *P. pyrifolia*) to identify the genes controlling russet formation. In addition, expression of genes controlling russet formation was compared in russet and non-russet exocarp. The microstructure of 'Minibae' (russet) and 'Whangkeumbae' (non-russet) showed that the cork layer was only developed in russet exocarp. As a result of RNA-seq, 2,081 and 4,344 differentially expressed genes (DEGs) were detected at 50 and 80 days after full bloom (DAFB), respectively. Most of DEGs were involved in suberin and lignin biosynthesis and stress response and the expression of the DEGs was begun at 50 DAFB. On the other hand, cutin biosynthetic DEGs were down-regulated or not detected during fruit development. Comparison of the DEGs controlling russet formation between 'Minibae' and 'Whangkeumbae' indicated that the expression levels of lignin and suberin biosynthetic genes were higher in 'Minibae' than 'Whangkeumbae'. Whereas, expression levels of cutin biosynthetic DEGs were lower in 'Minibae' than 'Whangkeumbae'. Therefore, the major components of russet in 'Minibae' exocarp are lignin and suberin and the up-regulation of lignin and suberin biosynthetic genes in early fruit development stage affects russet formation. Moreover, stress responsive genes also affect russet formation.

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PF-0048

Heritability of Stone Cell Content in 'Whangkeumbae' (*Pyrus pyrifolia*) × 'Minibae' (*P.* hybrid)

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Stone cells have thicker secondary cell walls than parenchyma cells formed by the deposition of lignin called sclerenchyma cells. Stone cells are mainly composed of lignin, cellulose, and hemicellulose, and stone cells are roughly chewed in the mouth giving gritty texture when eaten in a raw state. The existence of stone cells in pear leads to reduction of fruit quality and economic value. Therefore, control of stone cell content in pear is essential to improve fruit quality and economic value. In this experiment, fruits of 'Whangkeumbae' (*Pyrus pyrifolia*), 'Minibae' (*P.* hybrid), and their 130 F_1 individuals were examined as the material to investigate stone cell content in the fruit to determine heritability of stone cell content. 'Whangkeumbae', 'Minibae', and their 130 F_1 individuals were sampled 132 days after full bloom. Isolated stone cells of 'Whangkeumbae' and 'Minibae' were 0.044 and 0.226 g respectively. Stone cell content in F_1 individuals ranged from 0.025 to 0.320 g. The heritability of content of stone cells was 0.923. Knowing the information on the heritability of stone cell content as basis, identifying genetic traits related to stone cell formation in later works will contribute to pear breeding.

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PF-0049

수박 대목용 박과채소의 저온 발아특성 비교

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시설원예 재배지에서 연작을 하면 염류집적, 토양물리성 악화, 토양병원균 밀도 증가 등에 의해 장해가 발생하고, 이로 인해 생산물의 품질저하와 생산량 감소로 이어진다. 특히 수박은 연작피해가 상대적으로 심한 작물로 그중 토양전염성인 덩굴쪼김병으로 인한 피해가 크기 때문에 대부분 박이나 호박을 대목으로 이용하여 접목재배가 이루어지고 있다. 접목재배는 연작장해를 회피할 수 있을 뿐만 아니라 내냉성, 내서성, 내습성 등 불량환경에 대한 적응력을 높여 안정생산에도 도움이 된다. 본 연구는 수박 대목용 박과채소에 대한 저온 적응력 검정의 일환으로 저온조건에서 발아(출아)특성을 조사하였다. 시험재료는 호박, 박, 야생수박 각 10계통을 이용하였다. 1차 발아시험은 12, 15, 18℃에서 20일간 진행하였고 이때 호박은 12℃에서 2계통, 15℃에서 7계통이 발아되었다. 박과 야생수박은 12, 15℃에서 발아가 되지 않았고 18℃에서 각각 9계통이 발아되었다. 2차 발아시험은 17일간 진행하였고 호박은 16, 18, 20℃ 그리고 박과 야생수박은 18, 20, 22℃에서 진행하였다. 호박은 16, 18, 20℃에서 계통별 발아율 평균은 각각 40.5, 74.3, 91.4%, 발아세는 38.1, 70.4, 79.5%, 평균발아일수는 13.3, 9.5, 7.4일 이었다. 박은 18, 20, 22℃에서 계통별 발아율 평균은 각각 63.8, 86.2, 91.9%, 발아세는 38.1, 50.6, 67.6%, 평균발아일수는 14.1, 10.2, 9.7일 이었다. 야생수박은 18, 20, 22℃에서 계통별 발아율 평균은 각각 46.7, 82.9, 87.1%, 발아세는 24.8, 60.0, 61.0%, 평균발아일수는 13.9, 9.6, 9.3일 이었다. 결과를 종합해 보면 호박, 박, 수박 순으로 저온에서 발아력이 높게 나타났다.

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PF-0050

백색 녹심의 볼륨감 있는 중대형 국화 '프레시카펫' 육성

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전라북도 완주분 이서면 농생명로100 국립원예특작과학원 화훼과

국화는 장미, 나리와 더불어 세계 3대 절화 중 하나이며 국내에서도 전체 절화류의 30%를 점유하는 중요한 화훼작물이다. 2018년 국내 절화국화의 재배면적은 314ha로 그 중 스프레이 국화는 68.4ha로 약 21.8%를 차지하고 있다. 국화는 다양한 꽃색과 꽃모양을 가지고 있어 축하용이나 위문용등으로 그 쓰임새가 다양하다. 유통시장에서는 기존국화와 다른 동그란 공모양의 폼폰형, 여러 가지 꽃색의 중대형 디스버드형에 대한 요구도가 증가하고 있다. '프레이카펫(Fresh Carpet)'는 2013년 국립원예특작과학원 화훼과 국화육종온실에서 연녹색 폼폰형 겹꽃인 '07B1-145'를 모본으로 밝은 녹색 중대형 겹꽃인 'windmill green'를 부본으로 교배하였다. 2014년 종자를 파종, 육묘 후 실생묘를 정식하여 자연개화후 선발하여 '13B1-04' 계통번호를 부여받았다. 이후 1차, 2차 특성검정을 실시하였으며, 3차 특성검정을 실시하였다. 개화특성검정을 실시하고 촉성재배, 자연재배, 억제재배의 주년생산성 검정 및 절화수명 등 소비자 기호성에 대해 조사되었다.

국화 '프레시카펫' 품종은 10월 하순에 자연 개화하는 절화용 스프레이국화로 디스버드형으로 사용이 가능하다. 꽃색은 백색(W155C)으로 중심부가 녹색인 겹꽃이며 꽃크기는 9.3±1.5㎝이며 꽃당 설상화수는 232.7±20.9매로 볼륨감이 있는 중대형화이다. 초장은 100.9±1.5㎝로 균일하가 잘 자라고 볼륨감이 있고 고온기인 7~9월 개화작형에서 꽃색이 좋고 균일한 특성을 가지고 있다. 한줄기당 착화수는 약 16.8±2.3개 정도이며 절화수명은 약 21일로 길고 꽃잎 빠짐현상이 없어 소비자기호도가 높았다. 단일처리 후 연평균 개화반응은 7.5주이다. '프레시카펫' 품종의 재배시 주의할 점은 일교차가 있는 늦겨울에서 봄 재배작형에서 흰녹병이 발생되지 않도록 적극적인 환기가 필요하며 시설내습도가 70%이하가 되도록 관리해야 한다. 고온기에 생장성이 좋아 꽃목길이가 길어질 수 있어 생장조정제 처리 등 적절한 조절이 필요하다.

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PF-0051

Identification of diverse spray type chrysanthemum cultivars using SSR markers

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Chrysanthemum is the second most important ornamental plants after rose and is a popular cut flower across the global flower market. It is a commercially important crop for the floral industry in Korea. Several hundreds of chrysanthemum cultivars have been commercialized due to its trouble-free vegetative propagation and the presence of considerable amount of genetic variations resulting in a wide range of phenotypic variations. Considering the substantial number of cultivars, identification of the cultivars is highly essential to protect the intellectual property of the breeder and to guarantee the right labelling of the cultivar in the floral market. Morphological characteristics alone are not sufficient to identify the cultivars as they are often indistinguishable, not stable and are influenced by the environment. Hence, an effective and reliable method to identify and discriminate the cultivars is required. This study was aimed to identify the suitable molecular markers that can discriminate the diverse spray type chrysanthemum cultivars. SSR markers were employed to identify a collection of 61 spray type cultivars including both commercial and cultivars developed at NIHHS, RDA. Among the total 23 markers screened, polymorphism was detected in 10 SSR markers by ABI genetic analyzer. The PIC (Polymorphism Information Content) values of 10 SSR markers ranged from the low of 0.24 to the high of 0.65 with an average PIC value of 0.47. Among these 6 SSR markers were identified which could the detect polymorphism and could discriminate all the tested 61 spray type cultivars. Hence, 6 SSR markers are considered as informative markers for the identification of spray type chrysanthemum cultivars. Hence, these SSR markers can be effectively applicable to provide the data for cultivar discrimination and for assessing the genetic similarity among the chrysanthemum cultivars.

Key words: Chrysanthemum, cultivar discrimination, polymorphism, SSRs, variety protection

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PF-0052

A Mid-flowering Freesia 'Snow Candy' with White Double Petals

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A Freesia (*Freesia hybrida* Hort.) 'Snow Candy' with double white petals and mild scent was developed in the National Institute of Horticultural Herbal Science during 2019. The hybrid seedling was selected '12C3-1-3' resulting from the cross between 'Teresa' and 'Medeo' in 2012. Therefore, the growth and flowering characters of '12C3-1-3' were evaluated from 2014 to 2018. Superior performance was observed and the hybrid was named as 'Snow Candy' in 2019. Phenotypic characters were compared with the control cultivar 'Medeo'. Growth characteristics were vigorous with average plant height of 106.7 cm which was 10cm higher than that of the control 'Medeo'. Flower color was white (RHS, W155B) with flower stalk length of 12.6 cm which was superior to the control 'Medeo' (8.0 cm). Number of floret per stalk was 13.3 while it was 12 in control. Flower width was 6.9 cm with an average yield of 6.7. It takes 134 days to first flowering with average vase life of 8 days. They yield an average of 4.3 cormlets per plant. Flower scent of 'Snow Candy' was compared between two cultivars '10C3-894' and P16C3-68-11 which were strong and weak scented, respectively. In the principal component analysis (PCA) of 'Snow Candy' formed two components with 98.60% in PC1 and 0.99 % in PC2 of variance while discriminant functions displayed 98.60% in DF1 and 0.99 % in DF2.

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PF-0053

포드×무지개 F1 국화계통의 주요 농업 형질의 유전력 검정

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본 연구는 경지면적은 좁으나 양질의 노동력을 보유하고 있는 우리나라 농업의 수익 작물의 특징을 가지는 스프레이 국화 우수 품종의 교배조합 후대에 표현되는 중요 농업 형질의 유전력을 검증하기 위해 실시하였다. 독립적인 재배조건의 두 지역에서 식물재료로 소비자와 재배자가 가장 선호하는 모본 포드와 부본 무지개를 교배친으로 종자번식을 한 F1 21 계통을 이용 하였으며, 조사항목으로는 초장, 줄기직경, 측지수, 화경, 화심폭, 착화수, 꽃잎수, 꽃목길이, 개화일 등이다. 생육조사를 통해서 얻은 평균치를 대표치로 하여 형태적 특성의 차이를 확인하기 위해 유전변이계수(Genetic coefficient of variation, GCV), 표현형 변이계수 (Phenotypic coefficient of variation, PCV), 광의의 유전력 (Heritability, h^2), 유전적 진전(Genetic advance, GA), 유전적 진전율(Genetic advance as present of mean, GAM)등에 대한 통계적 분석을 수행하였다. 형태학적 특성별 품종 간 Tukey와 LSD를 검정한 결과 같은 지역 내에서도 표현형질의 평균 차이가 크게 났으며 두 지역 간의 각 계통에서 각 형질의 평균값은 매우 달랐으며, 고도의 유의차가 인정되었다. 표현 변이계수(PCV)는 개화일이 10.3%, 유전 변이계수(GCV)도 개화일이 7.4%로 가장 낮았으며 꽃목길이가 29.8-34.6%로 가장 높았으나, 광의의 유전력 (h^2)은 줄기직경이 11%로 가장 낮았고 화심폭 화경 꽃잎수가 84.4-86.3%로 가장 높았다. GA(유전적 진전)는 줄기직경이 0.2로 가장 낮았고 초장이 14.2%로 가장 높았으며 GAM(유전적 진전율)은 줄기직경이 3.4%로 가장 낮았으며 화심폭이 55.4%로 가장 높았다. 따라서 유전력 및 기타 양적유전지표에서 높은 값을 나타내는 화경, 화심폭, 꽃잎수 등의 형질들은 포드x무지개 교배조합에서 선발효율이 높을 것으로 사료된다. 향 후 본 연구는 고품질 스프레이국 우수중간모본의 개발에 유용하게 이용될 것으로 기대된다.

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PF-0054

상추 아삭함의 대량평가기술개발을 위한 물성측정방법 최적화 연구

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본 연구는 아삭함에 대한 요구가 증가되는 바, 상추의 조직감 특성을 나타내는 관능적 표현을 정량적으로 나타내기 위한 기계적 측정방법을 찾고자 Texture Analyser를 통해 측정방법을 확립하고, 아삭함 예측 물성회귀식을 도출하여, 대량평가를 위한 물성측정방법을 확립하고자 수행하였다. 상추품종은 '학교급식 상추선호도'인 선행 연구와 동일한 국내 유통, 향상된 잎상추 8종과 오크, 로메인등 10종류이다. 물성측정기(Rheometer (CR-100))로 상추 중륵, 잎 물성측정 최적화를 위한 probe를 선정 하고, 산출된 다양한 Texture profile로 평균비교와 상관관계를 통해 중요물성을 추출하여, 두 가지 방법으로 적합한 물성회귀식 모델을 선정하였다. 그 결과 상추 품종의 중륵, 잎 물성이 다르고 MaxG는 조직감을 구성하는 다양한 물성 인자 간에 중요 물성으로 관찰되었다. 모델은 선형회귀분석으로 Y= 3.0184 + 0.034 x leafMaxG와 로지스틱회귀분석으로 $\log(\pi/(1-\pi)) = -10.8437 + 0.4386$ x leafMaxG가 도출되었는데, 이에 의해 물성데이터인 leafMaxG로 아삭함 예측이 가능하며, 특히 데이터 값이 26일 때 아삭함의 예측력이 뚜렷해짐을 알 수 있어 선발지표로 활용될 수 있음이 사료된다. 확립된 물성측정 최적화방법을 핵심집단에 확대 적용을 통하여 아삭함이 우수한 상추 자원을 효율적으로 선발 관련 유전자 및 분자표지 마커 발굴을 위한 대량평가 기술로 유용하게 활용될 것으로 기대한다.

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PF-0055

수박 신품종 육성을 위한 단간종 F_2유전분리비 및 특성조사

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충청북도 음성군 대소면 대금로 326-8 충청북도농업기술원 수박연구소

수박은 관행 포복재배의 악성 노동환경 개선과 수경재배를 통한 연중생산 및 생산성 향상을 위해 최근 수직유인재배, 딸기 고설베드 활용 재배 등 재배방식의 다양화가 시도되고 있다. 이에 따라 하우스에서 줄기가 3m이상 자라는 기존 품종 외에 1.3~1.8m정도의 재배방식에 적합한 품종이 요구되는 실정이다. 본 연구에서는 줄기길이가 일반 수박의 1/3 정도(1m 이내)로 짧은 유전자원인 단간종 수박의 줄기길이 중단간화 및 외형, 과피두께 감소, 당도 향상 등 과실 고품질화를 통한 신품종 육종을 위해 수행되었다. 청피, 호피, 흑피의 단간종 유전자원 4계통에 각각 고당도 장간종 4계통을 교배하여 16계통의 F_1(단간종×장간종)을 만들었고, 이 중 우수형질을 보이는 6계통을 선발하였다. 선발된 F_1을 각각 자가수정하거나 여교배하여 F_2(자가수정: [단간종×장간종]×자가수정, 여교배: [단간종×장간종]×단간종) 12계통의 유전 분리비 및 특성검정을 실시하였다. F_1(단간종×장간종) 특성검정 결과, 16계통 모두 줄기길이 3m 이상의 장간형질이 발현되었으며, 과실특성은 과중, 당도의 경우 단간 유전자원과 차이를 보이지 않았으나 과피두께는 단간종이 1.5~1.6cm인데 비해 0.7~1.1cm로 매우 얇아졌다. F_2 분리비 및 특성검정 결과, 자가수정의 경우 장간형질:단간형질 분리비가 87:13, 여교배의 경우 26:64로 나타났다. 각 계통별 장단간 분리비의 경우, 다른 계통과 달리 흑피 계통인 231-2에 여교배된 2계통에서 모두 단간 경향이 강하게 나타났으며, 장간형질:단간형질 분리비가 0:100로 조사되었다. 줄기길이는 단간 유전자원이 0.96m로 가장 짧고, 여교배가 1.23m, 자가수정이 2.15m였으며, 이는 각각 단간 유전자원의 1.3배, 2.2배 해당하는 수치였다. 정식 32일 후, 암・수꽃 수 조사결과 단간종의 경우 암꽃은 평균 1개, 자가수정 2.9개, 여교배 2.3개였으며, 수꽃은 단간종의 경우 8개, 자가수정과 여교배는 단간종과 비교하여 각각 1.7배 많았다. 과중, 과피두께, 당도 등 과실특성은 단간종, 자가수정, 여교배 간의 차이가 없었다.

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PF-0056

Overexpression of *OsTZF8*, a CCCH-tandem zinc finger, improves drought tolerance in rice by regulating stress-related genes

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Background: Tandem CCCH zinc finger proteins (TZFs), one of the zinc finger protein family, is recently researched to participate in the regulation of stress responses and development via the posttranscriptional regulation of messenger RNA in animals, yeast and plants. However, the molecular mechanism of TZF-mediated drought tolerance is not fully understood.

Results: We analyzed the functions of *OsTZF8*, a member of the rice TZF family. *OsTZF8* is predominantly expressed in flowering stage, very specifically at seeds, and its expression levels rapidly declined during seed imbibition. The expression of *OsTZF8* was induced by 4 different abiotic stresses, drought, high salinity and abscisic acid (ABA). Subcellular localization analysis revealed that *OsTZF8* localization decreased from the nucleus and increased at the processing bodies and stress granules upon stress treatment. Root-specific overexpression of *OsTZF8* was insufficient to induce drought tolerance, while the overexpression of *OsTZF8* throughout the entire plant enhanced the drought tolerance of rice plants. Transcriptome analysis revealed that *OsTZF8* overexpression elevated the expression levels of genes involved in stress responses, including *LATE EMBRYOGENESIS ABUNDANT PROTEINs* (*LEAs*), *PATHOGENESIS RELATED GENEs* (*PRs*) and *GERMIN-LIKE PROTEINs* (*GLPs*).

Conclusions: Our results demonstrated that *OsTZF8* is involved in the regulation of the drought tolerance pathway by modulating the expression of stress-related genes.

Keywords: Tandem CCCH zinc finger, Rice, Drought tolerance, Processing bodies (PB), Stress granules (SG)

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PF-0057

Developing Inbred Line of 'Wonkyo20051ho' Showing Resistance for the Low Temperature Cultivation at Autumn Culture in Kimchi Cabbage (*Brassica rapa* L.)

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Kimchi cabbage(Chinese cabbage, *Brassica rapa* L) is one of the major 10 vegetables in Korea. Because the most famous fermented traditional food of 'Kimchi' is mainly produced using Kimchi cabbage. Besides its usage is increasing for instance, shabu-shabu, salad, and ssam. Due to the climate changing, the major cultivation method of autumn cultivation was restricted hot or cold temperature stress. Therefore, the crucifer breeders in the National Institute of Horticultural and Herbal Science decided to develop inbred lines showing resistance to the temperature stress using microspore cultivation of selected breeding plant material.

In 2014, 37 major summer F_1 cultivar planted at 15th May and investigated at 17th July in Suwon. Because of hot and humid weather, only 11 cultivar produced head and showed yellow inner leaf color. The selected plants was transplanted into small pot and managed to produce flowers to do bud pollination and microspore cultivation. In 2018, we developed 83 inbred lines and evaluated the horticultural trait through autumn cultivation. One inbred line of 'FH98' was selected as field resistance to cold temperature. The inbred was derived from Korean summer variety of 'Arari' and showed mild resistance to the low concentration (1.0 x 10^6spores/ml) clubroot 'Seosan' inoculumn. Breeders of 3 commercial companies selected this inbred as showing good heading traits under chilly autumn climate of 2018. Thus considered valuable breeding material showing low temperature and clubroot tolerant DH inbred.

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PF-0058

Comparative of radio sensitivity to Gamma-ray and Proton Beam in Coriander (*Coriandrum sativum*)

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Coriander (*coriandrum sativum*) is an annual herbal plant, belonging to the Apiaceae, is used for culinary and medicinal uses. Mutagenesis using ionizing radiation has been widely used for the development of breeding resources with novel characteristics. Although mutation breeding using gamma-rays has been attempted in crops, information on the effectiveness of other ionizing radiation and a comparative analysis of mutagenic effects of different forms of radiation is limited. Therefore, we investigated and compared the radio sensitivity of gamma-rays and a carbon beam (a heavy ion beam) in Coriander. Gamma-ray and proton beam irradiated to dry seeds with various doses (0 to 300 Gy). The survival rate obtained by irradiation at various doses showed that the median lethal dose (LD_{50}) was about 150 and 80 Gy, and the median reduction dose (RD_{50}) was about 80 and 40 Gy for gamma rays and carbon beams, respectively. The raido sensitivity showed that the mutagenic effect of the proton beam was higher than that of gamma-rays. This study provides basic information for mutation breeding using ionizing radiation in Coriander.

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PF-0059

Development of seedling screening method for selecting low-temperature tolerant pumpkin (*Cucurbita moschata*) and selection of tolerant genetic resources

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This study was conducted to establish a screening method of low-temperature tolerance using seedling and select the tolerance genetic resources of *Cucurbita moschata*. *C. moschata* is being used as a bloomless rootstock for cucumber that suppresses bloom formation on fruit skin, but due to its low chilling tolerance, it is not applied for long-term cultivation practices that include cold season in Korea. In solar greenhouse cultivation in the northern China, where non-heating cultivation is settled as a general cultivation practices, *C. moschata* is used as main rootstock for producing Chinese long green type cucumber, so the demand for low-temperature tolerant rootstock varieties are increasing. It is necessary to develop a screening method that can be efficiently applied for early evaluation because long-term cultivation tests are needed for evaluating chilling tolerance and it is difficult to impose uniform selection pressure in the field condition. The suitable temperature conditions for chilling tolerance selection was 17℃/7℃ (8h/16h light /dark, 100μmols-1m-2 light intensity), where the seedling growth rate showed the same pattern with the known chilling response of the Cucurbita species. Among the two screening methods of seedling culture and cut seedling culture under the low-temperature, the latter (r= 0.708) showed higher correlation than the former (r = 0.577). Overall, as low-temperature response of adult plants and seedlings under the low temperature were highly correlated, so it was thought that the seedling evaluation could be applied for effective screening of chilling tolerance. The photochemical efficiency (Fv/Fm) of PSII after continuous chilling light treatment (4℃, 100 μmols-1m-2, 24hrs or 48hrs) was not correlated with the seedling growth rate, so it seemed not to be applicable as a selection index. Applying the seedling screening method, four chilling tolerant genetic resources were selected among the 407 accessions collected from NPGS and National Agrobiodiversity Center, Rep. of Korea.

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PF-0060

뿌리가 작고 단단한 무 '원교10050호' 육성

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무(*Raphanus sativus* L.)는 한국의 주요 10대 채소 중 하나로 김치의 재료로 주로 소비되고 있으며, 전통적으로 국, 나물 등의 요리에 이용된다. 최근에 기능성 성분을 보유하고 있는 채소 품종에 대한 관심이 증가하면서, 유색 품종의 수요도 점차 증가하고 있다. 이에 본 연구에서는 무의 활용범위를 넓히기 위하여, 수요자 요구가 증가하고 있는 유색무 품종을 육성하고자 하였다. 2011년에 보유중인 다양한 유색 자원의 뿌리 특성 조사결과, 대부분 수집 자원의 진한 분홍색(마젠타색) 발현이 불균일하였으며, 열근과 바람들이 발생이 많았다. 이점을 개선하기 위하여 성숙모본의 형태로 선발하여 매 세대 자가수정으로 세대를 진전하였고, 2014년에 근육과 근피 색이 진한 분홍색으로 균일하며 열근과 바람들이에 강한 계통을 육성하였다. 이 선발 계통의 종자를 2년간 증식하고 특성평가를 실시하여, 이를 '원교10050호'로 품종보호출원(출원 2016-399) 하였다. '원교10050호'의 근형은 짧은 단타원형이며, 근미 맺힘이 우수하고 근피색과 근육색이 진한 분홍색이다. 품질특성 조사결과, '원교10050호'의 당도는 8.2 °Brix로 시판품종인 서호무(5.9 °Brix) 보다 2.3 °Brix 더 높으며, 바람들이는 3.1로 시판품종(서호무, 2.3)보다 0.8 더 우수하였다. 채종은 오염 수분을 방지하기 위하여 망을 씌워놓은 상태에서 채종하는 방법과 소형 망실에 뒤영벌을 투입하여 채종하는 방법을 이용하여 각각 4,130립과 34,970립을 확보하였으며, 기존 육성품종인 유색무 '원교10048호'(141립, 14,713립)와 비교해 우수한 채종 특성을 보였다. 또한 증식된 '원교10050호'의 종자를 이용하여 뿌리흑병 저항성 등 주요 병해저항성을 평가할 계획이다. 육성된 품종은 국내 무 시장의 다양성 확보 및 종자 수출 증진을 위한 육종 소재로써의 활용이 가능할 것으로 기대된다.

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PG-0001

Genetic diversity and population structure among Korean *Perilla* germplasms using SSR markers

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In this study, a total of 20 SSR loci were used to evaluate the genetic diversity and genetic relationships among 155 accessions of var. *frutescens* of *Perilla* crop collected in South Korea. The average GD and PIC values were 0.642 and 0.592, respectively, with ranges of 0.244-0.935 and 0.232-0.931. The genetic variability in the southern region of South Korea was higher than that in the central region. In the analysis of population structure, the 155 accessions of var. *frutescens* were divided into 3 main groups and an admixed group at K = 3. The UPGMA phylogenetic tree revealed that the 155 accessions of var. *frutescens* were clustered into seven major groups. The clustering patterns were not clearly distinguished between the accessions of var. *frutescens* from the central and southern regions of South Korea. In South Korea, the *Perilla* crop has been cultivated for a long time, but native landraces still exist in each region, and native landraces are frequently exchanged between the two regions. These results regarding the genetic diversity and population structure of the 155 accessions of var. *frutescens* from central and southern regions of South Korea provide useful information for understanding the genetic variability of this crop and selecting and managing core germplasm sets in the RDA-Genebank of the Republic of Korea.

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PG-0002

Evaluation of world wheat germplasms for major agronomic parameters in Korea

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Wheat is one of the most cultivated crops in the worldwide, and its consumption reaches about 32.4 kg per a person per year in Korea. Climate changes aggravated wheat growth and resulted in significant reduction of productivity in the world. Furthermore, wheat genetic resources are limiting factors for development of new cultivars throughout the world. Therefore, incorporation of wheat germplasms directly in the breeding program is needed. For this, adaptation is the priority factor among the numerous agronomic traits. In this study, 12 agro-morphological traits of 360 wheat germplasms (provided by the National Agrobiodiversity Center) were measured in the Korean environment. Analysis of variance showed significant variation among the yield related traits. Cluster analysis showed that the groups were divided by geological climate condition. These data will be directly used in the wheat breeding programs aiming at introduction of new genetic resources.

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PG-0003

Pepper CaAIPP1 interacting MAP3 kinase CaAIMK3 positively regulates ABA and drought responses

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Protein phosphorylation and dephosphorylation by kinase and phosphatase, respectively, are important mechanisms in response to drought stress. In this study, we isolated and functionally characterized the pepper MAP3 kinase *CaAIMK3* (*Capsicum annuum* CaAIPP1 Interacted MAP3 Kinase 3), which interacted with group A protein phosphatase CaAIPP1 in the nucleus. Kinase activity of CaAIMK3 was negatively regulated by CaAIPP1. Expression levels of *CaAIMK3* are increased by ABA, H_2O_2 and drought treatments. Subcellular localization of CaAIMK3-GFP fusion protein was detected in nucleus and cytoplasm. *CaAIMK3*-silenced pepper plants exhibited drought sensitive phenotypes, accompanied by increased transpiration rate, decreased evaporation and increased stomatal aperture. Overexpression of *CaAIMK3* in transgenic Arabidopsis displayed ABA sensitive and drought tolerant phenotypes, which characterized by high induction of stress-related genes. Taken together, these data indicate that the CaAIPP1 negatively regulates CaAIMK3, which play a role as positive modulator of ABA sensitivity and drought tolerance.

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PG-0004

The function of the pepper protein phosphatase 2C, CaADIP2, in abscisic acid signaling and drought tolerance

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Plant has developed tolerance mechanisms to endure and survive under unfavorable environmental conditions. Abscisic acid (ABA) is a key plant hormone for adaptation to environmental stress. Although ABA signaling pathway is well studied in model plants, it remains unclear in other plants. In this study, we found and functionally characterized the pepper protein phosphatase type 2C, CaADIP2 (Capsicum annumm ABA and Drought-Induced Protein phosphatase 2) containing protein phosphatase type 2C clade domain. CaADIP2 was localized in the nucleus and higher expressed in flower tissues. Moreover, CaADIP2 was significantly induced by ABA, dehydration and osmotic stress conditions. Virug-induced gene silencing of CaADIP2 in pepper plants showed ABA-sensitivity phenotypes and CaADIP2-overexpressed (OX) plants exhibited ABA-insensitive phenotypes. Furthermore, CaADIP2-OX plants showed the most sensitive phenotypes to ABA compared with wild-type and other pepper PP2C-OX plants. Taken together, our data indicate that CaADIP2 plays a major role as a negative modulator in ABA signaling.

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PG-0005

The pepper SUMO E3 ligase CaDRS1 improves drought tolerance via stabilizing the transcription factor CaDRHB1

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Sumoylation is a reversible post-translational modification that is associated with protein stability and activity, and modulates hormone signaling, abiotic and biotic responses in plants. In our previous study, we reported that the homeobox domain transcription factor CaDRHB1 acts as positive modulator of abscisic acid (ABA) and drought responses. Here, we show that the pepper SUMO E3 ligase CaDRS1 stabilizes CaDRHB1 by facilitating its sumoylation and positively modulates ABA signaling and drought response. Drought stress facilitated sumoylation of CaDRHB1 *in vivo* and enhanced the stability of CaDRHB1. A K138R substitution in CaDRHB1 inhibited sumoylation of the transcription factor *in vivo*, indicating that K138 is the principal site for SUMO conjugation. The loss-of-function of CaDRS1 promoted the degradation of CaDRHB1 protein, suggesting that CaDRS1 is involved in the drought-induced sumoylation of CaDRHB1. CaDRS1 physically interacted with CaDRHB1 and facilitated its SUMO conjugation. In addition, *CaDRS1*-silenced pepper plants exhibited reduced ABA sensitivity and decreased drought tolerance, whereas *CaDRS1*-overexpressing plants displayed ABA-hypersensitive and drought-tolerant phenotypes. Taken together, our studies suggest that CaDRS1-mediated sumoylation of CaDRHB1 contribute to ABA-mediated drought tolerance.

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PG-0006

키르기스스탄 적응 콩 선발 및 문제 잡초 조사

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중앙아시아는 동아시아와 유럽을 잇는 실크로드의 중간에 위치하여 향후 농산물 교역의 실크로드가 될 가능성이 높은 지역이다. 최근 육류소비가 늘어 중앙아시아에서도 단백질 원료에 필요한 콩의 생산과 소비가 늘어나고 있지만, 현지에 적합한 품종개발이 부족한 실정이다. 본 연구팀은 중앙아시아에 있는 키르기스스탄에 적합한 콩 품종육성에 필요한 자원을 선발하기 위해 중앙아시아, 미국, 캐나다, 중국 등에서 수집한 69개의 콩 유전자원에 대하여 현지 검정을 실시하고 있다. 키르기스스탄의 비슈케크(Bishkek)와 잘랄아바트(Jalal-Abad)에서 수집된 69자원을 2020년 4월 28일에 트레이에 파종 후 각각 5월 12일과 10일 본포에 정식하였다. 현재 키르기스스탄 현지의 도움을 받아 콩의 개화시기와 문제 잡초 조사를 하고 있으며, 추후 키르기스스탄에 적합한 우수한 자원을 선발하고, 조사한 잡초를 바탕으로 적합한 잡초 방제 시스템을 구명할 예정이다. 또한, 경상북도 군위의 경북대학교 농장에 카자흐스탄에서 수집한 58자원을 심어 종자 증식 및 농업적 형질을 조사하고 있다. 이들 자원의 평가를 통해 우수한 형질을 가진 계통은 국내외의 우수 품종과 교배하여 향후 현지에 적합한 품종육성에 이용할 것이다.

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PG-0007

Assessment of genetic diversity in Korean cowpea germplasm

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Cowpea is one of the most important legume crops that provides a cheap dietary protein and essential nutrients for the people in sub-Saharan Africa, East-Asia, and other developing countries. The aims of this study were to understand the genetic diversity and population structure of global and Korean cowpea germplasms. In this study, genetic diversity study was carried out using 35,116 SNPs within 376 cowpea germplasm including 229 Korean accessions. Based on the STRUCTURE and Principal Component Analysis (PCA), a total of 376 global germplasm were divided into four major populations. The cowpea origin of West-Africa and the sub-origin of India came out separately. In addition, 229 Korean accessions were divided into three major populations (1: Jeonnam, Jeonbuk; 2: Gangwon; 3: a mixture of provinces). Additionally, the neighbor-joining tree indicated the same results. Further genetic diversity analysis within the global and Korean population groups indicated low observed heterozygosity, low polymorphism information content, and high inbreeding coefficient in Korean cowpea germplasms. These results will provide useful knowledge to support the genetic potential for the cowpea breeding program, especially in Korea.

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PG-0008

Characterization of mutational effects of proton-beam in cowpea

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In this study, mutational effects were investigated in cowpea plants irradiated by proton-beam. Seeds of 'Okdang' cultivar were exposed to 100, 200, 300, 400 and 500Gy of proton-beam. The proton-beam irradiation significantly delayed emergence period, but had little effect on emergence rate. Compared to the control, a significant decrease in survival rate was confirmed from 200Gy. And the half-lethal dose (LD_{50}) of 'Okdang' was 200 ~ 300Gy. The plant height and fresh weight of shoot tended to decrease with increasing dose. The Reduction Dose 50 (RD_{50}) of the plant height was between 100 and 200Gy. And the RD_{50} of plant weight was expected to be 500Gy or higher. The APX activity increased in proportion to the dose up to 300 Gy, but tended to decrease from 400Gy to 500Gy. The POD activity showed a significant increase as the dose increased with the highest value observed at 500Gy. The MDA content decreased slightly to 200Gy compared to the control, but increased at 300Gy. However, for chlorophyll content, no significant differences were identified between all proton-beam treatments and the control. The mutation spectrum and frequency of 5,654 M_2 populations derived from M1 seeds irradiated with 300Gy of proton beam were investigated. As a result, several mutations were identified for chlorophyll (61), leaf variation (2), dwarf (17) and plant growth variation (17). A total of 61 chlorophyll mutations were classified as Albina (44.26%), Xhantha (19.67%), Aurea (1.64%), Chlorina (1.64%), Viridis (14.75%), Bright green (11.48%), other type (6.56%).

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PG-0009

A Study on Plant Lignan Composition and Content in Perilla frutescens and Characterization of Function of Lignan Synthesis Enzyme

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Plant lignans are a natural source of useful biologically secondary metabolites that show a various health-promoting effect in plant. The molecular structure of lignans is mono-lignol dimers, in which the phenylpropane units are linked by the central carbons of the side chains. The widely known plant lignans are pinoresinol, secoisolariciresinol, lariciresinol, sesamin and sesaminol. The present project reveals lignans composition and metabolic synthetic pathway in perilla frutescens. Perilla seeds were taken from our green house and the seed samples were extracted with hexane, ethanol and ethyl acetate. Extracted compound was analyzed by liquid chromatography-mass spectroscopy (LC-MS). The present study shows that perilla include several types of lignans (pinoresinol, lariciresinol). Next, evaluate an expression level of synthetic metabolic enzyme for lignan precursor using RT-PCR and confirm function of lignan synthetic enzyme with yeast expression system. This result confirms that plant lignans metabolic pathway exist in perilla and suggest the possibility large-scale production of health/functional lignan based on genome editing.

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PG-0010

마 신품종 육성을 위한 감마선 조사량 설정

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경상북도 안동시 북후면 북평로 613 경상북도농업기술원 생물자원연구소

본 연구는 감마선을 이용한 마 신품종 육성을 위한 적정 감마선 조사량을 설정하고자 실시하였다. 단마 절편과 주아를 시험재료로 각각 50Gy, 100Gy, 200Gy, 300Gy, 400Gy, 500Gy에 24시간 처리하였다. 포장 출현율은 주아처리구는 50, 100, 200Gy 에서 각각 77, 48, 11%, 300Gy 이상에서는 0% 였다. 절편 씨마 출현율은 50Gy에서 18%로 낮았고, 100Gy 이상에서는 출현율이 0% 였다. 주아의 LD_{50}은 100Gy, 절편 씨마는 50Gy 이하로 볼 수 있었다. 주아의 감마선 선량별 생육특성은 엽장, 엽폭, 엽면적 모두 무처리에 비해 감소하였고, 절편 씨마의 초장 및 경경도 감소하였다. 변이형태는 주로 잎 모양의 왜곡, 위축 및 확대와 줄기 자색의 농도 변이 형태로 나타났다. 주아와 절편 씨마의 괴경특성은 조사 선량이 높을수록 괴경장, 괴경중이 감소하였다. 선량 증가에 따른 출현율 및 괴경 생육 저하 정도는 주아보다 절편 씨마가 더 심하였다. 변이 발현 및 괴경 특성 평가를 토대로 LD_{50} 이상의 선량에서 26개체를 선발하였고, M_2세대를 증식 및 개체 선발 중이다.

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PG-0011

Identification of Cytoplasmic Male Sterile Factors in *Sorghum bicolor* with InDel Markers Based on the Complete Chloroplast Genome Sequence Analysis

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In sorghum, Cytoplasmic Male Sterile (CMS) is predominantly used for F1 hybrid breeding and seed production. For developing new sorghum F1 hybrid by using new resources, unique polymorphic markers are needed to distinguish normal male-fertile (CMS-N) and male-sterile (CMS-S) cytoplasm in sorghum. In this research, the complete chloroplast (cp) genome sequences of a CMS-N and CMS-S cytoplasm of sorghum were produced by next-generation sequencing. The *de novo* assembled genome sizes of ATx623 and BTx623 chloroplast was 140,644 and 140,754bp, respectively. And phylogenetic analysis with seven *Sorghum* species including wild species of complete cp genome revealed that CMS-S and CMS-N of *S. bicolor* cytoplasm had high similarity with *S. propinquum* and *S. sudanense*, respectively. The Bayesian inference analysis indicated that the *Sorghum* genus was diverged from *Miscanthus* about 19.5 million years ago (Mya). The comparative analysis with complete cp genome suggested that CMS-S and CMS-N had Milo and Kafir cytotype originated form *S. propinquum* and *S. Sudanese*, respectively. In compared to CMS-S and CMS-N the cytoplasm of chloroplast genomes showed 19 Single Nucleotide Polymorphisms (SNPs) and 142 Insertions and Deletions (InDels) were identified in genic region, which can be used for marker development for breeding, population genetics and evolution studies. Two InDel markers above 20bp sizes were developed to distinguish the cytotypes on the basis of the copy number variation of lengths as 28 and 22 tandem repeat, respectively. Additional each five CMS-S and CMS-N lines was also used for the validation of the InDel markers for determination of chlorotypes. The InDel markers also applied to a total 1,104 plants of 6 Korean sorghum cultivars for identify variant cytotypes. All of accessions were identified by assay, suggesting that these variations in cp genome sequence can be useful for breeding and genetic study of sorghum.

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PG-0012

한국 육성품종 콩의 E1, E2 및 E3 유전자형 분류

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콩(*Glycine max* [L.] Merr)은 한반도와 중국이 기원지로 동아시아에서는 사람의 식량으로 많이 소비되고 목적에 따라 다양한 품종들을 육종해 왔다. 성숙기는 콩의 수량에 크게 영향을 미치며, 농경지의 토지이용 효율을 높이기 위한 작부체계에서도 다양한 성숙기의 콩 품종이 필요하다. 최근 콩 성숙기를 조절하는 유전자 *E1, E2, E3*는 야생형 대립유전자가 성숙기를 늦게 하며, 돌연변이형 대립유전자는 성숙기를 앞당긴다는 연구가 진행 되었지만 국내에서 육성된 콩 품종에 대한 성숙기 유전자형에 대한 분류는 미비한 실정이다. 본 연구는 한국 육성품종 168개의 성숙기를 조절하는 유전자형을 조사하여 향후 관련 품종 육성에 기여하고자 실시하였다. 한국 육성품종 169개에 대한 E1, E2, E3 유전자형을 결정하고 이와 실제 개화기, 성숙기와의 관계를 분석하고자 하였다. 본 연구에서 얻은 결과를 이용한다면 성숙기 관련 육성품종의 효율성을 높일 수 있을 것으로 기대된다.

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PG-0013

녹색자엽 검정콩의 D1, D2 및 cytG 유전자 다양성 분석

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콩(*Glycine max* [L.] Merr)은 경제적인 주요작물로, 동아시아에서는 사람의 식량으로 많이 소비된다. 특히 한국에서는 녹색 자엽의 검정콩을 약콩으로 분류하여 선호도가 높고 일반콩에 비하여 높은 가격에 판매가 되고 있다. 식물에서 녹색 자엽 특성은 *STAY-GREEN* 유전자와 관련이 있고, 콩 자엽의 색깔은 핵 유전자 (*D1*, *D2*) 및 세포질 유전자 (*cytG*)로부터 조절되는 것으로 확인되었다. 콩 연구기관에서 녹색자엽 검정콩 품종육성을 하고 있지만 국내 자원에 대한 녹색자엽에 대한 유전자형 분류가 현재까지 되어 있지 않아 육종에 어려움이 있다. 본 연구는 농촌진흥청 유전자원센터에 있는 녹색자엽 검정콩의 유전자형을 조사하여 향후 관련 품종육성에 기여하고자 실시하였다. 녹색자엽 검정콩 467 개에 대한 *D1, D2, cytG* 유전자형을 결정하고 이와 엽록소 합량간의 관계를 분석하였다. 466중에 *d1d1d2d2*유전형인계통은 111개(23.8%) 이었고, *cytG*유전자형인 것은 355개(76.2%)로 *d1d1d2d2*와 *cytG*를 동시 가진 계통은 없는 것으로 나타났다. 유전자형별로 엽록소 a, b 및 전체 함량, lutein 함량을 비교해본 결과, lutein, 엽록소 a, 전체 엽록소에서 *d1d1d2d2*유전자형이, 엽록소 b의 경우 *cytG* 유전자형이 유의하게 높은 것으로 나타났다. 본 연구에서 얻은 결과를 이용한다면 녹색자엽 검정콩 품종육성의 효율성을 높일 수 있을 것으로 기대가 된다.

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PG-0014

Selection of hard wheat on HMW glutenin subunits and agricultural traits in wheat germplasm from abroad

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Although domestic demand for hard wheat is increasing, it is urgent to develop domestic hard wheat because most of them depend on imported wheat. Therefor this study was conducted to select and utilize elite resources of hard wheat among the wheat germplasm in Korea. We used as materials total 248 accessions collected from 29 countries including Mexico, Mongolia and China. For the characterization of agricultural traits, culm length, heading date and maturity date were investigated. In addition, the Glu-1 gene related to the High Molecular Weight(HMW) glutenin subunits that determines wheat elasticity, which is one of the important baking characteristics was evaluated. Glu-1 genes *Ax, Bx, By* and *Dxy* were calculated by Glu-1 score using PCR and SDS-PAGE. The materials used in this study were sown in the field of the National Institute of Crop Science in Jeonju city on October 25, 2018. Culm length was average 86cm, ranged from the shortest 45.3cm to the longest 126.3cm, and heading date was average May 2, 2019, distributed between April 23 and May 24. Maturity date was average June 10, ranged from earlies June 2 and July 3. The Glu-1 scores on HMW glutenin subunits were ranged from four to ten, and the total of ten were 131 accessions. Among them, 38 excellent genetic resources with characteristics of short culm length (less than 80cm) and early maturity (before June 10) were selected. This elite germplasm is planned to be used as materials for breeding of bread-making wheat.

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PG-0015

Anthracnose resistance evaluation of Pepper genetic resources with non-wound spray and field inoculation

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Pepper (*Capsicum* spp.) anthracnose, which is caused by *Colletotrichum* spp. such as *C. acutatum, C. capsici*, and *C. gloeosporioides*, leads to significant yield losses in many Asian countries, including Korea, Thailand, Indonesia, and India (Than et al., 2008). Resistance to Anthracnose (*Colletotrichum acutatum*) on pepper (*Capsicum* spp.) was evaluated *Capsicum* germplasm in National Agrobiodiversity Center. 222 *C. chinense* species were evaluated for anthracnose resistance by non-wound spray and field inoculation. The distribution of resources according to the Disease Index seemed to have not similar field results to the laboratory in the *C. chinense* group experiment. Thirty-three resistant accessions, which were resistant to both chamber and field evaluation, were selected. After a series of processes, several resistant genetic resources were selected. This pepper germplasm might be used as breeding resources for the anthracnose resistance breeding program.

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PG-0016

Examination of glucoraphanin content in broccoli seedlings over growth and the impact of hormones and sulfur-containing compounds

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In this study, we found that the glucoraphanin (GR) content in broccoli seedlings decreased before first foliage leaf emergence. Methyl jasmonate (MeJA) treatment significantly increased the GR content in broccoli, with effects being consistent over the period of application. Unlike MeJA, abscisic acid (ABA) and salicylic acid (SA) led to slight GR accumulation within 24 h of the application. The feeding of a sulfur-containing compound, MgSO4, via the root of broccoli caused accumulation of GR within 24 h. Thus, both the germination time and the duration of sulfur fertilization and MeJA application are important to maximize GR content in broccoli.

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PG-0017

Genome editing-based breeding of pepper inbred lines

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Consumers and growers of peppers (*C. annuum*) are demanding a low pungent green pepper varieties that are stable to environmental stress. However, the pungent taste of green pepper sold inside Korea is highly dependent on environmental stress (temperature, moisture, nutrients, etc.). However, there is a considerable difficulty in breeding low-pungent cultivars by applying existing traditional breeding techniques, as well as time and economic aspects. Therefore, in this project, we select the genes involved in the capsaicin biosynthetic pathway by environmental stress. We aim to cultivate a low-pungent green pepper inbreeding line that is stable in environmental stress by inhibiting the expression of these genes by applying gene-editing techniques (CRISPR / Cas9).

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PG-0018

Bi-, Tri- and Tetra-cistronic Expression Using Three 2A Sequences to the Stepwise Biosynthesis of Carotenoids in Rice Endosperm

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stPAC (stPsy-F2A-stCrtI) rice, the β-carotene-accumulated golden rice, was developed via a bicistronic expression of the codon-optimized synthetic two genes encoding Capsicum phytoene synthase (PSY) and bacterial carotene desaturase (CRTI) involving the ribosomal pausing 2A peptide (F2A, 20 aa) from mammalian virus. To overcome the limitation of a mammalian pathogenic viral origin, two recombinant genes of stPTAC (stPsy-T2A-stCrtI) and stPIAC (stPsy-I2A2-stCrtI) with replacement of F2A with either T2A (20 aa) or I2A2 (30 aa), which were selected among non-mammalian viral 2A peptides on the basis of their high ribosomal pausing efficiency, also generated the β-carotene enriched golden rice, suggesting their successful bicistronic expression activities with even better ribosomal pausing efficiency than F2A. To establish further polycistronic expression in crop plants using carotenoid metabolism, rice codon-optimized synthetic genes (stBch or stBkt) encoding Capsicum β-carotene hydroxylase (BCH) or Haematococcus β-carotene ketolase (BKT), required for transition to zeaxanthin and astaxanthin from β-carotene, were linked alone or in combination with stPTAC as a recombinant gene and with I2A1 (30 aa) as another non-mammalian viral 2A for tri-, tri- and tetra-cistronic expression, generating stPTAC-IABc (stPTAC-I2A1-stBch), stPTAC-IABk (stPTAC-I2A1-stBkt), and stPTAC-IABc-IABk (stPTAC-I2A1-stBch-I2A2-stBkt), respectively. All of three were successfully resulted in the accumulation of zeaxanthin, astaxanthin and astaxanthin in the transgenic rice endosperms. Collectively, this work clearly demonstrated that polycistronic expression system using 2A peptides could serve to accelerate multi-step metabolic engineering for the development of new biofortified crops.

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PG-0019

Validation of Optimization Method for Development of Korean Golden Rice

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As a proof of concept, we developed the β-carotene-enriched golden rice, PAC (Psy-F2A-CrtI) and its codon-optimized version, stPAC (stPsy-F2A-stCrtI), via a bicistronic expression of phytoene synthase (Psy) and bacterial carotene desaturase (CRTI) involving the ribosomal pausing 2A peptide (F2A) from mammalian virus. To develop β-carotene enriched rice events being able to be commercialized, further improvement should be carried out to pass the restrictions on genetically modified organisms (GMO). First, we changed ribosomal pausing elements 2A sequence from F2A (a mammalian pathogenic viral origin) to T2A (a non-mammalian pathogenic viral origin). Second, we replaced patent vector to patent-free ones. Finally, we compared the efficiency of endosperm-specific promoters and chloroplast targeting transit peptides (Tp) on carotenoids accumulation in rice endosperm. Covering all these changes, Golden Rice variants, GT::stPTAC (GT::stPsy-T2A-PTp-stCrtI), GB::stPTAC (GB::stPsy-T2A-PTp-stCrtI) and GB::stPTARC (GB::stPsy-T2A-R3Tp-stCrtI) rice were generated. Transgenic rice plants containing a copy of T-DNA which were located in intergenic site were selected. Among them, putative GMO event lines which exhibit the highest transgenic protein levels and carotenoids content were finally selected and their agronomic trait are now being evaluated.

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PG-0020

파종시기가 참깨 리그난 함량에 미치는 영향

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경상남도 밀양시 점필재로 20 국립식량과학원 남부작물부

참깨 종자의 리그난 성분은 대표적인 항산화 물질로서 체지방 및 콜레스테롤 감소, 항염증, 심혈관 질환 예방, 항당뇨 등에 효과가 있다고 보고되어 있다. 참깨 종자에는 sesamin, sesamolin, sesaminol, sesaminol glcucoside 등 리그난 성분이 다량 함유되어 있으며 국내 육성품종의 리그난 함량은 2.2~10.0mg/g이다. 본 연구에서는 참깨의 리그난 성분을 최대로 할 수 있는 재배환경을 검토하기 위해 2019년 4월 30일부터 20일 간격으로 6월 30일까지 4차례 파종하여 생육특성, 종실수량, 리그난 함량 등을 조사하고 파종기와 특성간의 관계를 분석하였다. 파종시기가 늦어짐에 따라 생육량은 줄어들고 삭수와 립중 등 수량 구성요소도 감소하였으며 이에 따라 수량도 감소하였다. 파종기에 대하여 수량과 천립중은 5월 20일 부근을 정점으로 하는 2차 회귀반응을 보여 기존의 연구결과와 다르지 않았다. 파종기가 늦어짐에 따라 개화일수는 4월 30일 파종 51일에서 6월 30일 파종 35일 까지 급격히 짧아졌다. 종실의 리그난 함량은 파종기가 늦어짐에 따라 증가하는 경향을 보였는데, 종실의 리그난 함량과 종실수량은 -0.847로 고도의 부의 상관을 보였으며, 리그난 함량은 파종기에 대해 5월 20일 파종일 부근을 저점으로 하는 2차 회귀 반응을 보였다. 파종시기 변화에 따라 리그난 함량이 변화한 원인이 개화기에서 성숙기까지의 온도 등 환경변화에 따른 것인지, 파종기가 늦어짐에 따라 생육이 감소하여 등숙 정도에 영향을 미친 것이 원인 인지에 대해서는 2년차 시험에서 추가로 분석할 예정이다.

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PG-0021

Quantitative Analysis of Sesaminol Glycosides in Defatted Sesame Seed Extracts

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Sesame (*Sesamum indicum* L.), considered to be an important oilseed, is composed of 50% oil and 20% protein. The most outstanding characteristic of sesame oil is its content of the major lignans, sesamin and sesamolin, which have attracted a lot of interest during last years because of health-promoting effects. Lignan glycosides are also abundant lignan in sesame seeds and considered to be beneficial compound for human health. An HPLC method was developed and validated for the quantification of water-soluble lignans, sesaminol triglucoside and sesaminol diglucoside, in seasame seeds. Sesame seeds (Goenbaek, Gomazou, Namback, Seongbun, Yangbaek), which were defatted with extraction n-hexane, were extracted first with 85% ethanol for 5h followed by 70% ethanol overnight at room temperature. The contents of sesaminol triglucoside ranged from 145 to 920 mg/100 g of sesame seed (mean 658±319) and that of sesaminol diglucoside ranged from 15 to 139 mg/100 g of seed (mean 75±53). Total content of sesaminol diglucoside was high in the order of Namback (1040 mg/100 g), Yangbaek (981 mg/100 g), Seongbun (883 mg/100 g), Gomazou (600 mg/100 g) and Goenbaek (160 mg/100 g). These results provide information that would be useful in developing high quality sesame varieties and using sesame cake, a by-product of the oil industry.

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PG-0022

Phenolic Compounds of *Hibiscus acetosella* Extracts and their Biofunctional Properties

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Hibiscus acetosella (Cranberry hibiscus), a member of the Malvaceae family, is an amphidiploid plant native to Africa and this plant is usually consumed as green vegetables. In traditional medicine, decoction drinks made from extracts of the leaves and shoot has been used for their anti-anaemia and antipyretic properties in Western and Central Africa. In the present study, we investigated the phenolic compounds of leaf extracts from 18 different *H. acetosella* accessions and evaluated their biofunctional properties such as antioxidant and antibacterial activity. The most abundant phenolic compounds in *H. acetosella* was caffeic acid, which levels ranging from 14.95 to 42.93 mg/100g. The antioxidant activity by ABTS assay divided into two groups, which formed the high activity group with red leaf varieties (74.71% - 84.02%) and relatively low activity group with green leaf varieties (57.47% - 65.94%). The antioxidant activity was significantly correlated with TAC (0.933), Dp3-Sam (0.932), Dp3-Glu (0.924), and Cy3-Sam (0.913) contents at P-value < 0.001. The *H. acetosella* phenolic extracts showed antibacterial activity against two bacteria, these zone of inhibition ranging between 2.00 to 2.83 mm (*S. aureus*) and 1.33 to 2.67 mm (*P. aeruginosa*), respectively. As results of *S. aureus* bacteria, all accessions were exhibited basal antibacterial activity level (2 mm), among which PI500758 and PI500764 has increased antibacterial activity (2.83 mm), on the other hand, gram-negative (*P. aeruginosa*) bacteria was showed dynamic antibacterial activity levels.

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PG-0023

Analysis of Genetic Diversity and Relationship in *Perilla frutescens* using New Developed EST-SSR markers

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Perilla frutescens is an annual plant that is widely distributed East Asia, but a lack of genetic information hinders genetic and molecular research on this crop. In this study, our research team aimed to develop EST-SSR markers from mutant cultivar (cv. Antisperill) and original plant, and to assess the genetic diversity of the *P. frutescens* germplasms/cultivars. A total 65Gb of nucleotide data comprising 632,970 unigenes were assembled by de novo RNA-sequencing of *P. frutescens var. crispa* (wild type) and *P. frutescens* var. *frutescens*. In total 102 polymorphic EST-SSRs were derived by pairwise comparison of the mutant and wild types based on in-silico analysis. Ninety-six worldwide collected genetic resources were assessed genetic diversity and characterized with newly developed 102 EST-SSR markers. Among these markers, 58 EST-SSR primer pairs exhibited good amplification patterns and polymorphisms. A total of 532 alleles were identified at all loci, with an average of 12.37 alleles per locus, ranging from 2 to 42 alleles. The average polymorphisms information content value was 0.66, ranging from 0.13 and 0.95. The genetic diversity ranged from 0.13 and 0.95, with an average value of 0.69. A phylogenetic tree was also constructed based on the UPGMA analysis, all accession were divided into 2 major groups; Group I and Group II. The new EST-SSR primers of perilla species reported in this study may provide potential genetic markers for population genetics to enhance our understanding of the genetic diversity and relationship.

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PG-0024

화장품소재 단백질 생산 유전자변형 콩의 생태계 침입성 평가

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유전자변형(genetically modified, GM) 작물의 생태계 침입성 또는 잡초화 가능성은 환경 측면에서 주요 우려사항의 하나이다. 인간 상피성장인자 유전자(egf, igf-1, trx)를 발현하는 GM 콩 3개 이벤트가 재배관리되지 않는 환경에서 지속할 수 있는지 여부를 평가하고, 토양에 매몰된 종자의 활력을 조사하기 위해 본 연구를 수행하였다. GM 콩과 비변형 콩 종자를 2017년 6월에 파종하고 연구기간 동안 물과 병해충 및 잡초 관리를 하지 않은 채 시험구에 출현한 콩 식물체 수를 조사하였을 때 GM 콩과 비변형 콩 식물체는 생장하고 종자 생산도 하였지만 17개월까지만 개체군을 유지할 수 있었다. 콩 종자를 2017년 11월에 매몰한 뒤 4, 6, 8, 10개월 후에 활력을 조사하였다. GM 콩과 비변형 콩 종자 모두 월동은 가능했지만, 모든 종자는 6개월 이내에 활력을 잃었다. 이와 같이 GM 콩과 비변형 콩 모두 정착에 성공하지 못했으며, 수명이 짧은 콩 종자는 일시적으로만 토양종자은행을 형성하였다. 따라서 3개 GM 콩 이벤트가 생태계에서 침입식물 또는 잡초가 될 가능성은 거의 없을 것으로 판단된다.

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PG-0025

인간 티오레독신 유전자 발현 형질전환 콩의 발현단백질과 대체단백질간 생물학적 동등성 평가 방법 개발

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유전자변형 작물의 인체 위해성 평가를 위해서는 대량의 순수한 단백질이 필요하다. 그러나 생물체 내에서 발현되는 단백질의 양은 극히 소량이라 이 단백질을 추출하여 위해성 평가에 사용하기에는 불가능하다. 이런 이유로 단회투여독성, 물리화학적 안정성 검정 등 단백질 관련 위해성 평가를 위하여 대장균 등 대량으로 단백질 생산이 가능한 숙주를 이용하여 평가용 단백질을 생산하고 있다. 본 연구에서는 인간 티오레독신 유전자를 도입한 형질전환콩의 인체위해성 평가를 위하여 사용된 미생물 유래 티오레독신 단백질과 형질전환콩에서 직접 정제한 단백질 간의 생물학적 동등성 평가 방법을 개발하였다.

본 시험에서는 형질전환콩의 도입단백질인 티오레독신과 위해성 평가를 위하여 사용된 미생물 유래 단백질간의 동질성을 조사하기 위하여 SDS-PAGE 및 Western immunoblot 분석, 펩타이드 질량 분석, N-말단 아미노산 서열 분석과 peptide ID분석을 진행하였으며, 분석 결과 미생물 유래 티오레독신 단백질과 형질전환콩에서 직접 정제한 단백질 간의 동등성을 확인하였다. 이와 같은 결과를 종합해 본 결과 미생물 유래 티오레독신 단백질과 형질전환콩에서 직접 정제한 티오레독신 단백질은 서로 동일한 것으로 예상되며 다른 형질전환작물의 인체위해성평가에 개발된 동등성평가방법 개발의 기초자료로 사용될 수 있을 것으로 사료된다.

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PG-0026

Brassinosteroids regulate circadian oscillation via the BES1/TPL-CCA1/LHY module in Arabidopsis thaliana

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Brassinosteroids (BRs) regulate a variety of physiological processes in plants via extensive crosstalk with diverse biological signaling networks. Although BRs are known to reciprocally regulate circadian oscillation, the molecular mechanism underlying BR-mediated regulation of the circadian clock remains unknown. Here, we demonstrate that the BR-activated transcription factor *bri1*-EMS-SUPPRESSOR 1 (BES1) is a key factor that integrates BR signaling into the circadian network in Arabidopsis. BES1 repressed the expression of *CIRCADIAN CLOCK-ASSOCIATED 1* (*CCA1*) and *LATE ELONGATED HYPOCOTYL* (*LHY*) genes at night by binding to their promoters, together with TOPLESS (TPL). The repression of *CCA1* and *LHY* by BR treatment, which is relevant during the night, was compromised in *bes1-ko* and *tpl-8* mutants. Consistently, long-term treatment with BR shortened the circadian period, and BR-induced rhythmic shortening was impaired in *bes1-ko* and *tpl-8* single mutants, and in the *cca1-1lhy-21* double mutant. These observations indicate that BR signaling is conveyed to the circadian oscillator mainly via the BES1/TPL-CCA1/LHY module, thus contributing to gating diurnal BR responses in plants.

Keywords: Brassinosteroid, circadian clock, BES1, CCA1, LHY, TPL

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PG-0027

Development of InDel markers generated from re-sequencing data for the identification of Korean sorghum cultivars (*Sorghum bicolor* L.)

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Sorghum is an important food crops in the worldwide that can be grown arid land and it have high functionality with anti-oxidant. Therefore the needs of production and consumption are dramatically increased in Korea. We have launched new breeding program of Sorghum highly adaptable in Korea by inbred line selection and F1 hybrid cultivars. To protect breeder's right, low-cost and simple gel electrophoresis DNA markers for cultivar identification is essential. The use of Insertion and Deletion (InDel) polymorphic markers could be one of the effective ways to allow Korean specific sorghum cultivars. This research was conducted to develop a method for the identification of Korean sorghum cultivars using InDel markers subtracted by re-sequencing. In order to develop the cultivar identification markers, we carried out Next Generation Sequencing (NGS), Illuminal Hi-Seq with average 20X coverages of four Korean sorghum cultivars (Nampungchal, Donganme, Sodamchal, Hwanggeumchal) and to detect InDel regions, NGS data was mapped to a reference genome about 820Mb. A total of 308,777 InDel were identified and the highest number of InDels was shown in Donganme as 217,333 and there were highly similarity between Nampungchal and Hwanggeumchal as 99.86% homology in sequence levels. The high quality score with above Q=20 and uniquely reads mapped to reference genome region were selected and large InDel above 20bp among four cultivars were selected for cultivar identification. A total of 130 InDel markers were designed and after validation with PCR amplification by eight Korean Sorghum cultivars, 41 InDels markers were selected with high fidelity in PCR amplification. Among the 41 InDel markers, we can identify Korean and China Sorghum cultivars with four markers (InDel_74, InDel_76, InDel_108, InDel_119). And we tested selected four InDel markers to 96 individual plants from each cultivars to analyze genetic variation within population. About 10% of genetic variation was shown in Nampunchal and Hwanggeumchal variety bred by pure line selection and there was no variation in other pedigree line selection varieties. The InDel markers developed in this study can be used not only to differentiate Korean sorghum cultivars but also to genetic characterization of Sorghum germplasm.

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PG-0028

OsPAP3-mediated chloroplast development in rice

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Chloroplast is a cellular organelle that affects broad aspects of plant physiology and growth, because chloroplast is the place where photosynthesis occurs, and a variety of plant hormones, amino acids and lipids are produced in plants. Thus, chloroplast development is closely connected to plant physiology and productivity. Transcription of chloroplast genes is an essential step for chloroplast development, and plastid-encoded RNA polymerase (PEP), a major RNA polymerase in chloroplast mediates this process. However, PEP requires PEP-associated proteins (PAPs) for its transcriptional activity. Recently, PAP3 was reported as a key PAP for regulation of PEP activity and chloroplast development in Arabidopsis. In this study, we identified *OsPAP3* in rice through amino acid homology search. To characterize this, we investigated *OsPAP3* expression pattern and localization. Similar to the transcription pattern of *OsrbcL,* transcription of *OsPAP3* was activated by light, and the transcript level of *OsPAP3* in shoot was much higher than that in root. In addition, OsPAP3 proteins specifically localized to nucleoid where PEP acts. To analyze its function in chloroplast development, we generated *osapap3* mutants using CRISPR/Cas9 system. The o*spap3* mutants showed abnormal whitening phenotype and the whitening phenotype is tightly linked to the mutation of the *OsPAP3* gene, suggesting that *OsPAP3* is an essential PAP that controls chloroplast development in rice.

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PG-0029

Characterization of genetic diversity of Korean peanut germplasm by 48K SNP chip analysis and selection of cultivar identification SNP marker set

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Peanut (*Arachis hypogaea* L.) has been grown widely in tropical and temperate zones as one of the major oilseed crops and is important as a rich source of unsaturated fatty acids. The objective of this study was to investigate genetic relationship and diversity among Korean peanut accessions mainly used for breeding materials. 48K Axiom Arachis SNP chip was used for genotyping and detected that 9,947 probesets representing polymorphism among 96 accessions, which was 497.35 SNPs per chromosome. The minor allele frequency ranged from 0.01 to 0.50 (average 0.16), and polymorphic information content was between 0.02 and 0.50 (average 0.23). The clusters were detected from the phylogenetic analysis (UPGMA), STRUCTURE, and principal component analysis (PCA). Those results indicated that Korean peanut germplasm could be divided into two main groups, Korean peanut cultivars and germplasm introduced from abroad, respectively. The genetic distance between Virginia, Spanish, and Shinpung plant types also well characterized. Furthermore, five SNP markers were selected from the robust polymorphic probeset for the identification in 17 Korean peanut cultivars, and those were successfully converted into KASP markers set based on the flanking sequences. These results suggested that high throughput genotyping approach with SNP chips is very effective on the genetic characterization and marker development in peanut breeding.

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PG-0030

Evaluation of Kenaf (*Hibiscus cannabinus* L.) Pedigrees for High Yield, Disease-Resistance and Wide Adaptability

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Kenaf (*Hibiscus cannabinus* L.) is multipurpose due to high biomass. So, the breeding of kenaf with high yield, disease resistance and wide adaptability is important strategy to improve production. The study was conducted to select the superior strains with higher biomass, resistance for anthracnose and adaptability to reclaimed land. The pedigrees was developed from the three-way cross, Jangdae/Hongma300//M191. It was possible to select the elite lines (F_2 generation) based on the agronomic performances at two fields, non-reclaimed and reclaimed land, in comparison with to the Control (Jangdae, Hongma300, and M191). At non-reclaimed land, a pedigree (no. 641-16) has a stem in deep red and resistance for anthracnose. It was blooming on July, 24 which is a significant difference from Jangdae (July, 9) and both (Hongma300 and M191) without flowering. 641-16 had the highest height with 184 cm in comparison with Hongma300 (153.5 cm), Jangdae (139 cm) and M191 (129.8 cm). Also, its stem diameter (27.04 mm) over 15cm of soil surface was higher than that of Hongma300 (25.2 mm), Jangdae (26.1 mm) and M191 (21.9 mm). At a reclaimed land, a strain (641-21) has shown red stem, anthracnose-resistance and flower bud initiation in late July. This line was shown a high significance for plant height and stem diameter. Its height was the best as 119 cm compared to the others containing the Controls. The diameter (18.57 mm) of this pedigree was the third thick after 641-40 of 20.73 mm and 641-24 of 20. 46 mm. Taken together, the two pedigrees of 641-16 at non-reclaimed land and 641-21 at reclaimed land would be useful resource for high production.

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PG-0031

Identification of *Cucumber mosaic virus* (ChiVMV) P1 resistance sources via *Capsicum* germplasm screening

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Cucumber mosaic virus (CMV) is one of the major devastating plant virus in pepper production worldwide. *Cucumber mosaic virus resistance 1* (*Cmr1*) gene had been deployed to breed resistant cultivar against CMV-P0 isolate. A few decades ago, *Cmr1*-derived resistance was overcome by evolved CMV isolate, CMV-P1. Even a few CMV-P1 resistant sources have been reported up to date, their commercial use was inadequate because of the limitation of genetic distance or QTL studies. To overcome this limitation, we screened 350 *Capsicum* core collection sets with CMV-P1. We found two CMV-P1 resistant accessions among 350 accessions. Inheritance study of two resistant accessions showed that all CMV-P1 accessions are inherited by single recessive mode. For complementation test, we executed test cross CMV-P1 accessions with CMV-P1 resistant cultivar 'Lam32' (*cmr2*/*cmr2*). It was revealed that *cmr2* gene is involved in CMV-P1 resistance in seven resistant accessions. Our results elucidate that *cmr2* gene have mainly conferred CMV-P1 resistance in *Capsicum* accession. Moreover, we provide additional CMV-P1 resistance sources in *Capsicum* accession for resistant breeding program.

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PG-0032

The ATXR2 protein represses *de novo* shoot regeneration by controlling cytokinin signaling in *Arabidopsis*

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Plants have evolved a high regenerative capability to ensure efficient tissue repair and *de novo* organogenesis. The regenerative potential has known to be determined by genetic contribution, and a few genetic components have been identified. Here we report that ARABIDOPSIS TRITHORAX-RELATED 2 (ATXR2) interacts with the type-B ARABIDOPSIS RESPONSE REGULATOR 1 (ARR1) protein and activates a subset of *type-A ARR* genes, *ARR5* and *ARR7*, to repress *de novo* shoot organogenesis during plant regeneration. The ATXR2-ARR1 complex directly binds to the *ARR5* and *ARR7* promoters and catalyzes H3K36me3 deposition, balancing *de novo* shoot organogenesis. Consistently, *atxr2-1* mutant calli showed enhanced shoot regeneration capability with low expression of *ARR5* and *ARR7*, which in turn ultimately leads to up-regulation of *WUSCHEL* (*WUS*). Genetic analysis further supports that type-A ARRs are epistatic to ATXR2. These observations indicate that ATXR2 elaborately regulates cytokinin signaling and prevents premature *WUS* activation for proper cell fate transition in plants, and this regulatory scheme can be applied to diverse crop plantsto improve shoot regeneration.

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PG-0033

Screening and validation of KASP markers set based on the 48K SNP chip analysis for Marker Assisted BackCrossing (MABC) in peanut (*Arachis hypogaea* L.)

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Peanut (*Arachis hypogaea* L.) is allopolyploid species mainly grown in tropical, subtropical and warm temperate climates, it is the fourth most important oilseed crop in the world. High yield and high oleic acid is a two major factor and key value-added trait in groundnut which improves the shelf-life of product besides offering nutrition and health benefits to the end-users. Marker-assisted backcrossing (MABC) is one of the most effective strategies widly used for pyramiding or introgressing the favourable trait from donor to elite line. Here we report, high-density SNP array 'Axiom Arachis' with 48K SNPs and their usefulness in the analysis of genetic diversity of groundnut. With the MABC approach, we are improving Korean cultivars Sinpalkwang, Haeol, and Sewon for oleic acid content and yeild. Based on the 'Axiom Arachis' 48 K SNPs genotyping we identified total 47837 SNP, out of it 2059 poly high-resolution SNP were identified throughout the genome. Furthermore, 708 SNPs were identified among the three genotypes based on high-polymorphism. From the cross between Sinpalkwang and Heaol, 78 SNP were selected for validation and we observed the 60% polymorphism. Where as from the second cross between Sewon and Haeol 45 SNPs were selected for validation and 50% polymorphisms were observed. The resulting polymorphic markers will be utilized for peanut MABC.

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PG-0034

Evaluation of Fruit Traits on Strawberry Genetic Resources for Various Utilization

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The strawberry domestic market is dominated by 87.6 percent of "Seolhyang", and export of fresh strawberry is concentrated on "Maehyang" more than 90 percent. As strawberry industries are concentrated on some cultivars, it is necessary to diversify the cultivars through the development and distribution of new cultivars. Therefore, this study was conducted to establish a foundation for breeding new cultivars through the collection and evaluation of characteristics on genetic resources and to promote the utilization of them. From February to March in 2019, Mother plants of 23 kinds of genetic resources from Korea, Japan, the United States, and the Netherlands were received from the National Institute of Horticultural Science. Daughter plants were raised from June to August, and transplanted on September 23 at hydroponic greenhouse in the Jeollabuk-do Agricultural Research and Extension Services. The first flower cluster was budding in order of "Seolhyang", "Ssanta", "Bennihoppe", "Tochiotome", and harvesting was initiated first in "Seolhyang", "Ssanta", "Camarosa". The average weight of each fruit was heavy in the order of "Akihime", "Keumhyang", "Daewang", "Ssanta", "Seolhyang", and was light in sequence of "Harunoka", "Aihime", "Sagahonoka", "Elsanta", "Tochiotome“. The fruit sugar content was high in the order of "Ssanta", "Daewang", "Tochiotome", "Akihime", and low in sequence of "Elsanta", "Harunoka", "Camarosa", "Amaou", "Camiroreal". On the other hand, the fruit firmness was high in the order of "Festival", "Camiroreal", "Camarosa", and low in sequence of "Yayohime", "Amaou", "Sachinoka". The resources derived from U.S. tended to be hard and resources derived from Japan tended to be soft.

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PG-0035

Evaluation on the Vegetable Leaf Characteristics of Accessions in Perilla Breeding Materials

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We evaluated the morphological characteristics of 140 accessions of perilla germplasm collected from diverse country. And it examined quantitative and qualitative characteristics in order to develop cultivars which is high yielding, quality and efficiency of harvest leaf. The days to flowering(DtoF), days to maturity(DtoM), size, shape and color of leaves were examined. Perilla germplasm can be classified as two groups. One group is generally called as "Deulke"(*Perilla frutescens.* var. *frutescens*) in Korea or "Egoma" in Japan. Those are generally used as oil seed cultivar or leaf vegetable. Another group is called as "Chajogi"(*Perilla frutescens.* var. *crispa*) in Korea or "Siso" in Japan. The total included 115 *P. frutescens* var. *frutescens*, 25 *P. frutescens* var. *crispa.* The type of *P. frutescens* var. *frutescens* showed variation in DtoF and leaf size. Days to flowering of accessions showed the range from 37 to 141 days with the highest frequency proportion was the group from 100 to 117 days, which occupied 41%. The leaf shape of most accessions had flat and cordate. Leaf length and width of accessions ranged from 7.4 to 16.3 ㎝, with average 12.9 ㎝ and from 5.4 to 13.5 ㎝, with average 9.6 ㎝, respectively. The type of *P. frutescens* var. *crispa* showed variation in leaf color and shape. Most accessions pigmented light purple on the abaxial (reverse) sides of leaves were green or purple pigmented on the adaxial (front) side of leaves. Leaf shape described as cordate or wrinkle was observed. We selected only one ideal resource of flowering date (25 Sep.), leaf size and color, and it used as parent for developing new cultivars with high yielding, quality and efficiency of harvest leaf.

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PG-0036

내습성 품종 육종을 위한 유채 계통별 유묘기 및 개화기 습해 피해 양상 비교

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전라남도 무안군 청계면 무안로 199 농촌진흥청 국립식량과학원 바이오에너지작물연구소

국내에서 주로 소비되고 있는 유채유는 주로 캐나다, 호주 등에서 수입되고 있는 실정이다. 최근 국내 유채유 수요 증가와 함께 건강한 먹거리에 대한 관심 증가로 국내에서 유채를 논에 재배하는 면적이 증가하고 있다. 그러나 유채는 습해에 취약한 작물로 내습성 품종을 육종하는 것이 필요하다. 이에 본 연구에서는 중간 모본으로 이용되고 있는 올레산 함량이 높은 'EMS26'과 내동성 계통인 'J8634-B-30' 유채 2계통을 대상으로 유묘기(본엽 4엽기)와 개화기에 7일간 침수를 실시하여 습해 피해 양상을 비교하였다. 유묘기 침수 처리로 'EMS26' 계통은 잎이 고사하고 광합성량이 감소하였으며, 처리 3일차에는 오래된 잎이 탈락하여 엽록소 함량을 측정할 수 없었으며, 새로운 잎에서는 엽록소 함량이 감소하였다. 반면 'J8634-B-30' 계통은 유묘기 침수 처리로 인한 광합성량에 변화가 없었으며, 오래된 잎에서도 엽록소 함량 변화가 관찰되지 않았으며, 침수 처리 7일차의 어린잎에서만 SPAD 함량이 대조구 대비 81.1% 수준으로 감소하였다. 개화기 습해 처리로 인한 꽃대 꺾임 피해율은 'EMS26' 계통에서 78.5%로 거의 모든 개체에서 꽃대 꺾임 현상이 관찰되었다. 반면 'J8634-B-30' 계통에서는 7.15%로 꽃대 꺾임 피해율이 낮았다. 최종 종자 생산량 또한 'EMS26' 계통에서는 대조구(무처리) 대비 92.3%가 감소하였으며, 'J8634-B-30' 계통에서는 42.4%가 감소하였다. 이러한 결과를 종합해 볼 때 'EMS26' 계통은 습해에 감수성으로 'J8634-B-30' 계통은 내습성으로 사료되어 내습성 품종 육종을 위한 중간모본으로 유용하게 사용할 수 있을 것으로 판단된다.

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PG-0037

Phenotypic Variation of Mutant Population induced by Ac/Ds Mediated Gene Tagging System in Rice

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Rice is one of the world's most important crops, particularly in Asia, for human consumptions. Rice consumption has been increased due to diversity of nutrients and tastes. In addition, Rice has taken a role of model plant since the whole genome was completely sequenced (Jun et al. 2002, Feng et al. 2002). To increase higher yield potentials of crops, the discovery of novel genes and the construction of QTL maps should be essential projects in genomic researches. This project has been performed to develop a large population of insertional mutations, and to construct databases of molecular information on Ds insertion sites in rice.

Currently, various insertional mutants are used for rice functional genomics. The insertional mutant pool of this research is stable knockout population for various screening studies. Through this research program, insertion sites of more than 33,157 Ds lines were exploited and their information has been released via a database.

Through this research program, phenotypic and agronomical characteristics of the population will be open for public and be expected to be useful in isolating agronomically important genes. A lot of mutant showing variation on phenotypic characters such as tiller number and seed size etc. were found through field test over the years, and genetic analysis of these lines are conducted. Currently, genomic resequencing strategy becomes very powerful in isolating rice genes. Our genetic materials will serve perfectly for the requencing project in the near future. Ultimate goals are to supply genetic materials and informations essential for functional analysis of rice genes and for breeding using agronomically important genes.

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PG-0038

Brazzein protein production from transgenic carrot cells by air-lift bioreactor culture

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Recombinant protein production in plants is effective system compared to mammalian cell system, because it is more easily scale-up, low production cost and animal pathogen-free. In this study, we established brazzein production system using air-lift bioreactor from transgenic carrot cells, which is introduced brazzein gene by Agrobacterium-mediated transformation. First of all, transgenic carrot callus (TC12) was cultured in liquid medium and the brazzein content was analyzed during entire culture period. After that, bioreactor type, volume, and culture period were compared to establish a bioreactor culture system. In addition, ABA was treated as elicitor to increase brazzein biosynthesis. During the suspension culture, cell proliferation was increased rapidly at 12-day, and at this time total soluble protein (TSP) and brazzein were 9.0 mg · gfw^{-1} and 1.2 mg · gfw^{-1} respectively. Brazzein content was 0.5 mg · gfw^{-1} (TSP 5.3 mg · gfw^{-1}) in balloon-type bioreactor, and cone and column-type bioreactors were produced 1.1 mg · gfw^{-1} (TSP 5.7 mg · gfw^{-1}) and 1.2 mg · gfw^{-1} (TSP 7.8 mg · gfw^{-1}), respectively. The brazzein productivity considering cell proliferation, cone-type was the most suitable, which was 6.1 g brazzein per bioreactor. After 8 hours of ABA treatment, brazzein content was 3.3-fold higher than non-treated. Overall, the results presented here demonstrate that brazzein could be produced from transgenic carrot cell culture and air-lift bioreactor system could be used for mass production.

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PG-0039

Comparative transcriptome analysis during direct somatic embryogenesis in *Tilia amurensis* Rupr

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Tilia species are valuable woody species due to their beautiful shape and role as honey trees. Somatic embryogenesis can be alternative methods for mass propagation of *T. amurensis*. However, the molecular mechanisms of *T. amurensis* somatic embryogenesis are yet to be known. Here, we conducted comparative transcriptional analysis during somatic embryogenesis of *T. amurensis.* RNA-Seq identified 1,505 differentially expressed genes, including developmental regulatory genes. Auxin related genes such as YUC, AUX/IAA, and ARF, signal transduction pathway-related genes such as LEA and SERK, and other transcription factors such as B3 domain family (LEC2, FUS3), VAL, and PKL are differentially regulated during somatic embryogenesis. Our results provide plausible pathway of signaling somatic embryogenesis of *T. amurensis*, and serve an important resource for further studies in direct somatic embryogenesis in woody plants.

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PG-0040

자가화합성이면서 탄저병과 혹응애에 강한 구기자 품종 '화강'

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자가화합성으로 수분수 품종과 혼식할 필요가 없으면서 탄저병과 혹응애에 강하고 색택이 양호한 구기자 신품종 '화강'을 선발하였다. 2013년도에 CBP11540-21 계통을 종자친(♀)으로, CBP11515-37을 화분친(♂)으로 교배하여 특성을 검정하여 2014년에 CBP13603-12 계통을 선발하였다. 선발된 계통은 2015년부터 2016년까지 생산력검정 예비시험과 생산력검정 본시험을 통하여 병해충 저항성, 자가수정율, 지표성분 함량, 수량성 등의 특성을 조사하였고 '청양 32호'로 계통명을 부여하였다. 2017년부터 2019년까지 3년간 청양군, 예산군, 금산군 등 3개 지역에서 지역적응성을 검정한 결과 자가화합성이며 수량이 많고 탄저병과 혹응애가 강하며 색택이 양호하여 최종 선발하였고, 국립종자원에 '화강(Hwagang)'으로 명명하여 품종보호 출원하였다. 선발된 품종의 주요특성은 다음과 같다. Flow cytometry 검정 결과 4배체이었ek. 수정양식은 자가화합성으로 꿀벌의 유입이 적은 비가림 하우스 재배에 적합하였다. 식물체 수형은 반개장형이고 잎은 둥근피침형이면서 농녹색이었다. 열매는 장타원형으로 대과종이고, 적색이며 과병 길이가 긴 편이었다. 개화기는 6월 20일로 대조품종에 비하여 5일 가량 늦었고, 착과수는 적은 편이었고 열매무게는 무거운 편이었다. 탄저병 이병과율은 12.5%로 강한 편이었고, 혹응애 피해엽율은 3.9%로 매우 강하였다. 지표성분인 베타인 함량과 당도, 산도는 대조품종에 비하여 높은 편이었다. 건구기자 수량은 대조품종에 비하여 생산력 검정시험에서 30%, 지역적응시험에서 23% 증수되었다.

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PG-0041

농업생명공학연구단 성과분석을 통한 가치증대 및 향후 활용방안 연구

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서울시 마포구 성암로 189 18,19층 ㈜윕스

전 세계적으로 농업 생산력 및 기후변화 대응을 위한 농업생명공학연구개발의 필요성이 대두되며 GM작물에 대한 상업화와 이에 대한 국가 정책, 기업의 역할에 대한 논의가 활발해지고 있다. 그러나 국내에서 GM작물의 개발과 상업화에 대한 사회적 합의는 초보단계에 머물러 있는 상황이다. 이에 본 과제에서는 국내 종자산업의 글로벌 경쟁력 확보를 위한 생명공학작물의 실용화 기반 구축 전략을 세우고자 한다. 농업생명공학연구단 사업은 1, 2단계('11~'17) 성과의 종합적 분석과 3단계('18~'20) 실용화 성과도출이 요구되는 시점으로, 성과확산운영을 위해 관련분야 시장동향, 국가별 생명공학작물 개발 정책동향, 특허동향, 최신 기술 개발동향을 비롯해 기업 수요기술 발굴과 기술마케팅 시스템 구축이 필요하며, 사업화 우수 후보과제 성과에 대한 실용화 갭 해소 및 중개연구가 필요하다. 또한 일반 시민들에게 GMO와 LMO에 대해 올바른 인식을 형성시키기 위한 적극적인 홍보 활동 및 자료발간으로 막연한 불안감을 해소할 수 있는 방법 연구가 필요하다.

농업생명공학연구단 성과 확산을 위한 3단계 과제소개서 및 사업화 유망기술 선별을 통한 유망기술 소개서를 발간하여 온-오프라인을 통해 기업・기관 관계자에게 배포하였으며, 이를 통해 발굴된 기술 수요기업을 대상으로 우수기술 설명회를 진행하였다. 2020년에는 현재까지 구축된 농업생명공학연구단 특허성과의 사업화 활동 효율성 제고를 위하여 기술정보를 데이터베이스화 하였으며, COVID-19로 인한 오프라인 행사 축소에 대비하고 기술수요자의 기술 접근성을 제고하기 위해 '농업생명공학연구단 TLO(Technology Licensing Office)' 온라인 플랫폼을 구축하였다. 이를 통해, 기술수요자는 간편하게 온라인으로 농업생명공학연구단의 특허 정보를 확인할 수 있으며, 관심 기술에 대한 기술이전 프로세스 확인 및 기술상담 신청이 가능하다. 또한, 농업생명공학연구자들에게 사업화 유망기술에 대한 기술사업화 컨설팅 및 기술가치평가를 지원하고 있다.

향후 농업생명공학연구단 온라인 플랫폼을 기술수요자나 소비자가 원하는 연구방향의 수용 및 사업화 가능기술의 선별, 활용으로 이어져 실질적 GM작물의 기술사업화 성과를 발굴하고자 한다.

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PG-0042

Keumgang wheat flour has a potential to identify optimum conditions for noodles using a Mixolab

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Mixolab is a useful device that determine the properties of dough and immediately analyze the protein and starch patterns in wheat flour. Mixolab has an advantage of being able to analyze the degree of softening and gelatinization of the dough at the same time when the heat is applied. In the case of farinograph and RVA (Rapid Visco Analyser), which were previously used, it is an analysis device that utilizes only the primary raw material, but in the case of Mixolab, it is possible to predict the secondary processing suitability with the dough heating system as well as the primary raw material analysis. Because of these advantages, Mixolab is dominantly used as a quality indicator in the flour milling and processing companies. In this study, multifaceted analyses through blending ratio were evaluated between high-quality imported noodles wheat and Keumgang wheat to identify optimized blending ratio for noodle by Mixolab. After analysis of starch properties with eight commercial imported wheat, a total of nine blending samples (the ratio for Keumgang wheat to imported wheat were 9:1, :8:2, 7:3, 6:4, 5:5, 4:6, 3: 7, 2:8, and 1:9, respectively) were analyzed with absorption, mixing, gluten, viscosity, amylase and retrogradation. The imported wheat and Keumgang showed similar value for absorption, viscosity, amylase and retrogradation except mixing and gluten. Especially, mixing value as low as 3 in imported wheat increased until 8 in the 5:5 blending sample. The Mixolab analysis can be useful program for wheat breeding and blending strategy because it can compare and test in domestic optimal noodles using finely digitized data without eating quality traits of noodles. Further experimental results will be discussed.

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PG-0043

LiDAR 활용 기반 잣나무 차대검정 및 개량효과 추정

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본 연구는 잣나무 육종재료 성적의 정확한 평가와 개량효과 추정을 위해 LiDAR를 활용하여 가계별 30년생 성적을 조사하고 유전모수를 추정하였다. 연구대상지는 춘천에 위치하며 잣나무 수형목 35클론의 반형매 차대 유전검정을 위해 대조구 10개 그룹과 함께 5반복 난괴법으로 설계되었다. 이동형 스캐너를 활용하여 개체목별 수고, 흉고직경 데이터를 취득하고 재적지수를 산출했으며 혼합모형과 Restricted Maximum Likelihood/Best Linear Unbiased Prediction(REML/ BLUP)에 의해 육종가와 개량효과를 추정하였다. 그룹간 평균 재적을 비교한 결과 대조구, 수형목 차대 35가계에 비해 상위 7개 우수가계의 평균 재적이 유의하게 높았다. 따라서 잣나무 육종재료의 반복선발(recurrent selection)을 통해 점진적인 개량효과를 획득할 수 있을 것으로 여겨졌으며, 향후 실현된 개량효과에 관한 연구를 위해 입지환경, 가계, 수령 등을 고려한 추가 분석이 필요할 것으로 판단되었다.

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PG-0044

Identification of Volatile Compounds in Freesia Cultivars by GC-MS

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Freesia (*Freesia hybrida* Hort.) is widely cultivated for its unique floral fragrance and attractive colors in many countries including South Korea. In the present study, four Freesia cultivars namely 'Shiny Gold', 'Yvonne', '10C3-894' and '10C3-424' with varied odor intensity were used to identify the volatile organic compounds (VOC). Based on sensorial analysis, 'Shiny Gold' and 'Yvonne' were classified as strong scented, '10-894' as very strong scented, while '10C3-424' as weak scented. The VOCs emitted from the flowers were collected by headspace solid-phase microextraction and analyzed by gas-chromatography-mass spectrometry. A total of 11 monoterpenes including Linalool, beta.-Myrcene, Octamethyl-Cyclotetrasiloxane, 2,6-dimethyl-2,4,6-Octatriene, D-Limonene, 3,6,6-trimethyl Bicyclo [3.1.1] hept-2-ene, 3-Carene, gamma- Terpinene,1-methyl-4-(1-methylethylidene)-Cyclohexene, 2,6-dimethyl-,(E,E)-2,4,6-Octatriene, 2,6-dimethyl-,(E,Z)-2,4, 6-Octatriene, alpha-Terpineol were detected. Among the compounds, linalool was identified as the major component in all the cultivars. This study showed that the relative proportion of volatile compounds varied among the cultivars and there is a great diversity of volatiles among the cultivars. Further research may lead to a better understanding of combination of compounds that gives a cultivar an exclusive fragrance.

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PG-0045

건식제분 전용 쌀가루 가루미 2의 이화학적 특성평가

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대내외적 여건 변화로 쌀소비형태가 가정 내의 '취반' 형태는 감소하는 반면, 간편한 '가공' 형태는 증가하고 있다. 하지만, 쌀가공산업에서 원재료인 쌀은 즉석밥류를 제외하면 쌀가루 형태로 유통되어 가공된다. 일반적으로 유통되는 쌀가루는 쌀을 물에 불리는 수침과정이 필요한데, 습식제분한 쌀가루의 수분함량은 건식 쌀가루에 비해 약 3배 가량 높기 때문에, 저장이나 유통을 하려면 냉동보관을 해야하는 번거로움이 있고, 가공과정에서 폐수가 발생한다. 본 연구에서는 수침과정이 필요하지 않는 건식제분에 적합한 벼 '가루미 2'의 주요 가공적성을 분석함으로써 건식제분 전용 쌀가루 품종 개발을 위한 기초자료로 활용하고자 한다. 쌀가루 품질 분석을 위해 가루미 2, 수원620호, 설갱을 수분함량 각 16%, 15%, 15%로 tempering 한 후 제분(Buhler Mlu 202, Buhler, Uzwil, Switzerland)하였다. 가루미 2, 수원620호, 설갱의 입도, 손상전분, 회분, 아밀로스, 단백질 함량을 측정하였다. 가루미 2의 입도는 77.40㎛로써, 수원620호와 설갱의 입도와는 유의한 차이가 있었고, 수원620호와 설갱의 입도는 각 82.44㎛, 82.59㎛로써 비슷한 수준이었다. 가루미 2의 손상전분은 6.47%로써 설갱에 비해 유의하게 낮았으나, 수원620호에 비하여 유의한 차이가 있지 않았다. 가루미 2, 수원620호, 설갱의 회분함량은 0.53g, 0.64g, 0.62g으로 가루미 2는 수원620호, 설갱 보다 회분함량이 낮았다. 가루미 2, 수원620호, 설갱의 아밀로스 함량은 17.75%, 17.42%, 18.05%로 유의한 차이가 없었다. 단백질 함량은 각 6.23, 5.94, 5.06%로 역시 유의한 차이가 있지 않았다. 가루미 2는 입도, 손상전분함량이 낮고, 주요 이화학적 형질이 같기때문에, 쌀가공산업에 다양하게 활용될 것으로 기대된다. 또한 가루미 2는 다양한 건식제분 전용 쌀가루의 품질설정 기준 및 육종소재로 활용할 것으로 예상된다.

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PG-0046

Identification and Analysis of Miliacin Content in the Millet Cultivars by GC-MS

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Although the consumption of different types of millet such as proso millet, foxtail millet, finger millet, and barnyard millet is less than that of rice, they have various functional and nutritious contents. In particular, miliacin, the main triterpenoid of millet, is known to stimulate the metabolism and proliferation of keratin cells and is very effective in the women's telogen effluvium by stimulating the cell proliferation in the hair roots. The aim of this study was to evaluate the miliacin content of millet cultivars so as to use it as a food and/or cosmetic material, and to use it as a specific breeding material. Different cultivars of proso millet (Geumsilchal, Manhongchal, Yeonheechal, Ollechal, Leebaekchal, Hallachal and Hwangsilchal), foxtail millet (Daname and Samdachal), finger millet (Finger1ho) and barnyard millet (Sodamjik and Borajik), which belong to the RDA, National Institute of Crop Science, Miryang, Korea, were used in this study. The miliacin content of millet cultivars were determined by GC-MS. In proso millet, the average miliacin content was 1,579.28 ㎍/g. In barnyard millet, trace amounts of miliacin were detected. However, miliacin was not detected in the foxtail millet and finger millet. Among the cultivars of proso millet, Geumsilchal and Hallachal showed the highest content of miliacin. Based on this analysis, proso millet and barnyard millet need to be considered for further research, analysis and validation.

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PG-0047

Terpene Synthase Gene Expression during Flowering Stages in Freesia 'Shiny Gold'

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Terpene synthase genes (*TPS*) plays major role in scented flowers, including *Freesia hybrida*. Six major *TPS* genes responsible for monoterpene synthesis were selected for gene expression study. Among the six genes, *TPS3* was highly expressed, followed by *TPS8, TPS6 and TPS2* while *TPS4* resulted in low expression in freesia 'Shiny Gold'. Based on sensorial analysis, 'Shiny Gold' and 'Yvonne' were classified as strong, '10C3-894' as very strong, and '10C3-424' as weak scented, respectively. *TPS4* and *TPS6* showed high expression in Bud (S1) and full bloomed (S2) whereas *TPS2, TPS3* and *TPS5* were down-regulated in S1 between 'Shiny Gold' and 'Yvonne'. All *TPS* genes were down-regulated in S1 between 'Shiny Gold' and '10-894'. In case of '10C3-424', all of *TPS* genes were up-regulated in both S1 and S2. Linalool, one of the result product of *TPS*2 and 3, is a major volatile compound of freesia scent. Linalool synthase (*LNS*) expression was found to be high in S1 and S2 in 'Shiny Gold'. Among the four cultivars, 'Shiny Gold' and 'Yvonne' exhibited similar levels of *LNS* expression while the expression was high in very strong scented cultivar '10C3-894' whereas sharply down-regulated in the weak scented cultivar '10C3-424'.

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PG-0048

Scent Analysis of Freesia Cultivars Using a Chemiresistive Electronic Nose sensor

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Floral scent is an important attribute made up of different combination of volatile compounds. Odor intensity is multifaceted which sometimes make human olfactory system unable to perceive the lowest intensity. Moreover, Electronic Nose (E-Nose) can perceive odor intensity in a similar way of human olfactory system by considering compound and concentration concurrently thereby overall fingerprint of volatile component is obtained. In order to analyze floral scent of eight freesia cultivars strong (‘10-322’, ‘10-335’, and ‘13-190-3’), medium (‘10-895’, ‘12-1-13’ and ‘10-157’) and weak (‘13-27-57’ and ‘13-151-4’) scented based on sensory analysis, E-nose with six metal oxide sensors were used. The fingerprint data was subjected to dimensionality reduction using principal component analysis (PCA) and discriminant function analysis (DFA). The first two principal components accounted for 98.97% (PC1) and 0.79 % (PC2) respectively. DFA was displayed in two-dimensional plot comprising of two discriminant functions, which accounted for 77.10 % (DF1) and 19.74 % (DF2) respectively. Distance between cultivar and control on the PCA score plot were used to classify the level of odor intensity. Unscented or weak scented cultivar cluster near control. The result showed that cultivars ‘10-322’, ‘13-190-3’, ’10-335’ and ‘12-1-13’ grouped together while ‘13-151-4’ and ‘13-27-57’ clustered separately and this result could indicate the separation of strong and mild scented cultivars. Therefore, this method could be useful to classify odor strength and to discriminate cultivars from germplasm for preliminary screening during breeding program.

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PG-0049

Expression profiles of the *CaCPR1* and *CaCPR2* in Hot pepper (*Capsicum annuum* L. cv. *Bukang*)

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The cytochrome P450s (CYP) play important roles in development and defense system in plant. CYPs require NADPH-cytochrome P450 reductase (CPR) enzyme for their functions. CPRs are required for electron transfer from NADPH to cytochrome P450. There are two CPR genes in the hot pepper (*Capsicum annuum* L. *cv. Bukang*) genome which are *CaCPR1* and *CaCPR2*. The *CaCPRs* expression levels were measured by quantitative real-time PCR in various development stages and stress conditions (Jasmonic acid, Salicylic acid, drought treatments). The *CaCPR1* expression level was gradually increased during fruit ripening. The *CaCPR2* gene was constitutively expressed in all the tested tissues but the expression level was lower than the *CaCPR1*. Under the stress conditions, both of the *CaCPR1* and *CaCPR2* expression levels were increased possibly because more CPR enzymes are needed against stress. To investigate the enzymatic properties, two *CaCPRs* were isolated from hot pepper and heterologously expressed in *Escherichia coli*. The enzymatic activities were assessed using protein and chemical substrates such as MTT and ferricyanide. *In vitro* assay showed that both CaCPR1 and CaCPR2 mediated electron transfer from NADPH to the substrates. These results suggest although CaCPR2 may plays minor enzyme in normal condition, the CaCPR1 and CaCPR2 could be involved in responses of plants under stress conditions.

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PG-0050

Comparative Transcriptome Analysis in Freesia 'Gold Rich' between Normal and Abnormal Flower

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Flowering is a complex process, influenced by external and internal factors and is accompanied by various morphological and physiological growth signals. Floral malformation occurring in tissue cultured plants has recently become a serious constraint in cut flower production, leading to economic losses. *Freesia* 'Gold Rich' is a popular domestic cultivar in South Korea for its attractive yellow color and fragrance. Floral malformation has caused reduction in cultivation area of this cultivar. In order to determine the genetic cause for floral malformation, comparative transcriptome analysis between normal and malformed flowers was performed. cDNA libraries from four tissues, namely normal bud, normal flower, malformed bud and malformed flower were prepared independently for Illumina sequencing. A total of 141,750,500 reads were generated out of which 88.6 % were mapped to the reference gene set. Around 916 transcripts specific to flower development was identified using BLAST and 420 differentially expressed genes (DEGs) were identified using DESeq. Among these DEGs, 26 transcripts associated with MADS-box gene were related to ABC model of flower development. The gene expression study helped to select candidate genes that are involved in number of biological, cellular and molecular functions that affect flower development in freesia. The data in our study will serve as a comprehensive resource for investigating the regulation mechanism involved in floral organ development in freesia 'Gold Rich'.

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PG-0051

Plant autophagy-related protein 8 (ATG8) protein is modified by pathogen effector PopP2

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Autophagy related proteins (ATG) are key players in maintaining cellular homeostasis and regulating immune system in eukaryotes. Autophagy is a highly conserved process that degrades certain intracellular proteins and contributes with both pro-death and pro-survival functions to specific pathogen infections. Several pathogens have evolved strategies to manipulate host autophagy pathways to suppress plant immunity. In this study, tomato StATG8 protein is coIPed and acetylated by *Ralstonia solanacedarum* effector PopP2 which has an acetyltransferase activity. PopP2 is partial relocalized in the autophagosome when coexpressed StATG8. PopP2 acetylates clade-specific ATG8 proteins but still is able to interact with other clade ATG8 proteins. Together, we demonstrate that autophagy ATG8 might be targeted by bacterial pathogen effector to manipulate host autophagy pathway. Regulation of Atg8 acetylation will provide new approaches in crop engineering.

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PG-0052

Autophagy-related protein regulates plant immune receptor

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Autophagy is an intracellular degradation system that evolutionally conserved in eukaryotes. Mechanistic understanding of autophagy function serves important roles in various biological processes. Autophagy-related (ATG) proteins have important roles in the plant immunity regulation. Recently, It has been reported that the ATG8 protein interacts with Arabidopsis orosomucoid (ORM) protein which acts as a selective autophagy receptor of Flagellin-sensing 2 (FLS2). Thus, protein accumulation of FLS2 immune receptor is regulated by selective autophagy. In our research, we found that ATG8 associated with the RPS4/RRS1 immune receptor in coIP. Using the iLIR autophagy database, we found some of the putative autophagy interacting motifs (AIM) in the RRS1 and RPS4. If coexpressed ATG8 with RPS4/RRS1 in the non-recognized or recognized condition, transient expression of StATG8 strongly suppressed hypersensitive response. These data indicate that the immune receptors seem to be regulated by autophagy by physical interaction. This study may be useful tools to regulate plant immune receptors in crop development.

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PG-0053

Characterization of the hot pepper ubiquitin conjugating enzyme 2

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The Ubiquitin proteasome system (UPS) is a critical actor of protein recycling during biotic/abiotic stress response in crop plant. In UPS, the role of E2 enzymes have been investigated but their biological roles are still unknown. To reveal the role of E2 in plant environmental stresses, we identified and cloned 10 hot pepper genes encoding ubiquitin E2 proteins. All the *CaUBC* genes were expressed in root, stem, flower, and leaf, although the expression of some of the genes was increased or decreased in several organs. Subsequently, the expression pattern of 10 *CaUBC* genes were investigated in response to multiples stresses. The gene expression of *CaUBC* is specifically induced by the specific abiotic stresses. Interestingly, *CaUBC2* was up-regulated all of the abiotic stresses. Base on protein sequence analysis, some of the CaUBC protein may contain the putative Autophagy Interacting Motif (AIM), suggesting that UBC protein might have physical interaction with autophagy pathway. These results indicated that the CaUBCs may play vital roles in different stress responses and could be useful target for gene transfer or engineering crop plant.

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PG-0054

Analysis of *Tos17* mutants with increased rice seed weight and size

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It is important to develop rice varieties with higher yield to cope with climate change, depletion of natural resources and population growth. In the previous study, we generated 1,500 mutants via insertion of *Tos17*, a mobile endogenous retrotransposon, using the Korean domestic rice Ilmibyeo. Here, we selected 6 mutants with a 16~36% increase in the 1000-grain weight compared with that of the wild type. In the 877, 878, and 884 mutant lines, *Tos17* was inserted into the exon of *phosphate transporter*, the 5' UTR of *Ammonium transporter*, and the exon of *retrotransposon*, respectively. Furthermore, the CRISPR/Cas9 system was employed to knockout each three genes, in order to increase seed weight. This study demonstrates the potential utility of *Tos17* mutants via an efficient tissue culture method in various rice cultivars for the improvement of agronomic traits including seed weight.

Tos17 has been a useful tool for insertional mutagenesis and the functional analysis of genes, but it can cause somaclonal variation during callus induction. For deletion of *Tos17* from the genome of rice, we designed CRISPR/Cas9 vector for the long terminal repeat sequences of *Tos17.* Through the genotype analysis of T0 and T1 transgenic rice plants, we succeeded in producing homozygous mutant lines carrying edited Tos17 without Cas9 genes. This variety could be used as original seed in rice transformation.

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PG-0055

Functional studies of hot pepper *CYP707A* family genes: Identification of their catalytic reaction and analysis of their roles in plant

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CaCYP707A1 Change of abscisic acid (ABA) homeostasis affect to various ABA mediated stress and developmental responses. Homeostasis of ABA is regulated by balance of biosynthesis and catabolism processes. The ABA catabolism pathway involves the *CYP707A* family, encoding ABA 8'-hydroxylase. Here we have identified that four Capsicum annuum cytochrome P450 genes (*, 2, 3,* and *4*) have ABA hydroxylation activity. Expressions of *CaCYP707A*s have been validated to increase under drought stress condition. To identify the catalytic function of the CaCYP707As, these proteins were cloned into *E. coli* expression vector and heterologously produced in *E. coli* system. These recombinant proteins were incubated with ABA in NADPH condition and catalyzed ABA to 8'-hydroxy ABA, phaseic acid. ABA hydroxylation activity was also demonstrated in *CaCYP707As*-overexpressing tobacco plants, which ABA level was lower than non-transgenic plant and exhibited drought sensitive phenotype. More interestingly, these transgenic tobacco plants showed that down regulated seed formation. The phenotypical analysis of pollen showed that the development of pollens were not complete. In addition, the pollen viability of transgenic tobacco plants were significantly lower than non-transgenic plant. Our results indicate that CaCYP707As regulate the seed formation and pollen viability through their ABA hydroxylation activity.

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PH-0001

Systemic silencing approach to rapidly identify disease resistance genes required for recognition of *Ralstonia solanacearum* effectors in *Nicotiana benthamiana*

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Ralstonia solanacearum (Rso) is the causal agent of bacterial wilt disease in Solanaceae family. This pathogen injects more than 70 effector proteins into host cells to enhance infection. The disease resistance (*R*) genes encoding the nucleotide-binding leucine-rich repeat (NLR) proteins detect the presence of effectors and activate the plant immune system. However, it remains challenging to identify NLRs due to the complex and large size of crop genomes. The solanaceous model plant *Nicotiana benthamiana* is well suited to identify new NLRs due to the availability of genome-wide annotation of NLRs and the application of functional genetic tools, such as virus-induced gene silencing (VIGS). Here, we selected 11 Rso effectors that induced cell death upon expression in *N. benthamiana* leaves. The cell death induced by Rso effectors was compromised in plants silenced for the NLR chaperone SGT1. We then screened a NbNLR-VIGS library consisting of concatenated constructs covering over 300 *NbNLRs*. This systematic screening allowed us to discover two NLRs required for effector-induced cell death. To confirm the specificity of the identified NLRs, we also performed alternative silencing to target different region of the NLRs and genetic complementation assays with synthetic version of the NLRs resistant to silencing. Further experiments aim to demonstrate that newly identified NLR confers resistance to pathogen. New NLRs from *N. benthamiana* might be used as a source of resistance in Solanaceae crops and provide mechanistic insight into plant NLR function.

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[식물분자육종사업단]

PI-0001

The rice transcription factor OsMYB102 delays leaf senescence by downregulating abscisic acid accumulation and signaling

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MYB-type transcription factors (TFs) play important roles in plant growth and development, and in the responses to several abiotic stresses. In rice (*Oryza sativa*), the roles of MYB-related TFs in leaf senescence are not well documented. Here, we examined the rice MYB TF gene *OsMYB102* and found that an *OsMYB102* T-DNA activation-tagged line (termed *osmyb102-D*), which constitutively expresses *OsMYB102* under the control of four tandem repeats of the 35S promoter, and *OsMYB102*-overexpressing transgenic lines (*35S:OsMYB102* and *35S:GFP-OsMYB102*) maintain green leaves much longer than the wild type under natural, dark-induced, and abscisic acid (ABA)-induced senescence conditions. Moreover, an *osmyb102* knockout mutant showed an accelerated senescence phenotype under dark-induced and ABA-induced leaf senescence conditions. Microarray analysis showed that a variety of senescence-associated genes (SAGs) were downregulated in the *osmyb102-D* line. Further studies demonstrated that overexpression of *OsMYB102* regulates the expression of SAGs, including genes associated with ABA degradation and ABA signaling (*OsABF4*, *OsNAP*, and *OsCYP707A6*), under dark-induced senescence conditions. OsMYB102 inhibits ABA accumulation by directly activating the transcription of *OsCYP707A6*, which encodes the ABA catabolic enzyme ABSCISIC ACID 8'-HYDROXYLASE. OsMYB102 also indirectly represses ABA-responsive genes, such as *OsABF4* and *OsNAP*. Collectively, these results demonstrate that OsMYB102 plays a critical role in leaf senescence by downregulating ABA accumulation and ABA signaling responses.

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PI-0002

Drought-Responsive Long Noncoding RNAs Alter the Expression of Abiotic Stress-Related Genes in Rice

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Long noncoding RNAs (lncRNAs) have appeared as critical regulatory factors of various biological processes in both plants and animals. In Rice (*Oryza sativa* L.), it has been known that several lncRNAs regulate key biological processes such as phosphate homeostasis, flowering and fertility. However, systematic examination of rice lncRNAs involved in abiotic stress responses has not been reported. Here, we re-analyzed the expression profile of lncRNAs in publicly available rice transcriptome datasets derived from abiotic stress treatments to unveil the potential roles of rice lncRNAs in abiotic stress responses. Overall, we identified 10,831 rice lncRNAs that were significantly altered in shoot and/or root tissues under four different abiotic stresses. Based on Venn diagram analysis, we observed strong cross-talks between different stress signaling pathways, showing transcriptional regulatory networks underlying lncRNA expression changes in response to abiotic stresses. In addition, we identified novel drought-induced lncRNAs (DRILs) through transcriptome analysis of drought-treated rice. Out of them, we examined some Long intergenic noncoding RNA (LincRNA) and Natural Antisense Transcripts (NATs). Real-time RT-PCR analysis confirmed the differential expression patterns of these lncRNAs under various stress conditions and developmental stage. To determine the regulatory role of lncRNAs in abiotic stress signaling, lncRNAs were transiently overexpressed in rice protoplasts. As a representative result, *DRIL4* overexpression increased the expression levels of stress marker genes such as *Rab16* and *Dip1*. Our results show the first comprehensive identification and functional characterization of a group of abiotic stress-responsive lncRNAs in rice.

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PI-0003

Construction of mutant population by gamma irradiation using the dwarf tomato cultivar Micro-Tom

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Diverse genetic resources are used by breeders to develop new and improved varieties with desired characteristics. Therefore, generating a mutant population is a effective tool for identifying functional genes. To generate a mutant population in tomato, we used the Micro-Tom variety which has reduced size and relatively short life-cycle compared to other commercial cultivars and gamma rays as a mutagen. To find optimal intensity of gamma rays for the mutagenesis, dry seeds of Micro-Tom were irradiated with different intensities of gamma rays, from 0 to 1000 gray (Gy) in 100 Gy increments. When the mutagenized seeds (M_1 seeds) were germinated onto MS media, the germination rate of M_1 seeds was not affected by the intensities of tested gamma rays. However, M_1 seedling growth was severely reduced as the intensities of gamma rays increased. Seedling growth rate on the eight days after germination showed that median gamma ray doses for hypocotyl and root length were 600 and 300-400 Gy, respectively. Survival test for 300, 400, and 500 Gy-treated M_1 seeds showed that survival rate significantly decreased as irradiation dose increased. Especially, the plant survival rate of the 400 Gy-radiated seeds was almost one half of the plants. These results suggest that the gamma rays of 300-400 Gy are good for tomato mutagenesis.

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PI-0004

Characterization of the *no trichome* mutant in tomato

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Trichomes are fine outgrowths derived from epidermal cells on the aerial part of plants. Trichomes exist in most plant species and are classified as either glandular or non-glandular. Glandular trichomes function in a chemical defense against herbivores, while non-glandular trichomes function as physical barriers to various biotic and environmental stresses. In this study, we describe a novel recessive mutation named *no trichome* (*nt*) which was identified based on the absence of trichomes on stems. *nt* plants exhibited lower density of trichomes on leaves, stems, and hypocotyls, compared with the wild-type (WT) plants. Types I, III, and V trichomes, especially, were not developed at all on the stems of the *nt* plants. In addition to trichome initiation, the length of Type I trichomes was shorter in the *nt* plants than in the WT plants. The growth of *nt* plants under greenhouse conditions showed that the mutant has shorter stems and fewer leaves than the WT plants. The identification of the *Nt* gene will provide a clue for understanding multicellular trichome development in tomato and the *Nt* gene can be used as a useful genetic resource to develop insect-resistant tomato.

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PI-0005

QTL mapping for α-glucosidase inhibitory activity at three different stages of leaf and one stage of fruit in pepper (*Capsicum annuum* L.) using genotyping-by-sequencing analysis

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Diabetes mellitus, a metabolic disorder characterized by high blood sugar level, is one of the most serious and common diseases in the world, leading to major complications such as diabetic neuropathy, retinopathy and cardiovascular diseases. The widely used treatment for non-insulin dependent diabetic mellitus is to disturb hydrolytic cleavage of carbohydrate and retard glucose absorption. Alpha-glucosidase inhibitors (AGI) such as acarbose have been used to lower blood glucose level by suppressing the activity of α-glucosidase and α-amylase in digestive organs. The ability to control blood sugar by the inactivation of α-glucosidase has been reported in pepper (*Capsicum annuum* L.). Therefore, we aimed to identify QTLs controlling AGI activity in pepper leaf and fruit using enzyme assay and genotyping-by-sequencing (GBS) analysis. A total of 17,427 SNPs were identified by GBS analysis and subjected to pepper genetic linkage map construction. The map contained 12 linkage groups with a total genetic distance of 2,379 cM and consisted of 763 SNP markers. The AGI activities at three different stages of leaf and one stage of fruit were analyzed using a segregating 96 F_2 individuals. QTL analysis revealed seven QTLs (*qAGI1.1*, *qAGI11.1*, *qAGI5.1*, *qAGI9.1*, *qAGI12.1*, *qAGI5.2*, and *qAGI12.2*) controlling AGI activity in pepper leaf and fruit. Two QTLs (*qAGI1.1*and *qAGI11.1*) were detected in leaves sampled in April. A major QTL *qAGI5.1* was identified in leaves sampled in July. In October analysis, two QTLs (*qAGI9.1* and *qAGI12.1*) and two QTLs (*qAGI5.2* and *qAGI12.2*) were identified in leaf and fruit samples, respectively. This QTL information will contribute to develop pepper varieties with high AGI activity.

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PI-0006

QTL mapping for agronomic traits using a high-density linkage map in maize RIL population

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In this study, 80 $F_{7:8}$ recombinant inbred line (RIL) population was derived from a cross between inbred lines of dent corn (Mo17) and waxy corn (KW7). These population was genotyped using the MaizeSNP50 BeadChip. The genetic map constructed using 2,904 SNP markers, and spanned 3,553.7 cM with an average genetic distance between markers of 1.2 cM, and the number of loci per linkage group ranged from 105 to 476. Based on this genetic map, the 12 quantitative trait loci (QTLs) for plant height (PH), ear height (EH), water content (WC), ear length (EL), setted ear length (SEL), amylose content (AC) in maize were detected in the Mo17/KW7 RIL population. They were mapped to chromosomes 1, 3, 4, 6, 8, and 9. Among these QTLs, only one QTL was associated with PH, EL, SEL, AC. While, each four QTL were related to EH and WC, respectively. Moreover, the 9 QTLs were major QTLs which had more than 10% phenotypic variation (3.79-82.10 %), and qAC9 had the highest phenotypic variance (82.10 %). The qEL6 and qSEL6 were co-located in same region on chromosome 6. This pleiotropy supported high correlation between EL and SEL traits. For marker-assisted selection (MAS) in breeding program, it is important to identify genes on the chromosomal segment linked to the target trait. Thus, the results of this study may improve the identification of genes or QTLs responsible for agronomic traits in maize.

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PI-0007

Molecular Analysis of *OsGT1* (*Oryza sativa Grassy Tiller1*) determining tiller branching in rice

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Enhancing yield has been a major challenge of agriculture. In rice, tiller number is one of the important biomass and yield components. A maize mutant *grassy tillers1* (*gt1*) increases lateral branches in maize. The *GT1* gene encodes a class I homeodomain leucine zipper (HD-Zip) protein. In maize, the *gt1* expression is dependent on the activity of *teosinte branched1* (*tb1*), a major domestication locus controlling tillering and lateral branching. To estimate the biological role and agricultural utility of *gt1* in rice, rice homologue (*OsGT1*) has been isolated and its overexpressors and RNAi lines were generated. Field data have shown that *OsGT1* overexpressors reduce the number of tillers and panicles while RNAi lines increase them, compared to ones of wild type. To establish the molecular relationship between *TB1* and *GT1*, the transcription activation of *GT1* by TB1 has been examined with EMSA, yeast one hybrid, and in vivo transcriptional activation assay. To Identify *GT1*-downstream genes, RNA seq has been performed with *tb1* and *GT1* RNAi. In order to establish relationships of *GT1*-mediated tillering mechanism with hormonal and *TB1* genetic factors, tillering phenotypes and gene expression patterns were examined in wild type and *GT1* RNAi treated with various treatments of hormones (e.g., strigolactone, cytokinin, and their inhibitors) that make influence on lateral branch formation. These researches could provide insights to understand how *OsGT1* takes action on branch development in rice. This research is supported by the Plant Molecular Breeding Center of PostBiogreen 21

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PI-0008

HIGH CROSSOVER RATE1 restricts the number of meiotic crossovers in Arabidopsis

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Meiotic crossover creates new combinations of genetic variation and ensures balanced chromosome transmission. Crossover numbers per meiosis are tightly restricted in most eukaryotes, despite a large excess of initiating DNA double-strand break precursors. The majority of crossovers in plants are dependent on the Class I interfering repair pathway. A minority of crossovers are formed by the Class II non-interfering pathway, which is normally limited by multiple anti-recombination pathways. However, similar pathways that limit Class I interfering crossovers are unknown. To identify regulators of crossover formation, we performed a forward genetic screen in Arabidopsis using fluorescent crossover reporters, to identify mutants with increased or decreased recombination frequency. This screen identified the p*HIGH CROSSOVER RATE1* (*HCR1*) gene as repressing crossovers. Using genome-wide analysis we show that *hcr1* crossovers are most strongly increased in the distal euchromatic chromosome arms. We observe a significant increase in MLH1 foci in *hcr1* and a decrease in the strength of crossover interference, which is consistent with a major effect on the Class I pathway. We used yeast two hybrid and *in planta* assays to demonstrate physical interaction between HCR1 and multiple proteins within the Class I interfering pathway, including HEI10, PTD, and MSH5. Our data identify HCR1 as limiting the number of interfering Class I crossovers in plants. We propose that HCR1 acts in opposition to pro-recombination DNA repair or cell division kinases, in order to limit crossover number per meiosis.

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PI-0009

Arabidopsis patatin-like phospholipas 2A involves in fertilization by regulating pollen tube growth and guidance

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Breeding using doubled haploids (DHs) reduces the time required to generate and evaluate new lines from 6-7 years to 2 years or less. Recently, few proteins including MATRILINEAL were identified as haploid inducers in monocot plants. However, it is still remained unclear in dicot plants. Here, we investigate the effects of Arabidopsis patatin-like phophpolipase 2A (AtPLP), a homologue of maize MATRILINEAL, on expression of the genes modulating pollen development and fertilization in Arabidopsis. The phenotypic analysis showed that T-DNA inserted *Atplp* mutants did not show big difference with wild type plants during vegetative and reproductive growth. Quantitative RT-PCR showed that the transcript levels of four pollen tube growth-related genes and six pollen guidance- or reception-related genes were increased in *Atplp* mutants. In addition, the transcript levels of four mitosis and meiosis-related genes were increased in *Atplp* mutants. Moreover, the transcript levels of two hormone-related genes and a calcium pump-encoding gene were increased in *Atpla2a* mutants. But, the expression levels of the genes encoding a synergid-secreted peptide AtLURE1.1 and ACA9 were decreased in *Atplp* mutants, suggesting that AtLURE1.1 and ACA0 can function in AtPLP-mediated haploid induction in Arabidopsis. Notably, phenotypic analysis showed that flowering time was significantly delayed in of *Atplp* mutants. These results suggest that AtPLP involves in fertilization through modulation of pollen germination, pollen tube growth and guidance as well as floral induction.

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PI-0010

Chronic γ-irradiation on tomato seedling changes plant growth and leaf morphology

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γ-phytotron is an enclosed research facility used for plant-environmental interactions. Morphological modifications and antioxidant-related gene expressions have been studied to examine the effects of chronic γ-irradiation on tomato seedling. Tomato seedings were continuously exposed to 50 to 200 Gy of γ-irradiation for 2 weeks. In comparison to non-irradiated plants, the size of plants irradiated with 150 and 200 Gy was greatly reduced. Based on the dissecting microscopic images, leaf surface of γ-irradiated plants appeared rougher than non-irradiated plants. In addition, 150 and 200 Gy irradiated plants reduced the number of type I trichome compared with non-irradiated plants. Type VI trichome also decreased depending on doses of γ-irradiation. These results suggest that chronic γ-irradiation on tomato seedlings negatively affect plant growth and trichome density. We are testing which genes are involved in changes after chronic γ-irradiation on tomato.

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PI-0011

Rice small protein OsSTR1 controls cell stability and stress responses

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Small peptides play important roles in plant development and responses to abiotic and biotic stresses. We have identified a novel *OsSTR1* gene encoding a small peptide comprised of 76 amino acids. *OsSTR1* is mainly expressed in the leaf, stem, and root, and its expression is induced by drought treatment. Fluorescence analysis shows that OsSTR1 localizes in inner nuclear membrane. Transgenic Arabidopsis plants overexpressing OsSTR1 exhibited enhanced drought stress tolerance as compared to the wild type. In addition, OsSTR1-overexpressing plants displayed enhanced expression of pathogen-related genes including *PR1* and *PDF1.2* and abiotic stress-related genes including *RDA29A* and *CPK6*, indicating that OsSTR1 is involved in the control of biotic and abiotic stresses. OsSTR1 directly interacts with rice E3 SUMO ligase and modified with SUMO (Small Ubiquitin-related Modifier), strongly indicating that the function and stability of OsSTR1 are modulated by sumoylation. OsSTR1 also directly interacts with an inner nuclear membrane protein SUN (SAD1/UNC-84 DOMAIN PROTEIN), indicating that OsSTR1 can function as a linker of nucleoskeleton and cytoskeleton complex. OsSTR1 forms homodimer itself and also heterodimer complex with a basic helix-loop-helix transcription factor, suggesting that OsSTR1 can regulate gene expression as a transcription factor. Our data indicate that OsSTR1 plays crucial functions in various stress responses by the establishment of cell polarity, cell migration, cell mechanosensing, and gene expression.

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PI-0012

OsMADSN-mediated floral repression is stimulated by intronic lncRNA *FLOWERING ASSOCIATED* in rice

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In plants, long noncoding RNAs (lncRNAs) are known to play important roles in flowering, organ development and stress response. However, the researches related to the diversity and complexity of lncRNA and their mechanism of gene regulation in plants are still far behind that of animals. Here, we show that a long intronic noncoding RNA called FLOWERING ASSOCIATED (FLA) is required for the long day-specific epigenetic activation of *OsMADSN* expression. FLA is produced from the first intron of *OsMADSN* gene and physically associates with a rice enhancer of zeste OsiEZ1, a homologue of Arabidopsis histone H3K27-specific methyltransferase CURLY LEAF (CLF). Under long day, *OsMADSN* expression is upregulated while the expression of both *OsiEZ1* and *FLA* are down-regulated. But, interestingly, FLA-overexpressing transgenic rice displays delayed flowering phenotype under long day, and the transcript levels of *OsMADSN*and *OsiEZ1* are increased in the transgenic plants. In addition, expression level of rice Trithorax1 (OsTRX1), a homologue of Arabidopsis histone H3K4-specific methyltransferase ATX1 (Arabidopsis Trithorax-like protein), is increased in FLA-overexpressing transgenic rice. FLA-interacting protein OsSAP blocks or interferes the binding of OsiEZ1 to FLA, strongly suggesting that OsiEZ1-mediated H3K27me3 production on *OsMADSN* chromatin is negatively regulated by OsSAP. These data indicate that FLA overexpression promotes OsMADSN-mediated floral repression by increasing H3K4me3 on *OsMADSN* chromatin without affecting on other phenoytypes.

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PI-0013

Arginine Catabolism for Nitrogen Mobilization: Lessons from Cyanobacteria

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Metabolic pathways for the nitrogen-rich arginine play a crucial role in nitrogen mobilization and storage in cyanobacteria. Two cyanobacterial enzymes, AgrE from *Anabaena* sp. strain PCC 7120 and ArgZ from *Synechocystis* sp. PCC 6803, contain an arginine dihydrolase in their N-terminal domains. These two enzymes catalyze the arginine catabolic pathway and produce an ammonia as well as ornithine and CO_2. In AgrE, the C-terminal domain contains additional enzyme, an ornithine cyclodeaminase that converts ornithine into proline and ammonia. Therefore, AgrE is a bifunctional enzyme that performs two sequential reactions for arginine catabolism. In plants, there are no enzymes for AgrE. In order to understand the proposed role of AgrE in nitrogen mobilization and storage, we initiated biochemical and structural analysis of the enzyme. Our recent study showed that AgrE is present in a tetrameric conformation. These structural data identified the binding sites for the substrate l-arginine and the product l-ornithine in arginine dihydrolase. The ternary complex of AgrE containing the coenzyme NAD(H) for ornithine cyclodeaminase and ornithine for arginine dihydrolase suggested a possible passage for substrate channeling that connects the active site of the N-terminal domain to that of the C-terminal domain. These studies unraveled biochemical and structural insights on AgrE for nitrogen mobilization.

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PI-0014

Analysis of glutenin relative gene in response to heat stress in wheat spike

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Common wheat (*Triticum aestivum* L.) is frequently exposed to high temperature during anthesis and ripening period, which resulted in yield loss and detrimental end-use quality. To study the effect of high temperature stress on wheat grain development, especially on wheat glutenin synthesis, glutens from the grains of Con (nine days after flowering, Zadok scale 71), DAT6-T (six days of treatment, Zadok scale 75) and DAT10-T (ten days of treatment, Zadok scale 77) were analyzed by 2DE-PAGE. Spots that showed unique decreased pattern as heat treatment augmented (DAT 6-T, DAT 10-T) showed strong similarities each other and most of the sequences fit to the glutenin relative gene. These glutenin relative genes were identified as possessing similar promoter and transcription factors binding motifs compare of common glutenin gene. The glutenin relative gene possess signal peptide, N-terminal, C-terminal and repetitive domain and one exon. QRT-PCR in de-hulled spikelet showed that glutenin relative gene showed decreased transcription level under the high temperature stress. Analysis of grain quality-related traits like seed storage protein can help to assess and understand breeding progress and selection

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PI-0015

Application of subgenome specific markers to develop wheat-rye translocation lines

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Bread wheat is one of the major cereal crops in the world, and a number of strategies have been applied to develop cultivars with preferable agronomic traits. Among those, introgression of rye chromatin into wheat genome background has been widely used thanks to agronomically useful genes located on the rye chromatin, which confers tolerance to biotic stress, high yield components, and increased root length. To facilitate breeding wheat-rye translocations, we developed each subgenome (A, B, D of wheat, and R of rye) specific markers using public genome database. The specificity of the markers was verified via PCR analysis using wheat aneuploid and wheat-rye chromosome addition genetic sources. Near-isogenic lines (NILs) were developed by crossing Korean wheat cultivar and 1BL.1RS translocation, followed by screening the translocation lines with the developed markers. Glutenin and gliadin fraction of the translocation and the non-translocation lines was observed via A-PAGE (Acid-PAGE) and SDS-PAGE, which represented that recombination occurred among the genomes. Furthermore, shoot and root biomass was measured during drought stress, which indicated superior drought tolerance of wheat-rye translocation lines. From this study, we developed subgenome specific markers on the short arm of chromosome 1 of wheat and rye, and produced the novel wheat-rye translocation lines, which will be helpful in breeding wheat-rye translocation lines.

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PI-0016

Overexpression of Rice *Expansin7* (*Osexpa7*) Confers Enhanced Tolerance to Salt Stress in Rice

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Expansins are key regulators of cell-wall extension and are also involved in the abiotic stress response. In this study, we evaluated the function of *OsEXPA7* involved in salt stress tolerance. Phenotypic analysis showed that *OsEXPA7* overexpression remarkably enhanced tolerance to salt stress. *OsEXPA7* was highly expressed in the shoot apical meristem, root, and the leaf sheath. Promoter activity of OsEXPA7:*GUS* was mainly observed in vascular tissues of roots and leaves. Morphological analysis revealed structural alterations in the root and leaf vasculature of *OsEXPA7* overexpressing (OX) lines. *OsEXPA7* overexpression resulted in decreased sodium ion (Na^+) and accumulated potassium ion (K^+) in the leaves and roots. Under salt stress, higher antioxidant activity was also observed in the *OsEXPA7*-OX lines, as indicated by lower reactive oxygen species (ROS) accumulation and increased antioxidant activity, when compared with the wild-type (WT) plants. In addition, transcriptional analysis using RNA-seq and RT-PCR revealed that genes involved in cation exchange, auxin signaling, cell-wall modification, and transcription were differentially expressed between the OX and WT lines. Notably, salt overly sensitive 1, which is a sodium transporter, was highly upregulated in the OX lines. These results suggest that *OsEXPA7* plays an important role in increasing salt stress tolerance by coordinating sodium transport, ROS scavenging, and cell-wall loosening.

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PI-0017

New DNA marker development to target major abiotic stress tolerance QTL/gene for rice

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World climate change incur various abiotic stress on crops. Rice breeders are trying to improve cultivar for abiotic stress tolerance coping with climate change. For quickly do that, MAS(marker assisted selection) is needed. We considered salinity, drought, anaerobic germination and submergence stress to develop DNA marker for various abiotic stress. Reference tolerance gene/QTL was targeted about these stress. Known major tolerance gene/QTL for salinity, drought, anaerobic germination and submergence stress are *Saltol* QTL, *DTY* (*DTY2.2, DTY4.1*) QTL, *AG1* gene, *Sub1A* gene, respectively. In this study, we developed KASP marker to replace existing gel-base marker over target these gene/QTL.

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PI-0018

Genotype analyse of North Korea rice varieties population base on phenotypic screening for salinity stress tolerance

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Salinity stress can cause damage to crops. Rice production can be decreased because of salinity stress when rice growing stage is early vegetative or reproductive stages. In this study, we are trying to find out genotype of new salinity tolerance using North Korea(NK) rice population of 190 varieties which have not been assessed. There are tolerance varieties for salinity stress in hydroponic screening. GWAS analysis and DNA marker validation were proceeded for the population base on screening phenotype result. It enables you to detect new salinity tolerance genotype of japonica type by using this population.

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PI-0019

Activation of a novel E3 ubiquitin ligase gene produces formation of coiled branches in Arabidopsis

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To investigate the molecular mechanism of stem coiling, a screening was carried out from Arabidopsis activation tagging lines obtained by activation T-DNA treatment. A mutant with a wavy and curly morphology, and coiling branches, named *cbr*, was identified. Plasmid rescue and genomic southern blot analysis revealed the site of T-DNA insertion in the genome. RT-PCR was performed to monitor expression levels of the genes adjacent to the T-DNA integration site and showed the activation of an E3 ubiquitin ligase gene. Database search revealed that the protein with the C3HC4 type RING domain belongs to a family of E3 ubiquitin ligases. Complementation test by overexpression and RNA interference of the gene showed that activation of the novel gene caused the *cbr* mutant phenotypes. Ubiquitination affects every cellular process including plant development. E3 ubiquitin ligase has been reported to recognize target proteins that are needing to be ubiquinated for further degradation by the proteasome complex. We have obtained eight candidate substrates for E3 ubiquitin ligase by performing a yeast two-hybrid screening. Currently we are performing correlation analysis between the selected substrates and CBR protein.

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PI-0020

Identification of two *S* haplotypes containing duplicate *SRK* genes in radish (*Raphanus sativus* L.) and integration of Korean *S* haplotypes controlling self-incompatibility into the unified nomenclature

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To integrate *S* haplotypes identified in previous studies of Korean radish (*Raphanus sativus* L.) breeding lines into a unified nomenclature system established using Japanese and Chinese breeding lines, the nucleotide sequences of *SRK* and *SLG* genes isolated by different research groups were compared with each other. Two radish accessions, 'WK10039' and 'Aokubi', whose draft whole genome sequences were previously reported, were shown to harbor class II *RsS-9* and class I *RsS-19* haplotypes, respectively. Nucleotide sequences of *SLG* and *S* domains of *SRK* genes were obtained from breeding lines using four degenerate and 13 haplotype-specific primer pairs. A total of 27 out of 31 *S* haplotypes isolated in our previous study showed that *SRK* and *SLG* sequences were almost identical with those reported by other research groups. In addition, eight novel putative *SRK* or *SLG* sequences showing high homology with other *SRK* genes were identified. As a result, 27 *S* haplotypes were successfully integrated into the unified nomenclature, and the four novel *S* haplotypes were renamed. In addition, full-length and partial genomic DNA sequences of duplicated putative *SRK* genes were obtained from the two *S* haplotypes to identify genuine *SRK* genes. Duplicate *SRK* homologs showed a high degree of homology with each other, and were closely related to the other known *SRK* genes, suggesting recent duplication of these genes. The nucleotide sequences of one of the duplicate *SRK* genes in these two *S* haplotypes were almost identical to those of class II *RsS-26* and class I *RsS-48* haplotypes.

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PI-0021

Pepper MAP kinase CaDIK2 functions as positive modulator of ABA signaling and drought tolerance

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Protein phosphorylation by kinase is one of important mechanism to adapt drought stress condition. Here, we isolated and functionally characterized the *CaDIK2* (*Capsicum annuum* Drought Induced MAP Kinase 2) gene from pepper leaves induced in dehydration treatment. Subcellular localization of CaDIK2 protein was transiently expressed in cytoplasm and nucleus. *CaDIK2*-silenced pepper plants by virus-induced gene silencing, exhibited drought susceptible phenotypes characterized by increased transpiration rate, low leaf temperatures and decreased stomatal closure. *CaDIK2*-overexpressing (OX) transgenic plants exhibited ABA hypersensitivity during seed germination and seedling growth stages. Moreover, *CaDIK2*-OX plants drought tolerant phenotypes. When quantitative RT-PCR analysis was given drought condition, the transcript levels of several stress-related genes were higher in *CaDIK2*-OX than wild-type platns. Taken together, these data unveil that the novel *CaDIK2* gene is a positive modulator of ABA signaling and drought tolerance in pepper plant.

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PI-0022

Pepper MAP3 kinase CaAIMK2 interacts with CaADIP1 and positively regulates ABA-mediated drought tolerance

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Mitogen-Activated Protein Kinase (MAPK) cascades play a key role in various plant regulatory responses. Moreover, several studies have established ABA signaling in which group A PP2Cs function as core components. Although group A PP2C inhibit ABA signal through PP2C-SnRK2 type kinase complex, it remains elusive if other inhibition mechanisms by PP2C exist. Here, we identified pepper MAP3 kinase CaAIMK2 (*Capsicum annuum* ADIP1 Interacting MAP3 Kinase 2), which interacts with group A PP2C CaADIP1. *CaAIMK2* transcripts were induced by ABA, drought and high salinity treatments. Furthermore, CaAIMK2 interacts with CaADIP1 in nucleus and weakly in cytoplasm. We verified that CaADIP1 inhibits auto-phosphorylation activity of CaAIMK2 by using in gel kinase assay. We used *CaAIMK2*-silenced pepper and *CaAIMK2*-overexpressing (OX) Arabidopsis plants for genetic analysis. *CaAIMK2*-silenced pepper plants showed drought-sensitive phenotype and *CaAIMK2*-OX Arabidopsis plants showed ABA-sensitive and drought-tolerant phenotypes. Substitution of Lys32 to Asn at ATP-binding site of CaAIMK2 showed recovered phenotype to ABA and drought stress. Taken together, CaADIP1 modulates kinase activity of CaAIMK2, which is positive regulator in ABA-dependent drought stress response.

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PI-0023

Evaluation of drought-tolerant lines in an EMS-induced population and core populations

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Drought is one of the major abiotic stresses that strongly limits crop productivity and yield. Soybean (*Glycine max* (L.) Merr.) is an important leguminous plant which is popularly known as drought-sensitive crop. The purpose of the present study is to screen of drought-tolerant accessions and utilize them as genetic resources for the development of high yielding drought-tolerant varieties. In the present study, index of leaf wilting score was used to isolate tolerant accessions. A total of 769 accessions (384 accessions of *G. max* and 385 accessions of *G. soja*) of soybean core populations in Korea and 1362 lines of EMS-induced Pungsannamul population were screened for drought tolerance at vegetative stage in greenhouse condition. Out of them, 6 very tolerant and 21 tolerant accessions were identified from *G. soja* core population, whereas only a single tolerant line was isolated from the *G. max* EMS population. Further, genome-wide association study was carried out to detect genome region that controls the quantitative trait loci (QTL) for drought-tolerance by using 131,620 SNP markers in genetically diverse sets of the 377 *G.max* and 318 *G. soja* soybean germplasm accessions. Association analysis identified 8 SNPs in *G. max* and 2 SNPs in *G. soja* that are associated with canopy wilting at the significance level of -Log10 (P) > 5. One chromosomal region on chromosome 17 correspond with previously reported QTL regions that were associated with canopy wilting. The chromosomal regions defined in this study can be used for further analysis to identify the causal gene(s) as well as to identify DNA markers that can be used in selection to drought tolerance soybean. In the other hand, drought stress caused reductions in biological yield, root length, lateral root, root weight and physiological indicators such as water relative content, water use efficiency, water retention capacity. The tolerant accessions in this study can be use to identify the drought-tolerant genotypes at different growth stages (germination stage, vegetative growth phase, reproductive growth phase) as well as evaluate the effectiveness and reliability of multiple phenotypic and yield-related characteristics in soybean.

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PI-0024

Screening for flooding tolerance in two soybean populations (EMS-induced 'Pungsannamul' population and Korean *Glycine soja* core population)

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Flooding is one of the most serious abiotic stresses that reduce productivity of crops in many important agricultural regions of the world. Soybean (*Glycine max* (L.) Merr.) is the important legume crop, which is generally sensitive to flooding stress. The present study is aimed to screen and isolate the flood-tolerant soybean lines/ accessions in EMS-induced 'Pungsannamul' mutant and Korean wild core populations. In this study soybean plants at V2 stage were subjected in conditions of submergence for 5-7 days, or waterlogging for 21 days. Foliar damage after the removal of water was used to evaluate the level of flooding tolerance. Evaluation data showed that 3 EMS mutant lines and 2 wild soybean accessions were tolerant to submergence and 2 other wild soybean accessions were very tolerant. Besides, 2 accessions and 10 others in the wild core population were very tolerant and tolerant, respectively, in a waterlogged soil condition. A genome-wide association analysis (GWAS) was conducted using the phenotypic data of the wild soybean population. Eighteen and fourteen single nucleotide polymorphisms (SNPs) were identified to be associated with submergence and waterlogging tolerance, respectively, at a significance level of -Log(P) $\geq$ 5.0. Four SNPs strongly associated with foliar damage reduction were found in the regions spanning approximately 630 kb of chromosome 10 under both flooding conditions. In further studies, the tolerant lines isolated will be utilized for the breeding program to identify the genetic resources involved in the flooding tolerance.

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PI-0025

Selection of drought tolerance lines for water limited environment in maize

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The impact of climate change is affecting the magnitude of rainfall and its distribution, which in turn has adverse effects on crop production. Plants exhibiting high drought tolerance are the most suitable targets of drought-related research and are the most promising sources of drought-related gene and gene regions to be used in the improvement of modern crop varieties. Maize (Zea mays), with its high photosynthetic rates and yields, is a particularly valuable agricultural resource, serving as a food source for humans and livestock as well as a biofuel and source of fiber in some parts of the world. However, continuously diversifying demands for maize production has led to the constant need for genetic improvement of various agriculturally and economically important traits. In this challenging scenario, molecular approaches offer novel opportunities for the dissection and more targeted manipulation of the genetic and functional basis of yield under drought conditions. present study, we intend to dissect genetic factors contributing to drought tolerance in maize based on Genome-wide association studies (GWAS). Our objective is to 1) Identify maize genotype tolerant to drought stress 2) To identify genetic regions contributing drought tolerance based on 55K SNP chip. We evaluated 150 maize inbred lines. The germination, survival and recovery rate were measured and we observed a significant difference between genotypes under stress environment. We shortlisted 15 maize inbred accessions categorized based on a) drought tolerant b) moderately tolerant c) Drought susceptible. Our further step is to perform a GWAS scan on the shortlisted inbred lines

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PI-0026

Development of perennial wheat lines by wide-crossing between wheat and *Leymus mollis*

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The objective of this study is to develop perennial wheat lines by wide-crossing between wheat varieties and *Leymus mollis* as wild species. We performed to compare protein expression pattern and function of *L. mollis* by two-dimensional electrophoresis and LTQ Velos mass spectrometer. *L. mollis* showed that most protein spots were expressed between 50 and 75 kDa and with 12S seed storage globulin 1. In Keumkang, Korean wheat showed many protein spots between 37 and 100 kDa. Among protein spots of Keumkang, the function of protein spots with higher protein score was serpin 3. One protein spot in only *L. mollis* was high molecular weight glutenin subunit HMW-GS, Glu-1St1.2. Also, we conducted to investigate composition of glutenin of *L. mollis* by RP-HPLC. *L. mollis* showed three major glutenin subunits(*L.m* 1, 2, and 3). *L.m* 1 had shorter retention time than the Dy10 glutenin subunit of Keumkang. *L.m* 2 had the retention time between the Dx5 and Bx7 of Keumkang. *L.m* 3 had longer retention time than the Bx7 of Keumkang. To develop perennial wheat lines, we produced 10 seeds between Chinese Spring and *L. mollis* by wide-crossing. Of the 10 seeds, five seeds were germinated with two shoots and one thicker root than major three roots. The five F_1 hybrids showed the perennial nature, *i.e.* new shoots appear on the ground by rhizome. Another F_1 hybrids showed the same nature. The other three F_1 hybrids showed inferior phenotype as the character of the haploid. Last one F_1 hybrid was naturally withered.

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PI-0027

Identification of Candidate Genes Controlling Non-pungency in the EMS-induced Pepper Mutant (*Capsicum annuum* L.)

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The pungency of pepper fruit is caused by capsaicinoid, the unique alkaloid mixture of *Capsicum*. The capsaicinoid is synthesized through many plant organelles and sequestered in the glandular regions on the epidermal tissues of fruit placenta, named blisters. Among the structural and regulatory genes in the capsaicinoid biosynthetic pathway, functions of only a few genes including *Pun1*, *pAMT*, *Pun3*, and *CaKR1* have been studied using loss-of-function mutants. However, many genes in the capsaicinoid biosynthetic pathway are still unknown due to the lack of natural variations. In this study, an EMS-induced non-pungent mutant line '221-2-1a' derived from pungent Korean landrace 'Yuwolcho' was used to reveal the novel genetic factors controlling capsaicinoid biosynthesis in pepper. The segregation ratio of an F_2 population derived from the cross between '221-2-1a' and pungent Indian landrace 'Lam32' fit to a 13:3. The segregation ratio indicated the non-pungency of '221-2-1a' may be controlled by two genes. To identify genetic loci controlling the non-pungency, genetic mapping was performed using genome-wide genotyping and MutMap analysis, and one locus on chromosome 6 was identified and named *Pun4*. Using SNP markers, the *Pun4* region was delimited to 655.1 kb region and 12 candidate genes were predicted.

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PI-0028

Assessment of the biomass potentials of algal communities in open pond raceways through mass cultivation systems for use as a potential resource of biofuel and biofertilizer

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This study explored the possibility of using algal biomasses from open pond raceways (OPRs) for biodiesel and biofertilizer production. The phenotype-based environmental adaptation ability of soybean plants was assessed for the latter. Metagenomics analysis using MiSeq identified approximately 127 eukaryotic phylotypes following mass cultivation with (OPR #1) or without (OPR #3) a semitransparent film. Of these, approximately 80 phylotypes were found in both systems, whereas 23 and 24 phylotypes were identified only in OPR #1 and OPR #3, respectively. The phylotypes belonged to various genus. Of these, the dominant algal species was *Desmodesmus* sp. The growth rate, biomass, and lipid productivity of the algae have been examined under mass cultivation. On average, OPR #1 and #3 produced approximately 8.6 and 9.9 g m^{-2} · d^{-1} of total biomass, respectively, of which 14.0 and 13.3 wt% were lipid contents. Fatty acid profiling revealed that the total saturated fatty acids (mainly C16:0) of the biodiesels obtained from these biomasses were 34.93% and 32.85%, respectively, whereas the total monounsaturated fatty acids (C16:1 and C18:1) were 32.40% and 31.64%, and the polyunsaturated fatty acids (including C18:3) were 32.68% and 35.50%, respectively. The fuel properties were determined by empirical equations and found to be within the limits of biodiesel standards ASTM D6751 (American) and EN 14214 (European). Additionally, culture solutions with or without the biomasses also enhanced the environmental adaptation ability of soybean plants, increasing their seed production. Hence, algal biomass produced through mass cultivation is an excellent feedstock for the production of high-quality biodiesel and biofertilizer.

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PI-0030

Development of optimized MALDI-TOF-MS method for High-throughput identification of HMW-GS with standard wheat varieties

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High-molecular-weight glutenin subunits (HMW-GS) are important determinants of wheat end-use quality as they confer visco-elastic properties to the dough. In order to cultivate the superior quality wheat, there is a great need for high-throughput identification of HMW-GS in many wheat genetic resources or in many breeding lines. For this purpose, we adopted matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF-MS) which can analyze all HMW-GS of one wheat variety in about 1 minute and optimized the machine to get the best resolution by adjusting alkylating reagent in protein extraction, solvent components, dissolving volume and matrix II components. 18 out of 22 subunits were successfully identified by clear difference of molecular weight or inferring tightly lined subunits using the optimized methods and standard wheat cultivars for HMW-GS analysis. 1Ax2* & 1Bx6 and 1By8 & 1By8*, which are difficult to distinguish due to very similar molecular weights, were easily identified using RP-HPLC. Among them, 1Bx7 and $1Bx7^{OE}$ were divided into two groups with molecular weight about 82,400 and 83,000 Da with about 600 Da difference and they were classified into 1Bx7 group 1, 1Bx7 group 2 and $1Bx7^{OE}$ using well-known DNA markers. To validate this method, HMW-GSs from 38 Korean wheat varieties were tested and successfully identified with reference to the molecular weight of each subunit of the standard wheat varieties above. The optimized MALDI-TOF-MS method used in this study will be useful as the best high-throughput tool for selecting desirable HMW-GS among genetic resources or wheat breeding lines.

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PI-0031

High-throughput analysis of high-molecular weight glutenin subunits in 665 wheat genotypes using an optimized MALDI-TOF-MS method

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Gluten protein composition determines the rheological characteristics of wheat dough and is influenced by variable alleles with distinct effects on processing properties. Using matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF-MS), we determined the high-molecular weight glutenin subunit (HMW-GS) composition of 665 wheat genotypes employed in breeding programs in South Korea. We identified twenty-two HMW-GS alleles, including three corresponding to the *Glu-A1* locus, fourteen to *Glu-B1*, and five to *Glu-D1*. The Glu-1 quality score, which is an important criterion for high quality wheat development, was found to be 10 for 105/665 (15.79%) of the studied genotypes, and included the following combinations of HMW-GS: 2*, 7+8, 5+10; 2*, 17+18, 5+10; 1, 7+8, 5+10; and 1, 17+18, 5+10. To select wheat lines with the 1Bx7 overexpression ($1Bx7^{OE}$) subunit, which is known to have a positive effect on wheat quality, we used a combination of MALDI-TOF-MS and published genotyping markers and identified 6 lines carrying $1Bx7^{OE}$ out of the 217 showing a molecular weight of 83,400 Da, consistent with $1Bx7_{G2}$ and $1Bx7^{OE}$. This study demonstrates that the MALDI-TOF-MS method is fast, accurate, reliable, and effective in analyzing large numbers of wheat germplasms or breeding lines in a high-throughput manner.

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PI-0032

Symptom severity of broad bean wilt virus 2 is associated with jasmonic acid/ethylene-mediated defense response in pepper

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Broad bean wilt virus 2 (BBWV2) is an emerging virus in various economically important crops, especially pepper (Capsicum annuum L.) in Asia. Recently, the emergence of various BBWV2 strains that induce severe symptoms has increased damages in pepper. While the symptomatic variations among virus strains should be associated with the differences in transcriptomic reprogramming of host plants upon infection, underlying molecular mechanisms and associated genes are largely unknown. In the present study, we employed transcriptome analysis to identify responsible host factors for symptom enhancement in the BBWV2-pepper pathosystem using two distinct BBWV2 strains, PAP1 (a severe strain) and RP1 (a mild strain). Comparative analysis of the differentially expressed genes revealed that various genes involved in defense responses were significantly up-regulated upon infection with the severe strain PAP1, but not with the mild strain RP1. Endogenous hormone analysis revealed that the levels of jasmonic acid (JA) and ethylene (ET) were significantly increased by infection with PAP1, while no difference was observed in the levels of salicylic acid induced by infection with either PAP1 or RP1. These observations implied that the activation of JA/ET-mediated defense response seems reinforce symptom formation during BBWV2 infection in a virus strain-specific manner. Our findings extend our understanding of the roles of plant hormones in symptom development during viral infection.

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PI-0033

Plant virus and disease control through RNAi mechanism induced from application of exogenous dsRNA

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RNA interference (RNAi) is a regulatory mechanism of gene expression mediated by various small RNAs. Small RNAs loaded to Argonaute protein form RNA-induced silencing complex (RISC), a key player in RNAi. RISC cuts target mRNA in a sequence specific manner, finally suppresses expression level of a target gene. On the one hand, application of exogenous double-stranded RNA (dsRNA) designed complementary to target mRNA sequence generates many kinds of small interfering RNAs (siRNAs), which can also induce RNAi. Therefore, RNAi technique applying dsRNA would be an effective method for plant virus and disease control. In this study, we select two genes of pepper mottle virus (PepMoV) and synthesize several dsRNAs based on the target gene sequences. By application of these dsRNAs to *Nicotiana Benthamiana* plants, we expect plant protection ability against the virus infection. Through adjustment of dsRNAs and virus treatment time, injecting dsRNA to a plant before virus infection was shown to be more effective. Furthermore, each dsRNA designed to target different regions within a transcript had different level of effects on suppression of virus replication. The underlying mechanism of dsRNA effect on virus is currently investigated. On the other hand, we design various dsRNAs targeting genes of *phytophthora infestans*, which causes serious problems in Solanaceae plants including pepper, tomato and potato. Research on these dsRNAs would contribute to plant disease control and RNAi would be an efficient tool for crop production improvement.

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PI-0034

Chrysanthemum Dihydroflavonol 4-reductases Function in Flavonoid Biosynthesis

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Dihydroflavonol-4-reductase (*DFR*) catalyzes a committed step in anthocyanin and proanthocyanidin biosynthesis by reducing dihydroflavonols to leucoanthocyanidins. However, the role of this enzyme in determining flower color in the economically important crop chrysanthemum (*Chrysanthemum morifolium* Ramat.) is unknown. Here, we isolated cDNAs encoding DFR from two chrysanthemum cultivars, the white-flowered chrysanthemum 'OhBlang' (CmDFR-OB) and the red-flowered chrysanthemum 'RedMarble' (CmDFR-RM), and identified variations in the C-termini between the two sequences. *CmDFR* transcript levels were consistent with the anthocyanin contents in different tissues of both cultivars. We also detected different levels of protein solubility between CmDFR-OB and CmDFR-RM. An enzyme assay using recombinant proteins revealed that CmDFR-RM catalyzes the reduction of dihydrokaempferol (DHK), dihydroquercetin (DHQ), and dihydromyricetin (DHM), whereas CmDFR-OB reduces DHK and DHQ but not DHM. An *in planta* assay using the *Arabidopsis thaliana tt3-1* mutant revealed complementation of the defective anthocyanin biosynthesis of this mutant at the seedling stage and proanthocyanidin biosynthesis in the seeds of transgenic plants harboring *CmDFR-RM* but not *CmDFR-OB*. An insertion/deletion (Indel) marker based on the sequence variation between *CmDFR-OB* and *CmDFR-RM* discriminated between ray florets of different colors, implying that allelic variation of *CmDFR* results in different levels of anthocyanin accumulation in chrysanthemum flowers. These observations indicate that CmDFR plays a crucial role in anthocyanin and proanthocyanidin biosynthesis in chrysanthemum.

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PI-0035

Targeted Genome Editing of the *eIF4E1* Gene in Tomato Confers Resistance to Pepper Mottle Virus

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Number of plant genes involved in the plant viral resistance confer recessive resistance. The eukaryotic translation initiation factors (eIFs), including eIF4E, eIF4G and their homologs are involved in potyvirus resistance. Plant pathogenic viruses are constantly emerging and pose sever threat to crop plants as plant resistance offered by the known resistance sources is often overcome by the emerging pathogens. Genome editing approaches facilitates the creation of novel genetic alleles in plants. In this study, we used CRISPR/Cas9 (Clustered Regularly Interspaced Palindromic Repeats/CRISPR-associated protein9) mediated targeted genome editing to create novel site-specific mutations in the *eIF4E1* gene from *Solanum lycopersicum* cv. Micro-Tom. Sequence analysis of the *eIF4E* gene from E_0 transgenic Micro-Tom plants uncovered sequence deletions of various sizes ranging from 11 to 43 bp in *eIF4E1*. Furthermore, transgene-free heritable, homozygous mutants were recovered in the E_1 generation. Genotyping of edited *eiF4E1* plants from E_0, E_1, and E_2 lines showed that the mutations were stably inherited to subsequent generations. Homozygous mono- or bi-allelic E_1 plants were screened for potyvirus resistance. *eIF4E1* edited mutant lines showed significantly enhanced resistance to Pepper mottle virus (PepMoV) with no accumulation of viral particles. However, *eIF4E1* edited plants were not resistant *Tobacco etch virus* (TEV), because TEV can use other homologs of *eIF4E1* for their replication and infectivity.

Keywords: CRISPR/Cas9, Eukaryotic translation initiation factor 4E (*eIF4E*), Genome editing, Potyvirus, *Solanum lycopersicum* cv. Micro-Tom, Transgenics

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PI-0036

Development of KASP markers for high-throughput genotyping with Korean *japonica* rice varieties

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Single nucleotide polymorphism (SNP)-based kompetitive allele-specific PCR (KASP) marker that have major advantage of improved time- and cost-effectiveness enable high-throughput genotyping for quantitative trait loci (QTL) mapping and gene identification. In previous studies, 740,566 SNPs were discovered by genome re-sequencing with 13 Korean *japonica* rice varieties, and 1,014 SNPs with polymorphism information content (PIC) > 0.4 per 200 kb were converted to 771 KASP markers. Additionally, in order to develop sufficient and stable KASP markers for genetic map construction with Korean *japonica* rice varieties, 740,566 SNPs were annotated by SnpEff program that can predict effects of variants on protein function, and selected SNPs validated by KASP assay system with 15 Korean *japonica* rice varieties. Of 740,566 SNPs, 703 (0.1%) and 739,863 (99.9%) SNPs were annotated as high and other impact effects, respectively. 357 SNPs were selected from 703 SNPs having high impact effects and converted to polymorphic 283 KASP markers (79.3%) resulting in development of polymorphic 1,054 KASP markers. Subsequently, in order to fill gaps on all chromosomes, 284 SNPs were selected from large gap regions and converted to polymorphic 171 KASP markers (60.2%). Totally, we developed successfully 1,225 KASP markers including previous 771 and present 454 KASP markers. The developed 1,225 KASP markers will be helpful for QTL/gene analysis as well as marker-assisted selection (MAS) in Korean *japonica* rice breeding.

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PI-0037

Molecular approach to develop crops with increased productivity by down-regulating the expression of the key regulators of the shade avoidance syndrome (SAS)

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Plants make use of the photosynthetically active radiation for the energy source. Plants under the shade condition display the hyponastic growth, hypocotyl elongation and petiole elongation, known as the shade avoidance syndrome (SAS). As plants respond to the shade by elongating hypocotyl and petioles through auxin production and transport, plants become tall and premature flowering, resulting in poor yields. In order to suppress the shade-avoiding phenotypes, the important regulators of the SAS such as the downstream genes of PIFs need to be modulated. It was found that, the overexpression of *TCP13*, one of TCP transcription factor family, displayed shade avoidance response even under normal condition. Shade-avoiding phenotypes were suppressed in transgenic *Arabidopsis* expressing an artificial microRNA against *TCP13,* and its homologs-TCP5 and TCP17 (amiR-*3TCP*), as well as in the triple mutant *tcp5tcp13tcp17*. Down-regulation of ATHB2 and its homologs, class II HD-Zip family members, by amiR-*3ATHB* also showed reduced SAS. In addition, artificial microRNA against 3 YUCCAs, genes for auxin-synthesizing enzyme, also showed diminished SAS. Transgenic tomato suppressing tomato orthologs of *ATHB2* and *TCP13* (amiR-*SlHB* and amiR-*SlTCP,* respectively) have been generated to test for minimizing shade avoiding phenotypes. We also investigate functions of ATHB2 downstream genes controlling shade avoidance. Altogether, these efforts should produce crop plants with reduced yield loss due to SAS.

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PI-0038

Changes in sugar availability and cellular energy status extensively cross-talk in transcriptomic adjustment in aerobically and anaerobically germinating rice embryos

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The global RNA profile of rice genes can be affected by the availabilities of sugars, oxygen, or the cellular energy in germinating seeds, all of which can fluctuate significantly under dynamic environmental conditions. In aerobically germinating rice embryo, the amount of upregulated genes is larger than that of downregulated genes in sugar deficient conditions, while it is reverse during anaerobic germination. Most of sugar-regulated genes also show the responsiveness to low energy and anaerobic conditions in both aerobically and anaerobically germinating rice embryos. Expression of those genes with aerobic sugar regulation is interfered similarly by anaerobic conditions and low energy conditions, suggesting that anaerobic response may result largely from the low energy conditions which it induces. However, the differential pattern of responses observed in anaerobically sugar down-regulated genes between two conditions also suggests the presence of distinctive anaerobic pathway to interfere with sugar regulation. Anaerobically downregulated genes are especially highly overlapped with those genes whose expression is repressed by low energy conditions. The very similar responsiveness between two conditions suggests that anaerobic down regulation is probably due to prevention of aerobic respiration due to the absence of the final electron acceptor, molecular oxygen. Among three conditions to be examined, low energy conditions perturb the expression of the highest number of genes, followed by anaerobic conditions and sugar status. Interference of regulation and co-responsiveness observed in the expression of numerous genes indicate that the signaling pathways activated by these conditions are closely interconnected with each other.

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PI-0039

Genetic diversity of tocols, squalene, and phytosterol contents in brown rice of 296 accessions of Korean rice core set (KRICE_CORE)

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To understand genetic diversity in lipophilic phytonutrients, 296 accessions of Korean Rice Core Set selected from 25,604 world-wide collections were cultivated in 3 separate fields in Korea, and harvested brown rice were used for determination of tocopherols (TP), tocotrienols (TT), squalene (SQ), campesterol (CA), sitosterol (SI), and stigmasterol (ST) contents by using a gas chromatography. The average contents (μg/g) of α-TP, γ-TP, α-TT, γ-TT, SQ, CA, SI, and ST were 11.31, 2.27, 8.74, 15.35, 31.44, 48.11, 171.68, and 21.13, respectively. Total vitamin E, squalene, and total phytosterol contents (μg/g) ranged 24.62 to 54.87, 7.87 to 78.37, and 162.93 to 392.77, respectively. Significant ecotype-dependent variations in phytonutrient contents were observed in that japonica-type rice showed significantly higher α-TP, α-TT, and subsequent ratios of α-TP/γ-TP and α-TT/γ-TT compared to indica-type rice. Total TP and TT contents, however, were not significantly affected by ecotypes. Similarly, higher SQ contents were observed in japonica-type rice, while no clear ecotype-dependent differences could be observed in CA, SI, and ST contents. Among phytonutrients tested, α-TT showed positive correlation with α-TP (r=0.845**) and SQ (r=0.606**), but negative with γ-TP (-0.801**) and γ-TT (r=-0.587**). All phytosterols exhibited positive correlation to each other in both japonica- and indica-type rice accessions. All these results showed diverse variations in phytonutrient property among 296 KRICE-CORE collection, which can be further used for development of a superior rice variety with high nutritional value.

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PI-0040

Hypolipidemic and Antidiabetic Effects of Keunnunjami embryo in C57BL/KsJ-db/db mice

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This study investigated whether Keunnunjami embryo improved plasma lipid profiles and suppressed hepatic glucose production in an animal model of type 2 diabetes. C57BL/KsJ-db/db mice were divided into three dietary groups: diabetic control (db/db-C), brown rice embryo (db/db-B) and Keunnunjami embryo (db/db-K). After 8 weeks of feeding, the diabetic control group exhibited substantially higher blood glucose, plasma insulin, total cholesterol, and triglyceride levels than the embryo groups, whereas plasma HDL-cholesterol and adiponectin levels were significantly increased in the db/db-K group. Furthermore, significantly higher glucokinase (GK) activity and lower phosphoenolpyruvate carboxykinase (PEPCK) activity were observed in db/db-K mice compared with that of the diabetic control group. It was also found that the glucose-6-phosphatase (G6pase) activity and hepatic glycogen concentration were considerably higher in db/db-K group, respectively, than that of the db/db-C group. These findings demonstrate that Keunnunjami embryo reduce the risk of hyperglycemia via regulation of hepatic glucose-regulating enzyme activities.

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PI-0041

약배양을 이용한 고추 재분화 연구

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반수체 식물은 단기간에 동형 접합체를 생산하기에 용이하므로, 식물 육종 프로그램에서 매우 중요하다. 현재 고추(*Capsicum annuum* L.) 조직을 이용한 재분화 유도는 매우 제한적인 용도로 사용되는 상황이다. 본 연구는 고추 약배양을 통해서 재분화 개체를 효율적으로 생산하는 방법을 제시하고자 한다. 본 실험에서는 식물 호르몬 (NAA, kinetin)과 열처리 (31°C, 33°C, 35°C)가 약배양을 통한 재분화에 어떤 영향을 미치는가를 조사하였다. 본 연구에서는 31°C 열처리 조건이 배 발생에 효과적이라는 결과를 얻었다. NAA (0.2mg/l) 와 Zeatin (0.2mg/l)을 혼용한 배지조건이 배 발생에 효과적이라는 결과를 얻었다. 전반적으로 호르몬 조성이 열처리 조건보다 배 발생에 큰 영향을 미치는 것으로 밝혀졌다.

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PI-0042

Genome editing-based breeding of pepper inbred lines

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Consumers and growers of peppers (*C. annuum*) are demanding a low pungent green pepper varieties that are stable to environmental stress. However, the pungent taste of green pepper sold inside Korea is highly dependent on environmental stress (temperature, moisture, nutrients, etc.). However, there is a considerable difficulty in breeding low-pungent cultivars by applying existing traditional breeding techniques, as well as time and economic aspects. Therefore, in this project, we select the genes involved in the capsaicin biosynthetic pathway by environmental stress. We aim to cultivate a low-pungent green pepper inbreeding line that is stable in environmental stress by inhibiting the expression of these genes by applying gene-editing techniques (CRISPR / Cas9).

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PI-0043

The drooping leaf (dr) gene encoding GDSL esterase controls leaf morphology in rice (Oryza sativa L.)

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Leaf morphology is one of the most important agronomic traits in rice breeding because of its contribution to crop yield. The drooping leaf (dr) mutant was developed from the Ilpum rice cultivar by ethyl methanesulfonate (EMS) mutagenesis. Compared with the wild type, dr plants exhibited drooping leaves accompanied by a small midrib, short panicle, and reduced plant height. The phenotype of the dr plant was caused by a mutation within a single recessive gene on chromosome 2, dr (LOC_Os02g15230), which encodes a GDSL esterase. Analysis of wild-type and dr sequences revealed that the dr allele carried a single nucleotide substitution, glycine to aspartic acid. RNAi targeted to LOC_Os02g15230 produced similar phenotypes to the dr mutation, confirming LOC_Os02g15230 as the dr gene. Microscopic observations and plant nutrient analysis of SiO2 revealed that silica was less abundant in dr leaves than in wild-type leaves. This study suggests that the dr gene is involved in the regulation of silica deposition and that disruption of silica processes lead to all drooping leaf phenotypes.

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PI-0044

HOS1 activates DNA repair systems to enhance plant thermotolerance

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Plants possess an astonishing capability of effectively adapting to a wide range of temperatures, ranging from freezing to near-boiling temperatures. Yet, heat is a critical obstacle to plant survival. The deleterious effects of heat shock on cell function include misfolding of cellular proteins, disruption of cytoskeletons and membranes, and disordering of RNA metabolism and genome integrity. Plants stimulate diverse heat shock response pathways in response to abrupt temperature increases. While it is known that stressful high temperatures disturb genome integrity by causing nucleotide modifications and strand breakages or impeding DNA repair, it is largely unexplored how plants cope with heat-induced DNA damages. Here, we demonstrated that HIGH EXPRESSION OF OSMOTICALLY REPONSIVE GENES 1 (HOS1) induces thermotolerance by activating DNA repair components. Thermotolerance and DNA repair capacity were significantly reduced in HOS1-deficient mutants, in which thermal induction of genes encoding DNA repair systems, such as the DNA helicase RECQ2, was markedly decreased. Notably, HOS1 proteins were thermostabilized in a heat shock factor A1/heat shock protein 90 (HSP90)-dependent manner. Our data indicate that the thermo-responsive HSP90-HOS1-RECQ2 module contributes to sustaining genome integrity during the acquisition of thermotolerance, providing a distinct molecular link between DNA repair and thermotolerance.

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PI-0045

Identification of Citrus Varieties Bred in Korea Using Microsatellite Markers

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More than 30 citrus varieties have been developed in Korea over almost four decades. Despite the economic importance of citrus fruit production, reliable technologies for the identification of citrus varieties bred in Korea have not been established. In this report, we developed 53 polymorphic nuclear microsatellite markers fully covering the nine pseudo-chromosomes of citrus and applied them to the discrimination of the 32 available citrus varieties bred in Korea. Most of Korean citrus varieties were clearly discriminated by a total of 245 alleles derived from the polymorphic microsatellite loci. However, nucellar or bud sport mutant varieties originated from Citrus hybrid 'Shiranuhi' were not able to be discriminated from each other by sharing identical genotypes on all of the microsatellite loci investigated. The microsatellite markers developed in this study will be an efficient molecular genetic tool to protect breeders' rights and guarantee the quality of nursery plants in the citrus industry.

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PI-0046

Virus infectivity related gene expression analysis of pepper by multiple plant virus infections

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Pepper is one of the major vegetables over the world. It is easy to be infected by multiple plant viruses during growing in greenhouse and nature. During virus infection, interaction response between pepper and viruses is sophisticated and results in compatible response or incompatible response. To characterize a gene expression which are involved in compatible and incompatible response against virus infection, we utilized SRA database of CM334 cultivar showing two distinct symptoms against tobacco mosaic virus (TMV) and pepper mottle virus (PepMoV) infection. Furthermore, we prepared the RNA-seq library constructs using chili veinal mottle virus (ChiVMV) infected tissue on same cultivar, CM334. We analyzed the transcriptome files using DEBrowser software. TMV infection, compatible interaction showed over 600 genes up- or down-regulation at two days after virus inoculation. On PepMov-infected pepper, however, less than 40 genes were reacted by PepMoV infection. For the ChiVMV infection on CM334, about 150 genes expression were changed against virus multiplication on local leaves. Based on RNA seq analysis, we amplified several genes which were related to virus infection. One of them, carboxylesterase 120 (NbGID) gene was cloned from N. benthamiana. Silencing of NbGID on N. benthamiana inhibited cell death induced by Pvr4 and PepMoV-NIb interaction. We will further investigate the function of NbGID gene related to plant resistance response against virus infection.

Key words: Plant virus, Pepper, Transcriptome

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PI-0047

Homeobox transcription factor OsZHD2 promotes root meristem activity in rice by inducing ethylene biosynthesis

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Root meristem activity is the most critical process influencing root development. Although several regulatory factors that regulate meristem activity have been identified in rice, studies on the enhancement of meristem activity in roots are limited. We identified a T-DNA activation tagging line of a zinc-finger homeobox gene, *OsZHD2*, which has longer seminal and lateral roots due to increased meristem activity. The phenotypes were confirmed in the transgenic plants overexpressing *OsZHD2*. In addition, the overexpressing plants enhanced grain yield under low nutrient and paddy field conditions. *OsZHD2* was preferentially expressed in shoot apical meristem and root tips. Transcriptome analyses and qRT-PCR experiments on roots from the activation tagging line and wild type (WT) showed that genes for ethylene biosynthesis were up-regulated in the activation line. Ethylene levels were higher in the activation lines compared to the WT. ChIP assay results suggested that OsZHD2 induces ethylene biosynthesis by controlling *ACS5* directly. Treatment with ACC, an ethylene precursor, induced the expression of *DR5* reporter at the root tip and stele. Whereas an ethylene biosynthesis inhibitor treatment, AVG, decreased that expression in both WT and *OsZHD2-D*. These observations suggest that OsZHD2 enhances root meristem activity by influencing ethylene biosynthesis and, in turn, auxin.

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PI-0048

The *in vivo* functions of ARPF2 and ARRS1 in ribosomal RNA processing and ribosome biogenesis in Arabidopsis

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Yeast Rpf2 plays a critical role in the incorporation of 5S rRNA into pre-ribosomes by forming a binary complex with Rrs1. The protein characteristics and overexpression phenotypes of Arabidopsis Ribosome Production Factor 2 (ARPF2) and Arabidopsis Regulator of Ribosome Synthesis 1 (ARRS1) have been previously studied. Here, we analyze loss-of-function phenotypes of ARPF2 and ARRS1 using virus-induced gene silencing to determine their functions in pre-rRNA processing and ribosome biogenesis. ARPF2 silencing in Arabidopsis led to pleiotropic developmental defects. RNA gel blot analysis and circular reverse transcription-PCR revealed that ARPF2 depletion delayed pre-rRNA processing, resulting in the accumulation of multiple processing intermediates. ARPF2 fractionated primarily with the 60S ribosomal subunit. Metabolic rRNA labeling and ribosome profiling suggested that ARPF2 deficiency mainly affected 25S rRNA synthesis and 60S ribosome biogenesis. ARPF2 and ARRS1 formed the complex that interacted with the 60S ribosomal proteins RPL5 and RPL11. ARRS1 silencing resulted in growth defects, accumulation of processing intermediates, and ribosome profiling similar to those of ARPF2-silenced plants. Moreover, depletion of ARPF2 and ARRS1 caused nucleolar stress. ARPF2-deficient plants excessively accumulated anthocyanin and reactive oxygen species. Collectively, these results suggest that the ARPF2-ARRS1 complex plays a crucial role in plant growth and development by modulating ribosome biogenesis.

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PI-0049

Molecular characterization of Oryza sativa Arsenic-Induced RING Finger E3 ligase 3 (OsAIR3)

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In plants, high concentrations in arsenic (As) contaminated environments are a serious threat to plants, human health, and animal. In this study, we characterized one As-responsive Really Interesting New Gene (RING) E3 ubiquitin ligase gene under As(V) stress condition. We named it *Oryza sativa* As-Induced RING E3 ligase 3 (OsAIR3). Under As(V) condition, the expression pattern of the *OsAIR3* gene was highly induced. The OsAIR3 was localized to the nucleus in rice protoplasts and possesses an E3 ligase activity. A yeast hybrid screen, bimolecular fluorescence complementation, and pull-down assay showed that OsAIR3 clearly interact with *Oryza sativa* sulfate transporter in the cytoplasm. In addition, using an *in vitro* cell-free degradation assay, we identified that OsAIR3 degraded the protein level of OsSulfate via the 26S proteasome system. Heterogeneous overexpression of OsAIR3 in *Arabidopsis* exhibited As(V) insensitive phenotypes in the cotyledon, root elongation, and fresh weight compared with control plants. Collectively, these findings suggest that OsAIR3 plays a positive role regulator of As(V) stress tolerance.

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PI-0050

Ralstonia solanacearum avirulence gene confers resistance against bacterial wilt disease in solanaceous plant

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Ralstonia solanacearum (*Rso*) is one of the major phytopathogens for solanaceous plants such as tomato, pepper and potatoes. The bacterium enters the plant through roots, wounds and natural openings and, devastates the whole plant irreversibly. *Rso* translocates type III effectors into host plant cells to dampen the host immune system. Plants carry disease resistance proteins that recognize corresponding effector proteins. These effectors triggering host immune responses are termed avirulence proteins. We aim to discover a *Rso* avirulence protein that triggers defense responses in a wild *Solanum* species, *S. americanum*. We used 30 isolates of *Rso,* acquired from different geographic regions of Republic of Korea. We identified resistant strain that carries avirulence determinant in the wild *S. americanum*. Based on the *S. americanum* SP2273-specific avirulence phenotype of *R. solanacearum* strain Pe_1, Pe_26, Pe_51, To_7, 15candidate avirulence T3Es were selected for further analysis. *Agrobacterium*-mediated transient expression of the candidate Rso effectors is planned to be carried out in a resistant accession SP2273. Through this screening, we aim to identify an avirulence determinant that confers bacterial wilt resistance in SP2273. We hope that this discovery would accelerate the development of BW resistant crops.

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PI-0051

배가 반수체 옥수수 육종효율 향상을 위한 염백체 배가방법 비교

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강원도 홍천군 두촌면 장남길 26, 강원도농업기술원 옥수수연구소

옥수수 계통육종은 우량 교잡종을 육성하기 위한 필수단계로서, 99% 이상의 순도를 가진 계통을 육종하기 위해서는 전통적인 방법에 의해 7회 이상의 인공교배(selfing)를 실시하여야 한다. 많은 노동력과 시간이 소요되는 전통육종의 이러한 단점을 보완하고자 선진국을 중심으로 배가반수체(Doubled Haploid) 방법에 의한 계통육종 방법이 실용화되고 있다. 배가반수체 방법에 의하면 2~3작기에 순도 100%의 계통을 육성할 수 있다. 선진기술인 배가반수체 기술을 도입하여 국내 옥수수 계통육종의 효율성을 향상시키고자 강원도농업기술원 옥수수연구소에서는 국제옥수수・밀연구소(CIMMYT)와 협력하여 배가반수체 기술 이용에 필수적인 반수체 유기체(Inducer)의 사용 권리를 확보하였고, 2014년부터 이 기술을 국내 환경에 맞게 정착시켜오고 있다. 국내에 적합한 배가반수체 기술은 유기체와의 교배를 통한 반수체 유기 및 종자선별, 염색체 배가 및 인공교배를 통한 계통 육성, 그리고 육성 계통의 특성평가 및 종자증식 등 3단계로 이루어진다. 이 중에서 2단계인 염색체 배가는 가장 중요시되며, 배가 반수체 육종기술을 활용한 옥수수 계통육성의 효율성 향상과 밀접한 관련이 있는 단계이다. 염색체 배가는 발아 종자 침지, 유묘 침지 및 유묘 주사 등 3가지 방법이 주로 이용되고 있다. 옥수수연구소 자체 시험 결과 발아종자 침지보다는 유묘침지의 효율성이 높은 것으로 확인하였다. 본 연구는 유묘침지와 유묘주사 방법을 비교하여 최적의 반수체 배가방법을 찾고자 수행하였다. 찰옥수수 및 종실용 2집단(17모A/P7709, 17자원/HW3)의 염색체 배가처리 방법에 따른 계통육성 비율은 유묘침지 13.4%, 유묘주사 9.5%로 유묘침지 방법의 효율성이 높게 나타났다. 그러나 배가처리 과정은 유묘침지 6단계, 유묘주사 4단계로 유묘침지 처리과정이 더 복잡하고 소요시간도 길다. 작업의 효율성을 고려할 때 비교 집단수를 확대하여 추가적인 검토가 필요할 것으로 생각된다.

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PI-0052

Transcriptomic profiling in leaf tissues of two soybean cultivars showing contrasting responses to drought stress at early development stage

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The growth, development, and thus yield of soybean, are severely affected by various environmental stresses, especially drought. In our study, eleven soybean cultivars were screened for their response to the drought stress by measuring the relative water content of leaves under drought stress. Among them two cultivars showed tremendous water loss differences under drought treatment: SS2-2 and Taekwang, which was drought resistant and sensitive, respectively. To reveal the genes responsible for drought resistance, transcriptomic profiling of these two cultivars in leaf tissues at early development stage was surveyed under both normal and drought stress by RNA-seq. The GoMapman protein function analysis, gene ontology enrichment and KEGG pathway results revealed that differentially expressed genes were enriched in signaling, lipid metabolism, phosphorylation and gene regulation. Among these pathways, lipid signaling pathway genes including non-specific phospholipase (NPC), phospholipase D (PLD) and phosphatidyl inositol monophosphate 5 kinase (PIP5K) were highly induced in SS2-2 aiding its response to drought stress by generating secondary messengers from the substrate of membrane lipids to transfer drought signal. The function of PIP5K in drought stress tolerance were confirmed in its homolog Arabidopsis thaliana mutant which showed lower survival rate and germination under drought stress compare to wild type. Our study supplements the mechanism in plants response to drought stress and provides valuable information for developing soybean drought tolerant cultivars.

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PI-0053

식물분자육종사업단 연구 개발 성과물의 기술이전 및 실용화 추진 체계 구축

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차세대바이오그린21사업 식물분자육종사업단 (2011~2020) 과제수행으로 창출되어 누적된 대량 연구성과물(논문, 특허, 신품종, 생명정보 등)의 국내 농생명바이오산업 분야로의 성과 확산 및 실용화 추진 체계 구축을 위해, 식물분자육종사업단 TLO(Technology Licensing Office, 그린국제특허법률사무소)는 과제책임자별 보유기술 분석, 연구성과의 권리 확보를 위한 신규 특허 출원 및 IP R&D 기술상담 지원, 식물분자육종 분야 글로벌 특허동향조사 보고서 발간, 산학연 네트워크 연계 지원, 수요기업 대상 온-오프라인 기술마케팅 및 기술이전 중개 등을 지원하고 있음.

식물분자육종사업단 TLO는 산업적으로 실용화 유망한 신품종, 특허 및 노하우 기술들을 선별, 응용 분야별로 기술패키징하고 IP 포트폴리오가 강화된 총 22건의 기술마케팅용 SMK(Sales Material Kits)를 제작하였음. SMK 기반 기술마케팅 및 성과확산 노력은 연중 수시로 수요기업/기관을 대상으로 온-오프라인에서 동시 진행되고 있으며, 연 1회 오프라인으로 개최되는 식물분자육종사업단 우수기술설명회에서는 기술개발 연구자들이 다수의 기업/기관/개인육종가들을 대상으로 직접 보유기술을 설명하고 R&D 네트워크 연계를 진행할 수 있는 기회를 제공하고 있음. 한편, 변리사, 회계사 등 전문가그룹으로부터 객관적 시장가치 및 실용화 가능성을 평가 받는 기술가치평가 서비스를 연 1회 사업단 중점 실용화 추진 우수성과에 대해 추가 지원하여, 기술마케팅 및 기술이전 조건 협상 과정에서 기술의 가치를 객관적으로 평가한 기술거래용 자료로 기술가치평가 보고서를 활용할 수 있도록 지원하고 있음.

최근, COVID19 확산으로 인해 수요기업과 1:1 대면 기술마케팅이 제한됨에 따라, 효율적인 온라인 비대면 기술마케팅 시스템을 확립하고 활용할 필요성이 대두되었음. 이에, 식물분자육종사업단 TLO는 2020년 5월 기준, 권리가 확보되어 기술이전이 용이한 국내외 특허 329건와 신품종 96건의 상세 정보를 키워드 검색이 용이한 데이터베이스(DB)로 신규 구축하고 TLO 홈페이지(http://pmbc-tlo.or.kr)를 통해 공개하였음. 대량 연구성과 정보 검색을 용이하게 하고, IP R&D 온라인 기술상담 및 비대면 기술마케팅 시스템으로 활용하는 식물분자육종사업단 TLO 홈페이지(http://pmbc-tlo.or.kr)는 사업단 연구성과물의 기술이전 및 실용화를 촉진하고 산학연간 협력연구 네트워크 연계의 장으로도 활용될 수 있을 것으로 기대함.

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PI-0054

Evaluation of Control Effect of Bacterial Stalk Rot in Maize using Chemical or Microbial bactericides

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Edible corn, such as waxy corn or super sweet corn, is one of the very important crops in Korea. Recently, the damage of bacterial stalk rot caused by *Dickeya zeae* has increased due to climate change. However, there are no solution to control against this pathogen. In this study, six antibacterial chemicals(validamycin, oxytetracycline, streptomycin, copper sulfate, kasugamycin, oxolinic acid) and one microbial(*Bacillus subtilis*) bactericides were evaluated against *D. zeae* under *in vitro* condition. To confirm the effect of bactericides on *D. zeae*, two experiments were conducted in a Luria-bertani solid medium and a liquid medium. When inoculated with standard amount and double amount in LB agar, oxytetracycline and oxolinic acid were formed clear zone in both treatments, and streptomycin was formed disinfected area in double amount. Amongst chemicals, oxolinic acid showed most effective antibacterial activity in solid medium. After confirming the control effect in agar plates, we tested the pathogens with antibiotics in the liquid medium. Four bactericides with standard concentration showed effective antibacterial activity which disinfected the population of *D. zeae*. Although there are no results *in vivo* condition because experiments are currently underway, our results may provide information on the selection of bactericides for the control of bacterial stalk rot caused by *D. zeae*.

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PI-0055

FSD3S negatively regulates chloroplast development

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Chloroplast development largely depends on the activity of plastid-encoded RNA polymerase (PEP), which is responsible for transcription of chloroplast genes. The activity of PEP is tightly regulated by PEP-associated proteins (PAPs), and approximately 12 PAPs including FSD3/PAP4 have been identified. Here, we identified *FSD3S*, a splicing variant of *FSD3*. The *FSD3* and *FSD3S* transcripts encode proteins with identical N-termini, but different C-termini. Transcript level of *FSD3* was higher than that of *FSD3S* in young leaves carrying well-developed chloroplasts, but lower in old leaves carrying senescent chloroplasts. Characterization of FSD3 and FSD3S proteins revealed that the C-terminal region of FSD3S contains a transmembrane domain, which promotes FSD3S localization to the chloroplast membrane but not to nucleoids. Unlike FSD3S, FSD3 localizes to the chloroplast nucleoid. We also found that overexpression of *FSD3S* negatively affects photosynthetic activity and chloroplast development by reducing expression of genes involved in photosynthesis. These results suggest FSD3 and FSD3S, with their distinct localization patterns, have different functions in chloroplast development, and FSD3S negatively regulates expression of PEP-dependent chloroplast genes, and development of chloroplasts.

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PI-0056

Investigation of intra-specific genetic diversity on *Peucedanum japonicum* utilizing chloroplast genome based KASP marker

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Peucedanum japonicum, a perennial herbal plant species of Apiaceae family, was initially cultivated as oriental medicine is nowadays being cultivated as healthy edible vegetable. In previous study, we have discovered two types (Long: L/ Short: S) of inverted repeats (IRs) variation along with the InDel & SNP polymorphisms in chloroplast (cp) genomes through comparative analysis of collected wild accessions. The polymorphisms, demonstrated intraspecific variation pattern in the long type *P. japonicum* had lesser variation than the short type *P. japonicum*. To evaluate further, we employed genotype assessment of the collected *P. japonicum* accessions and breeding lines with, newly developed eight Kompetitive Allele Specific PCR genotyping system (KASP) marker from SNP polymorphism for faster and efficient approach. Eight KASP markers have successfully distinguished the genotype of each accessions and once again verified that S type has more variable alleles than L type. Through the genotype of KASP markers, each type of *P. japonicum* alleles is separated as a group; L type into two groups while S type into four groups. Application of the KASP marker with morphological feature from breeding lines would provide useful phenotype assessment on each group of *P. japonicum*. Taken together, the identified intra-specific diversity from newly developed KASP marker in this study will be valuable resources that can be applied for future molecular breeding of *P. japonicum*.

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PI-0057

Assessment of Resistance to Bacterial Stalk Rot Caused by *Dickeya zeae* in Maize Doubled Haploid Lines

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Doubled haploid(DH) breeding system in maize is a rapid line development technology. Therefore, many foreign maize research institutes have been positively using this system. This DH breeding system is sensational, labor-saving, and time-efficiency procedure. Bacterial stalk rot(BSR) caused by *Dickeya zeae* has recently emerged as an crucial corn disease in Korea. However, there is no information about BSR management methods. For this reason, we induced DH lines using “Mibaeck2”, “Gangwonchal39”, and “HW9/HW11” to select BSR resistant strains. So, through this study, we evaluated the resistance of BSR using our 48 DH lines. We estimated the DH lines resistance using disease score 1-5 scales, which is based on symptomatology 7 days after BSR inoculation. DH strains were used 3-week-old plants and inoculated with 1ml of cell suspension containing 10^8 cfu/ml using syringe in the stalk internode. Among 48 DH lines, 11 lines were categorized as resistance, 3 line as moderate resistance, 34 lines as susceptible to BSR. Moreover, “HW9/HW11” DH lines to evaluation of resistance were currently inoculated with *D. zeae* in field test. The results are expected to come out in about a month. Therefore, our results will be expected useful for the development of BSR resistance varieties. In addition, these results show the possibility that it could be used for the development of molecular marker for the selection of resistance strains.

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PI-0058

Dissecting cellular mechanism of the plant immunity by using pathogen effectors

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The plant defense response is composed of a well-orchestrated system of cellular and molecular mechanisms. Subcellular responses, including phytochemical changes and molecular signaling, have been studied extensively in plant-pathogen interaction. Recently, dynamic changes in organelle structure and function were also identified as key component of the plant immune response. Chloroplast are a primary production site of pro-defense signaling molecules and their morphology actively changes during plant immune responses to generate a tubular structure a stromule that connects the chloroplast with the nucleus. Although the stromule has been demonstrated to provide a passage to transfer molecules from chloroplast to nucleus during immune responses, detail cellular and molecular mechanism of organelle immune responses and intercommunication between organelles are mainly unknown.

To understand the detail molecular mechanisms of organelle immune responses, we screened several effectors from *Phytophthora infestans* that are capable of inducing hypersensitive response (HR) cell death as well as suppressing HR cell death by co-expressing with specific cell death inducers in *N. benthamiana*. We also examine the subcellular localization of these effector proteins. Investigation of the target molecules of these cell death inducers and suppressors might provide us more detail mechanism of organelle immune responses.

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PI-0059

GmPAP2.1 encoding the purple acid phosphatase conferred strong resistance against soybean mosaic virus

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Soybean mosaic virus (SMV) is one of the most prevalent viral pathogen that infects soybean plants and occurs all around the world. Management of SMV is depends on a good agricultural practices and uses of resistant cultivars. However, the emergence of resistance-breaking strains of SMV urges the characterization of alternative resistance genes on soybean pants. GmPAP2.1 is member of purple acid phosphatases (PAPs) in soybean cultivar L29 which carrying an *Rsv3* resistance gene. Overexpression of *GmPAP2.1* on cultivars that susceptible to the infection of SMV strain G5H resulted in significantly reduced viral RNA accumulation in inoculated leaves and prevented virus spread into upper systemic leaves. GmPAP2.1-overexpressed plants also showed less severe mosaic symptom in inoculated leaves. In addition, coexpression of GmPAP2.1 delayed infection of more virulent SMV strain G7H. Construction of deletion and amino acids substitution mutants identified C-terminal region as important region for maintaining resistance to SMV strains. Transient expressions of GmPAP2.1 in experimental host *Nicotiana benthamiana* revealed that this protein is localized exclusively in the chloroplast. Furthermore, expression analyses of endogenous salicylic acid (SA)-related genes in GmPAP2.1-overexpressed soybean cultivar Lee74 exhibited higher expression levels of SA-related genes compared to those in the mock plants. Together, our finding provides new evidence and insight of the host protein which is GmPAP2.1 as a resistance factor in the defense response against SMV strains.

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PI-0060

The development of broad spectrum rice blast resistant rice varieties by introducing the race-nonspecific susceptibility gene

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A well-characterized hemibiotrophic fungal pathogen *Magnaporthe oryzae* causes rice blast disease which is associated with a global food shortage and security. Thereby the detail mechanism of the pathogenesis and resistant cultivar breeding become top priority. Here, we find a transcriptional factor RSG which is involved in the plant immunity responses by regulating the defense related genes expression during the pathogen infection process. The *RSG* gene deletion mutants show typical broad spectrum resistance to diverse rice blast pathogen races. *RSG* gene deletion mutant showed ferroptotic cell death is induced in the mutants, which plays crucial role in the hypersensitive responses in plant resistance. The exact role of RSG is needed to elucidated to understand the rice blast disease resistance phenotype against diverse *M. oryzae* races. The RSG mutant will provide a new resistant genetic resource for breeding to control the rice blast disease.

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PI-0061

Development of "Miscover", a new *Miscanthus* variety for soil erosion protection and vegetation restoration

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Exotic plant species are commonly used for vegetation restoration and soil erosion protection after constructing a new motorway, particularly on a hilly side along the motorway. However, they have a potential threat of disturbing natural vegetation and ecosystem. Once they escape from the site where they are artificially planted and spread into other ecosystems, it becomes very difficult to control and manage them. For this reason, Korea Forest Service recommends using native plant species for erosion protection works, but there are not many suitable plant varieties from the native plant species. Therefore, we developed a new *Miscanthus* variety called "Miscover" with outstanding abilities in ground covering and root formation due to its fast horizontal canopy growth. The Korean native grass *Miscanthus sacchariflorus* grows fast and form broad and deep root system. "Miscover" was thus developed by hybrid breeding by bulk crossing among *Miscanthus sacchariflorus* parents in 2012. A total of 121 hybrid seedlings were cultivated from 2013 to 2017 at Suwon and Yeoju fields to evaluate agronomic traits, productivity and genetic stability. CALS-M-21 line was finally selected and named as "Miscover". "Miscover" showed shorter (1.3 m tall) and dense shoot (253 stems per 0.25 m^2) compared to *Miscantus* x *giganteus* (Mxg; 3.5 m and 123 stems per 0.25 m^2, respectively). Moreover, "Miscover" has shorter vegetative growth period and earlier flowering (240 Julian days) than Mxg (286 Julian days), thus more suitable for soil erosion protection and vegetation restoration.

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PI-0062

신규 유전자원을 이용한 고추 탄저병 저항성 분자표지 개발 및 국내외 품종 육성 과제 진도 보고

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국내외적으로 고추 탄저병 및 바이러스병을 포함한 복합내병성 품종 요구도가 증가하고 있고, 고추 탄저병균의 다양한 변이가 보고되고 있으며, 국립유전자원센터 및 AVRDC 등을 중심으로 신규 저항성 유전자원이 지속적으로 보고됨에 따라, 새로운 병원균과 저항성 유전자원을 이용한 유전학적 연구를 통해서 신규 유전자 발굴(분자표지) 및 이를 이용한 품종 육성이 필요한 상황이다. 신규 저항성 소재를 발굴하기 위해서 탄저병 저항성이라고 확인된 *Capsicum baccatum* 계통을 도입하였고, 기존에 개발된 분자표지 분석과 포장에서 탄저병 발병정도를 조사하여 탄저병 저항성을 확인하였다. 또한 신규 도입자원을 균주별로 접종하고 포장저항성 및 분자표지(Anth12, Anth9, qCaR3.1, qCaR3.2, qCaR4.2, qCaR6.1, qCaR6.2) 분석결과를 토대로 저항성을 평가한 후, 기존 PBC81 유래 탄저병 저항성과 다른 유전자원을 선발 중에 있다. 선발된 신규 자원은 기 육성된 탄저병 계통들과 교배하여 저항성 유전자를 집적하여 탄저병에 강한 새로운 계통을 육성한다. 복합 내병성 육성 계통으로는 GMS 계통으로 F_2 분리세대에서 F_9 고정계통까지 시험 중이며 병저항성으로는 탄저병, TSWV, CMV 및 역병저항성을 주요 목표로 선발 중이다. CMS 및 CGMS 계통으로는 F_3에서 F_7세대까지 시험 중이며 여교잡 후대는 BC_1F_6 세대까지 진행되었다. 탄저병, TSWV, CMV 및 역병저항성인 B, C계통을 선발중이며 선발된 계통들은 조합능력검정을 위해 각각 조합을 작성하였다. 선행연구결과를 토대로 우수 계통과 조합을 선발하고 선행연구에서 우수조합으로 선발된 품종들을 시교사업으로 진행하고 있다.

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PI-0063

Discovering quantitative trait nucleotides associated with flowering of *Miscanthus*

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Miscanthus species has multifunctional traits, so has been used for various purposes such as biomass, ornamental, forage, bioremediation, and vegetation restoration. Among traits that make it a promising crop, flowering time is one of the most important traits which affects both functions. Flowering time decides the biomass production as well as the seasonal lifespan as a gardening plant, and thus can be set as a new objective of breeding. Since *Miscanthus* requires a considerable period of time (3-4 years) to show its fully developed phenotype, a marker assisted breeding is essential to facilitate *Miscanthus* breeding. However, due to its short history as a crop, trait-related genetic markers are very limited, so still many new trait-related genetic markers are urgently required. Two F1 mapping populations of *Miscanthus sinensis* were established by reciprocal outcrossing of two parent *M. sinensis* lines. Five traits related to flowering time were phenotyped for three successive years from 2017 to 2019 and all individual lines in two F1 populations were genotyped using NGS method. Genome-wide association study was conducted, and trait-related markers were selected as a candidate when the marker was recurring for multiple years in multiple traits. A total of 79 SNPs were significantly related to flowering traits assessed in 2019. Among them, 8 SNPs were repeatedly selected from the analyses with earlier phenotyping data, so we could finally select 2 SNPs as a candidate QTN associated with flowering. Therefore, it is expected that some reliable trait-associated markers would be developed from this study.

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PI-0064

Identification of genetic variances and application of KASP markers to MABC for developing good eating quality lines in rice

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With the continuous improvement of people's living standards, the rice grain quality, especially the eating quality of cooked rice is attracting more and more attention from the rice-eating consumers. Development of high eating quality rice varieties has become one of top breeding priorities to meet the highly competitive international and domestic rice market demand. Molecular markers have been used to enhance the precise breeding strategy in conventional breeding programs using DNA markers that are closely linked with specific genes of interest for crop improvement. Marker-assisted backcrossing(MABC) uses molecular markers for selecting favorable lines having highly recovered genome of a recurrent parent. Foreground and background selections are carried out at the same time during the MABC processes. A target gene can be detected through the foreground selection and the lines having highly recovered genome ratio of recurrent parent can be identified by background selection process. So we have applied MABC technology for developing high eating quality rice lines to backcross 'Samgwang' as a recurrent parent, which is a Korean elite variety, and 'Milky Queen' as a donor that has low amylose content.

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PI-0065

혈당강하 활성이 높은 잎전용 고추 우수계통 육성

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고추는 비타민, 카로티노이드, 캡사이신 등 다양한 기능성 성분이 함유된 채소로서, 대표적인 대사성 질환인 당뇨병 예방에도 효과가 있는 것으로 알려져 있다. 당뇨병은 대표적인 대사질환의 하나로 한번 발병하면 평생 관리해야 하며, 다양한 합병증을 야기하므로 치료뿐만 아니라 예방적 차원에서 접근이 중요하다. 당뇨병 치료제 중의 하나로 사용되고 있는 당질 흡수 억제제(α-glucosidase inhibitor, AGI)는 이당류를 단당류로 분해하여 소장에서의 탄수화물 흡수를 촉진시키는 효소인 α-glucosidase를 억제하여 식후 고혈당을 낮춰주는 기능을 한다. 고혈당이 심하지 않고 식후 고혈당이 문제가 되는 노인환자에게 저혈당의 우려 없이 처방이 가능하며 탄수화물 섭취량이 많고 고혈당이 문제가 되는 우리나라 당뇨병 환자에게 적합하다고 알려져 있다. 고추 잎에는 이러한 AGI 활성이 높은 것으로 보고된 바 있고, 국립원예특작과학원에서는 기존 고추 잎보다 AGI 활성이 4배 정도 높은 원기1호를 육성하였다. 본 연구는 기존 연구결과를 보완하고 상업용으로 보급이 가능한 항당뇨 잎전용 고추 품종 개발을 위해 기존 육성계통 및 도입 자원을 대상으로 2018년부터 AGI 활성 및 원예적 특성을 평가하여 상업용 품종 개발에 사용이 가능한 우수계통을 육성하고자 수행하였다. AGI 활성분석은 전북대학교가 기존에 보고된 AGI 활성 분석방법에서 α-glucosidase 및 기질(pNPG) 용량, 추출방법, 희석 배수 등을 조정하여 보완한 방법을 기준으로 하였다. 3분지 수확 잎을 55℃에서 건조하여 만든 분석샘플을 이용해 기존 육성 계통, 도입자원, 시판품종 등 총 150점에 대해 분석을 수행하였다. 분석결과 당뇨병 치료제인 Acarbose와 비슷한 수준의 활성을 보인 AGI29, 22, 23 등 3계통을 선발하였다. 선발한 계통은 올해 하반기 직무육성품종으로 출원하여 향후 항당뇨 잎전용 고추품종 육성 재료로 보급할 계획이다.

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PI-0066

Functional study of CbNLR genes from pepper related to enhanced anthracnose resistance

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Pepper (*Capsicum*) is one of the most valuable economic crops in the world, but its yield is damaged seriously by anthracnose caused by *Colletotrichum* species. Plant intracellular nucleotide binding leucine-rich repeat (NLR) immune receptors which can recognize the pathogen effectors play critical roles in resistance response to pathogens. To study the function of NLR genes from pepper *Capsicum baccatum* (*C. baccatum*) PBC80 and PBC81, we identified the three leucine-rich repeat (NLR) genes, *CbNLR09*and *CbNLR12* (from PBC80), *CbNLR819* (from PBC81) using the genome-wide comparative analysis. The transcriptions of these genes and pathogenesis-related (*PR*) genes such as *CaPR1* and *CaPR2* were increased highly in resistance variety PBC80 and PBC81 related to susceptibility variety An-S (*C. annum*) after *Colletotrichum acutatum* (*C. acutatum*) K1 treatment. To elucidate the function of these genes, we generated overexpressing tobacco lines, respectively. We revealed the upregulated expression levels of *NbPR1*and *NbPR2* in overexpressing plants after *C. acutatum* treatment. Moreover, we confirmed the downregulated expression levels of the *CaPR1* and *CaPR2* in virus-induced gene silencing An-S, PBC80 and PBC81 fruits. These results suggest these NLR genes are involved in regulation of PR genes and disease resistance to anthracnose in tobacco and pepper.

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PI-0067

콩에서 GWAS분석 및 BSA분석을 통한 싸리수염진딧물 저항성 연관 유전자 탐색

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최근 대기 중 이산화탄소, 메탄 등의 농도 변화로 인해 폭우, 가뭄과 같은 이상기후와 작물 재배지에서 급격한 병해충 발생이 증가하고 있다. 더불어, 해충의 발생 양상은 기존 대다수를 차지하던 식엽해충 보다 흡즙해충의 발생빈도가 높아지고 있다. 국내 콩을 가해하는 싸리수염진딧물은 콩 진딧물에 비해 크기가 크며 콩 전체를 가해하고 흡즙에 대한 피해증상이 심각하다. 그러나 진딧물에 대한 방제 연구와 콩진딧물에 대한 유전연구가 대부분이고 싸리수염진딧물 저항성 관련 유전연구나 저항성 품종 육성에 대한 연구는 미비하다. 이에 본 연구는 국내 콩 유전자원을 활용하여 싸리수염진딧물 저항성 연관 GWAS 분석 및 저항성 자원의 교배집단을 활용한 BSA(Bulk segregant analysis) 분석을 통해 저항성 연관 QTL을 규명하고자 하였다. 농업유전자원센터에서 분양을 받은 356점의 유전자원을 사용하여 싸리수염진딧물 저항성 검정과 Axiom® 180K SoyaSNP genotyping을 완료하고, GAPIT R package를 사용해 GWAS분석을 실시하였다. 추가로 저항성이 확인된 유전자원을 대풍콩과 인공교배한 F_2집단을 활용하여 BSA분석을 실시하였다. 유전자원에 대한 싸리수염진딧물 저항성 검정 결과 소수의 자원만 저항성을 보이며 대부분 감수성을 보였고, GWAS 분석 결과 14번 염색체에서 싸리수염진딧물 저항성과 연관 있는 영역을 탐색할 수 있었다. F_2집단 183개체에서 싸리수염 진딧물 저항성 유전분석 결과에서는 저항성과 감수성이 9:7의 분리비를 보여 1~2개 유전자가 관여함을 확인하였고 저항성과 감수성이 강하게 나타난 개체들을 선발하여 BSA 분석한 결과 7번 염색체에서 후보유전자 영역을 탐색할 수 있었다.

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PI-0068

Rapid breeding of determinate tomato to indeterminate tomato using CRISPR-mediated homology-directed repair

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CRISPR-mediated homology-directed repair could directly provides precise sequence editing in the target site related with interest traits in crop such as tomato. A determinate variety, S.lycopersicum cv M82, have been bred as indeterminate tomato by introgressing about 1Mb of chromosome 6 from S. pennellii via conventional crossing breeding for more than 5 years. In this study, we induced homology-directed repair (HDR) in determinate M82, using CRISPR/cas9-geminiviral replicon to gain determinate growth trait by editing sp mutant. Forteen independent T0 plants showed over 50% rate of homology-directed repair (HDR) indicating DNA double strand break (DSB) and donors copied by geminiviral replicon effectively complemented sp mutant into *SP* wild type in determinate M82. T1 progenys two succesively inherit the wild type *SP* edited in the two independent T0 parents. It takes just one and half year until we get the new indeterminate M82 by engineering sp target with finalizing off target assays indicating any unexpedted editions were absent in the new lines. Thus, we suggest that our HDR induction system provide the efficient and rapid processes of genome editing for genetic researches and tomato breeding.

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PI-0069

기능성 유색미 품종 '슈퍼자미'와 '슈퍼홍미'의 농업형질 개량

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본 연구는 기능성 쌀인 슈퍼자미와 슈퍼홍미의 농업 형질을 개량하여 기능성 성분의 함량은 유지하며 고품질 내재해성 계통 및 품종을 육성하기 위해 수행하였다.

'슈퍼자미'는 항산화성분인 안토시아닌의 함유량이 기존의 유색미인 '흑진주'에 비해 8배 ~ 10배 많은 기능성 유색미 품종이다. 그러나 출수기가 8월 25일로 만생종이며 간장이 82.0 cm 로 길어 장마 후 태풍과 등숙기간의 기후환경에 취약한 상태이다. 당뇨억제 성분인 탁시폴린(Taxifolin)을 함유한 만생종 슈퍼홍미는 출수기는 9월 5일로 슈퍼자미보다 10일 늦은 만생종이며, 간장은 94.7 cm 로 슈퍼자미보다 13 cm 큰 장간이다. 이러한 기능성 유색미의 농업특성을 개선하기 위해 돌연변이 처리와 선발, 교배집단육성 및 후대 계통 육성을 통해 내도복성이 우수한 계통을 육성하였다.

돌연변이 처리는 원자력연구소에서 감마선을 100Gy 200Gy 그리고 300Gy 처리하여 그 후대의 특성을 조사하여 개체 선발 및 계통 육성을 하였다. 교배집단은 기존의 기능성 유색미 품종에 찰성 유색미 품종과 찰성 우수 품종과의 교배집단을 만들어 선발 및 세대진전을 통해 고세대 계통을 마련하였다. 또한 기존의 '슈퍼자미'와 '슈퍼자미2호'를 교배하여 안토시아닌 함량은 유지하고 출수기를 8월 중순으로 앞당기며 초장을 줄이는 선발육종을 수행하였다.

선발 및 세대진전을 통해 간장이 75 ~ 77 cm 이며 안토시아닌의 주 성분중 하나인 C3G 함량이 이미 육성된 품종과 비슷한 F_6 9계통을 선발하여 생산력 예비시험 중이며, 결과를 토대로 품종출원을 준비중이다. 유색현미의 식감을 개선하기 위해 찰성을 도입한 계통 육성을 통해 22 계통 및 돌연변이 후대 48계통을 육성중이다.

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PI-0070

Studying of tomato yield effects from reciprocal hybrids between *Solanum lycopersicum* cv. M82 and Micro-Tom

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Hybrids possess a greater potential for agricultural productivity and higher commercial value among seed producers due to sustained marketability. Plant breeders took advantage of the phenomenon "Heterosis" for nearly 20 decades' even though they had a limited understanding of the genetic effects. Later, plant breeders hypothesized that the genetic loci resulted by crossing two independent inbred lines causes the genetic locus responsible for the enhanced performance may possess multiple factors which are equally contributed to the final effect. Due to the increased demand for food, reduction of cultivable land and climate change, plant breeding strategies must discover novel principles and materials to optimize the productivity of crops. In this study, we took advantage of the model plant *Solanum lycopersicum cv.* "Micro-Tom" to optimize the productivity of commercial cultivar *Solanum lycopersicum cv.* M82. Prominent mutations in Micro-Tom such as "*dwarf*", putative "*mnt*" and putative flowering time mutations make the model cultivar more compact and causes early flowering by reducing the generation time. Plant size and flowering time is widely associated with the yield of field grown crops. We hypothesized that the resulting hybrid of M82 and Micro-Tom genetic interaction may modify the flowering time, plant architecture and ultimately yield to increase the productivity of field tomatoes. Our results suggested that the mutations in Micro-Tom caused multiple inheritance patterns in F1 generation and modified the plant architecture and flowering time. The Plant size and flowering time was intermediate of that the parents and plants showed relatively early maturing of fruits resulting in a semi-dominant inheritance. Unexpectedly, the yield of F1 hybrids resulted in similar yield of the M82 cultivar regardless of the reduced photosynthetic biomass, resulting an overdominant effect in Harvest index. However, the fruit weight and Brix showed semi-dominant and underdominant inheritance in the F1 respectively. The results were similar under reciprocal F1 hybrids where the paternal and maternal materials are switched, indicating the non-nuclear genes does not contain any considerable variations or effects.

Induced mutations are excellent materials to explore novel alleles which can increase the crop productivity and favorable agronomic characters. TOMATOMA database provides EMS and Gamma induced mutants with potential productive mutations. We also took advantage of the current understanding of the M82 and Micro-Tom hybrids and hybridized with 13 Micro-Tom flowering time mutants to screen any overdominant alleles which can further increase the productivity of field tomatoes. We found two mutants with increased yield which possess mutations related to flowering time and floral architecture. Based on the understanding of these mutations, it's possible to breed plants with increased productivity by taking advantage of genetic materials present in Micro-Tom and discover novel high yielding alleles with inducted mutations.

Keywords: Micro-Tom, Plant growth, Tomato yield, Heterosis, Hybrids

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PI-0071

CRISPR/Cas9-targeted mutagenesis of *F3′H*, *DFR* and *LDOX*, genes related to anthocyanin biosynthesis in black rice (*Oryza sativa* L.)

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Altering a trait by CRISPR-Cas9-targeted mutagenesis offers great advantages in identifying gene function and crop improvement. In the present study, three genes (*OsF3′H*, *OsDFR* and *OsLDOX*) in the anthocyanin biosynthesis pathway were successfully edited on the Heugseonchal or Sinmyungheugchal variety using the CRISPR/Cas9 system. As a result, the ratio of the edited plants in the transformed early generation was 56.7%. These edited mutant lines were observed with the changes of seed color and anthocyanin content. All mutations were stably inherited to the T_2 progeny. In addition, we could select edited homozygous mutant lines lacking the T-DNA already in the first offspring generation. Also the insertion of vector backbone sequences in f3′h-9, dfr-4 and ldox-16 lines was not detected in the whole genome resequencing. These results demonstrated that the CRISPR/Cas9 system can induce clearly gene-specific mutations with a high efficiency in rice and null plants selected from these mutants cannot be distinguished from non-GMO plants even under strict GMO regulation.

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PI-0072

HXK5 is essential for starch metabolism in pollen grains and fertility

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There is little known about the function of rice hexokinases (*HXKs*) in planta. We characterized *hxk5-1*, a Tos17 mutant of *OsHXK5* that is up-regulated in maturing pollen, a stage when starch accumulates. Progeny analysis of self-pollinated heterozygotes of *hxk5-1* and reciprocal crosses between the wild-type and heterozygotes revealed that loss of *HXK5* causes male sterility. Homozygous *hxk5-1*, produced via anther culture, and additional homozygous *hxk5-2, hxk5-3* and *hxk5-4* lines created by CRISPR/Cas9 confirmed the male sterility. Pollen tube growth rate were significantly reduced in the *hxk5* mutant pollen. Biochemical analysis of anthers with the mutant pollen revealed significantly reduced hexokinase activity and starch content, although they were sufficient to produce some viable seed. However, the mutant pollen was unable to compete successfully against wild-type pollen. Expression of the catalytically inactive OsHXK5-G113D did not rescue the *hxk5* male-sterile phenotype, indicating that its catalytic function was responsible for pollen fertility, rather than its role in sugar sensing and signaling. Our results demonstrate that OsHXK5 contributes to a large portion of the hexokinase activity necessary for the starch utilization pathway during pollen germination and tube growth, as well as for starch biosynthesis during pollen maturation.

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PI-0073

Development of Late-bolting Variety in *Brassicaceae* by CRISPR-Cas9-mediated Genome Editing System

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Brassica crops are one of the major crops used for human diet. Among the *Brassica* crops, *Brassica rapa* L. ssp. *pekinensis* (Chinese Cabbage) is one of the most important leafy vegetables in Korea. For the successful productivity of Chinese cabbage, it is essential to inhibit bolting until harvesting. Thus, the present study aims to develop a late-bolting variety in Chinese cabbage to be mutated by CRISPR/Cas9-mediated genome editing system. In order to generate a late-bolting variety in Chinese Cabbage, we focused on three *BrVIN3* genes namely, *BrVIN3a, BrVINb,* and *BrVINc;* these *BrVIN3* genes are the homologues to *Arabidopsis thaliana VIN3* (*VERNALIZATION INSESITIVE3*), which plays a vital role in accelerating the flowering phenomena after vernalization process. As *A. thaliana vin3* mutant shows strong late-flowering phenotype, we expected that *BrVIN3* mutants to be generated would also show strong late-bolting phenotype. Thus, *BrVIN3*-targeting sgRNA to induce mutation were constructed, and subsequently introduced to the genome of Chinese cabbage inbred line by *agrobacterium*-mediated transformation. As a result, there were totally 16 regenerated plants obtained in which 4 out of the 16 plants have confirmed integration of sgRNA-Cas protein transgene. Unfortunately, until now, no mutation was occurred in those transgenic lines. Meanwhile, we are developing additional sgRNA to target other sites of *BrVIN3* genes with higher efficiency, confirmed by *in vitro* sgRNA efficiency test. That parallel approach will enhance the efficiency on developing a late-bolting variety in Chinese cabbage in near future.

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PI-0074

야생벼 수량안정성 유전자 분리 및 품종 개발

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기후변화 대응 야생 유전자원으로부터 다수성, 수량안정성 형질 관련 유전자를 탐색하고 활용하기 위하여, 근동질계통을 육성하고 관련형질 연관 QTL을 탐색하였다. 종자중 조절 유전자, *gw9.1* 의 후보유전자 Ascorbate peroxidase 9 (*APX9*)은 화성/*O. rufipogon* 조합 계통을 이용한 고밀도지도 작성으로 염색체 9번에서 탐지되었다. 유전자 발현 분석 및 근동질계통을 이용하여 *gw9.1*이 수량성 및 출수기 특성에 관여함을 밝혔다. 이들 *APX9* 유전자는 다른 APX family와 같이 항산화 능력이 높고 여러 스트레스 조건에서 발현이 증가되었다. 또한 *APX9* 과발현 형질전환체에서 수량이 증가되는 것을 확인하였다. 직파적응성 관련형질 중, 저온발아성 관여 QTL, *qLTG1*이 염색체 1번에서 탐지되었다. 화성/*O. rufipogon* 조합의 근동질계통과 고밀도지도 작성을 통하여 후보 유전자들을 선발, 발현분석을 통하여 후보 유전자 *OsD2*을 선발하였다. *OsD2*은 Brassinosteroid (BR) 생합성경로 관여 유전자로 화성과 *O. rufipogon* 의 염기서열 비교 결과, 코딩 서열부위에서 5개의 SNP가 발견되었고 이들 중 3개의 SNP는 아미노산 변이를 일으켰다. *OsD2* 유전자의 T-DNA 돌연변이체와 과발현 형질전환체의 저온발아성 검정 결과 *OsD2* 유전자가 저온발아성에 관여하는 것을 확인하였다. 화성/*O. rufipogon* 조합의 근동질계통을 이용하여 저온발아성 조사 결과, 조절 유전자 *qLTG1*와 *qLTG3*가 집적됨에 따라 저온 발아율이 상가적으로 증가하였다. 중배축 신장성은 직파적응성 관련 주요 형질로 알려졌다. 중배축 길이 조절 QTL, *qMel-1* 과 *qMel-3*은 Nipponbare/Kasalath 조합 근동질계통을 이용하여 염색체 1번과 3번에서 탐지되었다. 이 중*qMel-3*의 고밀도 지도를 작성하여 *qMel-3*의 약 6.7Mb 구간에 2개의 QTL이 연관되어 있음을 확인하였다. Microarray 분석 결과를 바탕으로 이들 두 지역에서 각각 후보유전자 13개, 7개가 선발, 발현분석을 실시하였다. 신형질 다수성품종 개발을 위하여 종자중 관여 유전자 *gw2*, *gw9*의 집적 계통을 육성하였고, 저온 발아성 우수 계통 육성을 위하여, *O. rufipogon* 유래 유전자*qLTG1, qLTG3, qLTG10*을 집적한 계통을 선발, 높은 저온발아성을 확인하였다.

사사: 본 연구결과는 농촌진흥청 차세대 바이오그린21사업 (과제번호: PJ01321401)의 지원에 의해 이루어졌다.

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PI-0075

Evaluation of Potato Germplasm Resistant to Bacteria Wilt (*Ralstonia solanacearum*) Disease Using Soil Drenching Inoculation

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Bacterial wilt (*Ralstonia solanacearum*) is a soil-borne disease that affects more than 200 crop species, including the potato (*Solanum tuberosum*) and is difficult to control once the disease occurs. This study was carried out to investigate potato germplasm resistant to bacterial wilt (BW) disease. A total of 38 germplasms collected and maintained at Highland Agriculture Research Institute were tested with 22 strains of *R.solanacearum* using soil drenching inoculation method. 20 days after inoculation, the resistance was evaluated as the range from 0 (resistance) to 4 (susceptible). In the first screening, 22 strains were inoculated into Lz3.2(*S.commersonii* line) known as BW resistance. 3 strains were selected that showed resistance and sensitivity, respectively. In the second screening, 6 strains selected at the first screening were tested for disease resistance againt 13 potato wild species, 5 *S.commersonii* lines, and 20 cultivated potatoes. Among the 22 strains, Pe_1, Pe_57, and To_22 strains caused disease in all of Lz3.2, and the pathogenicity was very strong. On the other hand, To_7 showed the weakest pathogenicity. In the *S.commersonii* lines, Lz3.2 and Lz3.4 were resistant to Pe_4, Pe_42 and To_7. *S.vernei* was resistant to Pe_4 and Pe_42 strains and all other wild species were susceptible. Among the 20 cultivated potato, CT08-4 showed the highest resistance to Pe_4, Pe_42 and To_7. The result have revealed that Lz3.2, Lz3.4, *S.vernei* and CT08-4 are resistant to *R.solanacearum*. Furthermore, the selected potato germplasm could be used as parent germplasm in bacteria wilt resistance breeding program of potatoes.

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PI-0076

Development of transgenic plants exhibiting flower color stability through RNAi suppression of CmDFR gene expression in chrysanthemum

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Chrysanthemum (*Chrysanthemum morifolium* Remat.) is one of the most important cut flowers and pot plants grown in many parts of the world. Chrysanthemums can be cultivated four times a year, but the flower color can be changed due to high and low temperature during cultivation and distribution process. The changes of flower color cause economic loss due to quality deterioration and decrease in commerciality. Therefore we tried to develop transgenic chrysanthemums exhibiting flower color stability through RNAi suppression of *DFR* expression. Leaf explants of chrysanthemum 'Baekgang' were infected with *Agrobacterium tumefaciens* LBA4404 harboring a binary vector pB2GW7 which carries CmDFR-RNAi regulated by the NtANS (*Nicotiana tabacum* anthocyanidin synthase) promoter, which is involved in the anthocyanin biosynthesis of tobacco. The explants were co-cultivated for 3 days on regeneration medium composed of MS salts and vitamins, 0.25 mg/L BA, 1.0 mg/L NAA with 100 μM acetosyringone. Then the explants were transferred to selection medium containing 0.75 mg/L phosphinothricin (PPT) and 250 mg/L cefotaxime. After 8 weeks of culture, adventitious shoots were generated from the transformed explants. The shoots were detached from the explants and cultured on the same selection medium. After 12-20 weeks of culture, the regenerated shoots were elongated and rooted successfully in shoot elongation medium with 0.75mg/L PPT. In transgenic plants the integration of transgene was confirmed by PCR analysis. After flowering, we will examine anthocyanin contents and flower color stability of transgenic plants.

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PI-0077

Development of Chloroplast InDel Markers from *Angelica gigas* Nakai

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The chloroplast is a multifunctional and essential organelle which has an independent genome that encodes important proteins required for carbon fixation, photosynthetic activity, and various housekeeping functions. Chloroplast DNA (cpDNA) is highly conserved in plants, consisting of homogeneous circular double stranded DNA molecules of quadripartite structure comprising two copies of inverted repeat (IR) regions that separate the large single-copy (LSC) and small single-copy (SSC) regions. The cpDNA size in most angiosperms ranges from 115 to 165 kbp. Recently, many researchers have focused on chloroplast genome sequencing for various plant genetics studies. In this study, we designed 25 AgCpInDel primer pairs from the comparison of chloroplast sequences of *A. gigas* genetic resources. Twenty-five primer sets were tested for intact, polymorphism, and reproducible amplification in *Angelica* species. Finally, 24 AgCpInDel markers were developed and one remaining primer showed unexpected amplification. Subsequently, 24 AgCpInDel markers were tested for intraspecific and interspecific comparison. The number of genotypes, frequency of major alleles, availability, and polymorphic index content values were measured using PowerMarker software. As a result, 24 AgCpInDel markers with polymorphism in *A. gigas* at the intraspecific level were developed and classified by chloroplast genotype in the analysis of 88 *A. gigas* accessions. Furthermore, the 24 developed AgCpInDel markers were able to identify diversity at the interspecific level for 13 *Angelica* species including *A. gigas*. These markers could be useful tools for exploring variations in *Angelica* species and for evolutionary study, molecular breeding of *A. gigas* and genetic diversity analysis.

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PI-0078

분자마커를 이용한 일품벼 내병성 근동질 계통 육성

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경남 밀양시 점필재로 국립식량과학원 남부작물부 논이용작물과

최근에 유전체 분석기술의 범용화에 따라 분자육종기술이 비약적으로 발전하고 있으며, 신품종 육성에 적극적으로 활용되고 있다. 특히, 기존 품종의 단점을 개량하는 여교배 육종에 가장 효율적으로 활용되고 있다. 최근 국내 벼 품종은 일품벼, 오대벼, 신동진벼 등 고품질 브랜드미를 중심으로 보급되고 있다. 하지만 이들 품종은 밥맛은 우수하지만 내병성이 약한 단점이 많다. 특히, 일품벼는 경북지역으로 명품 브랜드쌀로 정착되어 있지만, 내병성이 약해 기후변화에 따른 잦은 재해로 농가 피해가 우려되고, 농업현장에서는 이들 단점 개량에 대한 요구가 증가되고 있다. 본 연구에서는 일품벼의 내병성 단점을 개량하고자 완전미율이 우수하고 복합내병성인 새일미와 일품벼가 교배하였으며, 여교배 계통에서 줄무늬잎마름병, 흰잎마름병 및 이삭도열병 저항성에 대한 분자마커를 이용하여 선발하였다. YR33080조합 BC2F1세대의 22개식물체에서 줄무늬잎마름병, 흰잎마름병, 목도열병 저항성 분자마커로 MAS를 실시한 결과 저항성 유전자가 집적된 계통은 YR33082-13 및 YR33080-20이였다. BC2F1세대 2 계통은 YR33082-13 및 YR33080-20을 KASP마커를 이용하여 반복친인 일품의 게놈회복율(Recurrent parent recovery ratio)를 분석한 결과, YR33080-13과 YR33080-20의 반복친 회복율은 각각 80.8%, 및 54.8%이였다. 따라서 반복친의 회복율이 높았던 YR33080-13을 BC2F1 식물체에서 종자를 채종하여 BC2F2 식물체 310개체를 육성하였다. BC2F2식물체에서 DNA 샘플을 채취하여 다시 줄무늬잎마름병, 흰잎마름병, 목도열병 저항성 분자마커로 foreground 선발을 실시하였으며, YR33080-13-3을 선발하였다. 2020년 하계 포장에 이앙하여 생산력검정 시험을 수행하였으며, 생육초기 초장 및 경수는 비슷하였다.

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PI-0079

Type 2 Diabetes Management-related Antioxidant and α-Glucosidase Inhibitory Activities of Bioactive Ingredients Isolated from Colored Rice Keun-nun-jami (*Oryza sativa L.*) Inhabited in Korean Peninsula

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In the previous screening of antioxidant and anti-hyperglycemic bioactive compounds from the ethyl acetate extraction of Keun-nun-jami Bran (KBE), several bioactive fractions were isolated and compared to selected specific phenolics using HPLC and Prep-LC systems. Therefore, their structures were elucidated by extensive spectroscopic analysis, including 1D and 2D NMR, and FTICR-MS, LC-MS/MS in this study. To prove the anti-hyperglycemic potential of purified KBE fractions inhibitory activities of fractions against rat small intestinal α-glucosidases (sucrase, maltase, glucoamylase) were evaluated. Additionally, antioxidant activities of isolated fractions from KBE were also assessed by oxygen radical absorbance capacity (ORAC) method. The active components of fractions can be roughly divided into A and B. Fraction B had a high antioxidant and intestinal α-glucosidase inhibitory activities. Fraction A had an intestinal sucrase, maltase, glucoamylase inhibitory activities relevant for potentially managing post-prandial hyperglycemia. Although we need further *in-vivo* and clinical trials, these results indicate that KBE have dual anti-diabetic and antioxidant effects by suppressing carbohydrate absorption from intestine, and thereby reducing the postprandial increase of blood glucose and oxidative complications due to the excessive oxidative stress in diabetic patients.

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PI-0080

Apoptosis induction of moscatilin through JNK pathway in human head and neck squamous cell carcinoma cells

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Moscatilin, a bibenzyl derivative isolated from *Dendrobium* species, showed potent cytotoxicity against a FaDu human pharyngeal squamous carcinoma cell line. Thus, the apoptotic mechanism of moscatilin in FaDu cells was invetigated. Moscatilin (5 μM) induced FaDu cell death by mediating apoptosis, whereas cell proliferation following treatment with 1 μM of moscatilin was not suppressed to the same levels as by the anti-cancer agent, cisplatin. Consequently, we analyzed the apoptosis-related protein expression (cleaved caspase-8, cleaved caspase-7, cytochrome c, cleaved caspase-9, cleaved caspase-3, and poly (ADP-ribose) polymerase (PARP)) after treating with 5 μM of moscatilin. These results showed that moscatilin-mediated apoptosis is associated with the extrinsic and intrinsic apoptotic signaling pathways. In addition, moscatilin-induced apoptosis was mediated by the c-Jun N-terminal kinase (JNK) signaling pathway. Overall, the present study provided an additional mechanism of action on the pro-apoptotic effect of moscatilin and supported its application as a cancer chemotherapeutic agent for head and neck squamous cell carcinoma.

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PI-0081

Inhibitory effects of furanocoumarins on radiation-induced migration in human lung cancer cells

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Radiotherapy is routinely used in the treatment of advanced human lung cancer. However, ionizing radiation (IR) often causes malignant effects in non-small cell lung cancer (NSCLC), such as promoting cancer cell migration and invasion. As part of our ongoing search for radiotherapy enhancers from natural sources, a chloroform-soluble fraction of the roots of *Angelica dahurica* was subjected to phytochemical investigation, leading to the isolation of 8 furanocoumarins, psoralen (1), xanthotoxin (2), bergapten (3), imperatorin (4), phellopterin (5), isoimperatorin (6), cnidilin (7), and (*R*)-(+)-oxypeucedanin (8). Of these, compounds 1–3 inhibited IR-induced migration at a non-cytotoxic concentration (50 μM) in human NSCLC A549 cells. This study is the first report on the inhibitory activities of the constituents of *A. dahurica* against IR-induced cancer metastasis.

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The Korean Society of Breeding Science's Award

The Korean Society of Breeding Science's Award
2020년 사단법인 한국육종학회 학회상 시상

ㅇ 시상일 : 2020년 8월 18일(화) 11:00~12시

ㅇ 장　소 : 대전 ICC

ㅇ 시상내용

1. 농우육종학회상 (10호)

- 수상자　윤진영((전)농우바이오)
- 수상내용　채소류 유전자원 연구개발과 실용화 분야에서 탁월한 실적을 남겼을 뿐만 아니라 국내 종자가공 기술 발전과 육종 관련 학술단체 활성화에도 공헌하여 육종연구 및 종자산업 발전에 기여함
- 포상내용　상장 및 부상 500만원 (농우바이오)

2. 한국육종학회상 연구상 (34호)

- 수상자　지현소 (국립농업과학원 농업생명자원부)
- 논문제목　Single Nucleotide Polymorphism (SNP) Discovery and Kompetitive Allele-Specific PCR (KASP) Marker Development with Korean Japonica Rice Varieties (Plant Breed. Biotech. 2018;6:391-403)
- 포상내용　상장 및 부상 100만원 (한국육종학회)

3. 한국육종학회상 품종상 (30호)

- 수상자　김현태(국립식량과학원 밭작물개발과)
- 품종명　선풍(콩), 품종등록번호: 5931
- 포상내용　상장 및 부상 100만원 (한국육종학회)

4. 코레곤품종상 (5호)

- 수상자　이용직(하나종묘)
- 품종명　PR911고추(고추), 품종등록번호: 02-0004-2015-83
- 포상내용　상장 및 부상 200만원 (코레곤)

5. 우수논문상 다피인용부문

- 한국육종학회지 -

- 수상자　오성덕 (농촌진흥청 국립농업과학원 농업생명자원부)
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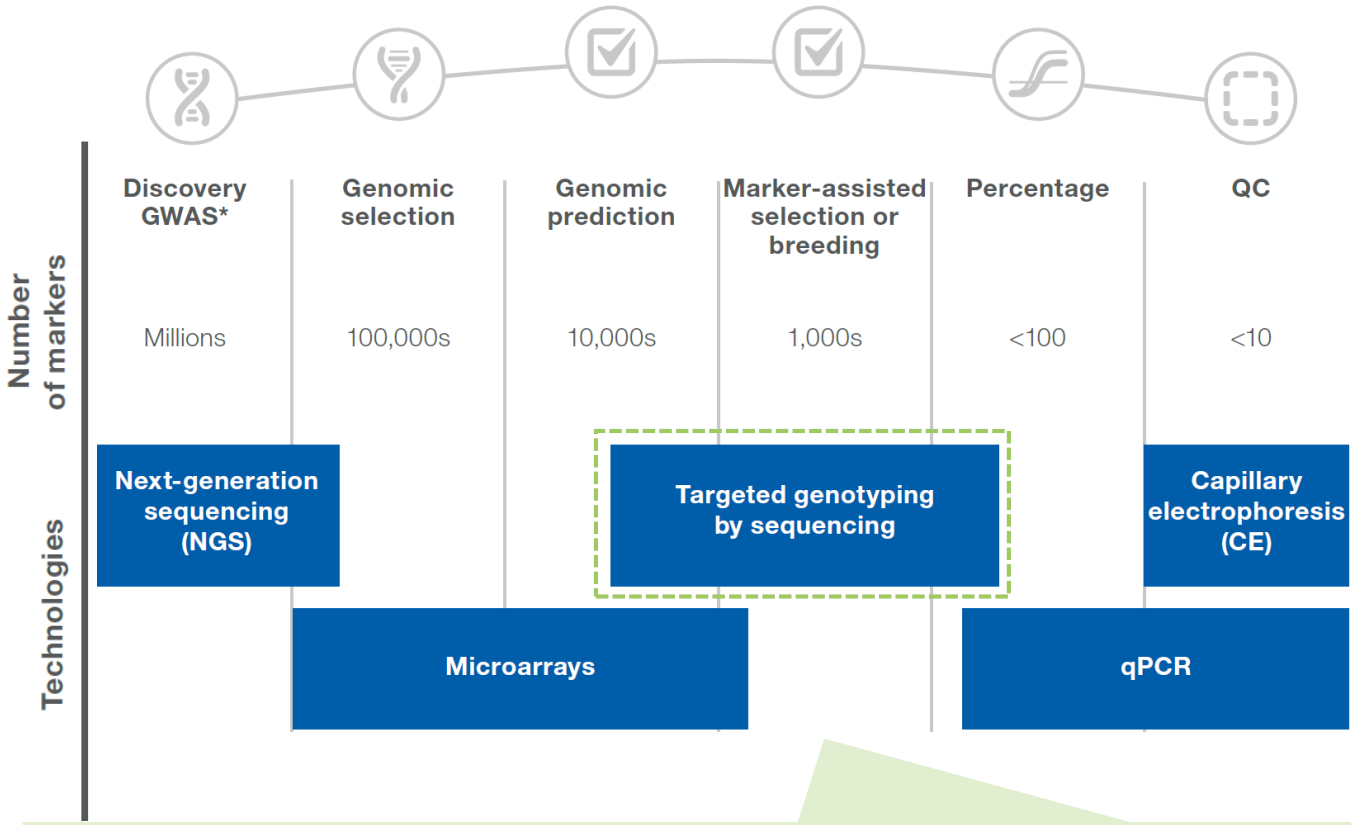

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